MicroImaging Manual

Paravision
User Manual

Version 006

The information in this manual may be altered without notice.

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Introduction 1

General 1.1

This manual is for the **engineer** who needs to **install the imaging accessory**, as well as the **user** to asssit in **performing existing experiments** and for the **creation of new experiments**.

Two different user interfaces exist for imaging experiments, the so called 'high resolution' style (HR-style) and the 'ParaVision' style (PV-style).

1. With the classical **HR-style** an automation program exists for each method, which queries the user sequentially for each of the imaging experiment parameters and sets the acquisition and processing parameters based on these entries. This style is described in a separate manual.
2. The newer **PV-style** uses menus for each experiment, whereas the imaging and processing parameters have been setup in a comfortable and intuitive way.

The support of both styles guarantees that imaging methods from A*X spectrometers can be easily installed on AVANCE spectrometers. It also makes the creation and handling of new and old methods easier for those who are used to working with the 'high resolution' style or with the 'ParaVision' style.

This manual describes the PV-style of imaging experiments. It is only a guide and may not include all the information you would like. On the following pages you find the shortest pathway through this manual for:

- The installation of the imaging accessory.
- The first image acquisitions.
- For the creation of new methods.

Contact Information 1.2

If you have any suggestions, please send them to:

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Checklist for Installation of the Micro-Imaging Accessory 1.3

Table 1.1. Installation Checklist

	Chapter Action	Date/Installed by
Connection of the imaging rack to the console.	***"Installation of the Imaging Rack" on page 14*** ***"Installation of the GREAT Bo Shift Compensation Unit" on page 16***	Not yet available
ParaVision and XWIN-NMR software installation.	***"Software" on page 75***	
Start of ParaVision as NMR super-user (**nmrsu**).	***"Step 3: Configuration of ParaVision" on page 78***	
Configuration of ParaVision, cf, Edit & Save Config.	***"Step 3: Configuration of ParaVision" on page 78***	
Installation of the „Micro-Imaging Patch CD“	***"Step 4: Installation of the Micro-imaging Patch CDROM" on page 82*** .	
Definition of directories for data storage.	***"Disk Selections" on page 85***	
Creation of routing parameter sets.	***"Generation of routing parameters" on page 93***	
Acquisition of a FID with the m_onepulse method.	***"Spectrum Acquisition (m_onepulse)" on page 98***	
Adjustment of the gradient loop adaptation.	***"Loop Adaptation" on page 103***	
Offset adjustment of the GREAT amplifiers.	***"Offset Adjustment" on page 108***	
Adjustment of the pre-emphasis.	***"Pre-emphasis Adjustment (m_preemp)" on page 113***	
Adjustment of the Bo shift compensation.		
Calibration of the gradients.	***"Gradient Calibration (m_msme)" on page 128***	
image acquisition with the m_msme method.		
Store the system configuration and create a CDROM.	Run the script ..../prog/service/storePvConfigData	

GREAT Imaging Hardware 2

Imaging Accessories IG40 and IG60 2.1

The new imaging accessories consist of the following components:

- The **Gradient Controller GCU** calculates the gradient pulses in real-time allowing for an infinite number of gradient switching points during experiments without limitation of waveform memory size. The intelligent gradient controller has several modes to control gradient waveforms which can be configured for complex gradient shapes, waveform lists, or just fast throughput. The gradient controller provides 16-bit resolution output for the X, Y, Z gradients with a time resolution of 25ns.
- The **GREAT Master Unit** is the interface between the gradient controller and the gradient current amplifiers. The digital gradient pulse information is routed to the individual gradient amplifiers and to the Bo compensation unit. The temperature of the gradient coils is controlled during the experiments as well as the state of the individual current amplifiers in order to protect the gradient coils and the imaging accessory.
- The **Gradient Power Supplies GREAT40 and GREAT60** provide 40A and 60A maximum current respectively and 120V.

  The current amplifiers get **digital gradient pulse input**, which is converted to analog signals in the amplifiers and not in a separate analog unit. Such a design prevents distortions, caused by analog signal transfers.

  The **pre-emphasis correction** is generated and applied inside the amplifiers. Four exponential time constants and amplitudes are available for each gradient. The adjustments are under software control and settings for variousgradients, magnets or methods can be stored on disk in the same manner as for shim settings.

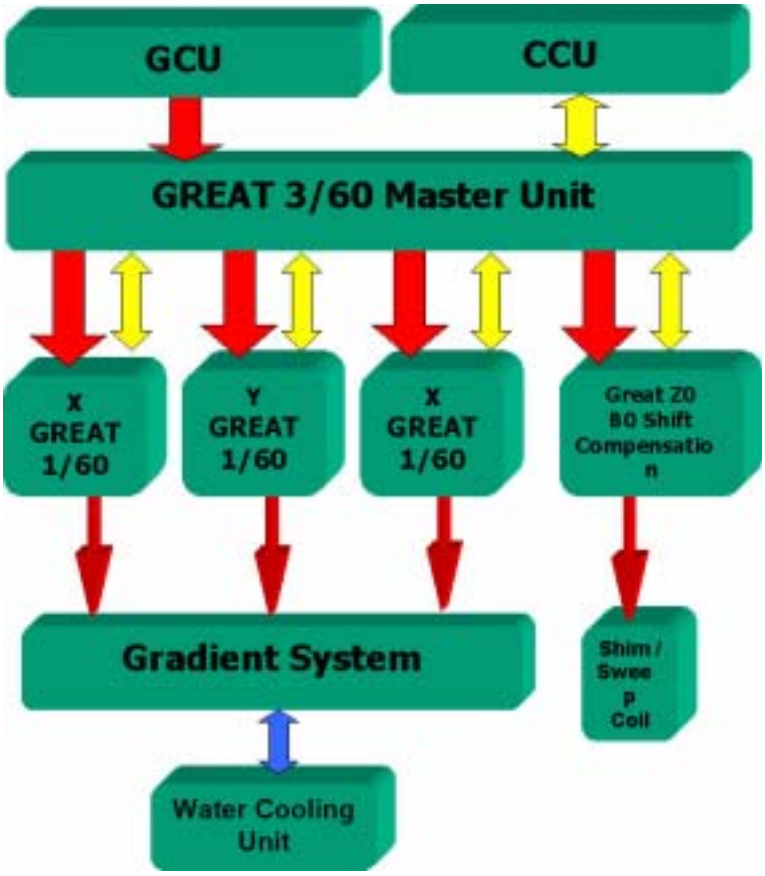
  The maximum current output stage of the amplifiers can be set in **steps of 10 A**, which reduces noise and increases the dynamic range of the output current.

  The amplifiers include **blanking units** for dedicated applications.

  Offset adjustment is under software control as well as **impedance matching** for a wide range of gradient coil loads.
- The **Bo Shift Compensation Unit, GREATZ0** features four exponential time constants and amplitudes for each gradient. The adjustments are under software control and settings for various gradients, magnets or methods can be stored on disk in the same manner as for shim settings.
- The **Gradient Water Cooling Unit, BCU20** provides cooling water for the gradient systems. The temperature can be adjusted manually or under software

control. The unit can be used for temperature adjustments of the sample up to approximately 50° C.

- Various **probes** and **gradient systems** with a large number of single or double tuned RF-coils and with different diameters from approximately 2 mm up to 64 mm are available, as well as additional accessories for in vivo experiments and special sample holders.



Imaging Hardware Parts List ***2.1.1***

Table 2.1. GREAT Imaging Hardware Parts List

Description	Part Number
IG40 GREAT Imaging Accessory with 40 A GREAT40 amplifiers	BH0354
Upgrade to IG60 with 60 A GREAT60 amplifiers	BH0358
GREAT Master Unit	H9402
GREAT Z0 compensation Unit	W1212776 (W1212287 old version)
GREAT 60 Amplifier	W1209612
GREAT 40 Amplifier	W1211690

Installation of the Imaging Hardware *2.2*

The installation of the imaging hardware is accomplished in two steps:

1. Check the wiring of the imaging rack and install the rack as described in the following sections.
2. Then connect the probe with the gradient system. This is described in chapter ***"Probes and Gradients" on page 51***.

Figure 2.1. GREAT Imaging Rack with Accessories

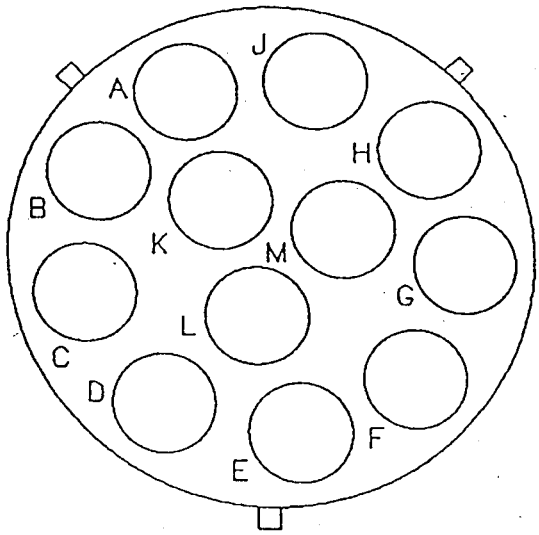
Once the hardware is installed, adjustments must be made as described in the chapter ***"Tests and Adjustments" on page 89***.

Checking the Gradient Wiring 2.3

The gradient cable HZ0969 connects the output of the GREAT40/60 gradient amplifiers with the gradient coil systems. The pins of the burndy connector are used for the gradient currents and for temperature measurements as described in the following table.

Table 2.2. Burndy Connector for the Gradient Cable

Polarity	-	+
Z-Gradient	A	B
X-Gradient	C	D
Y-Gradient	E	F
PT-100	L	M



Installation of the Imaging Rack 2.4

The imaging rack contains the GREAT Master Unit, three GREAT40 or GREAT60 amplifiers and the GREAT Zo Unit as an option. The wiring between the units in the imaging rack should be completed upon delivery as follows:

1. Connect the RS232 cable between the GREAT Master Unit and the console.
2. Connect the gradient cable between GRAD IN of the GREAT Master Unit and the Gradient Control Unit GCU in the console.
3. Connect the PT-100 temperature cable between the GREAT Master Unit and the gradient system.
4. Connect the cable between „Amplifier X“ of the GREAT Master Unit and the „GRAD IN + COMMANDS“ of the X-GREAT amplifier.
5. Connect the cable between „Amplifier Y“ of the GREAT Master Unit and the „GRAD IN + COMMANDS“ of the Y-GREAT amplifier.
6. Connect the cable between „Amplifier Z“ of the GREAT Master Unit and the „GRAD IN + COMMANDS“ of the Z-GREAT amplifier.
7. Connect the gradient cable at the OUTPUT of the GREAT40/60 amplifiers.
8. Connect the cable between „Z0 COMPENSATION“ of the GREAT Master Unit and the „GRAD IN + COMMANDS“ of the GREAT Zo Unit.

Follow the instructions in the section ***"Installation of the GREAT Bo Shift Compensation Unit" on page 16***.

Some parameters for the GREAT amplifiers, e.g. amplifier output current stage, loop adaptation, offset compensation have to be configured. This is described in ***"GREAT40/60 Amplifier Test (m_grdpulse)" on page 100***.

Activation of the GREAT40/60 Amplifier Blanking. *2.4.1*

A blanking unit is integrated in the GREAT amplifiers. It is controlled by blanking pulses, generated from the spectrometer console during the pulse program. The blanking pulses are created by setting special bits in the **NMR control word 0** as shown in the following table.

Table 2.3. Blanking Pulses on AVANCE

Back Panel I	AVANCE Rectangular Connector	AV Circular Connector
Blanking X gradient: c32 or set NMR0 | 32	C	b
Blanking Y gradient: c33 or setNMR0 | 33	H	c
Blanking Z gradient: c34 or setNMR0 | 34	M	d

Note: On AVANCE instruments all NMR controls are active low. Therefore, the blanking pulse selector switch at the blanking unit must be set to active low.

Note: The older pulse programs must be modified in order to make use of the blanking feature. The new version of programs contain these modifications.

A number of macros are defined in the file **Grad_Blank.incl** for a comfortable handling of the blanking features. Some examples are shown in the chapter for the BAFPA 40 gradient amplifiers.

Installation of the GREAT Bo Shift Compensation Unit *2.5*

The Zo (Bo) Shift Compensation Unit creates a correction signal for the compensation of Bo field shifts, caused by gradient switching. This signal is applied to the sweep coil of the magnet.

Different versions of the GREAT Bo Shift Compensation Units exist.

- The new version (***W1212776***) can add both signals from the Bo shift compensation and from the BSMS and apply them to the shim system (sweep coil).
- The older versions (**W1210128, W1212287**) can apply to either the Bo correction signal, created in the Bo shift compensation unit or the field signal (field offset, drift compensation, lock) created in the BSMS shim unit.

The installation of the units is different and is described in the following sections.

Installation of the GREAT Bo Shift Compensation Unit Version W1212776 *2.5.1*

1. Remove the Jumpers from the front panel of the BSMS/2.
2. Connect the cable HZ12200 between the BSMS/2 „Z0 Compensation Interface“ and the GREAT Bo Compensation Unit „Ho IN/OUT“.
3. Connect the GREAT Bo Compensation Unit „GRAD IN PLUS COMMANDS“ and the GREAT Master Unit „Zo - Compensation“.
4. Check the configuration parameters for the activation of the GREAT Zo (Bo) compensation unit as described in ***"Bo Shift Compensation Unit Functionality Test" on page 111***.

Installation of GREAT Bo Shift Compensation Unit Version **W1210128 & W1212287** *2.5.2*

In the version **(W1210128, W1212287)** of the Zo (Bo) shift compensation unit the signal from the shim unit is switched off, if the Bo compensation signal has to be applied. The switch is made in an external Bo switch box or in the BSMS, depending on the type of the shim system in use

As a consequence, the field cannot be shifted any more, when the system is switched to the Bo shift compensation mode. Then the frequency SFO1 must be adapted to the resonance conditions.

1. Check the configuration parameters for the activation of the GREAT Zo (Bo) compensation unit as described in ***"GREAT40/60 Amplifier Test (m_grdpulse)" on page 100***.
2. Connect the cable between the OUTPUT of the GREAT Zo Unit and the BSMS or the Bo switching box. Note, that this cable **must not contain a resistor** as it is used for the BAFPA40 amplifier. Different cables and Bo switch boxes exist, depending on the type of the shim system. The following table contains the part numbers for the various configurations.

Table 2.4. Zo Cables and Boxes

Shim System	Shim Unit	Cables/Boxes
BOSS1 or BOSS WB, HU057	BSMS	Zo Unit ECL00 Switch box H5996/1 Cable from Master Unit to Zo Unit HZ10202 Cable from Zo Unit to switch box HZ3538
BOSS WB99	BSMS	Zo Unit ECL00 Cable from Master Unit to Zo Unit HZ10202 Cable from Zo Unit to BSMS shim adapter HZ10213/1
BOSS WB99	BSMS	Zo Unit ECL01 Cable from Master Unit to Zo Unit HZ10202 Cable from Zo Unit to BSMS shim adapter ### with included switch under software control

For BSN18 and BSMS with WB17 or SB shim systems:

1. Disconnect the shim cable from the shim amplifier (BSN18 or BSMS) and connect it to the switch box.
2. Connect the cable from the switch box to the shim amplifier.
3. Set the switch on the box to the shim mode or to the Bo shift compensation mode.

For BSMS/2 and WB99:

1. Switch the BSMS off.
2. Set the jumpers at the front panel of the BSMS/2 to the Bo compensation operation mode.
3. Connect the cable HZ10213 between the BSMS/2 front plate and the gradient amplifier for the Bo compensation in the imaging rack.

External Variable Temperature Unit *2.6*

The external Variable Temperature Unit (**BVT H 3700**, part number **W1208444**) produces air of a adjustable temperature outside from a probe. The unit can be used for temperature adjustments of objects in probes with animal or object handling systems, where no dewar and heater is built in, e.g. in the Mini0.5 and Mini0.26 imaging probes. The principle is the same as the one used in most other probes. The unit contains a dewar, a heater and a temperature sensor (type E), which must be connected to a temperature control unit in the spectrometer console.

B-AFPA Imaging Hardware

3

General 3.1

The **imaging accessory** consists of the basic hardware units, including the gradient control unit (GCU), the pre-emphasis and Bo correction unit (BGU-II), three gradient amplifiers (B-AFPA-40) and a gradient water cooling unit. An additional amplifier for the Bo compensation and a amplifier blanking unit are available as options. These parts are common to all imaging accessories and independent of the NMR frequency.

A number of various imaging probes with gradient coils can be connected to the same imaging accessory.

The **GCU** is an intelligent VME bus slave controller board. Digital gradient values of the experiment are calculated at run-time and loaded into the BGU-II within less than 5 μs. The resolution of the gradient amplitude is 16 bit.

The **BGU-II** converts the digital gradient amplitude values into analog signals and modifies them by exponential shapes for eddy current and B0 shift compensation. Four amplitudes and time constants for corrections are available in the hardware. Three of them can be selected for simultaneous adjustments under software control. In practice this is sufficient for excellent pre-emphasis and B0 shift adjustments. The values for the amplitudes and time constants are stored for individual probes with gradient coils.

The BGU-II controls the gradient coil temperature and switches the amplifiers off when the temperature exceeds a safety value.

The **current amplifiers** drive the gradient coils. They include a matching unit for optimal adoption of the various gradient coil systems with different inductivities and resistance. An efficient safety unit is included in the current amplifiers to prevent amplifier and gradient coil damage.

The **B0 shift compensation** hardware in the BGU-II and one additional amplifier are optional, since most of the imaging applications do not need B0 shift compensation.

The **Gradient Blanking Unit** is mainly used in diffusion experiments, in order to separate the gradient amplifiers from the probes during data acquisition. It is also available as an option.

Various **probes** and **gradient systems** with a big number of single or double tuned RF-coils and with different diameters from approximately 2 mm up to 64 mm are available as well as additional accessories for in vivo experiments and special sample holders.

Installing the Imaging Hardware 3.2

The installation of the imaging hardware is accomplished in two steps.

1. First, check the wiring of the imaging rack and connect the rack as described in this chapter.
2. Then connect the probe with the gradient system. This is described in the chapter ***"Probes and Gradients" on page 51***.

Continue with the adjustments as described in the chapter ***"Tests and Adjustments" on page 89***.

Imaging Hardware Parts Lists 3.3

Table 3.1. Imaging Accessory

Option No.	Description
BH0354	D*X, COMPLETE MICROIMAG. W/O (NO) PROBE

Table 3.2. Imaging Accessory Parts

Part Number	Description	Quantity
H002165	MICRO IMAGING ACC D.X BASIC NO PROBE	
H2546	AQX GCU BOARD	1
H5577	AQX BUS 5 CONNECTOR BOARD	1
HZ2969	CABLE FLK 64P40	1
W1206288	BAFPA40 FOR BGU2 GRASP	1
W1206288	BAFPA40 FOR BGU2 GRASP	1
W1206288	BAFPA40 FOR BGU2 GRASP	1
H5380	BGU2 GRADIENT UNIT XYZ	1
H5517	CABLE COAX RG316 40CM SMB/SMB	2
H5496	CABLE SET MICRO IMAG BGU2	1
Z31247	MAN BGU2 GRAD.UNIT REMOTE CON.	1
H9015	MAN MICROIMAG AVANCE	1
H8087	SINGLE CABINET M AUFSATZ O FAN	1
H10960	PRINTER DESK JET 660C	1y
O001009	GRADIENT WATER COOLING UNIT	1

Table 3.2. Imaging Accessory Parts

Part Number	Description	Quantity
H5496	CABLE SET MICRO IMAG BGU2	1
HZ2691	CABLE KOAX 150 BNC/TWIN-BNC/SF	3
P1567	CABLE KOAX 2000MM SFT/SFT	3
HZ2690	CABLE KOAX 2P2000 BNC/TWIN	3
HZ0409	CABLE KOAX 2P3000 TWIN BNC/BNC	1
HZ3202	CABLE KOAX 2P5000 BNC/TWIN	1
HZ0969	CABLE RD 6P8700 MIRI AMPL PH	1
HZ04055	CABLE RD 9P4500 BU/BU	1
H5509	CABLE RD 25P2000 SFT/BU MINI-D	3
H5510	CABLE RD 50P8000 BU/BU	1
3000	CABLE RD ST NETZ SCHUKOZU.3122	1
19457	ST ADAP 9P SFT/SFT	1
14110	PNK SCHLAUCH PA HART SW 10X8	20
3033	ST BU 2 G KURZSCHLUSS JUMPER	30
CALIBRATION SAMPLES DEPENDENT ON THE PROBE TYPE		
H3695	GRAD CALIBRATION SAMPLE MICRO	1
H9018	GRAD CALIBRATION SAMPLE MINI	1

Gradient Cable *3.4*

The gradient cable HZ0969 connects the output of the B-AFPA-40 gradient amplifiers with the gradient coil systems. The pins of the burndy connector are used for the gradient currents and for temperature measurements as described in the following table.

Figure 3.1. Burndy Connector of the Gradient Cable

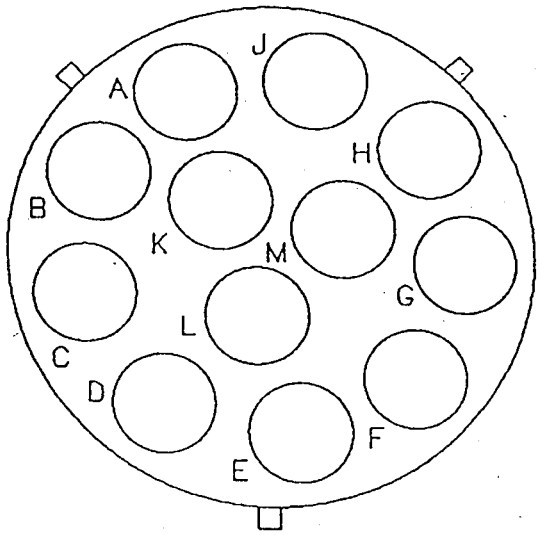
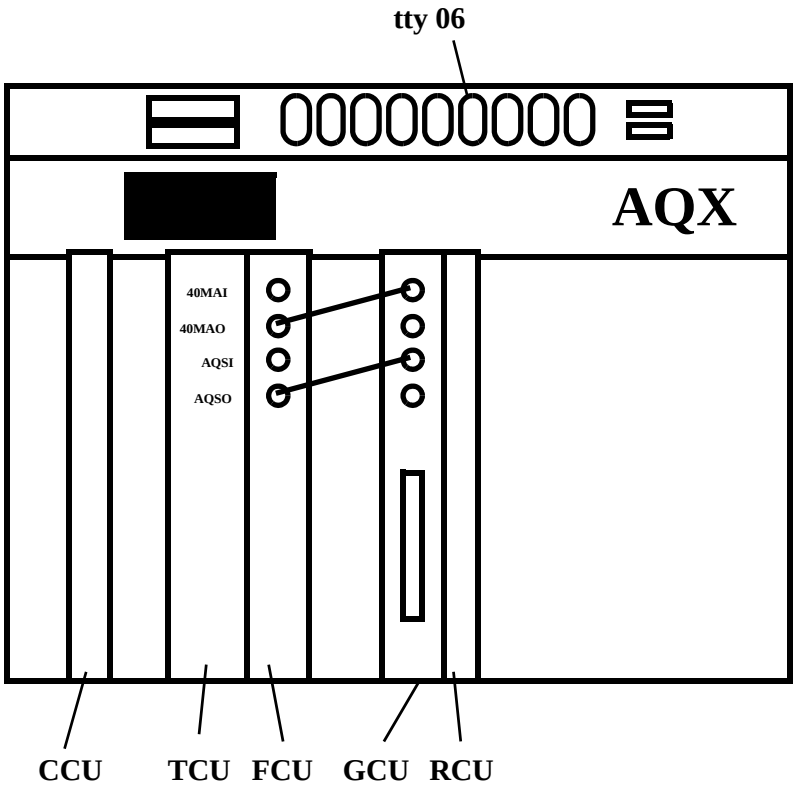


Table 3.3. Burndy connector of the gradient cable

Polarity	-	+
Z Gradient	A	B
X Gradient	C	D
Y Gradient	E	F
PT-100	L	M

Installation of the Gradient Control Unit GCU *3.5*

Figure 3.2. Installation of the GCU



The GCU is mounted in a slot between the frequency control units FCU's and the receiver control unit RCU as shown in the figure.

If there is no free slot available between the FCU and RCE, move the RCU to another position using the following steps:

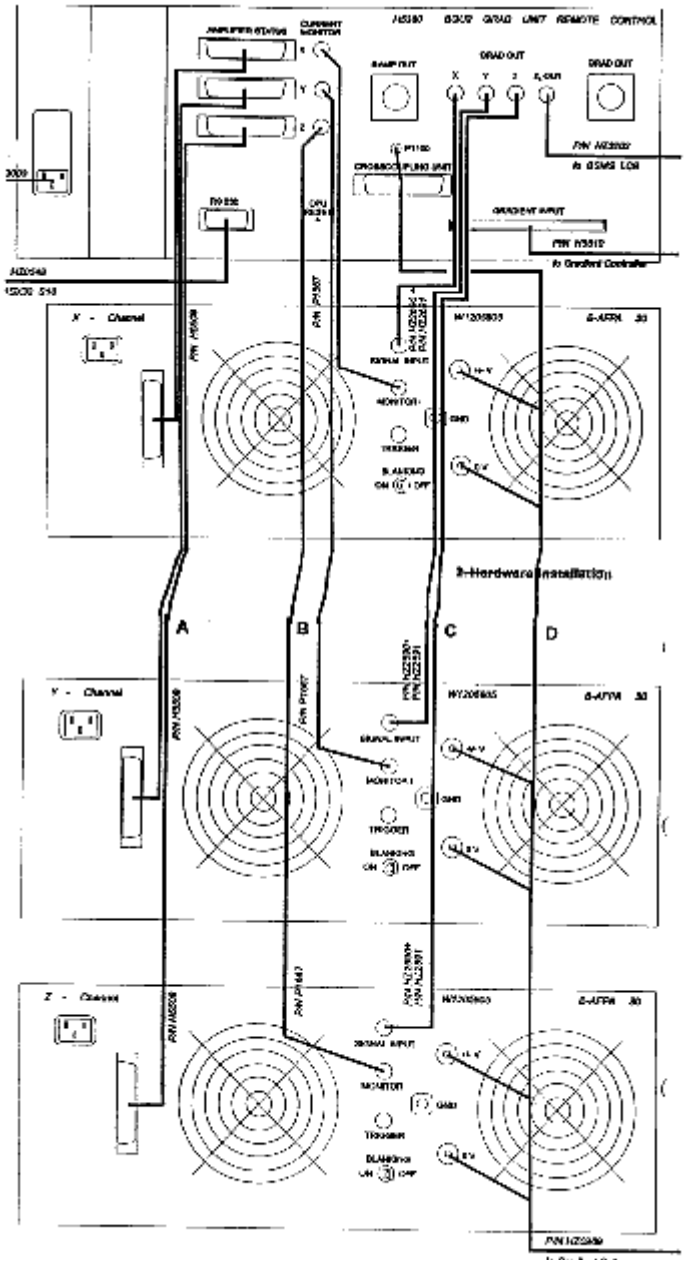
- Mount the pick-up board H5577 and the cable HZ2969 on the motherboard.
- Move the bus terminator resistors from the old to the new pick-up board.
- Take care, that the jumpers are set on the motherboard at the positions of the empty slots.

When the GCU is the last board next to the RCU, the 40 MHz lines 40MAO and AQSO must end in 50 Ohms on the GCU board. Therefore set the jumpers W1 and W2 on the GCU board and remove the jumpers W2 and W3 on the neighboring FCU board.

- Insert the GCU board into the free slot of the AQX rack and remove the jumpers on the motherboard.
- Connect the 40 MHz coax cable H5517 between 40MAO on the FCU board and 40MAI on the GCU board.
- Connect the H5517 coax cable between AQSO on the FCU board and AQSI on the GCU board.

Imaging Rack Wiring *3.6*

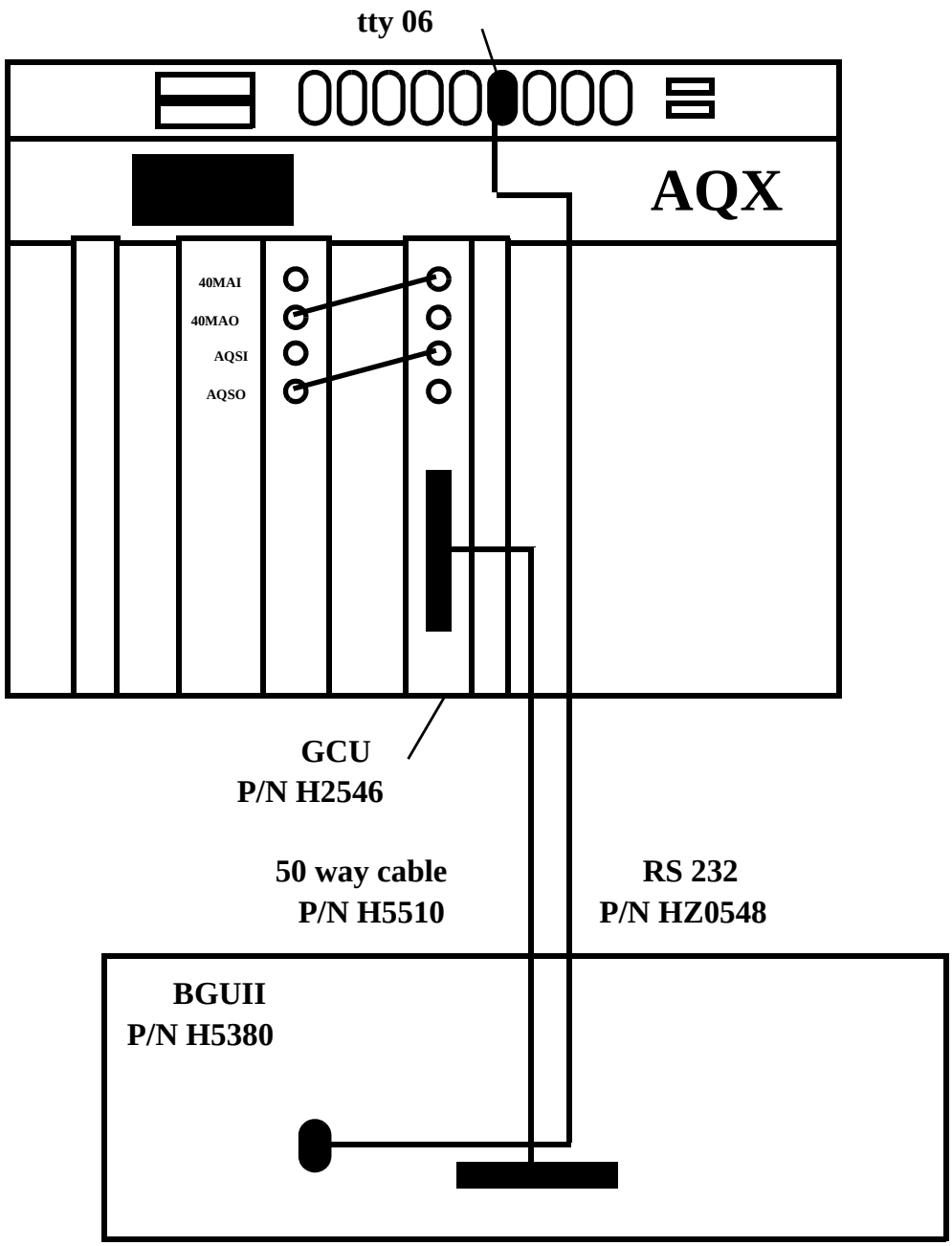
Figure 3.3. Imaging Rack



The imaging rack contains the BGU-II and the gradient amplifiers. Check to see if the wiring is correct between the BGU-II and the B-AFPA-40 amplifiers as shown in the figure above.

Connections Between the GCU and the Imaging Rack *3.7*

Figure 3.4. AQX and BGU-II



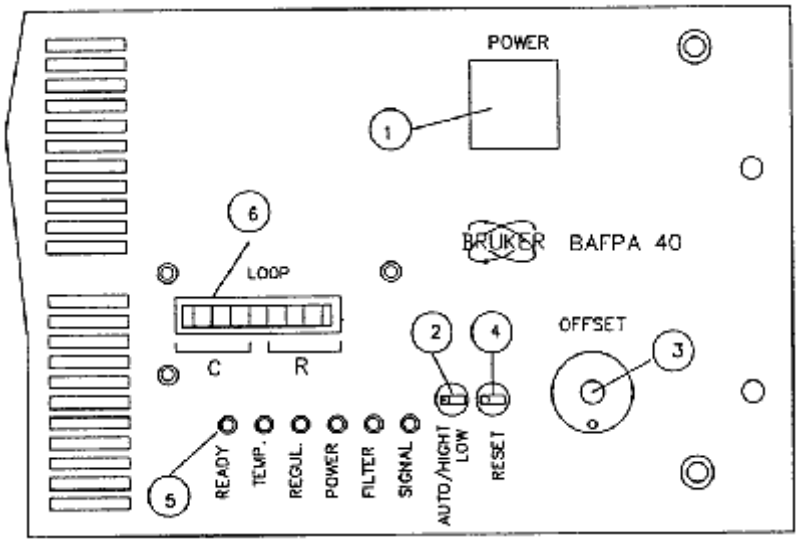
- Connect the RS232 cable HZ0548 between the BGU-II and a free TTY input on the SIB board in the AQX rack. *TTY06* is reserved for the BGU-II.
- Connect the 50 way cable H5510 between the GCU and the BGU-II.

Installation of the Gradient Amplifiers B-AFPA-40 *3.8*

A number of different gradient coils are used with the imaging accessory. The coils differ in inductance and resistance. In order to optimize the gradient pulse shape and gradient switching speed the B-AFPA-40 amplifiers provide the adoption of the load by adjusting RC-combinations on a feedback circuit.

The values for R and C are set by dip switches on the front panel of the amplifiers, marked as label (6) in the figure below.

Figure 3.5. B-AFPA-40 Front Panel with Dip Switches (6)



The following table shows the recommended dip switch settings for some gradient coils delivered from Bruker. The values in the table have been determined in the Bruker laboratories. They can be modified by the adjustment procedure, described in the following. Contact the Bruker imaging application group, when other gradients, not included in the table, are used.

Table 3.4. B-AFPA-40 Dip Switch Setting (up to ECL 5, 0 = open)

Gradient system	Gradient	C Dip Switch	R Dip Switch	C	R
Diff30	Z	0000 0001	0100 0000	0.22 nF	100 kΩ
Micro5	X, Y, Z	0000 0001	0100 0000	0.22 nF	100 kΩ
Micro2.5	X, Y, Z	0000 0001	0100 0000	0.22 nF	100 kΩ
Mini0.5	X, Y, Z	0000 0001	0100 0000	0.22 nF	100 kΩ
Mini0.36	X, Y, Z	0000 0001	0100 0000	0.22 nF	100 kΩ

B-AFPA-40 Dip Switch Setting (ECL 6 or higher, 0 = open)

Gradient system	Gradient	C Dip Switch	R Dip Switch	C	R
Diff30	Z	0001 0000	0001 0000	0.22 nF	100 kΩ
Micro5	X, Y, Z	0001 0000	0001 0000	0.22 nF	100 kΩ
Micro2.5	X, Y, Z	0001 0000	0001 0000	0.22 nF	100 kΩ
Mini0.5	X, Y, Z	0001 0000	0001 0000	0.22 nF	100 kΩ
Mini0.36	X, Y, Z	0001 0000	0001 0000	0.22 nF	100 kΩ

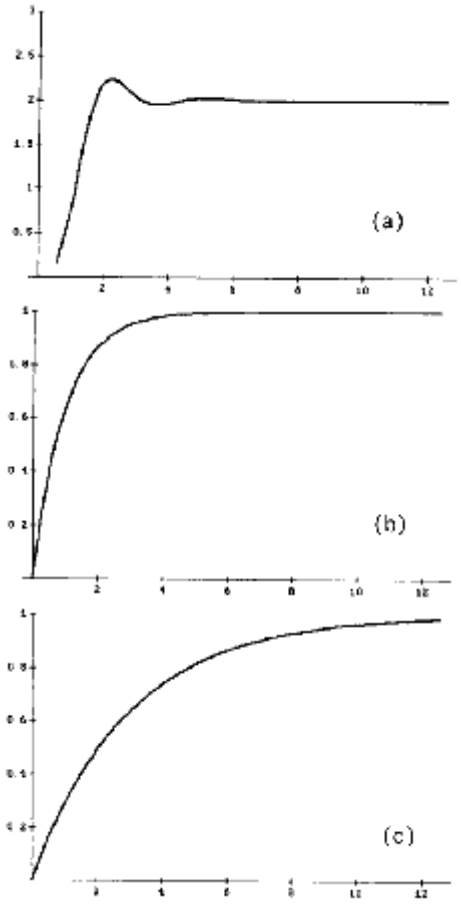
Adjustment procedure:

Do not set all dip switches to zero while the B-AFPA-40 is switched on! Select at least one switch for R and one for C. Otherwise the gradients and/or the amplifiers can be damaged.

- Install the probe for imaging applications as described in the chapter ***"Probes and Gradients" on page 51***.
- Set the B-AFPA-40 dip switches for the imaging probe (see the previous table).
- Set the parameters for the "**m_grdpulse**" test program as described in chapter ***"GREAT40/60 Amplifier Test (m_grdpulse)" on page 100***.
- Check that all gains of the pre-emphasis parameters are set to zero.
- Start the acquisition with **gsp**.
- Observe the gradient shapes on the oscilloscope.
- Modify the dip switches until the best shape is reached (see ***Figure 3.6.*** below).

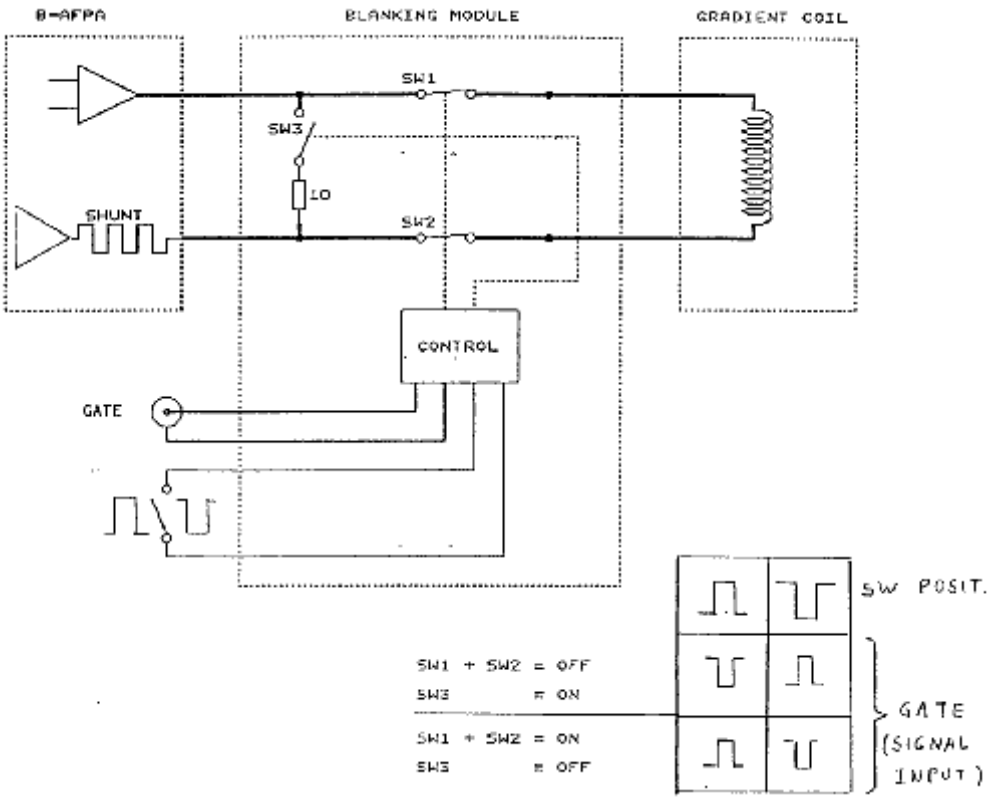
The best pulse rise behavior is shown in the following figure (b). Incorrect adjustments can cause an overshot of the pulse (a) or too slow gradient rise times (c).

Figure 3.6. Gradient Pulse Adjustment



Installation of the Gradient Blanking Unit *3.9*

Figure 3.7. Gradient Blanking Unit BGB3x40A (W1207793)



The gradient blanking unit is used to disconnect the gradient amplifiers from the gradient coils during the data acquisition e.g. in diffusion experiments with very strong gradient coils. The blanking unit exists with one or three channels. A hardware manual is available and can be ordered under part number W1207893/01.

- Connect the cables from the B-AFPA-40 current amplifiers to the input of the blanking unit.
- Connect the cable from the gradient coil to the output of the blanking unit.
- Connect the "**Blanking Control**" cables to the corresponding BNC sockets "**Signal Input**" (see following table).
- Set the selector for positive or negative logic of the gating pulse.

How to use the BGB Blanking Unit

The blanking unit is controlled by blanking pulses, generated from the spectrometer console during the pulse program. The blanking pulses are created by setting special bits in the NMR control word 0 as shown in the following table.

Table 3.5. Blanking Pulses on AVANCE

Back Panel I	AVANCE Rectangular Connector	AV Circular Connector
Blanking X gradient: c32 or set NMR0 | 32	C	b
Blanking Y gradient: c33 or set NMR0 | 33	H	c
Blanking Z gradient: c34 or set NMR0 | 34	M	d

Note: On AVANCE instruments all NMR controls are active low. Therefore the blanking pulse selector switch at the blanking unit must be set to active low.

Note: The older pulse programs must be modified in order to make use of the blanking feature. The new version of programs contain these modifications.

A number of macros are defined in the file **Grad_Blank.incl** for a comfortable handling of the blanking features. The file is listed in the following.

```
;Grad_Blank.incl - include file to handle the Gradient blanking unit
#define BLKGRAMP_ALL setnmr0^32 setnmr0^33 setnmr0^34
#define UNBLKGRAMP_ALL setnmr0|32 setnmr0|33 setnmr0|34
#define BLKGRAMP_X setnmr0^32
#define BLKGRAMP_Y setnmr0^33
#define BLKGRAMP_Z setnmr0^34
#define UNBLKGRAMP_X setnmr0|32
#define UNBLKGRAMP_Y setnmr0|33
#define UNBLKGRAMP_Z setnmr0|34
```

An example of an imaging pulse program, where the blanking unit is connected and when no gradient blanking must be applied, is given below. The modifications of the pulse program are the lines which include: #include <Grad_Blank.incl> and UNBLKGRAMP_ALL.

```
; images for Gradient-Echo-Single-Slice
#include <Grad_Blank.incl>
        1s ze                   ; zero data NBL blocks
        10u UNBLKGRAMP_ALL
        10      d31:ngrad       ; slice gradient on
        d2 fq1:f1               ; gradient stabilization delay
        p3:sp0 ph1              ; slice selective pulse
and so on.
```

An example of a diffusion pulse program, where the blanking unit is connected and when gradient blanking is applied, is given below. The modifications of the pulse program are the lines which include: #include <Grad_Blank.incl>, BLKGRAMP_ALL, UNBLKGRAMP_Z and BLKGRAMP_Z.

```
;diffse ;2D Steiskal Tanner sequence
#include <Grad_Blank.incl>

1s ze
 10u BLKGRAMP_ALL
 5m pl1:f1                  ;set rf power level
1 d1                        ;relaxation delay/2
 d11 UNBLKGRAMP_Z           ;unblank gradient amplifier
 p1 ph1                     ;90 degree pulse
d3:ngrad                    ;gradient on time
d2:ngrad                    ;gradient ring down time
 d9 BLKGRAMP_Z              ;tau
 d11 UNBLKGRAMP_Z           ;unblank gradient amplifier
 p2 ph2                     ;180 degree pulse
 d3:ngrad                   ;gradient on time
 d2:ngrad ph3               ;gradient ring down time
 d10 BLKGRAMP_Z             ;tau
aq adc ph0                  ;acquisition
rcyc=1                      ;ns=1
d1 st                       ;relaxation delay/2 increment echo pointer
```

```
lo to 1 times nbl          ;nbl=number of projections
 5m ip0                    ;phase cycle
 5m ip0                    ;phase cycle
5m ip1                     ;phase cycle
 5m ip1                    ;phase cycle
 lo to 1 times l1          ;# of averages
 d1 wr #0                  ;write data to disc
exit

ph0=0
ph1=0
ph2=1
ph3=0
```

Note: The following will work for the **AMX** spectrometers. This style is not used on AVANCE spectrometers.

It is recommended that you use **bit0** from the NMR control word 2 for the blanking of the gradients. The signal is available on pin JJ at the back panel connector BPI.

- Connect pin JJ from BPI at the spectrometer console with the one or three signal input BNC connectors at the blanking unit.
- Set the selector switch for positive/negative logic at the front panel of the blanking unit to negative logic (switch down).
- Modify the pulse program as shown in the following example:

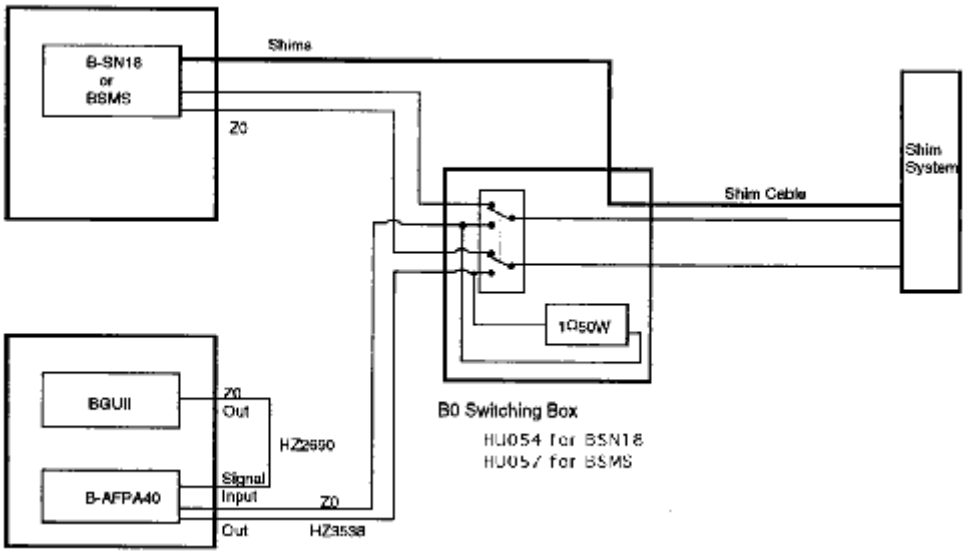
```
;file: imblank
;version 221096 DGR
;pulse sequence to show the use of the BGB3x40A gradient blanking unit.
;use bit0 from nmrcntl word 2 on pin JJ from BPI


#define BLKGRAMP_ALL setf2 ^0
#define UNBLKGRAMP_ALL setf2 |0
```

```
        ze
        1s BLKGRAMP_ALL             ;       blank all gradients
10      d1                          ;relaxation delay
        5m UNBLKGRAMP_ALL           unblank all gradients
        10u:ngrad                   ;dephasing read gradient on
        3m                          ;dephasing delay
        10u:ngrad                   ;gradient off
        1m
        1m ph3 BLKGRAMP_ALL         ;blank all gradients
        go=10 ph0
        wr #0
        exit

ph0 = 0
ph1 = 0
ph3 = 0
```

Figure 3.8. Bo Shift Compensation Accessory Wiring



The Bo shift compensation accessory consists of a B-AFPA-40 current amplifier and a switch box. The switch box disconnects the sweep coil signal from the shim amplifier and connects the Bo compensation signal from the BGU-II and the current amplifier to the sweep coil of the shim system. As a consequence, the field cannot be shifted any more, when the system is switched to the Bo shift compensation mode. Then the frequency SFO1 must be adapted to the resonance conditions.

Table 3.6. contains some part numbers for cables and Bo switch boxes.

For BSN18 and BSMS

- Disconnect the shim cable from the shim amplifier (BSN18 or BSMS) and connect it to the switch box.
- Connect the cable from the switch box to the shim amplifier.
- Connect the Bo output from the BGU-II to the input of the B-AFPA-40 current amplifier.
- Connect the current amplifier output to the switch box input.
- Set the switch on the box to the shim mode or to the Bo shift compensation mode.

For BSMS/2 and WB99

- Switch the BSMS off.
- Set the jumpers at the front panel of the BSMS/2 to the Bo compensation operation mode.
- Connect the cable HZ10213 between the BSMS/2 front plate and the gradient amplifier for the Bo compensation in the imaging rack.

Table 3.6. Zo Cables and Boxes

Shim system	Shim Unit	Cables/Boxes
WB17, HU054	BSN18	Switch box H5948 Cable to switch box HZ3538
BOSS1 or BOSS WB, HU057	BSMS	Switch box H5996 Cable to switch box HZ3538
WB99	BSMS	Cable to BSMS shim adapter HZ10213

Gradient Cooling Units

4

Gradient Cooling Unit BCU20 4.1

All the new gradient coil systems are water cooled for a better and safer performance. The cooling is accomplished through a closed loop water circuit, driven by a water pump. The temperature of the out flowing water is adjustable. A water filter and a pressure reduction device are added after the output of the water pump housing. A three way valve is added, where one input can be used to press forced air into the cooling circuit. This is used in order to remove the water from the gradient coil, when the gradient system has to be disconnected from the experimental setup.

The cooling unit can also be added as a heater for the gradient system for the temperature adjustment of the sample in the range between 5° C and 50° C. This helps to prevent convection in the sample during diffusion experiments, because the sample is inside of the gradient system with a very homogeneous temperature environment. Another application is to keep the body temperature of a animal during in vivo experiments at a convenient value, e.g. by setting the water temperature to 35 °C.

The BCU20 can be controlled by buttons at the front panel of the unit or under software control within XWINNMR by the „edtg“ command, if the BCU20 is connected to the console by a RS323 cable.

Some specifications of the BCU20 are the following:

Temperature range:	+5 to +50° C
Temperature stability:	+/- 0.1° C with internal sensor selected
Coolant:	3 liters of distilled water
Coolant flow rate:	0.2 to 1 l / min. (adjustable manually by a needle valve, and a flow meter on the front panel)
pump pressure:	maximum 0.3 bar
Two temperature sensors:	PT-100 in probe or bath, selectable by manual switch
Cooling power:	250 Watt at 20° C bath temperature
Compressor bath capacity:	0.4 Kg R124A gas
Draining gas requirement:	air, 4 to 6 bar, the draining pressure is factory set to 0.3 bar Byan internal pressure regulator

For more details see the BCU20 manual.

Fill distilled water into the chiller.

Connect the water hoses to the gradient system at the back panel of the unit.

Connect the air at the back panel of the unit.

Connect the RS232 cable to the console at the back panel of the unit.

Switch the unit on.

Check the proper operation by observing the flow display at the front panel.

Check the water flow from time to time by observing the pressure at the pressure reduction device. When the pressure is zero no water is flowing. Another way to check the water flow is simply to disconnect the water hose for a short moment at the output of the gradient system.

The water flow can be blocked, when the filter element is polluted e.g. by algae, which may grow in the water after a while.

The growing of algae can be stopped by adding a water conditioner (Art.9025.1 ROTH), available under part number “69663”.

The recommended concentration is 0.6 ml water conditioner for 4 l of water

(0.15 ml/l or 1.5 ml/10l or 1.8 ml/HAAKE-UWK45)

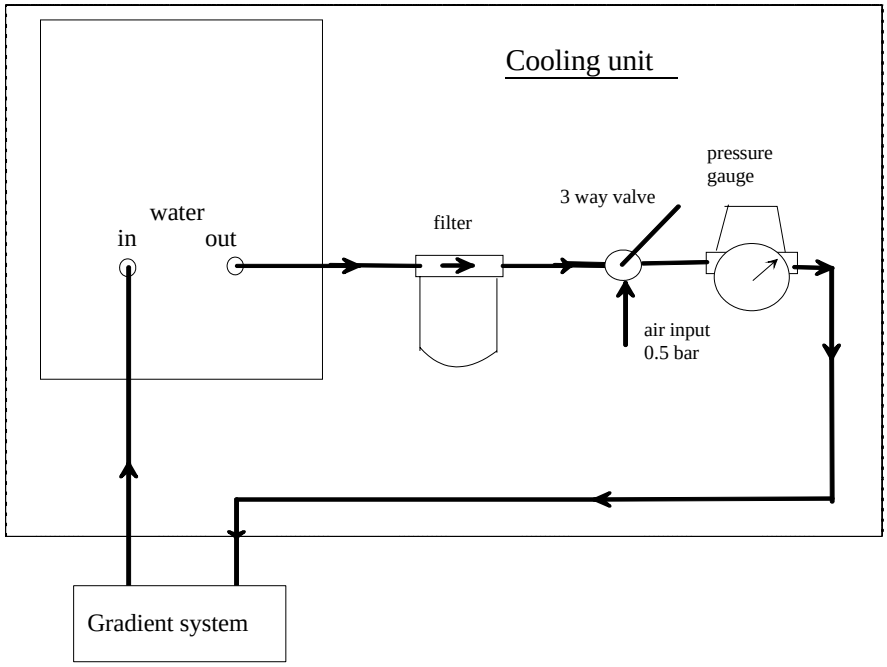
A package of 10 filter elements for replacement is available under part number “H9531”.

The complete filter unit, including the filter housing and one filter element is available under part number 68318.

Gradient Cooling Unit HAAKE UWK45 *4.2*

All the new gradient coil systems are water cooled for a better and safer performance. The cooling is accomplished through a closed loop water circuit, driven by a water pump. The temperature of the out flowing water is adjustable. A water filter and a pressure reduction device are added after the output of the water pump housing. A three way valve is added, where one input can be used to press forced air into the cooling circuit. This is used in order to remove the water from the gradient coil, when the gradient system has to be disconnected from the experimental setup. The connections of the individual parts are shown in the following drawing.

Figure 4.1. Gradient Cooling Accessory



Check the water flow from time to time by observing the pressure at the pressure reduction device. When the pressure is zero no water is flowing. Another way to check the water flow is simply to disconnect the water hose for a short moment at the output of the gradient system.

The water flow can be blocked, when the filter element is polluted e.g. by algae, which may grow in the water after a while.

The growing of algae can be stopped by adding a water conditioner (Art. 9025.1 ROTH), available under part number “69663”.

The recommended concentration is 0.6 ml water conditioner for 4 l of water

(0.15 ml/l or 1.5 ml/10l or 1.8 ml/HAAKE-UWK45)

A package of 10 filter elements for replacement is available under part number “H9531”.

The complete filter unit, including the filter housing and one filter element is available under part number 68318.

Monitoring and Triggering 5

BioTrig 5.1

Biotrig is a PC based (Laptop) monitoring and triggering system. A manual for the BIOTRIG is coming with the Biotrig software on CDROM.

For the connection between Biotrig and the console please read chapter ***"Connecting BioTrig/Physiogard and the Console" auf Seite 44***.

Physiogard 5.2

The **Physiogard SM 785 NMR** (part number **U88221**) is used to monitor ECG and/or respiratory signals during in vivo experiments. The unit can produce output signals for ECG and/or respiratory gated data acquisitions.

A detailed description is available in the manual delivered with the unit.

1. Pinout of the DB25 connector at the Physiogard:

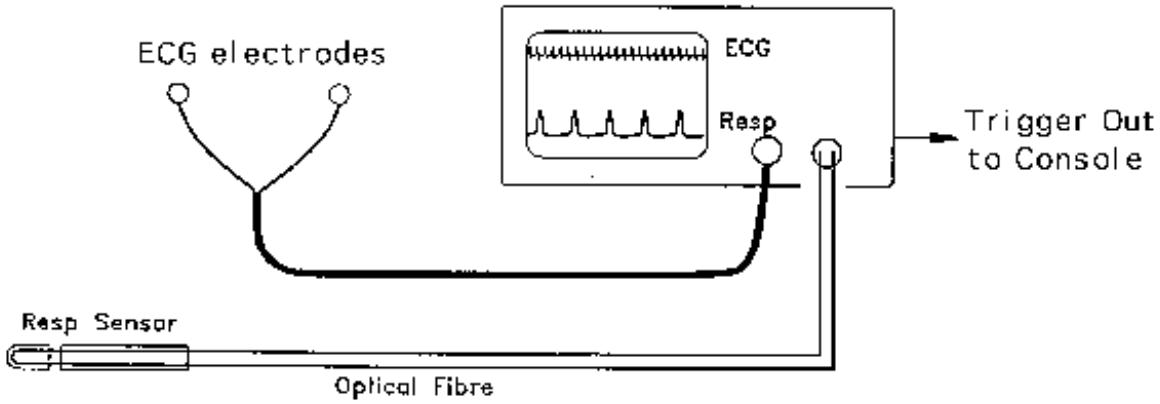
Details: Physiogard 25 pin connector

Pin 3-4:	shortcut
Pin 5:	Trigger output
Pin 6:	Ground for trigger output

For the connection between Physiogard and the console please read chapter *"Connecting BioTrig/Physiogard and the Console" auf Seite 44*.

2. Connections between the sensors and the Physiogard

Figure 5.1. Connections Between the Sensors and the Physiogard



3. Modifications of pulse programs for triggered acquisition:

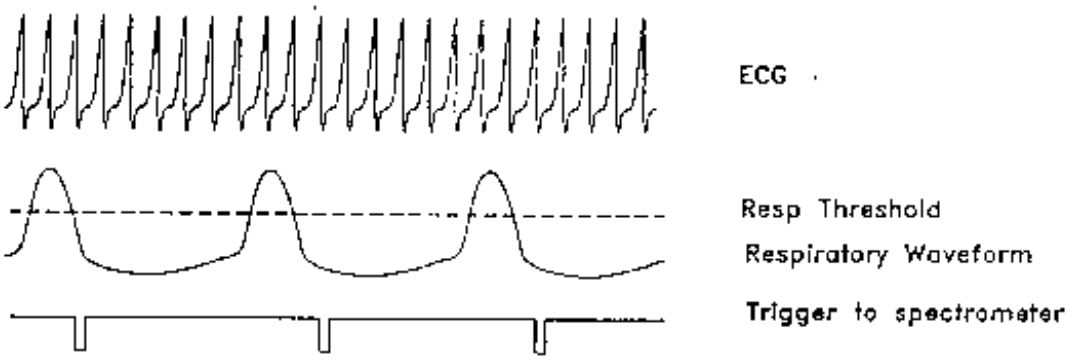
Insert the appropriate trigger command for the experiments in the pulse programs.

The following commands are available:

trignl1	wait for negative level on channel TRIG0
trigpl1	wait for positive level on channel TRIG0
trigne1	wait for negative edge on channel TRIG0
trigpe1	wait for positive edge on channel TRIG0
trignl2	wait for negative level on channel TRIG1
trigpl2	wait for positive level on channel TRIG1
trigne2	wait for negative edge on channel TRIG1
trigpe2	wait for positive edge on channel TRIG1

4. Adjustment of the trigger levels with the Physiogard

Figure 5.2. Adjustment of the Trigger Levels with the Physiogard



Select the trigger mode for the ECG trigger or respiratory trigger or for a combined mode of ECG/respiratory. In the combined mode, the first ECG peak after the falling respiratory signal peak is used for the trigger pulse.

Adjust the trigger levels to a appropriate value, using the buttons on the front panel of the Physiogard.

With the Software-Modification dated Sept. 22nd, 1993 the following features have been changed or added:

1. Possibility of choosing the QRS-trigger-mode
2. Possibility of choosing the displaying of the heart-frequency
3. Possibility of choosing the trigger-mode in the Combi-Mode

1. Possibility of choosing the QRS-Trigger-Mode

   At power-on of the device the possibility is provided to choose between QRS-Trigger-Mode by **hardware** or by **software**.

   The selection is done by the appropriate „+“-key.

   10 seconds after the last us of the „+“-key the monitor starts its normal processing.

   When software-triggering is selected one has additionally to „**learn**“ a QRS-complex.

   This is not necessary when hardware-triggering has been chosen.

2. Possibility of choosing the displaying of the heart-frequency

   At power-on of the device the possibility is provided to choose if the heart frequency should be displayed in **„Hf/min.“**or **„RR/ms“**.

   The selection is done by the appropriate „+“-key.

3. Possibility of choosing the trigger-mode in the Combi-Mode

At power-on of the device the possibility is provided to choose if one **QRS-complex** or multiple **QRS-complexes** should trigger during one respiration-cycle.

The selection is done by the appropriate „+“-key.

Connecting BioTrig/Physiogard and the Console *5.3*

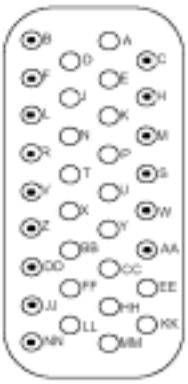
Connecting the Trigger Output to the Console *5.3.1*

The Physiogard/Biotrig can be used to control the pulse program. This means, the pulse program waits, until the Physiogard/Biotrig detects a trigger (ECG, respiration or combined ECG/respiration trigger). As soon as the monitoring system detects a trigger, it’s trigger output (Pin5 at Physiogard, Trig.Out at BioTrig) becomes 0 volt. The synchronization between the monitoring system and the console is done via the TCU signal Trig0. The connection itself is a single cable (Part HZ04532 for the Physiogard; for BioTrig) that has to be connected to the back panel connector BP1 of the console.

AVANCE Electronics

Connect the trigger out cable to pin NN on the back panel connector BP1:

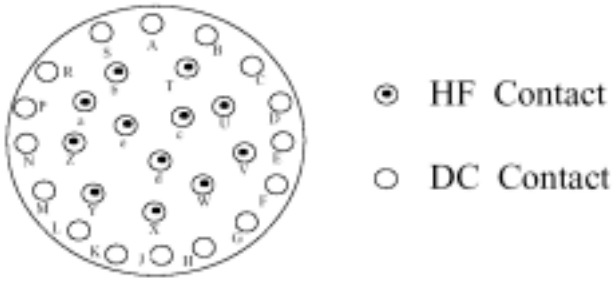
Figure 5.3. Back Panel Connector on AVANCE Instruments (front view)



AV Electronic

Connect the trigger out cable to pin Y on the back panel connector BP1:

Figure 5.4. Back Panel Connector at AV Instruments (front view)



Connecting Time Stamping Input to the Console *5.3.2*

This feature is available on Biotrig only. The pulse program can control a hardware output of the console, that give signals to the BioTrig system. BioTrig can put a mark to the physiological data, whenever it gets this signal. So the physiological data and the NMR data can be correlated.

Unfortunately, this signal is not available on the back panel of the system that are delivered before BioTrig, so it must be connected directly to the TCU front plate.

AVANCE Electronics

There are several Burndy connectors available at the front panel of the TCU. To connect the BioTrig T.Stamp output, Pin E from T5 must be connected to the BTCM. This means a short cable (Burndy-BNC) must be build into the housing of connector T5. This output can be controlled by the NMR word 3, Bit 8.

AV Electronic

There are a lot of SMB connectors visible on the front panel of the TCU. There are different groups (A,B,C,...,I) with 6 pins each. The T.Stamp output of the BioTrig must be connected to the output C1. To do this, an adapter is needed that can normally be found attached very close to the TCU or in the „blue service box“. This output can be controlled by the NMR word 3, Bit 6.

Gradient Calibration Samples

6

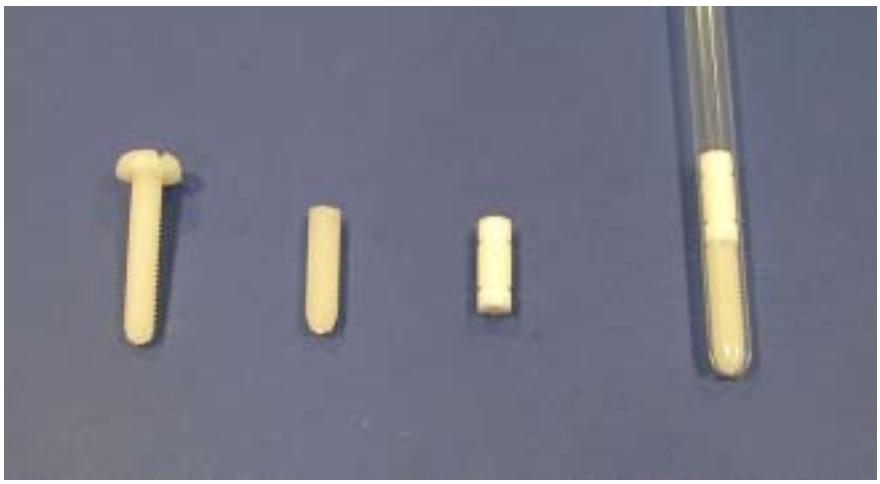
A number of different gradient calibration samples exist, adapted to the various RF-coil diameters and gradient coil sensitivities.

Gradient Calibration Sample, GC5 6.1

The gradient calibration sample **„GC5**“ fits into a 5 mm RF-coil. It is used for the **Micro5** gradient systems.

The sample is made from a M4 nylon screw and a teflon plug in a 5 mm NMR tube. Contact the micro-imaging group for such a sample or make one by yourself. Cut off the top of the screw and put the remaining part with the thread into the 5 mm NMR tube. Fill some doped water (1 g/l CuSO4) into the tube. Push a teflon plug into the tube to press the part of the screw to the bottom of the tube and to fix it well.

Figure 6.1. Gradient calibration sample “GC5“



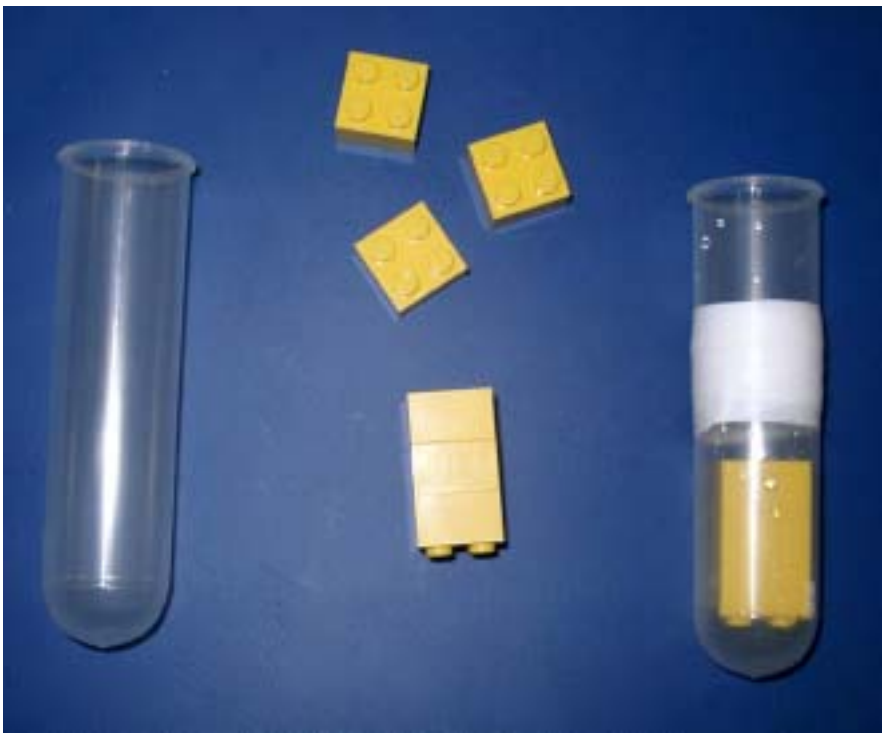
Gradient Calibration Sample, GC25 *6.2*

The gradient calibration sample **„GC25**“fits into a 25 mm RF-coil. It is used for the **Micro2.5** and the **Mini0.5** gradient systems.

The sample is made from three Lego blocks in a 23 mm plastic tube, filled with some doped water (1 g/l CuSO4).

Contact the micro-imaging group for such a sample or make one by yourself. Stick three lego blocks on top of each other and push them into a plastic tube as shown on the picture below. Make sure, that they fit tightly. Fill some doped water (1 g/l CuSO4) into the tube. It is recommended to drill some small holes into the Lego’s, that the air can escape, when the water is filled into the tube.

Figure 6.2. Gradient Calibration Sample “GC25“

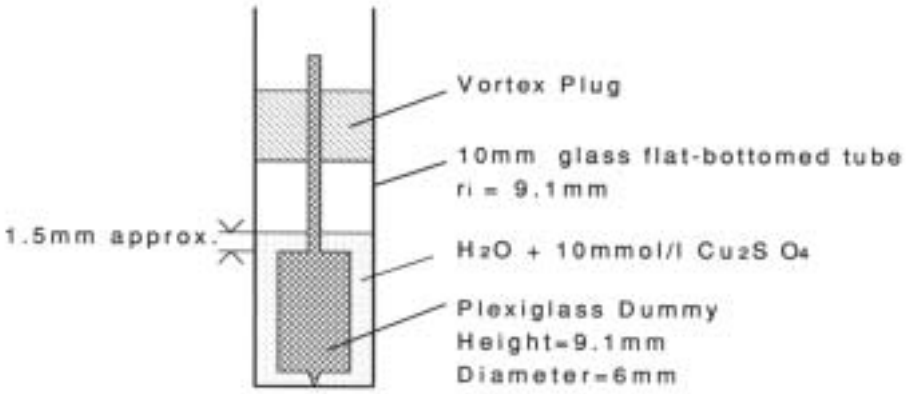


Old Gradient Calibration Samples *6.3*

The following gradient calibration samples are not produced anymore, but may still be available in some laboratories.

The calibration sample "**microcal**" (part number H3695) is recommended for the Micro5 and Micro2.5 probes.

Figure 6.3. Gradient Calibration Sample "microcal"



The calibration sample "**minical**" (part number T5893) is recommended for the Mini0.5 and Mini0.36 probes. The inner diameter is 30 mm and the length is 25 mm.

Figure 6.4. Gradient calibration sample "minical"

Gradient Calibration Samples

Probes and Gradients

7

The Micro5 Probe 7.1

Figure 7.1. Micro5 Probe, rf Inserts and Gradient Security Box

The Micro5 probe consists of a probe body with exchangeable rf coils of different diameters and type, an actively shielded XYZ gradient coil and a gradient coil security box.

The specifications are shown in the following table.

Table 7.1. Micro5 Probe and Gradient Specifications

Gradients	XYZ
Gradient strength	4.8 G/cm/A
ID/OD	19/40 mm
Linearity +-1.3% peak-peak +- 1.6% peak-peak +- 2.1% peak-peak	 18 mm sphere 19 mm sphere 20 mm sphere
Inductance	10 - 20 μH
Resistance	=< 120 mΩ
Rise time, 0-40A, 120V	< 50 μs
Cooling	air or water
Maximum current tested	40 A
Exchangeable rf coil types	solenoid, saddle
Rf-coil diameters	2 - 10 mm
Nucleus	1H and/or X

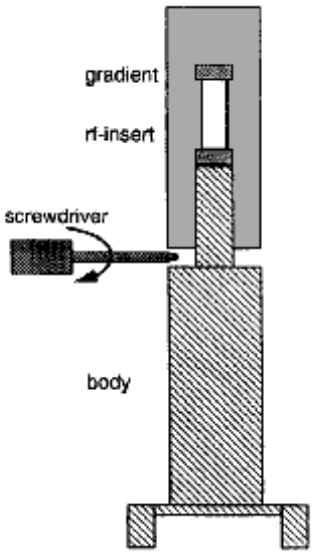
Handling the Micro5 Probe *7.1.1*

Mounting the rf inserts on the probe body must be made very carefully, because the inserts are very small and some of them are made of glass. They can break during the exchange. The most important step is the removal of the gradient coil from the probe body. **The gradient should not be tilted, when it is taken off the probe body!**

Removal of the Gradient Coils from the Probe Body

- When the gradients were previously used with water cooling, it is recommended that you remove the water in the gradient system with forced air, before the gradient coil system is disconnected from the probe body.
- The gradient is plugged onto the probe body and screwed down by a ring. Rotate the ring to disconnect the gradient coils.
- Carefully detach the gradient from the probe body by using a screw driver as shown in the figure below. Remove the gradients completely without tilting it, as the glass on the rf insert will break!

Figure 7.2. Gradient Coil Removal



1. Exchanging the RF-Inserts

- The saddle coil type inserts are not fixed with screws. You must only pull the insert off from the probe body. The solenoid coils are fixed by one or two screws. Remove the screws and pull the insert off.
- Mount another insert on the probe body. Fix it as in the case of solenoid inserts by the screws.
- Make sure that there is no water droplets from the gradient cooling at the probe body. Remove potential water drops with a tissue or a fan.

2. Mounting the Gradient Coils

- Push the gradient coil system carefully over the rf inserts. Do not tilt the gradients, as the glass of the rf insert will break!
- Screw down the ring to tighten the gradients on the probe body. The gradient system fixes the glass type rf inserts on the probe body. Do not use too much force to fix the ring.

3. Gradient Impedance Adaptation

- Set the dip switches at the front panel of the B-AFPA-40 amplifiers in order to match the load of the gradient coils as shown in the following table. Contact the Bruker imaging application group, when other gradient amplifiers are used.

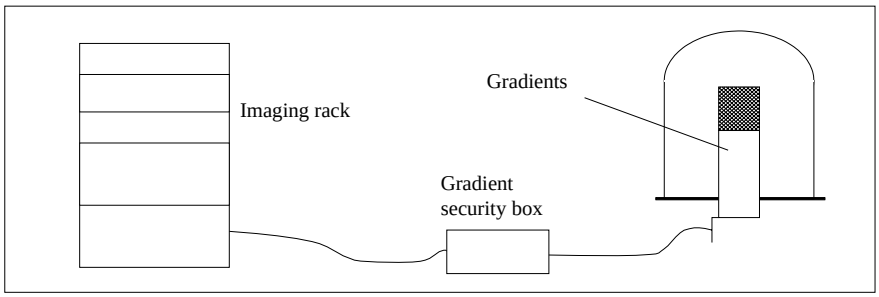
Table 7.2. B-AFPA-40 Dip Switch Setting

Gradient system	Gradient	C Dip Switch	R Dip Switch	C	R
Micro5	X	0000 1000	0001 0000	1.5 nF	20 kΩ
Micro5	Y	0000 0100	0001 0000	1.0 nF	20 kΩ
Micro5	Z	0000 1000	0000 1000	1.5 nF	15 kΩ

4. Gradient security

- Connect the gradient security box between the imaging rack and the gradient coils as shown below.

Figure 7.3. Gradient Cable Connections



5. Gradient cooling

Air or water cooling for the gradients is highly recommended, depending on the gradient currents and duty cycles. The temperature of the gradient system is displayed at the front panel of the BGU-II. The BGU-II switches the gradients off, when the temperature reaches 50°C.

- Connect the hoses for the gradient cooling as shown below and switch the cooling on.

Exchange the cooling water at least once a month and check the filter element of the cooling unit!

Figure 7.4. Air Cooling of the Gradients

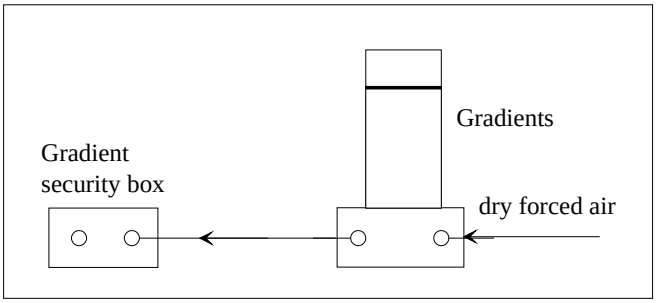


Figure 7.5. Water Cooling of the Gradients

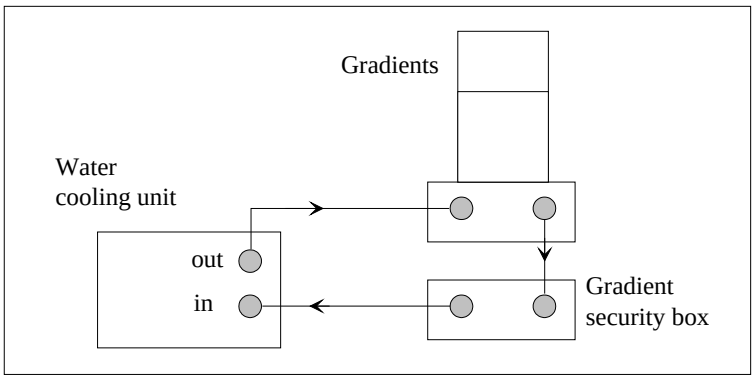


Table 7.3. Values for the Gradient Cooling

Air pressure	ca. 1 bar
Water pressure	< 0.5 bar
Water temperature	10 - 20 °C

8. Experiment Start

- Connect the RF-cable and start with the experiments. Observe the gradient system temperature and modify the cooling conditions of the experiment, if necessary.

9. Temperature adjustment with the Micro5 probe

The temperature behavior of the Micro5 probe is different from other probes, used in high resolution or solids NMR. The reason for this is the different type of heater and dewar, mounted in the micro-imaging probe, because there is less space available compared to other probe.

It is recommended to use the following parameters for temperature regulation, to be set by the **edte** command within XWIN-NMR:

Gas Flow:	500 to 900 l/h
Maximum Heater Power:	5 to 10%

and by clicking in the **edte** menu Setup

Sensors	Thermocouple E

and by clicking in the **edte** menu **Control** / **Self tune**:

Proportional Band:	130
Integral Time:	90
Derivative Time:	22

The temperature of the incoming gas should be at least 20° C below the “Target Temperature”.

It will take at least 10 minutes until stable conditions are achieved.

For more information read the manual of the temperature control unit, e.g. the chapter about manual tuning.

The Micro2.5 Probe *7.2*

Figure 7.6. Micro2.5 Probe, Gradients, Fuse Box, RF-Insert

The Micro2.5 probe consists of a separate RF- probe body with exchangeable rf coils of different diameters and type, an actively shielded XYZ gradient coil and a gradient coil security box.

Table 7.4. Micro2.5 probe and gradient specifications

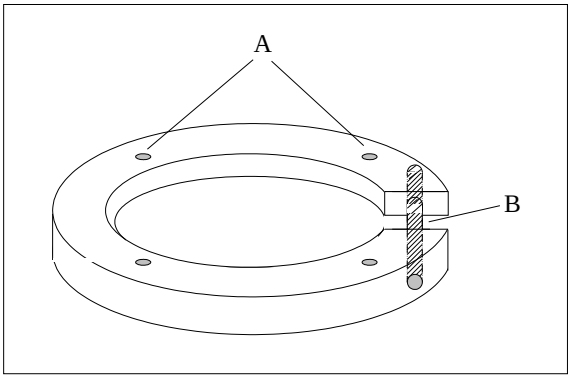
Gradients	XYZ
Gradient strength	2.5 G/cm/A
ID/OD	40/72 mm
Linearity +-1.8% peak-peak +- 2.2% peak-peak +- 3.0% peak-peak	 36 mm sphere 38 mm sphere 40 mm sphere
Inductance	=< 100 μH
Resistance	=< 400 mΩ
Rise time, 0-40A, 120V	< 110 μs
Cooling	air or water
Maximum current tested	40 A
Exchangeable rf coil types	solenoid, saddle, birdcage
RF-coil diameters	2 - 25 mm
nucleus	1H and/or X

Table 7.5. Micro2.5 Part Numbers

Frequency	Part Number
200 MHz	H8134
300 MHz	H8135
360 MHz	H8136
400 MHz	H8137
500 MHz	H8138
600 MHz	H8139
750 MHz	

Handling the Micro2.5 Probe *7.2.1*

1. Wide bore shim system modification



The Micro2.5 gradient coil system is longer than the wide bore probes for other applications. This was designed in order to increase the linearity of the XYZ gradients (2% peak-peak variation in a sphere of 38 mm diameter!).

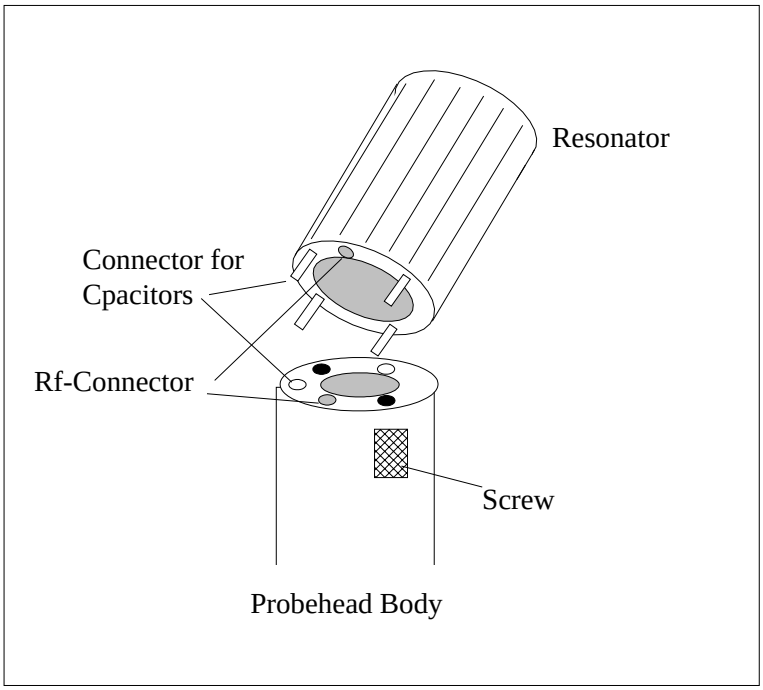
The upper part of the wide bore shim system must be shifted up by approximately 5 cm, to match the centres of the gradient coils, of the wide bore shims and of the rf coil. A modification of the wide bore shim system is required to fulfil these condition. The modification is made by a Bruker engineer.

After this modification the spinner turbine is fixed at the upper part of the shim system (top of the magnet).

2. Mounting of the gradient coil system

- Open the screws A and B at the upper part of the shim system as shown in the following figure and pull the upper part approximately 5 cm out of the magnet. Fix it then by the screws B.

Figure 7.7. Wide Bore Shim System Holder at the Magnet Top



- Remove the three screws from the bottom plate of the wide bore shim system and use them to connect the Micro2.5 gradients. Then the gradients are fixed very well, so that vibrations, caused by the gradient pulses in the magnetic field, are suppressed.

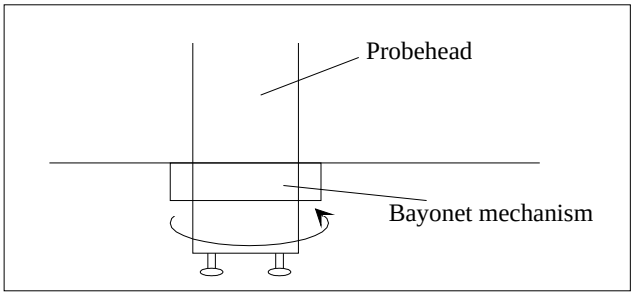
3. Exchanging the RF-inserts

- Set the RF-resonator insert on the probe body as shown in the following figure. Take care, that the connections for the RF-line, the capacitors and the two screws match.
- Rotate the two screws simultaneously, so that the RF-insert is slowly moved towards the probe body until it is completely fixed.

4. Mounting of the probe into the gradient system

- Insert the rf probe into the gradient coil system and fix it with the bayonet mechanism as shown below.

Figure 7.8. Bayonet Mechanism at the Probe Bottom



For some experiments the sample is mounted directly to the rf coil, for others the air lift can be used.

5. Gradient impedance adaptation

- Set the dip switches at the front panel of the B-AFPA-40 amplifiers to match the load of the gradient coils as shown in the following table. Contact the Bruker imaging application group, when other gradient amplifiers are used.

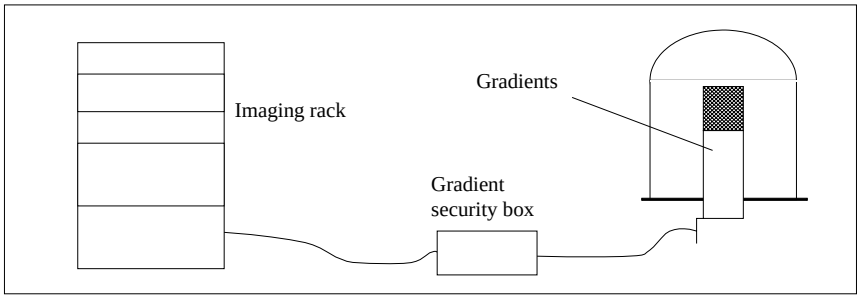
Table 7.6. B-AFPA-40 Dip Switch Setting

Gradient system	Gradient	C Dip Switch	R Dip Switch	C	R
Micro2.5	X	00001100	00010000	2.5 nF	20 kΩ
Micro2.5	Y	00001100	00010000	2.5 nF	20 kΩ
Micro2.5	Z	00001100	00010000	2.5 nF	20 kΩ

6. Gradient security

- Connect the gradient security box between the imaging rack and the gradient coils as shown below.

Figure 7.9. Gradient Cable Connections



7. Cooling of the gradients

Air or water cooling for the gradients is highly recommended, depending on the gradient currents and duty cycles. The temperature of the gradient system is displayed at the front panel of the BGU-II. The BGU-II switches the gradients off, when the temperature reaches 50°C.

- Connect the hoses for the gradient cooling as shown below and switch the cooling on.

Figure 7.10. Air Cooling of the Gradients

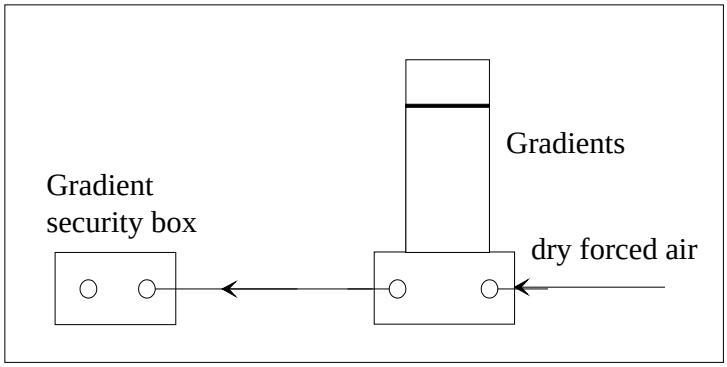


Figure 7.11. Water Cooling of the Gradients

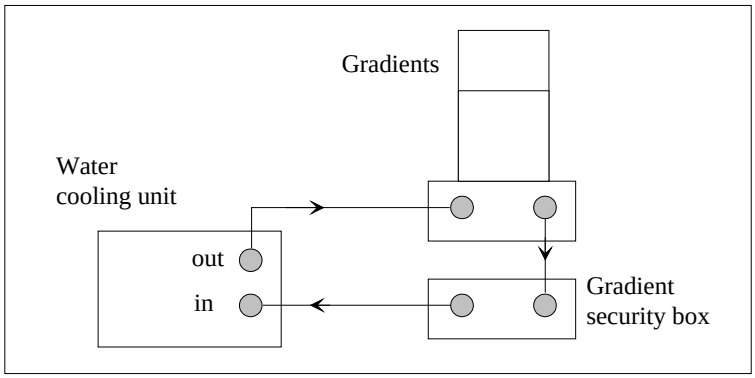


Table 7.7. Values for the Gradient Cooling

Air pressure	ca. 1 bar
Water pressure	< 0.5 bar
Water temperature	10 - 20 °C

Note: When the gradients were previously used with water cooling, it is recommended that you remove the water in the gradient system with forced air, before the water hoses are disconnected from the gradient system and from the gradient security box.

Exchange the cooling water at least once a month and check the filter element of the cooling unit!

8. Experiment start

- Connect the rf cable and start with the experiments. Observe the gradient system temperature and modify the cooling conditions of the experiment, if necessary.

Troubleshooting

Water leakages of the gradient system:

Replace the O-rings between the gradient system and the holder of the gradient system. The o-rings (3.50 mm x 1.20 mm) can be ordered under the part number 61643.

The Mini0.5 Probe *7.3*

Figure 7.12. Mini0.5 Probe with Gradients and Animal Handling System

The Mini0.5 probe contains a separate RF- probe body with exchangeable rf coils, an actively shielded XYZ gradient coil and depending on the experiments an animal or object handling system.

Table 7.8. Mini05 Probe and Gradient Specifications

gradients	XYZ
gradient strength	0.5 G/cm/A
ID/OD	57/72 mm
linearity +-2% peak-peak, Z / XY +- 10% peak-peak, Z / XY	 30 / 43 mm 40 / 52 mm
inductance	=< 70 μH
resistance	=< 1.6 Ω
rise time, 0-40A, 120V	< 150 μs
cooling	water
maximum current tested	50 A
exchangeable rf coil types	birdcages
RF-coil diameters	38 mm
nucleus	1H and/or X

1. Wide bore shim system modification

The Mini0.5 gradient coil system is longer than wide bore probes for other applications. This was designed in order to increase the linearity of the XYZ gradients.

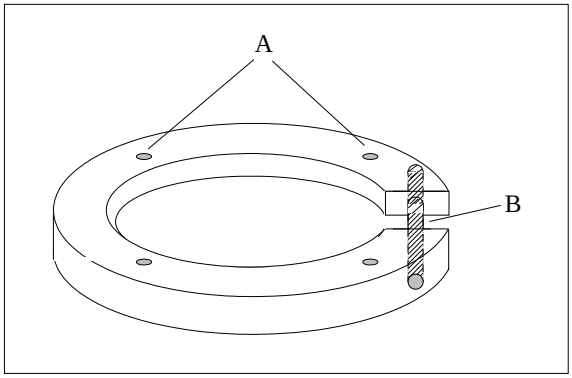
Therefore the upper part of the wide bore shim system must be removed, in order to match the centers of the gradient coils, of the wide bore shims and of the rf coil. A modification of the wide bore shim system is required to fulfill these condition. This modification must be made by a Bruker engineer.

After the modification the lower part of the wide bore shim system is fixed at the bottom of the magnet and the spinner turbine is fixed at the upper part of the shim system. Then the upper part of the shim system can be removed from the magnet when the lower part remains in the magnet at the same orientation relative to the magnet.

2. Mounting of the gradient coil system

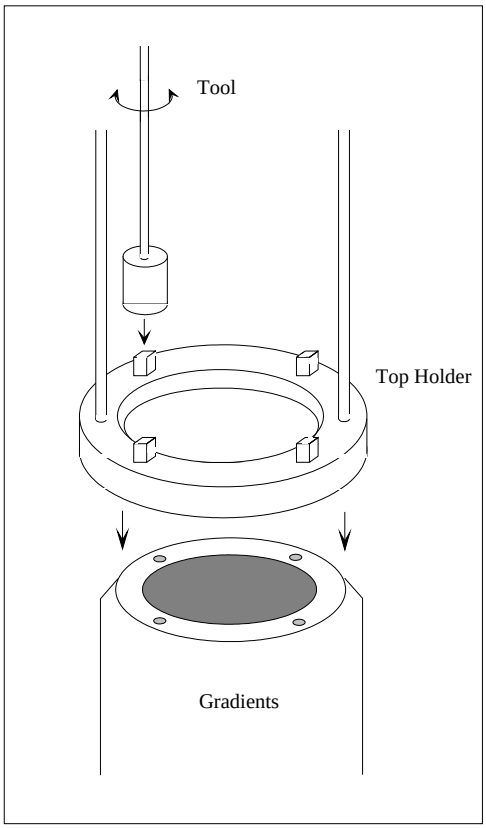
- Unscrew the screws A and B at the upper part of the shim system as shown in the following figure and pull the upper part of the shim system out of the magnet.

Figure 7.13. Wide Bore Shim System Holder at the Magnet Top



- Remove two or three screws from the bottom plate of the wide bore shim system and use them to connect the Mini0.5 gradients. A holder is mounted on the top of the gradients for a additional fixation of the gradient system in order to prevent vibrations, caused by the gradient pulses in the magnetic field.
- Mount the holder on the gradient top as shown in the following figure. Insert the holder from the top of the magnet and fix the 4 screws carefully on the gradient top with the special tool, which is delivered together with the gradients.

Figure 7.14. Mounting of the Gradient Top Holder

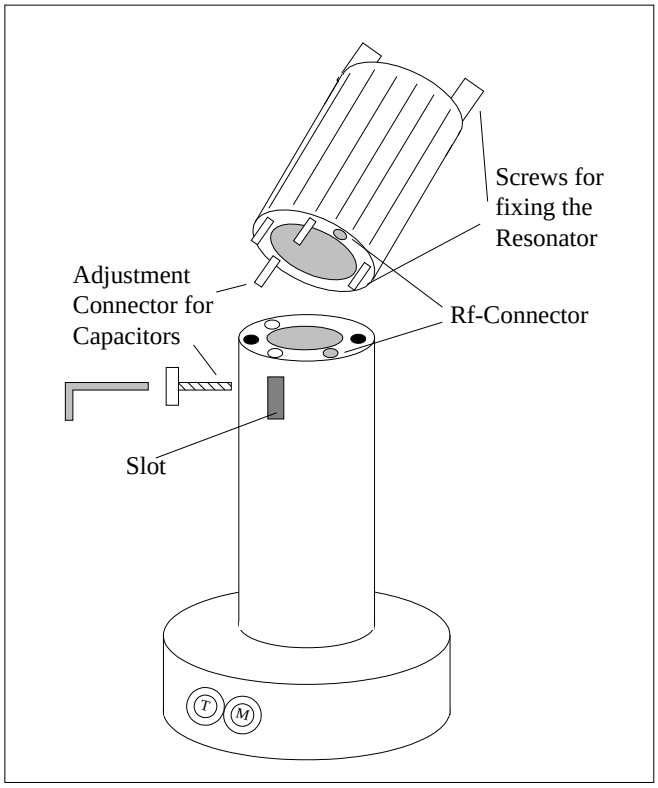


3. Exchanging the RF-inserts

This step can be skipped, when the resonator is already mounted on the probe body.

- Set the RF-resonator insert on the probe body as shown in the following figure. Take care, that the connections for the RF-line, the capacitors and the two screws match.
- Rotate the two screws on the resonator top simultaneously, so that the RF-insert slowly moves towards the probe body.
- Rotate the tuning and matching knobs at the bottom of the probe so that the connectors of the capacitors fit into the holders, which are visible through the small slots at the top of the probe body.
- Fix the capacitor rod at the holder with the small screws as shown in the figure.
- Check too see if the tuning and matching knobs move easily.

Figure 7.15. Mounting the RF-Insert on the Probe Body



4. Mounting the probe into the gradient system

- Insert the rf probe into the gradient coil system and fix it with the bayonet mechanism.

5. Mounting the Animal (AHS) or Object (OHS) Handling System in the probe.

- Put the animal or another sample into the handling system and then introduce it into the probe. Pull out the rod at the probe bottom until the AHS or OHS is introduced nearly completely. Then push the rod inside so that it fits into the gear at the bottom of the AHS or OHS. Then the sample can be shifted up and down within a small range for a fine adjustment of the vertical position.

The probe can be left in the magnet, when the object is exchanged. Only the AHS or OHS must be removed from the probe.

6. Gradient impedance adaptation

- Set the dip switches at the front panel of the B-AFPA-40 amplifiers to match the load of the gradient coils as shown in the following table. Contact the Bruker imaging application group, when other gradient amplifiers are used.

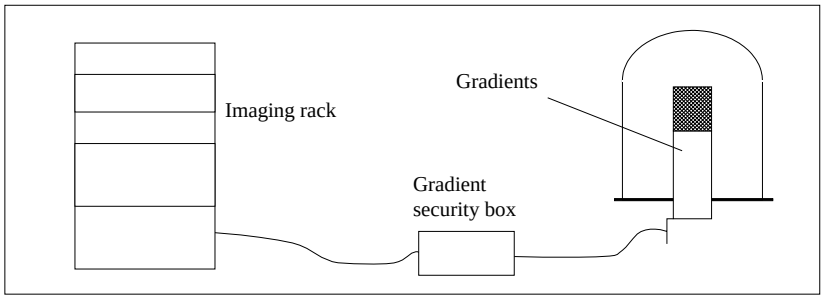
Table 7.9. B-AFPA-40 Dip Switch Setting

Gradient system	Gradient	C Dip Switch	R Dip Switch	C	R
Mini0.5	X	0001 1100	0000 1000	4.7 nF	15 kΩ
Mini0.5	Y	0001 0000	0000 1000	2.2 nF	15 kΩ
Mini0.5	Z	0001 0000	0001 0000	2.2 nF	20 kΩ

7. Gradient cable connection

- Connect the cable from the imaging rack with the fuse box and the gradient coil system.

Figure 7.16. Gradient Cable Connections



8. Cooling the gradients

Water cooling for the gradients is mandatory in order to prevent gradient coil overheating and damage. The temperature of the gradient system is displayed at the front panel of the BGU-II. The BGU-II switches the gradients off, when the temperature reaches 50°C.

- Connect the hoses for the gradient cooling as a closed circuit between the gradients and the cooling unit and switch the cooling on.

Figure 7.17. Water Cooling of the Gradients

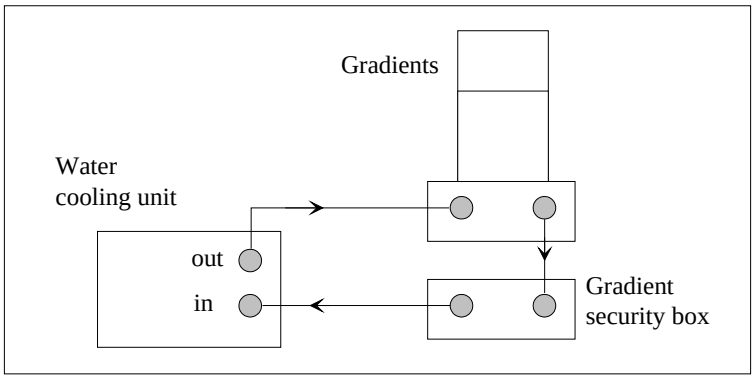


Table 7.10. Values for the gradient cooling

Air pressure	ca. 1 bar
Water pressure	< 0.5 bar
Water temperature	10 - 20 °C

Note: When the gradients were used previously with water cooling, it is recommended that you remove the water in the gradient system with forced air, before the water hoses are disconnected from the gradient system and from the gradient security box.

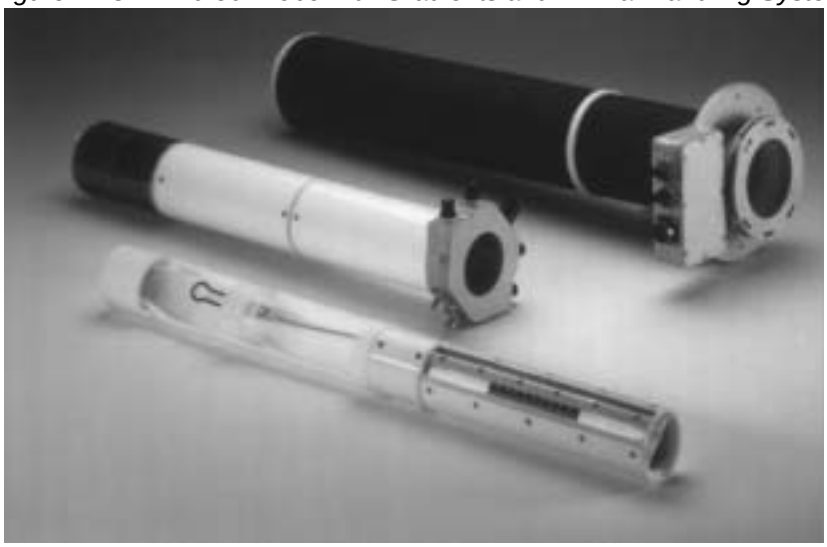
Exchange the cooling water at least once a month and check the filter element of the cooling unit!

9. Experiment start

- Connect the rf cable and start with the experiments. Observe the gradient system temperature and modify the cooling conditions of the experiment, if necessary.

The Mini0.36 Probe *7.4*

Figure 7.18. Mini0.36 Probe with Gradients and Animal Handling System



The Mini0.36 probe contains a separate RF- probe body with exchangeable rf coils, an actively shielded XYZ gradient coil and depending on the experiments an animal or object handling system.

Table 7.11. Mini0.36 Probe and Gradient Specifications

gradients	XYZ
gradient strength	0.36 G/cm/A
ID/OD	85/115 mm
linearity +-2% peak-peak, Z / XY +- 10% peak-peak, Z / XY	 44/ 60 mm 60/72 mm
inductance	=< 70 μH
resistance	=< 2 Ω
rise time, 0-40A, 120V	< 150 μs
cooling	water
maximum current tested	50 A
exchangeable rf coil types	birdcages
RF-coil diameters	64 mm
nucleus	1H and/or X

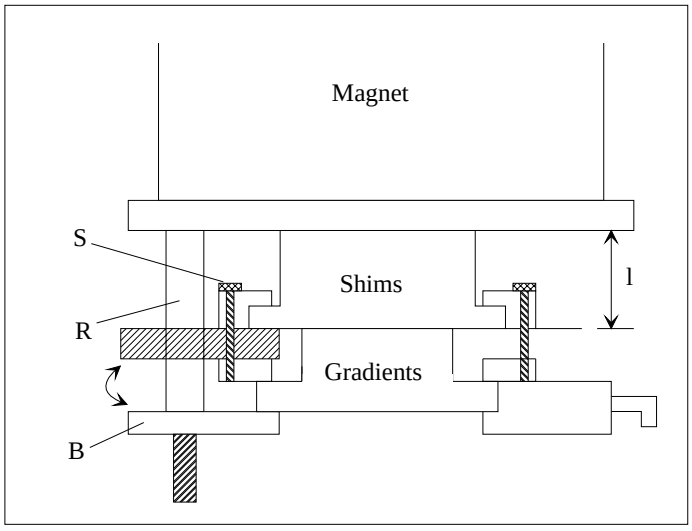
1. Mounting of the gradient coil system

Two persons should be present for mounting the Mini0.36 gradient coil system.

The gradients are shifted into the Standard Wide Bore (SWB) shim system. The shim system is fixed by a horizontal cross bar B, connected to a vertical rod R at the bottom plate of the magnet (see the following figure). This bar must be rotated off the shim base plate, while one person is holding the shim system to prevent a change of its position. Then the gradients are pushed inside the shim system and fixed together with the shims by the cross bar B. The vertical position of the bar must be changed by approximately 10 mm, so that the shim system remains in its original position “l”.

Two screws S connect the shim and the gradient system at the bottom in order to provide a good mechanical stability during the experiments.

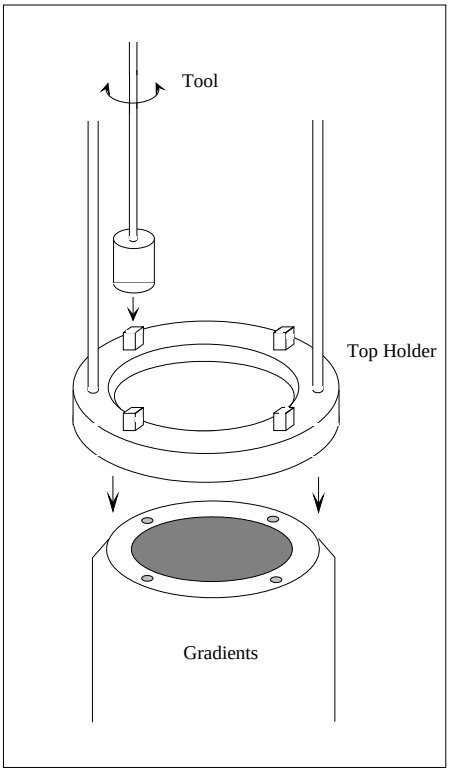
Figure 7.19. Bottom of the SWB Shim and Gradient Systems



A holder is mounted on the top of the gradients for a additional fixation of the gradient system in order to prevent vibrations, caused by the gradient pulses in the magnetic field.

Mount the holder on the gradient top as shown in the following figure. Insert the holder from the top of the magnet and fix the 4 screws carefully on the gradient top with the special tool, which is delivered together with the gradients.

Figure 7.20. Mounting of the Gradient Top Holder

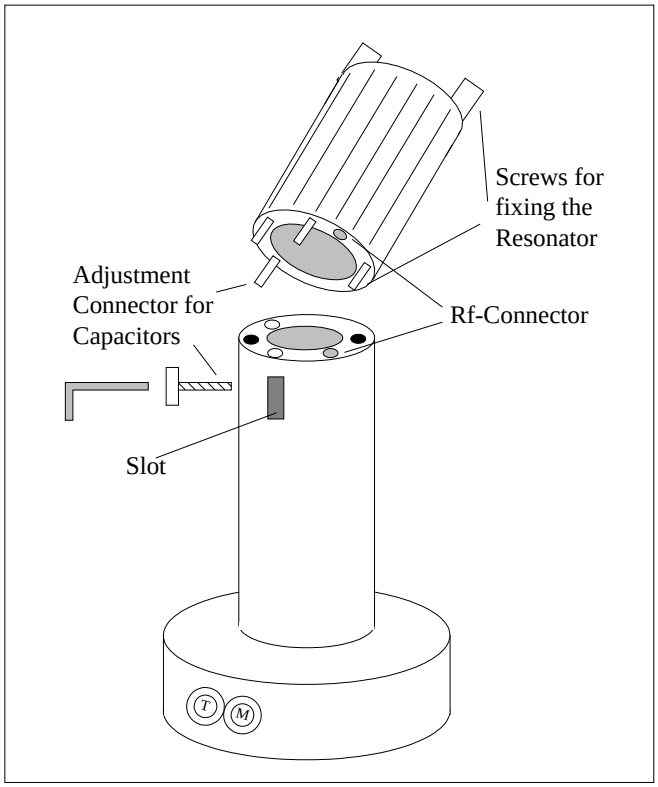


2. Exchanging the RF-inserts

This step can be skipped, when the resonator is already mounted on the probe body.

- Set the RF-resonator insert on the probe body as shown in the following figure. Take care, that the connections for the RF-line, the capacitors and the two screws match.
- Rotate the two screws on the resonator top simultaneously, so that the RF-insert slowly moves towards the probe body.
- Rotate the tuning and matching knobs at the bottom of the probe so that the connectors of the capacitors fit into the holders, which are visible through the small slots at the top of the probe body.
- Fix the capacitor rod at the holder with the small screws as shown in the figure.
- Check too see if the tuning and matching knobs move easily.

Figure 7.21. Mounting the RF-Insert on the Probe Body



3. Mounting of the probe into the gradient system

- Insert the rf probe into the gradient coil system and fix it with the bayonet mechanism.

4. Mounting the Animal (AHS) or Object (OHS) Handling System in the probe.

- Put the animal or another sample into the handling system and then introduce it into the probe. Pull out the rod at the probe bottom until the AHS or OHS is introduced nearly completely. Then push the rod inside so that it fits into the gear at the bottom of the AHS or OHS. Then the sample can be shifted up and down within a small range for a fine adjustment of the vertical position.

The probe can be left in the magnet, when the object is exchanged. Only the AHS or OHS must be removed from the probe.

5. Gradient impedance adaptation

- Set the dip switches at the front panel of the B-AFPA-40 amplifiers to match the load of the gradient coils as shown in the following table. Contact the Bruker imaging application group, when other gradient amplifiers are used.

Table 7.12. B-AFPA-40 Dip Switch Setting

Gradient system	Gradient	C Dip Switch	R Dip Switch	C	R
Mini0.36	X	0000 0001	0100 0000	0.22 nF	100 kΩ
Mini0.36	Y	0000 0001	0100 0000	0.22 nF	100 kΩ
Mini0.36	Z	0001 0000	0001 0000	2.2 nF	20 kΩ

6. Gradient cable connection

- Connect the cable from the imaging rack with the fuse box and the gradient coil system.

7. Cooling the gradients

Water cooling for the gradients is mandatory in order to prevent gradient coil overheating and damage. The temperature of the gradient system is displayed at the front panel of the BGU-II. The BGU-II switches the gradients off, when the temperature reaches 50°C.

- Connect the hoses for the gradient cooling as a closed circuit between the gradients and the cooling unit and switch the cooling on.

Table 7.13. Values for the Gradient Cooling

Air pressure	ca. 1 bar
Water pressure	< 0.5 bar
Water temperature	10 - 20 °C

Note: When the gradients were used previously with water cooling, it is recommended that you remove the water in the gradient system with forced air, before the water hoses are disconnected from the gradient system and from the gradient security box.

Exchange the cooling water at least once a month and check the filter element of the cooling unit!

8. Experiment start

Connect the rf cable and start with the experiments. Observe the gradient system temperature and modify the cooling conditions of the experiment, if necessary.

Software 8

Overview 8.1

The installation and configuration of ParaVision is made in three steps.

Step 1: Installation of the licenses

Step 2: Installation of ParaVision.

Step 3: Configuration of ParaVision.

Step 4: Installation of Micro-imaging Patch CDROM.

Step 1: Installation of the Licenses 8.2

Create the license file **license.dat** for both XWIN-NMR and ParaVision in

/usr/local/flexlm/Bruker/licenses

An example is shown in the following:

```
SERVER imagelx.applik.bruker.de 000103e290c6 1700
DAEMON bruker_ls /usr/local/flexlm/Bruker
DAEMON bbmri_ls /usr/local/flexlm/Bruker

FEATURE XWINNMR3 bruker_ls 0.0 4-apr-2017 uncounted \
        3B3E6031F8425150E83B HOSTID=000103e290c6 vendor_info=“ for \
        hostid(s) : 000103e290c6“ \
        ISSUER=690963087b16wT8Tw58r888485p7T8iwFdfRReI5j
# D4 73 5B F5 F1 98 B1 E7 1C FF 08 6D D2 70 7C 52
FEATURE XWINPLOT bruker_ls 0.0 4-apr-2017 uncounted \
        9B1EB0410305A7D83AD4 HOSTID=000103e290c6 vendor_info=“ for \
        hostid(s): 000103e290c6“ \
        ISSUER=690963087b16wT8Tw58r888485p7T8iwFdfRReI5j
# 04 80 13 66 85 AD AA 11 E4 86 0E 7A DF F8 1B 5E
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    610F 1DD7 CF79 F313“
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    764E 8CF6 9EA5 315B“
# NOTE: You can edit the following items:
#       - hostnames in the SERVER line(s),
#       - port number(s) (TCP/IP) in the SERVER line(s), or
#       - pathnames in the DAEMON line
#       Any other changes may invalidate your license!
```

Step 2: Installation of ParaVision *8.3*

Possibility A:

Login as **nmrsu** and install ParaVision with the SWIM Tool as described in the ParaVision installation guide on the ParaVision CDROM ***(pv_inst_guid_linux.pdf).*** Be sure that you choose ***nmrsu*** when you are asked for the NMR Super!

Possibility B (Quick guide):

Select the KDE startmenu / System / User Manager

Click User Name = FLEXLm

Click Properties, Login Shell = /bin/sh

Mount the CDROM

Start the script ***startme***

The SWIM menu is opening.

Change the XWIN-NMR destination directory to ***/opt/pv***

Select the programs for installation: ***XwinNmr, ParaVision, XwinPlot, ICONNMR***

Select ***diskless*** only if the version on the CD is newer than the version on disk

Select FLEXLm

Click the Start button

Enter in the upcoming window **Installation of XWINNMR *nmrsu*** and quit the menu by ok. Do not select another user at this position. Now the programs are installed on disk.

Answer the question ***„Do you want to make the xwinnmr path available to all users“*** with ***NO***.

Quit the FLEXLm menu with ***Quit***.

Reboot the computer.

Step 3: Configuration of ParaVision *8.4*

Start ParaVision by typing the command ***/opt/pv/paravision*** in a shell.

ParaVision asks, whether a completely new configuration should be done or an existing configuration should be copied from an earlier installation. Select the option, you need.

If the computer is connected to a spectrometer, the configuration of the actual hardware has to be done.

Answer the upcoming questions in the ParaVision startup console:

Would you like to skip the hardware configuration...? No

ParaVision starts up and a new console window appears (maybe behind the ParaVision windows). Continue with answering the question.

Configure Scanner? Yes

This is the ***cf*** command in XwinNmr. A detailed description of the cf configuration steps can be found in the XWinNMR Manual. After finishing this configuration step, you will be asked in the Console, if you want to do the „Configure Scanner?“ again. If everything was OK during the first run, than there is no need to do it again, the question can be answered with „No“. Otherwise you can repeat this configuration step by answering „Yes“

Configure external devices? Yes

Note: This is ***cfsbsb*** in XwinNmr.

Configure FGSV...? No

Configure GPSCU...? No

Configure MFB...? No

Configure BGU-II...? Yes

Note: Yes must be entered, even if a GREAT Master Unit is used.

Which device is used for BGU-II...? /dev/tty06

Configure RFSVR...? No

Configure TOSY...? No

Configure PHT...? No

Configure external devices...? No

You have a hardware list and shim unit...? No

Configure Spectrometer Parameters...? Yes

Note: This is ***edscon*** in XwinNmr.

Typical values are:

BLKTR	3 us
BLKPA	3 us
PHASPR	3 us
SHAPPR	1.6 us
PHASP4	0.5 us
DE1	2 us
DE2	2 us
DERX	3 us
DEADC	4 us
DEPA	2 us

Configure Spectrometer Parameters...? NO

Now the window of ***edasp*** with the routing parameters appears.

Select 1H for the nucleus NUC1 and off for all other nuclei.

Click on ***default*** and ***save***.

Edit & Save Config...? Yes

Some recommended parameters are the following:

Table 8.1. Parameters for Edit & Config

Parameter Name	Parameter Value
Institution name	e.g. Bruker
Instrument/Station Name	spect
Instrument Type	AVANCE
Reco scratch directory	none
Type of magnet	Cryogenic
Type of shim unit	BSMS
Maximum Shim Value	130000 or 400000
Auto-tuning available	no
Power-tuning available	no
Type of tuning	_Reference

Table 8.1. Parameters for Edit & Config

Parameter Name	Parameter Value
Rf supervisor connected	no
FGSV connected	no
GPSCU connected	no
User Type	Research
Size of buffer for transfer of acq data	2048 KWords
Basic spectrometer frequency	e.g. 500.13
Standard digitizer	HADC_2MHz
20 MHz FADC Digitizer available	yes or no
Default mode of digitizer	digital_mode
Default acquisition mode	qdig
Firmware used for digital filtering	DSP_medium
Routing Mode	default
Preferred RF-pulse	Shaped_Pulse
Length of Transmitter Enable	5 µsecs
System status	select S019 for Micro5 select S040 for Micro2.5 select S057 for Mini0.5 select S085 for Mini0.36
Type of pre-emphasis	BGU_II or GREAT60 for GREAT40 and GREAT60
Probe encoding installed	no
Dual DDS installed	no or DDS_3_4_MHz

Edit & Save Config...? No

Install PP‘s and GP‘s...? Yes

Installation for DBX Tomography Systems

Install pulse programs

Install Bruker library Au programs

Install library cpd programs

Install library gradient files

Install library shape files

Now the ParaVision hardware configuration is complete.

All data, acquired in ParaVision will be stored under the home directory of ParaVision. The data may be lost, if a new version of ParaVision is installed under a new path and if the old version will be removed. Therefore it is recommended to store the data under separate data paths, which are independent from the ParaVision data paths.

The definition of data paths is described in ***"Disk Selections" on page 85***.

Step 4: Installation of the Micro-imaging Patch CDROM 8.5

The latest developments for micro-imaging applications are collected on the CD:

„Micro-imaging Patch CD“

The CD contains protocols, macros, au programs, and more. The CD is permanently updated by the micro-imaging application group. The CD of the latest version is added to the imaging accessory at the end test period of a micro-imaging system.

If the CD is missing, send a message to applik@bruker.de.

The directory uImagAddon on the CD contains a README.txt file with a description of the contents and installation procedure of the patch CD.

Exit from ParaVision.

Install the patch CD as nmrsu!

Installation from the Micro-imaging CDROM:

Additional features and methods for micro-imaging applications are available on the Micro-Imaging CD. To install them:

1. Mount the CD-ROM by the command ***mount /mnt/cdrom***
2. Go to the cdrom directory, Type ***cd /mnt/cdrom/LINUX/***
3. Install the additional features by ./m_install

Installation of ISA fit functions for micro-imaging methods:

Some micro-imaging methods need adapted ISA fit functions for T1, T2, or diffusion data fitting. Copy the fit functions from CD to disk

1. Select the ParaVision Home directory. Type e.g. ***cd /opt/pv***
2. change into your **curdir** directory, e.g. ***cd prog/curdir/<user>/ParaVision*** and unpack the file isa.tar from the CD.

   tar xvf /mnt/cdrom/LINUX/isa/isa.tar

Parallel Installation XWinNMR 3.x and ParaVision 3.x

If you want to install XWinNMR 3.x/TopSpin and ParaVision 3.x in parallel, you have to modify one file by hand to start XWin3.x/TopSpin by typing 'xwinnmr'/'topspin' in a shell, and ParaVision by typing 'pv'.

You can do this globally, means for all users. Open the file /etc/profile and at the end of this file, you will find a line like this:

PATH=/opt/xwin31/prog/bin/scripts:$PATH; export PATH

This makes the path /opt/xwin31/prog/bin/scripts for XwinNMR 3.1 public for all users. If you want to add a public path for ParaVision to allow to start it from the shell (recommended), please change the line as follows:

PATH=/opt/xwin31/prog/bin/scripts:/opt/pv/prog/bin/scripts:$PATH;export PATH

If you have the line like this and type in 'xwinnmr' the system first searches in the directory */opt/xwin31/prog/bin/scripts* for this file, finds it and starts XWin3.1. if you type in 'pv', the system don't find this file in this directory and searches in the second path */opt/pv/prog/bin/scripts*, and here it finds ParaVision 3.x.

This PATH settings can also be done for each user individually in the file *~/.bashrc* or *~/.cshrc*.

Loading an image for processing *8.6*

Images can be loaded from disk into the ParaVision Image Display & Processing Windows (XTIP window), by clicking the button for browsing through the image containing directories. Some images should be available now e.g. in:

../nmrsu/nmr/filename/...

The processing features are described in the chapter ***"Image Processing" on page 213***.

Preferences 9

Disk Selections 9.1

This description is only valid for ParaVision programs with version numbers 2.0 or higher and for XWIN-NMR versions 2.5 or higher

It is recommended that the data, acquired or processed in ParaVision, should be stored under

/disk unit/data/user name/nmr/filename

In principle each user can define his own disk unit(s) where the data are written or read. This information has to be set in the file units.ini.

Create the data directory by ***mkdir /opt/data,*** if it does not yet exist

Edit the file:

/opt/pv/prog/mr_user/units.ini

Now define the disk unit(s) for read and write of ParaVision data, e.g. set the **readable and writeable and visible** disk units to:

/opt ; /mnt/cdrom

In addition set the other variables **admin, retrieve, writelist** to ***/opt***.

Copy this units.ini file to **/opt/pv/prog/curdir/nmrsu/ParaVision/units.ini** in order to activate it for nmrsu.

ParaVision has to be restarted after the units.ini file was changed.

Display and Processing Defaults 9.2

Display Image Scaling 9.2.1

The Image Display & Processing routine (Xtip) allows the user to specify the way images are scaled during display.

Xtip uses <automatic> scaling for the image display as default. This means that each individual frame (e.g. of a T2 sequence) will be displayed with its full dynamic range. Each frame is mapped between its individual minimum and maximum. Using the <global user> scaling, all frames will be scaled between the minimum and maximum of the whole series of images.

To set the default scaling, the following command line has to be added to the file ***lpStatus***:

1. If the scaling should be done for **all users**:

For <global user> scaling the command line **pvcmd tImRescale** has to be added to the file:

/xwinnmrhome/exp/stan/nmr/ProcStatPref/xtip.1/***lpStatus***

For <automatic> scaling the command line **pvcmd tImRescale a** has to be added in the file:

/xwinnmrhome/exp/stan/nmr/ProcStatPref/xtip.1/***lpStatus***

2. If the scaling should be done for **a particular user**:

For <global user> scaling the command line **pvcmd tImRescale uGlobal** has to be added in the file:

/XWINNMRHOME/prog/curdir/<user>/ParaVision/ProcStat/xtip.1/Pref/***lpStatus***

For <automatic> scaling the command line **pvcmd tImRescale a** has to be added in the file:

/XWINNMRHOME/prog/curdir/<user>/ParaVision/ProcStat/xtip.1/Pref/***lpStatus***

Parameter Display *9.2.2*

The Parameter Display can be configured either for all users or for any particular user. The following command line has to be added to the file ***lpStatus***:

1. If the configuration should be done for **all users**:

To display **no** parameters the command line **pvcmd tiDsetMaskPar -off ALL_TOPIC** has to be added in the file:

/xwinnmrhome/exp/stan/nmr/ProcStatPref/xtip.1/***lpStatus***

To display **all** parameters the command line **pvcmd tiDsetMaskPar -on ALL_TOPIC** has to be added in the file:

/xwinnmrhome/exp/stan/nmr/ProcStatPref/xtip.1/***lpStatus***

2. If the configuration should be done for **a particular user**:

To display **no** parameters the command line **pvcmd tiDsetMaskPar -off ALL_TOPIC** has to be added in the file:

/XWINNMRHOME/prog/curdir/<user>/ParaVision/ProcStat/xtip.1/Pref/***lpStatus***

To display **all** parameters the command line **pvcmd tiDsetMaskPar -on ALL_TOPIC** has to be added in the file:

/XWINNMRHOME/prog/curdir/<user>/ParaVision/ProcStat/xtip.1/Pref/***lpStatus***

Tests and Adjustments 10

After the wiring of the imaging hardware is finished ***"GREAT Imaging Hardware" on page 11***, ***"B-AFPA Imaging Hardware" on page 19*** and the ParaVision software is loaded and for the first time as described in the chapter, ***"Software" on page 75***, the following tests and adjustments have to be performed:

- Check the acquisition of a FID.
- Check the hardware for correct gradient pulses.
- Adjust the pre-emphasis and the Bo shift compensation.
- Calibrate the gradient strength for the X,Y and Z gradient.
- Determine the S/N of a resonator.

The Bo shift compensation unit is an option and is not available on all the imaging systems.

A number of protocols are available for the tests and adjustments in ParaVision. The protocols come with the „Micro-imaging Patch CDROM“ and are installed as described in ***"Step 4: Installation of the Micro-imaging Patch CDROM" on page 82***. Contact the micro-imaging application group, if you cannot find the protocols, used in the following installation procedure.

The tests and adjustments are performed in individual data sets, where experiments are carried out and where the results are stored.

This chapter describes an important feature, how a new data set is created. This step is often used for various tasks, e.g. for testing hardware, adjusting pre-emphasis parameters, calibrating gradients, acquisition of images. Read this chapter, when you are creating a new data set for the first time.

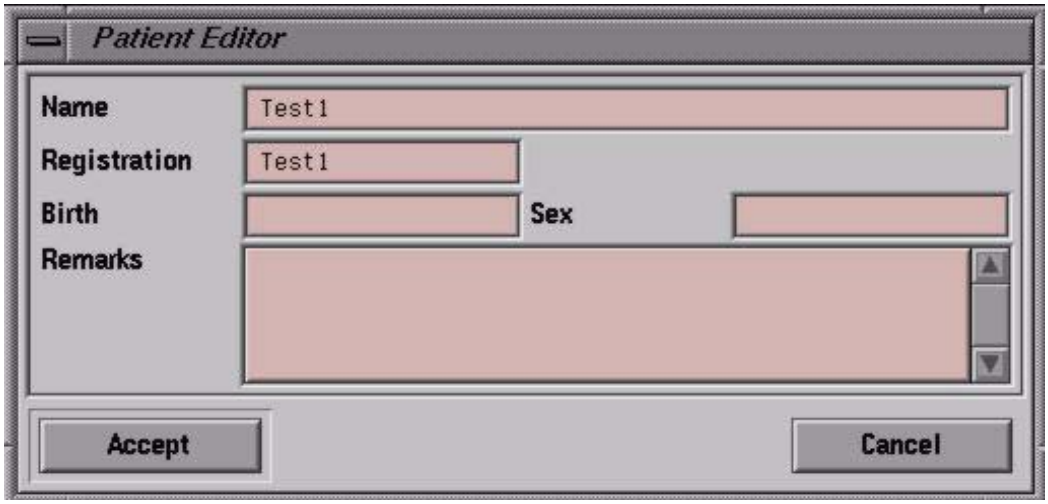
Creation of a new data set *10.1*

The following steps describe the creation of a new data set in a common way. The decision for the specific application has to be made in step 7, where a protocol with parameters, such as pulse program, gradient program, delays, RF-pulses for the requested application is selected.

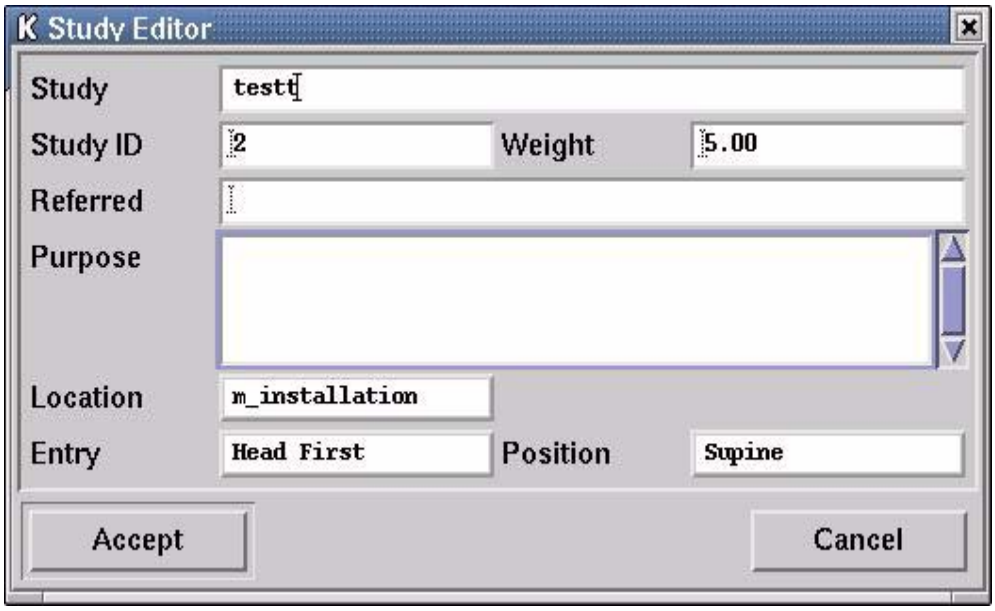
1. Click in the ParaVision Scan Control window the button ***New Patient***[1].

1. Note: ParaVision considers all objects as patients. They might have a sex, a weight, head and feet, even when they are stones, wood, polymers, plants or liquids.

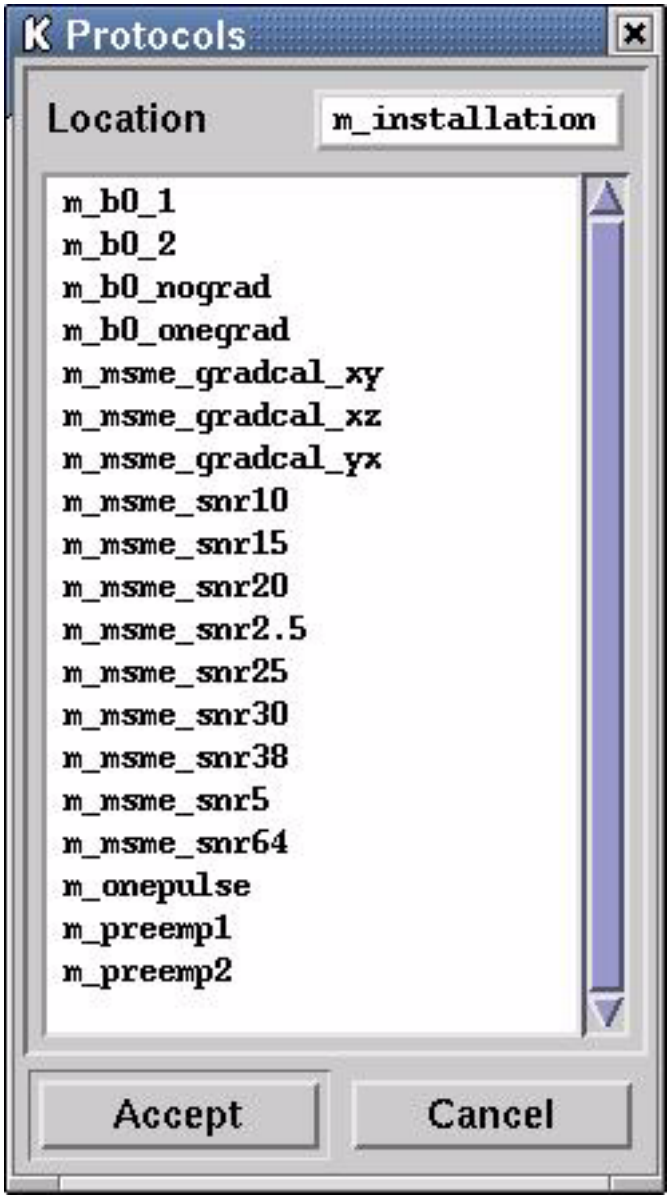
2. Enter a data set name in the fields ***Name*** and ***Registration*** of the appearing new window.



3. Click ***Accept***.
4. Enter a number or a name in the fields ***Study*** of the appearing new window.
5. Select a location, e.g. Bruker for applications or ***m_installation*** for the installation procedure.



6. Click ***Accept.***
7. A new window, called **Protocols** is coming up. Click ***Accept***.
8. Select a protocol from the list e.g. ***m_onepulse***.



9. Click ***Accept***.
10. Click in the ParaVision Scan Control window the button with the ***hammer and screw driver***.

11. Modify acquisition parameters for the selected method, if necessary.
12. Before the acquisition can be started, the routing parameters for the RF-channels must be defined, if it was not yet done before. This procedure is described in the following chapter ***"Generation of routing parameters" on page 93***.
13. Now the acquisition can be started.

Generation of routing parameters *10.2*

The routing parameters control the generation and application of the RF-pulses with the correct frequencies.

A comfortable user interface supports the generation of the routing files in ParaVision3.0 and higher versions. In earlier versions of ParaVision the generation of these files is more complicated. Both possibilities are described in the following.

*Generation of Routing Files for ParaVision 3.** *10.2.1*

Each experiment needs a well defined way of RF-transmission and signal acquisition pathways. They are described by routing parameters. Routing parameter sets can be created for different RF-coil types and operations.

Definition of the Routing Mode:

The following cases exist for the routing mode:

Single RF-coil for transmit and receive operation. This is called ***default***.

Array of RF-coils, where more coils are used simultaneously for transmit and receive. This is called ***coil-array***.

Decoupled RF-coils, where one coil is used for transmit and a separate coil for receive. This is called ***cross-coil***.

The type of RF-coil and operation has to be set as a configuration parameter.

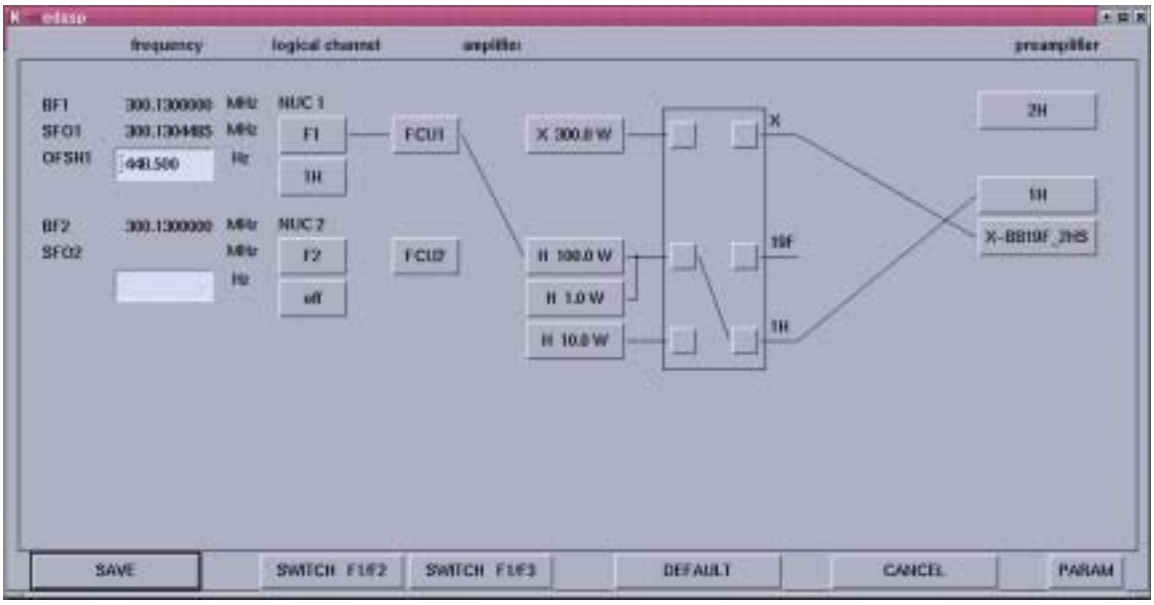
- Select the menu ***Tools / Edit & Save Config*** in the ***Spectrometer Control*** menu.
- Set the parameter ***Routing Mode*** to default or coil array or cross-coil.

Creation of the routing parameters:

Select ***Tools / Create Routing*** in the ***Spectrometer Control*** menu.

Select ***Create Routing***.

The following menu appears:



Generate some typical routing configurations, e.g. for 1H, 13C, 23Na, 1H/13C,... and save them. The parameters are stored under the filenames, created from the combination of the selected nuclei, e.g. 1H, 13C, 23Na, 1H/13C,...

These parameter files are automatically activated in PVM methods, according to the nuclei, defined in the PVM parameters.

Showing the active routing:

Select ***Tools / Create Routing*** in the ***Spectrometer Control*** menu.

Select ***Show Routing***.

The activated routing parameters are displayed in the same menu, shown above.

Read a predefined routing:

Select ***Tools / Create Routing*** in the ***Spectrometer Control*** menu.

Select ***Read Routing***.

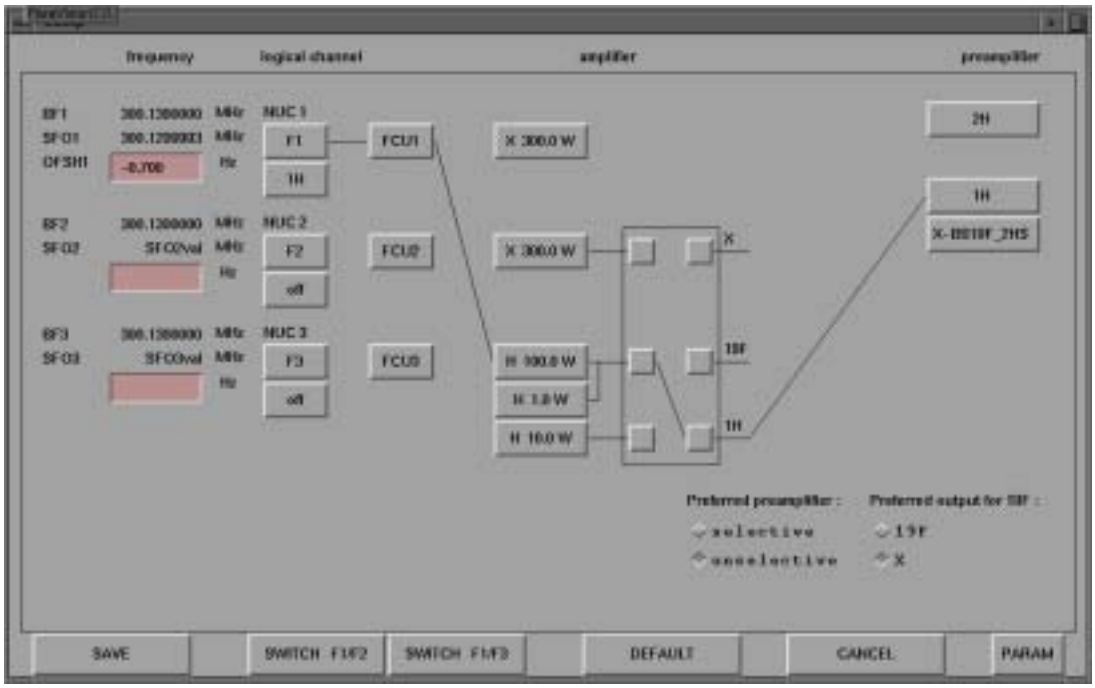
A menu with a list of existing routing files shows up and one of the parameter files can be selected.

Generation of Routing Files for ParaVision 2.1.1 *10.2.2*

Set the routing parameters by exporting the data set from the ***ParaVision Scan Control*** window to ***XWIN-NMR*** (Drag and drop with the middle mouse button).

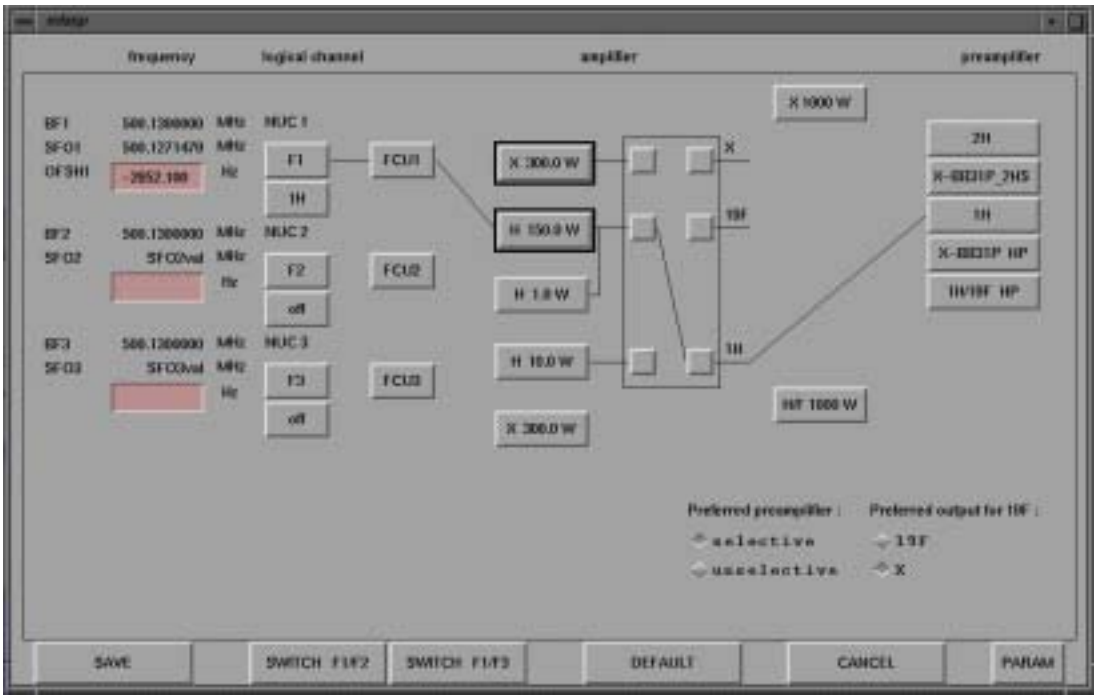
- Type ***edaspp*** in the XWIN-NMR Window
- Click ***DEFAULT*** in the now appearing window to set the correct connections

Figure 10.1. Routing Window for AVANCE Hardware



- For AVANCE proceed as follows, if a TOMOFCU (TFCU) is installed in the spectrometer. Note, that the TFCU must be installed in the F1 channel. Route the F1 channel through FCU1, as shown in the following figure.:

Figure 10.2. Routing Window for AVANCE DSX Hardware



- Click the PARAM button, then you will get new window

- Some of this numbers must be transferred into ParaVision. To find the correct numbers, follow the described procedure.

  Start in line 1 (FCUCHAN): The first number tells, which column from the 2nd has to be used. In the example, the 1st entry is 1, so in the second line (RSEL) the 1st column is the used one, number 3 in this example.
  The number in the selected column points to the column of the following row, and so on.
  Note the numbers for RSEL, SWIBOX and PRECHAN (in this example: 3 5 2).

  Press **Seen** and the windows will be closed.

- press the save button, and quit the appearing window by **OK**

Figure 10.3. Saving the Routing Parameters

- Store the routing parameters for later use on all experiments. Click the button ***WriteClass*** in the Spectrometer Control Tool Window and select the entry ***CONFIG***. Press ***OK*** and then insert the filename ***<$XWINNMRHOME>/conf/parx/default/config*** under ***Selection***. Press ***OK***. If an error message about 'Permission... was denied' shows up, then change the permissions to a super user chmod 666 /$XWINNMRHOME/conf/parx/default/config and repeat the 'WriteClass' in the Spectrometer Control Tool Window.
- Enter a UNIX shell and edit the file
  /$XWINNMRHOME/conf/parx/default/RoutingTable
  with your favorite text editor. The file will look like this

##TITLE=Parameter List

##JCAMPDX=4.24

##DATATYPE=Parameter Values

##ORIGIN= Bruker Medizintechnik GMBH

##OWNER=vml

$$ Thu May 27 15:21:32 1999 MESZ (UT+2h) vml

$$ /w/pv2.0.51/prog/curdir/vml/ParaVision/RoutingTable

##$PVM_Routing=(5)

(**<1H>, 3, 5, 2**) (<13C>, 1, 1, 3) (<31P>, 1, 1, 3) (<19F>, 2, 3, 4) (<23NA>, 1, 1, 3)
##END=

- Enter the numbers you noted before (RSEL, SWIBOX and PRECHAN) behind the nucleus you had selected in edaspp and save the file.

Spectrum Acquisition (m_onepulse) *10.3*

High resolution spectra can be acquired by using the m_onepulse method. The following steps should be made:

- Mount the probe and a sample in the magnet as described in the chapter ***"Probes and Gradients" on page 51***.
- Tune and match the probe by the wobble command in

  Spectrometer Control Tool / Acq / Wobble.

- Create a new data set as described in ***"Creation of a new data set" on page 89***.
- **If the protocol *m_onepulse* exists**, select it as described before. This is a protocol for the acquisition of a free induction decay (FID) after the application of a RF-pulse. Default parameters are already included in the protocol, but some of the parameters should be optimized depending on the properties of the sample as described in the following. If you want to modify parameters, click in the ParaVision Scan Control window the button with the ***hammer and screw driver*** to enter the ParaVision Spectrometer Control Tool. Enter the PVM parameter menu by clicking on the „***Edit Method***“ button in the ***Spectrometer Control Tool*** menu.
- **If the *m_onepulse* protocol is not available**, then exit from the menu with cancel and set the parameters as described in the following steps. Click in the ParaVision Scan Control window the button with the ***hammer and screw driver*** to enter the ParaVision Spectrometer Control Tool. Enter the PVM menu by clicking on the „***Edit Method***“ button in the ***Spectrometer Control Tool*** menu. The Parameter Editor for the PVM methods is opened. Click on the ***Measuring Method*** button and select the ***m_onepulse*** method.
- The parameters from the protocol show up and can be modified e.g. as suggested in the following table.

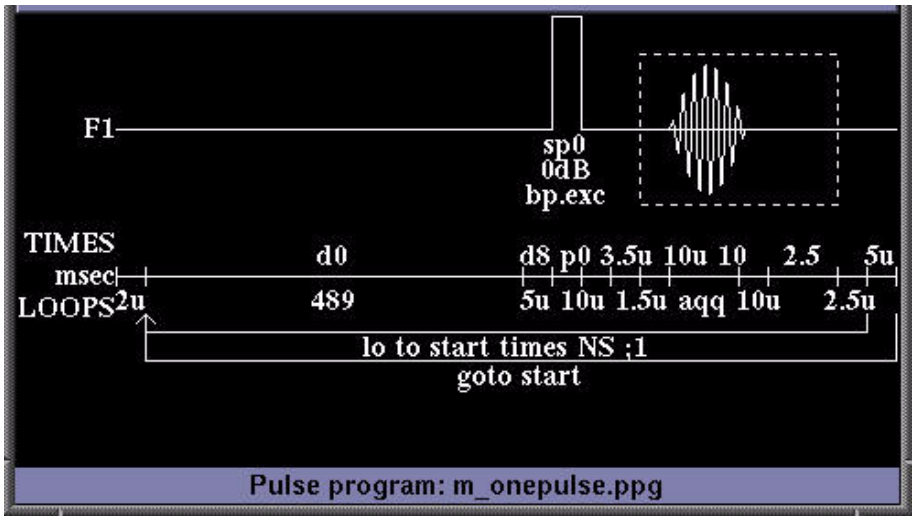
Table 10.1. m_onepulse Parameters

Parameter	Value
Measuring Method	m_onepulse
Nucleus	_1H
bf1	300.13 MHz
Effective Spectral Bandwidth	10000 Hz
Pulse Bandwidth	128000 Hz
ExcPulseLength	0.010 ms
Acquisition Size	4096
Repetition Time	1000 ms
Number of scans	1
Estimated total scan time	is set by ParaVision

Table 10.1. m_onepulse Parameters

Parameter	Value
Excitation Pulse	Expand
Select Excitation Pulse Shape	bp
Excitation Pulse Length	0.010 ms
Excitation Pulse Gain	0.0 dB
Excitation Pulse Attributes	Are set by ParaVision
Method Customization	Expand
Number of Repetitions	One or higher numbers when more experiments should be performed one after the other
Derive Pulse Gain	No, for manual adjustments
Modules	Expand
ECG Trigger Module Switched	Off
Info	Is set by ParaVision

- Click in the **Spectrometer Control Tool** menu the buttons ***Tools, Pulse Program Too***l and check the correct parameter settings, e.g.



- Click ***GSP*** in the ***Spectrometer Control Tool*** menu to start the setup of the acquisition.
- Adjust the 90° RF-pulse and the receiver gain by the ***TX Attenuator 0***, and the ***Receiver Gain*** sliders in the ***Spectrometer Control Tool*** menu. The FID should be visible in the acqDisplay and the Fourier transformed spectrum in the recoDisplay. Click ***STOP*** when the parameters are adjusted.
- Click ***GOP*** in the ***Spectrometer Control Tool*** menu to start the data acquisition.

GREAT40/60 Amplifier Test (m_grdpulse) 10.4

The installation of the GREAT imaging rack is handled by the pre-emphasis feature of ParaVision and the **setpre** feature of XWIN-NMR. ParaVision 2.1.1 needs the Patch 16 for proper functioning. Make sure, that this patch is installed, before starting the installation.

A number of different gradient coils are used with the imaging accessory. The coils differ in inductance and resistance. In order to optimize the gradient pulse shape and gradient switching speed the GREAT40/60 amplifiers provide the adoption of the load by adjusting **RC-combinations** on a feedback circuit.

The values for R and C are set under slider control in the „**setpre**“ menu of ParaVision or XWIN-NMR.

The „**setpre**“ menu contains additional features for the **offset adjustment** and for setting of the **current output stages** of the amplifiers.

Verifying Configuration Parameters 10.4.1

Setpre contains parameters for the actual gradient amplifier types. These parameters were set, by downloading files from the „Micro-imaging Patch CDROM“, as described in ***"Step 4: Installation of the Micro-imaging Patch CDROM"***.

The parameters should be checked in the following way:

1. Open ***Spectrometer Control Tool -> Config -> Edit & Save Config***.
2. Set the ***Type of Pre-emphasis*** parameter to GREAT_60
3. And return by ok.

4. Open ***Spectrometer Control Tool -> Edit Class -> PRE-EMPHASIS.***
5. Set the parameter ***Pre-emphasis type*** to GREAT_60.
6. Set the first three parameters of ***Gradient amplifiers*** to

   PREEMP_AMPLIFIER_60A or PREEMP_AMPLIFIER_40A, if GREAT60 or GREAT40 amplifiers are mounted in the imaging rack.
7. Set the fourth parameters of ***Gradient amplifiers*** to

   PREEMP_AMPLIFIER_60A, if a GREAT Zo Unit is available or to PREEMP_AMPLIFIER_NONE, if no GREAT Zo Unit is available.

If you made any changes in the parameters, save these parameters in the menu

Spectrometer Control Tool -> Tools -> Save Pre-emphasis Values

Store the parameters as default.

Creation of a Data Set for m_grdpulse. *10.4.2*

The gradient pulse test protocol ***m_grdpulse*** is used for testing the output of the gradient control unit (GCU), the GREAT Master Unit and amplifiers, or the pre-emphasis unit (BGU-II) and the BAFPA gradient amplifiers. This method creates rectangular positive and a negative gradient pulse.

- Create a new data set as described in ***10.1***, ***"Creation of a new data set"***. Check, if protocols exist already and select the protocol ***m_grdpulse***. Default parameters for the creation of the two gradient pulses are already included in the protocol, but some of the parameters can be modified as described in the following. If this protocol is not available, then exit from the menu with cancel and set the parameters as described in the following steps.
- Click in the ParaVision Scan Control window the button with the ***hammer and screw driver*** to enter the ParaVision Spectrometer Control Tool.
- Enter the PVM menu. The parameters from the protocol show up and can be modified e.g. as suggested in the following table. When no protocol was available, then select the method ***m_grdpulse*** by the ***Measuring Method*** button in the PVM menu and set e.g. the following parameters:

Table 10.2. m_grdpulse Parameters

Parameter	Value
Measuring Method	m_grdpulse
Nucleus*	_1H
bf1*	e.g. 300.13 MHz
Effective Spectral Bandwidth*	100000 Hz
Acquisition Size	1024
Repetition Time	100 ms
Gradient amplitude**	30%
Gradient duration**	2 ms
Gradient direction**	x or y or z
Gradient ramp mode**	Constant time
Gradient ramp time**	100 us
Gradient rise time**	180 us
Excitation Pulse*	expand

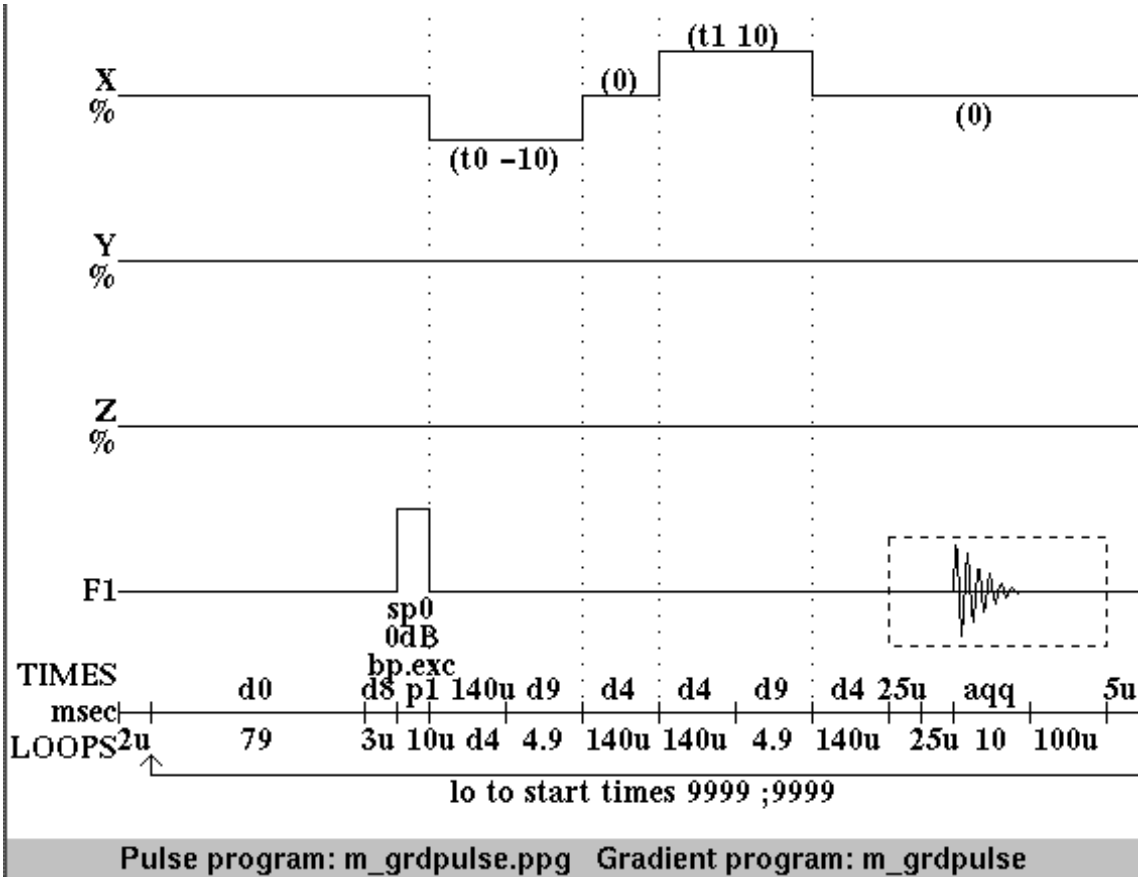
Table 10.2. m_grdpulse Parameters

Parameter	Value
Select Excitation Pulse Shape*	bp
Excitation Pulse Length*	0.010 ms
Excitation Pulse Gain*	6.0 dB
Excitation Pulse Attributes	are set by ParaVision
Info	is set by ParaVision

* Some of the parameters for the frequency and RF-pulse are only important, when the RF-pulse should be used for triggering a oscilloscope.

** The gradient pulses are programmed as rectangular block pulses. The pre-emphasis parameters can change them into trapezoidal pulses with additional overshots for eddy current compensation. The overshots can be varied in amplitude and exponential decay as described later.

- Click in the **Spectrometer Control Tool** menu the buttons ***Tools, Pulse Program Too***l and check the correct parameter settings, e.g.



Loop Adaptation 10.4.3

The GREAT amplifiers must be matched to the impedances of the different gradient systems. A RC combination is set in a feedback loop of the amplifier regulation. Default values are already loaded for the selected gradient system.

The following table shows the recommended settings for some gradient coils delivered from Bruker. The values in the table have been determined in the Bruker laboratories. They can be modified by the adjustment procedure, described in the following. Contact the Bruker imaging application group, when other gradients, not included in the table, are used.

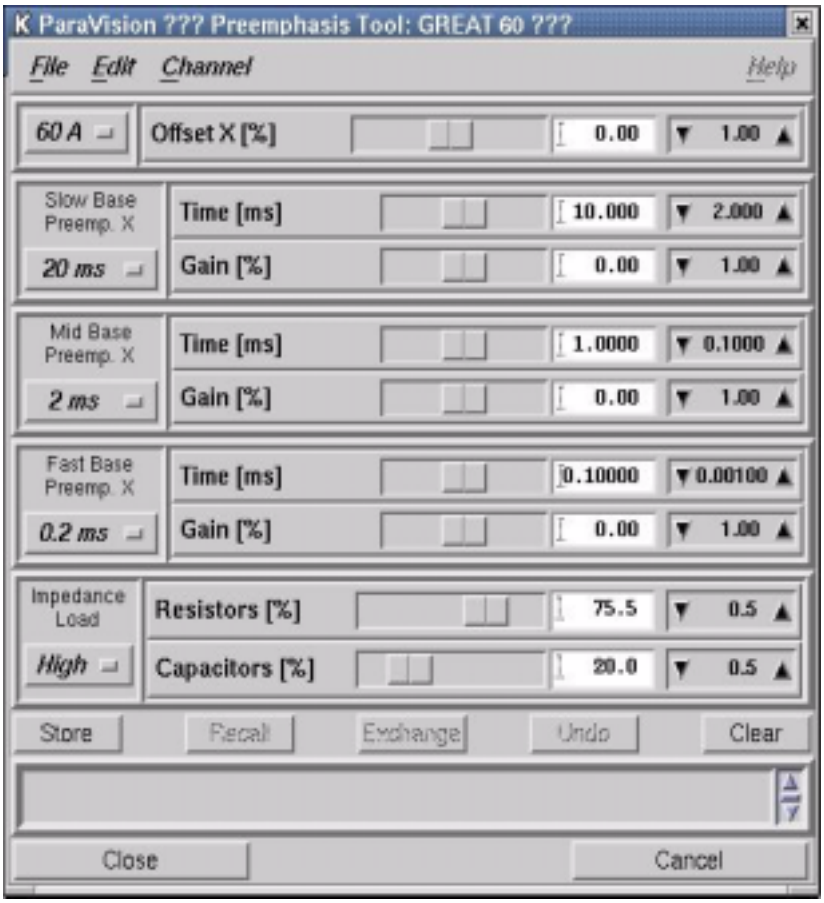
Table 10.3. GREAT Impedance Setting

Gradient system	Gradient	Capacitors	Resistors	Impedance Load
Diff60				
Diff30				
Diff25	Z			
Micro5	X			
Micro5	Y			
Micro5	Z			
Micro2.5	X	20%	75%	High
Micro2.5	Y	20%	75%	High
Micro2.5	Z	20%	75%	High
Mini0.5	X	20%	75%	High
Mini0.5	Y	20%	75%	High
Mini0.5	Z	20%	75%	High
Mini0.36	X			
Mini0.36	Y			
Mini0.36	Z			

These values can be modified in order to change the gradient pulse rise times. The RC values are set under slider control.

Warning: Wrong values can bring the amplifiers to an oscillation behavior and may destroy the amplifiers and/or the gradient system!

- Click ***Tools*** and ***Adjust Pre-emphasis Values*** to load the menu for the pre-emphasis parameters.



- Click ***Channel*** in the ***Pre-emphasis Tool*** menu and activate the X,Y or Z gradient pulses by clicking ***x pre-emphasis, y pre-emphasis or z pre-emphasis***.
- Set all ***Gain*** parameters in the ***Pre-emphasis Tool*** menu to zero, in order to get pure trapezoidal gradient pulses.

Activate the gradient water cooling as described in ***"Gradient Cooling Units" on page 37***, before you start pulsing the gradients.

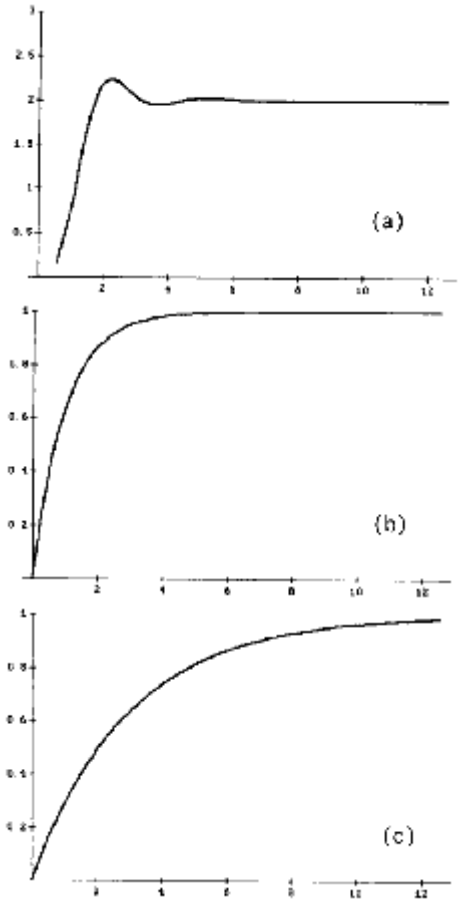
Open the sliders by ***Edit -> Impedance and loop editing***.

Adjustment Procedure

1. Install the probe for imaging applications as described in the chapter ***"Probes and Gradients" on page 51***.
2. Check and/or set the values for Impedance Load, Capacitors and Resistors in the for the mounted gradient system (see the previous table).
3. Check and/or set the parameters for the "**m_grdpulse**" test program as described before.
4. Check that all gains of the pre-emphasis parameters are set to zero.
5. Start the acquisition with **gsp**.
6. Observe the gradient shapes on the oscilloscope, connected to the monitor outputs of the gradient amplifiers.
7. Fine tune the values of the Capacitors and Resistors until the best shape is reached (see figure below).
8. Save the parameters by ***File -> Write default***.

The best pulse rise behavior is shown in the following figure (b). Incorrect adjustments can cause an overshot of the pulse (a) or too slow gradient rise times (c).

Figure 10.4. Gradient Pulse Adjustment



Check of pre-emphasis gain and time constants. *10.4.4*

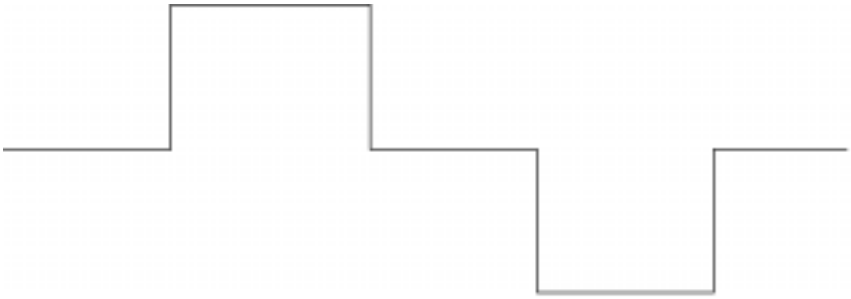
The data set with the loaded m_grdpulse method (see previous chapter) can be used to check the behavior of the pre-emphasis gain and time constant parameters on the gradient pulse shapes.

Activate the gradient water cooling as described in ***"Gradient Cooling Units" on page 37***, before you start pulsing the gradients.

- Connect a oscilloscope to the monitor output of the gradient amplifiers.
- Click ***Tools*** and ***Adjust Pre-emphasis Values*** to load the menu for the pre-emphasis parameters, if this is not already opened.

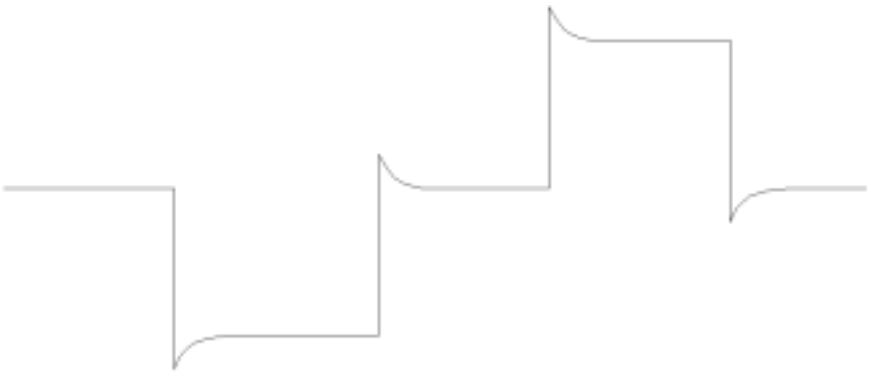
- Click ***GSP*** in the ***Spectrometer Control Tool*** menu to start gradient pulsing and observe the output signal from the gradient amplifiers on the oscilloscope. When all pre-emphasis parameters are set to zero, the gradient pulses should look like the following figure.

Figure 10.5. Oscilloscope View



- Modify the time and gain parameters for the X,Y,Z gradients, so that they are no longer zero. The gradient pulse shape should change as shown below.

Figure 10.6. Oscilloscope View with Pre-emphasis



- Click ***STOP*** in the ***Spectrometer Control Tool*** menu to stop the gradient pulse tests.
- Exit from the ***Pre-emphasis Tool***.

Setting of the Output Current Stage *10.4.5*

1. Open ***Spectrometer Control Tool -> Tools -> Adjust Pre-emphasis Values,*** if this menu is not open already.
2. Click the button with the selected current output stage and set a new value or keep the selected value, e.g. at 60 A.

Offset Adjustment *10.4.6*

The offset adjustment of the current amplifiers is made by observing the FID's e.g. from a water sample, when the amplifier is switched off and on. The Pre-emphasis menu contains features for the modification of the offset current.

Automatic Adjustment

1. Open ***Spectrometer Control Tool -> Tools -> Adjust Pre-emphasis Values,*** if this menu is not open already.
2. Click Enable / Offset Adjustment
3. Select a gradient channel.
4. Click Auto and wait some seconds.
5. The offset value shown in the field next to the slider may change during the adjustment.
6. Select the next gradient channel and click on Auto
7. Click Disable / Offset Adjustment

Manual Adjustment

1. Open ***Spectrometer Control Tool -> Tools -> Adjust Pre-emphasis Values,*** if this menu is not open already.
2. Click Enable / Offset Adjustment
3. Insert a sample in the imaging probe.
4. Switch all GREAT amplifiers off.
5. Shim to a reasonable linewidth and observe the FID in GS (XWINNMR) or GSP (ParaVision)
6. Switch the first GREAT amplifier on.

7. Observe the shape and/or the integral of the FID. The Shape changes and the integral gets lower, if an offset is applied by the amplifier.
8. Modify the offset under slider control until the FID returns to the same shape and the integral returns to the same value, where the GREAT amplifier was shut off.
9. Switch the second GREAT amplifier on and repeat steps 5 to 6.
10. Switch the third GREAT amplifier on and repeat steps 5 to 6.
11. Click Disable / Offset Adjustment

Activation of the GREAT Gradient Blanking *10.4.7*

The gradient blanking hardware is included in the GREAT amplifiers. It is used to disconnect the gradient amplifiers from the gradient coils during the data acquisition e.g. in diffusion experiments with very strong gradient coils.

- Connect the "**Blanking Control**" cables to the corresponding BNC sockets "**Gate**" at the front pannel of the GREAT40/60 amplifiers (see following table).

How to use the Blanking

The blanking is controlled by blanking pulses, generated from the spectrometer console during the pulse program. The blanking pulses are created by setting special bits in the nmrcontrol word 0 as shown in the following table.

Table 10.4. Blanking Pulses on AVANCE

Backpanel I	pin
Blanking X gradient: c32 or set NMR0 | 32	C
Blanking Y gradient: c33 or setNMR0 | 33	H
Blanking Z gradient: c34 or setNMR0 | 34	M

Note: The older pulse programs must be modified in order to make use of the blanking feature. The new version of programs contain these modifications.

A number of macros are defined in the file **Grad_Blank.incl** for a comfortable handling of the blanking features. The file is listed in the following.

```
;Grad_Blank.incl  -  include file to handle the Gradient blanking unit
#define BLKGRAMP_ALL setnmr0^32 setnmr0^33 setnmr0^34
#define UNBLKGRAMP_ALL setnmr0|32 setnmr0|33 setnmr0|34
#define BLKGRAMP_X setnmr0^32
#define BLKGRAMP_Y setnmr0^33
#define BLKGRAMP_Z setnmr0^34
#define UNBLKGRAMP_X setnmr0|32
#define UNBLKGRAMP_Y setnmr0|33
#define UNBLKGRAMP_Z setnmr0|34
```

An example of a diffusion pulse program, where the blanking unit is connected and when gradient blanking is applied, is given below. The modifications of the pulse program are the lines which include: #include <Grad_Blank.incl>, BLKGRAMP_ALL, UNBLKGRAMP_Z and BLKGRAMP_Z.

```
;diffse ;2D Steiskal Tanner sequence
#include <Grad_Blank.incl>

1s ze
 10u BLKGRAMP_ALL
 5m pl1:f1              ;set rf power level
1 d1                    ;relaxation delay/2
 d11 UNBLKGRAMP_Z       ;unblank gradient amplifier
 p1 ph1                 ;90 degree pulse
d3:ngrad                ;gradient on time
d2:ngrad                ;gradient ring down time
 d9 BLKGRAMP_Z          ;tau
 d11 UNBLKGRAMP_Z       ;unblank gradient amplifier
 p2 ph2                 ;180 degree pulse
 d3:ngrad               ;gradient on time
 d2:ngrad ph3           ;gradient ring down time
 d10 BLKGRAMP_Z         ;tau
aq adc ph0              ;acquisition
rcyc=1                  ;ns=1
d1 st                   ;relaxation delay/2 increment echo pointer
lo to 1 times nbl ;nbl=number of projections
```

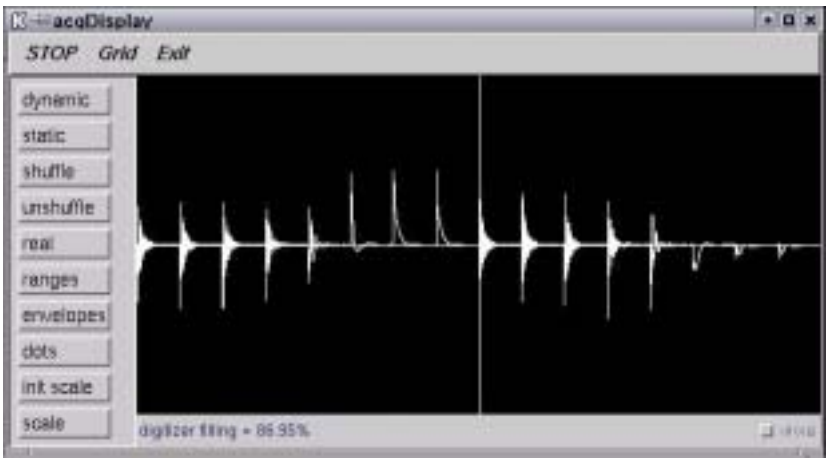
```
 5m ip0              ;phase cycle
 5m ip0              ;phase cycle
5m ip1               ;phase cycle
 5m ip1              ;phase cycle
 lo to 1 times l1    ;# of averages
 d1 wr #0            ;write data to disc
exit

ph0=0
ph1=0
ph2=1
ph3=0
```

Bo Shift Compensation Unit Functionality Test *10.5*

The field value from the BSMS is always connected to the Bo shift compenzation unit, version **W1212287** and from there back to the sweep coil of the shim system, even if the Bo shift compenzation unit is switched off.

- Create a new data set.
- Load the protocol ***m_preemp***.
- Adjust the system frequency to „***on resonance***“ condition.
- Start the acquisition with ***GSP***.
- Click in Spectrometer Control Tool / Tools / ***Adjust pre-emphasis values***.
- ***Enable*** „***Bo compensation***“.
- Change the field value at the BSMS keyboard and check if the frequency of the nmr signal is changing.
- Set the frequency back to „***on resonance***“. Select the „unshuffle“ style in the acqDisp for a easier observation of the effect.

- Connect an oscilloscope to the monitor output of the Bo shift compenzation unit.
- Select in the setpre menu ***channel X Bo compensation***.
- Set the time bases and the time parameter of the three sliders to 20 ms and the gains of all sliders to 100%.
- The frequency of the 8 FIDs in the acqDisplay must change during this operation. The effect depends on the parameters for the gains and time constants.



- The voltage Bo correction pulses at the monitor output should be approximately 10 V peak, if the gradient amplitude is 100 % and if all three gains are set to 100% for the selected channel. The actual m_preemp protocol sets a gradient of 30 %, resulting in a voltage of approximately 3V.
- Click „***Disable / Bo compensation***“. The Bo correction peaks must disapear at the output monitor and all FIDs must look almost the same. The Field offset must still be visible on the scope and the value is still changing, if the Field is changed at the BSMS keyboard.

Perform these tests also for the Y and Z channels.

Pre-emphasis Adjustment (m_preemp) *10.6*

The shape of an FID or an echo, acquired with only a short delay after gradient pulses, may be distorted by eddy currents caused by gradient switching. The influence of the eddy currents *can* be decreased by modifying the shape of the gradient pulses.Three exponential functions, with amplitude and time constants, are available to accomplish this.

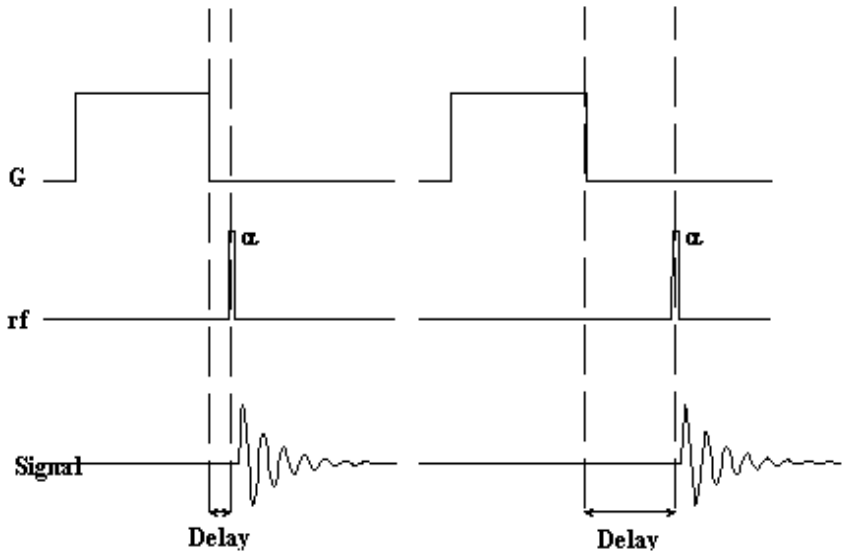
The amplitudes and time constants are set in a control window and are stored for individual gradient systems. This is described in the following section.

Adjustment with Variable Stabilization Delays *10.6.1*

The pre-emphasis parameters are *adjusted* by observing fids at different times after a gradient pulse. Typical time variations after gradient switching, are in the range between 100 µs and 1 sec, depending on the type of gradient system.

The standard parameters from the adjustment method are set so, that 8 Fids and spectra are displayed simultaneously. Each individual signal is created after a different delay between the end of the gradient pulse and the start of the data acquisition. All 8 signals cover the range e.g. between 100 µs and 1 sec. Therefore it is immeadiatelly visible, in which time range any modification of a pre-emphasis parameter is causing a change. The pre-emphasis adjustment is made by observing the 8 signals and by modifying the adjustment parameters until all signals look the same in amplitude and signal decay.

Figure 10.7. Pre-emphasis Adjustment Program



Activate the gradient water cooling as described in ***"Gradient Cooling Units" on page 37***, before you start pulsing the gradients.

- Mount the probe and a sample e.g. a 5 mm nmr tube or a sphere filled with water in the magnet as described in the chapter ***"Probes and Gradients" on page 51***. A recommended sample is 20% H2O, 80% D2O, 1 g/l CuSO4.
- Tune and match the probe.
- Shim the sample e.g.with the ***m_onepulse*** method.
- Create a new data set as described in ***"Creation of a new data set" on page 89***. Select the protocol ***m_preemp1***. This is a protocol for the acquisition of 8 free induction decays (FID) after the application of 8 gradient pulse with different delays between the end of the gradient pulses and the start of the acquisitions. The protocol sets parameters for weak but long gradient pulses.

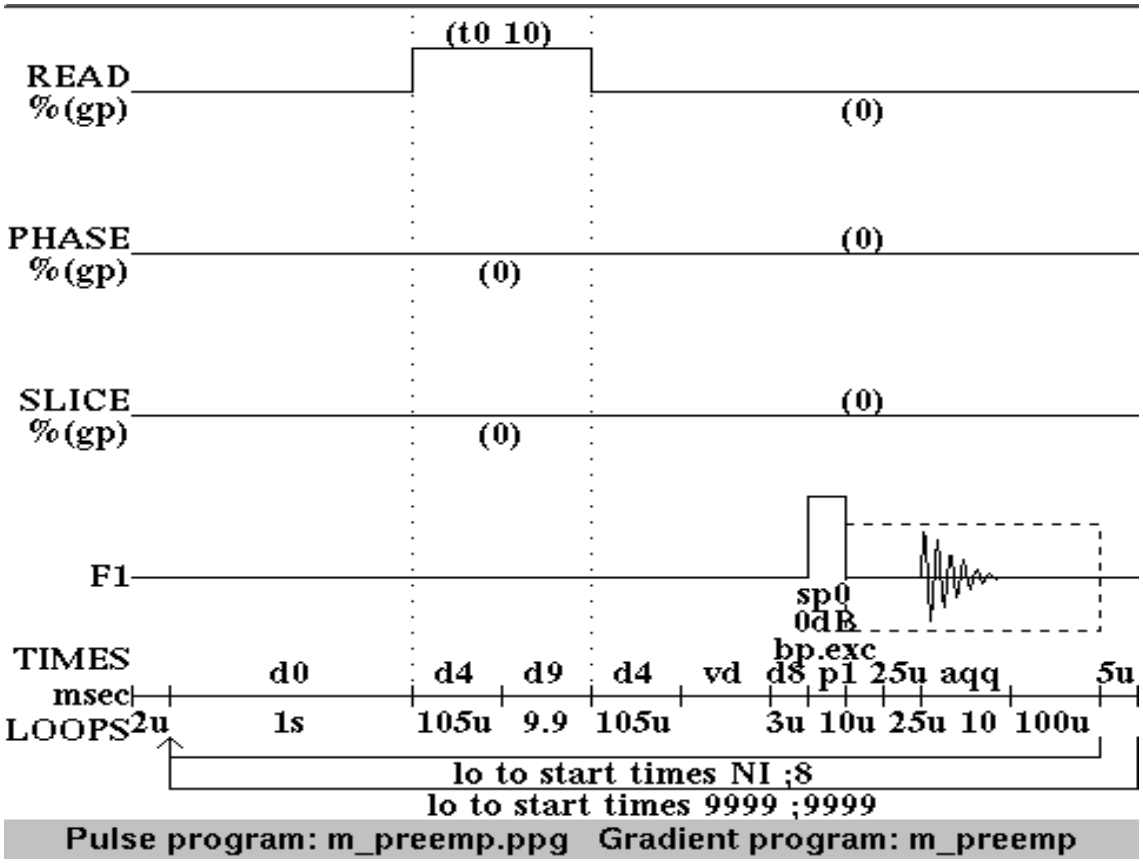
Table 10.5. m_preemp Parameters for Pre-emphasis Adjustments

Parameter	Value
Measuring Method	m_preemp
Nucleus	_1H
Eff. Spectral Bandwidth	100000 Hz
Acquisition Size	1024
Repetition Time	300 ms
Gradient Direction	x or y or z
Gradient Amplitude	20 %
Gradient Duration	50 m
DelayListType	AcqDelayList_Exp for exponetial delay list
Min. Max. ListValue	0.1 and 300
Number of experiments	8
Delay list	created by ParaVision, but can be modified by the user, when AcqDelayList_User is specified
Number of averages	1

Table 10.5. m_preemp Parameters for Pre-emphasis Adjustments

Parameter	Value
Excitation Pulse	expand
Select Excitation Pulse Shape	bp
Excitation Pulse Length	0.010 ms
Excitation Pulse Gain	0.0 dB
Excitation Pulse Attributes	are set by ParaVision
ECG Trigger Module Switched	off
Info	is set by ParaVision

- Click in the **Spectrometer Control Tool** menu the buttons ***Tools, Pulse Program Too***l and check the correct parameter settings by observing the drawn pulse program scheme as shown below.



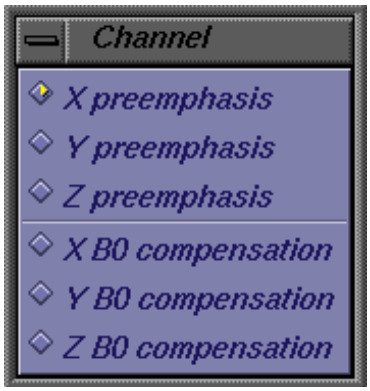
The pulse program and gradient program parameters for the pre-emphasis adjustment are set. The parameters for the gradient pulse shape modifications are described in the following.

- Go into the ParaVision Scan Control window the button with the ***hammer and screw driver*** to enter the ParaVision Spectrometer Control Tool.
- Check the correct Basic Frequency ***BF1*** value in the ***Spectrometer Control Tool*** and go off resonance by 2000 Hz.
- Activate in the ***Spectrometer Control Tool*** the pre-emphasis menu by the button ***Tools*** and ***Adjust Pre-emphasis Values*** if this is not already activated.

Three time bases out of a choice of four can be specified for the time constants of the exponential functions. The precise values of the time constants and the amplitudes are adjusted under slider control in the Time and Gain bars. Values can also be typed in directly after clicking on the buttons with the actual values at the right side of the menu.

The parameters X Grad, Y Grad, Z Grad from the ***Channel*** menu are used to select the pre-emphasis values for the x, y or z gradient respectively.

The parameters X B0 Mod, Y B0 Mod, Z B0 Mod from the ***Channel*** menu are used to select the Bo compensation parameters for the x, y, or z gradient respectively (see the following chapter ***10.7***, ***"Bo Shift Compensation (m_preemp)"***). These parameters show only up, if a Bo compenzation unit is connected.



After all parameters have been adjusted, they should be saved for the gradient system. The parameters can be loaded later in the same way as shim values for different probes. Use the ***Write default*** or the ***Write to*** buttons in the File menu.

- Check the values for the gradient calibration constant, gradient ramp mode, gradient ramp time, gradient rise time for the installed gradient system in the ***Edit*** menu according to the following table. These values are set already during the installation of the „Micro-imaging Patch CDROM“.

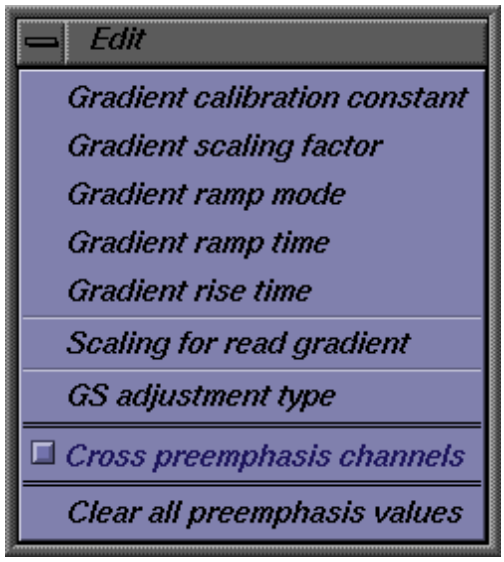


Table 10.6. Gradient Calibration Start Values with B-AFPA-40 Amplifiers

		Micro5	**Micro2.5**	**Mini0.5**	**Mini0.5S**	**Mini0.36**
Gradient calibration constant, [Hz/cm]	GCC	85000	425700	85000	85000	61000
Gradient scaling factors	Sx Sy Sz	1.0 for X 1.0 for Y 1.0 for Z	1.0 for X 1.0 for Y 1.0 for Z	1.0 for X 1.0 for Y 0.7 for Z	1.0 for X 1.0 for Y 1.0 for Z	1.0 for X 1.0 for Y 1.0 for Z
Gradient ramp mode		Constant time	Constant time	Constant time	Constant time	Constant time
Gradient ramp time [us]		100	100	100	100	150
Gradient rise time		180	180	180	180	230

Adjustment Procedures

1. Select the one gradients in the PVM menu to start with the adjustment (x, y or z) in the PVM menu.
2. Check the excitation pulse angle for the experiment so that **no saturation effects** show up. Saturation would make the signals look different in the same style as caused eddy curents. But this difference would not be caused by eddy

currents and thus lead to a complete confusion during the correction precedure. Therefore ***set the gradient amplitude to zero*** for the first run in order to adjust the excitation pulse angle. The power of the excitation pulse should be low enough to avoid saturation effects. Adjust the power with the sliderl in the Spectrometer control tool. Click ***GSP*** in the ***Spectrometer Control Tool*** menu to start the setup of the acquisition. 8 FIDs are visible in the acqDisplay and the 8 corresponding Fourier transformed spectra are visible in the recoDisplay windows, when the parameters from the previous table are used for the acquisition parameters. The O1 frequency should be off resonance.

3. Adjust the excitation pulse (e.g. increase the pulse attenuation by the ***TX Attenuator 0*** slider) and the receiver gain (by the ***Receiver Gain*** slider) in the ***Spectrometer Control Tool*** menu. 8 FIDs should be visible in the acqDisplay and the Fourier transformed spectrum in the recoDisplay. All signals must look the same as shown in the following figure. Click ***STOP*** when the parameters are adjusted. The 8 FIDs can be compared by the integrals, activated by Clicking the ***more*** button in the ***AcqDisplay*** window. If the integral values do not show up in the window, stop the acquisition, click ***Edit GS*** in the ***Spectrometer Control Window*** and change the parameter ***CalculateNormalized Area*** to ***Of_raw_data***. Then restart GSP.

The FIDs and the integral values should look as in the following figures.

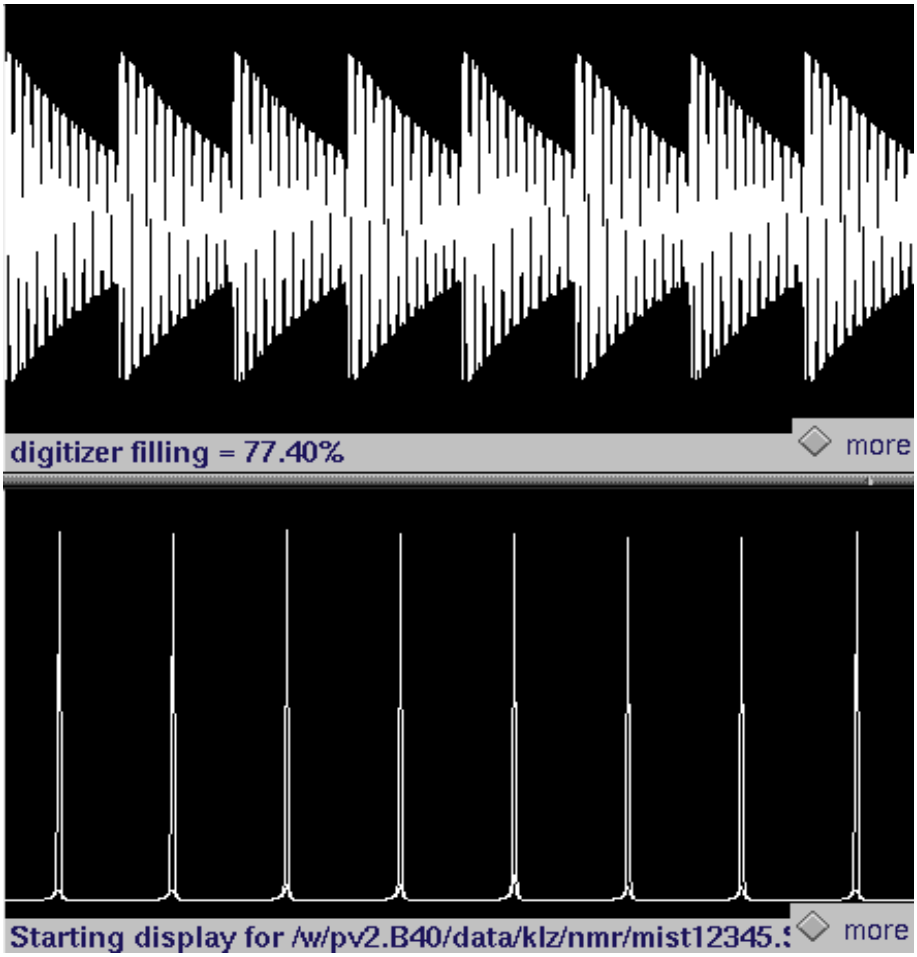
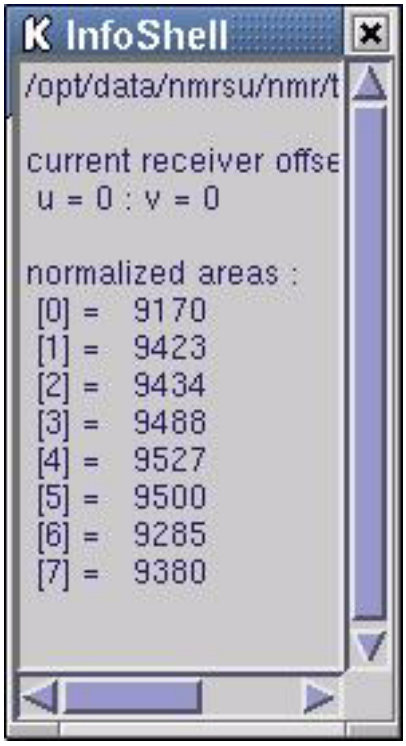
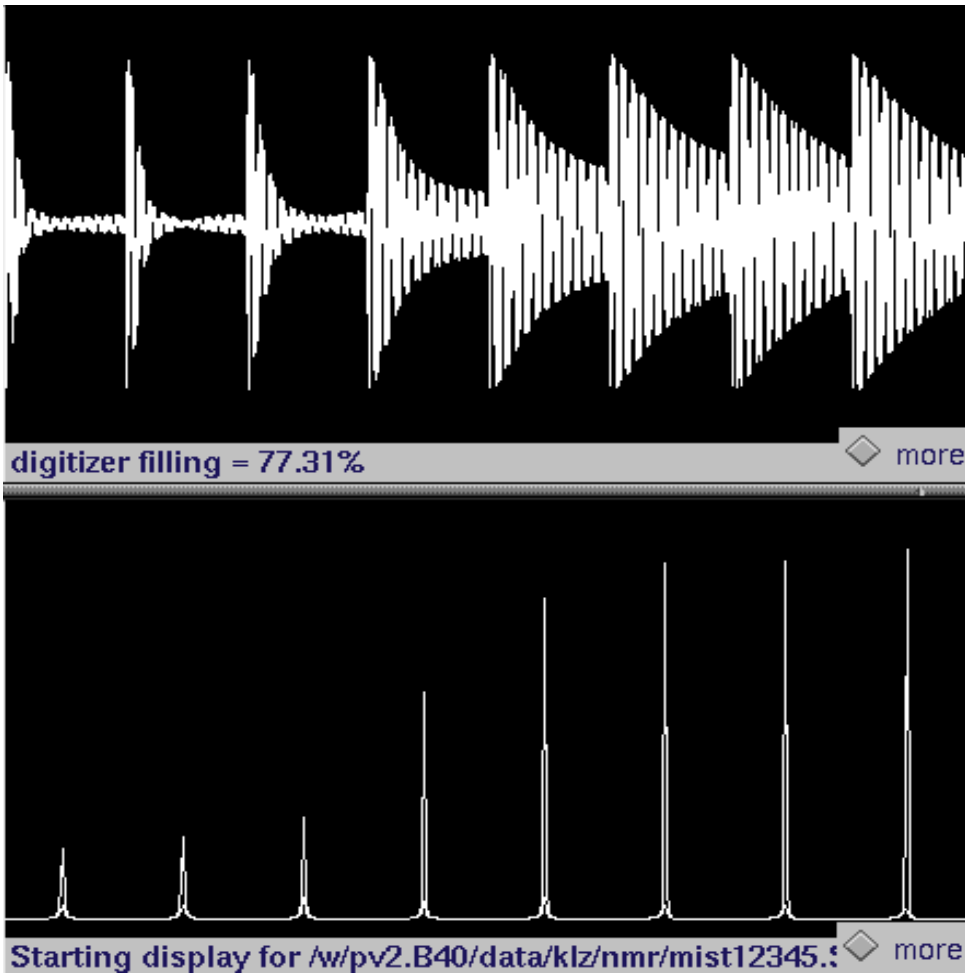


Figure 10.8. Window with iNtegral Values of 8 FIDs



4. Set the amplitude for the x gradient to 20% again in the PVM menu and restart the acquisition by ***GSP***.

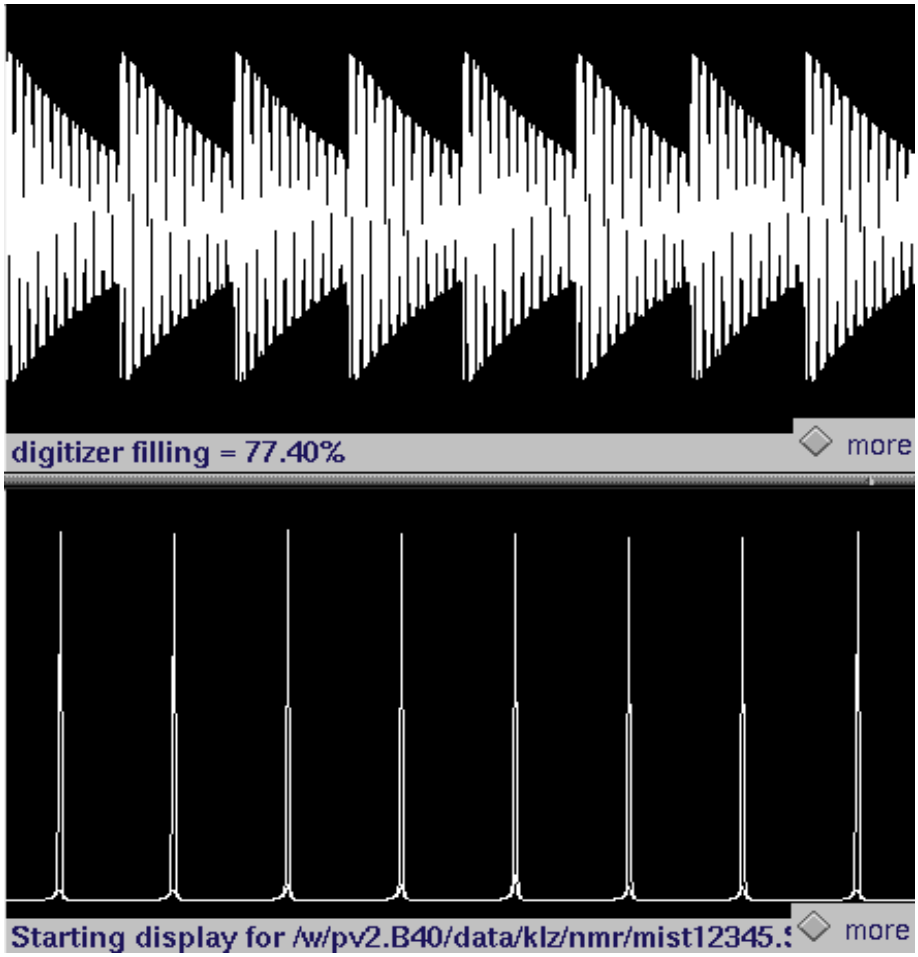
The screen should now look like the figure below.



5. Modify the gradient pulse shape by changing the ***time and gain parameters*** in the ***pre-emphasis menu*** until all fids are identical. Make sure, that the correct gradient channel is selected. The FID on the right side is used as a reference, since the delay between gradient switching and start of data acquisition is the longest for this FID. It is assumed that all eddy currents are gone for the last fid.

   During the adjustment it is recommended that you start with the long time constants and continue with the middle and short time constants afterwards. This procedure corrects the shape of the fids from right to the left.

After the correction the fids should look as shown in the figure below.



6. Store the adjustment parameters as ***default*** with the command under the **File** pull down menu in the pre-emphasis adjustment menu.
7. ***Stop*** the acquisition.
8. Create and scan and select the protocol ***m_preemp2***. This protocol sets parameters with stronger but shorter gradient pulses.
9. Perform steps 5 to 7.

10. Select the next gradient in the PVM menu and repeat the procedure (steps 5 to 7) for the y and z gradients with the protocols ***m_preemp1*** and ***m_preemp2***.

Save the pre-emphasis values in addition under a different file name by the Write to button in the File menu of the Pre-emphasis Tool window.

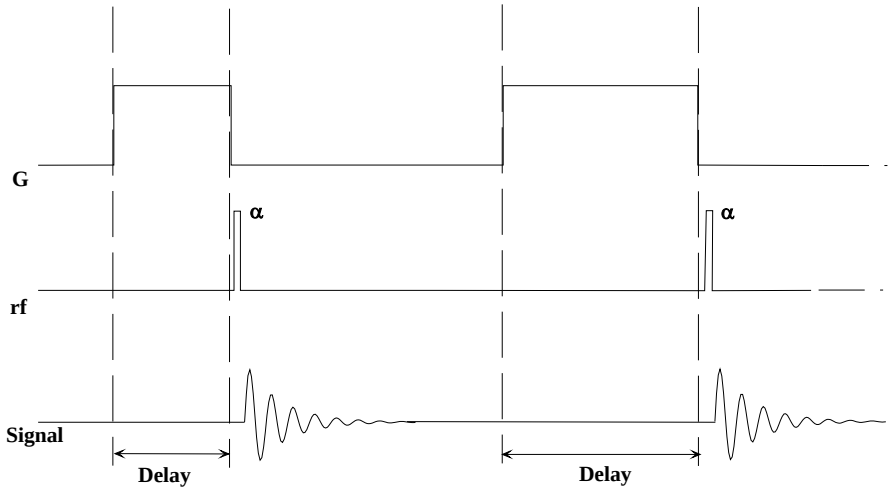
Adjustment with variable gradient durations *10.6.2*

A slightly different style for pre-emphasis adjustments is described in the following. This step is optional and usually not necessary during installations.

The pre-emphasis parameters are *adjusted* by observing FID's at fixed times after gradient pulses of variable durations. Typical durations are in the range between 1 and 20 ms, depending on the type of gradient system.

The standard parameters from the adjustment method are set so, that 8 FID's and spectra are displayed simultaneously. Each individual signal is created after a different duration of the gradient pulse. The pre-emphasis adjustment is made by observing the 8 signals and by modifying the adjustment parameters until all signals look the same in amplitude and signal decay.

Figure 10.9. Pre-emphasis Adjustment Program



Typical parameters for this adjustment are shown in the following table:

Table 10.7. m_preemp Parameters For Pre-emphasis Adjustments

Parameter	Value
Measuring Method	m_preemp
Nucleus	_1H
Eff. Spectral Bandwidth	10000 Hz
Acquisition Size	4096
Repetition Time	1000 ms
Gradient Direction	x or y or z
Gradient Amplitude	20 %
Acquisition Delay	e.g 100 us or 50 ms
DelayListType	GradDelayList_Lin for linear delay list or GradDelayList_Exp for exponetial delay list or GradDelayList_User for user defined delay list
Min. Max. ListValue	Minimum and maximum for DelayList_Lin or DelayList_Exp
Number of experiments	8
Delay list	created by ParaVision, but can be modified by the user, when GradDelayList_User is specified
Number of averages	1
Excitation Pulse	expand
Select Excitation Pulse Shape	bp
Excitation Pulse Length	0.010 ms
Excitation Pulse Gain	0.0 dB
Excitation Pulse Attributes	are set by ParaVision
ECG Trigger Module Switched	off
Info	is set by ParaVision

The optimization of the pre-emphasis adjustment are made in the same way as described in the previous chapter.

Bo Shift Compensation (m_preemp) *10.7*

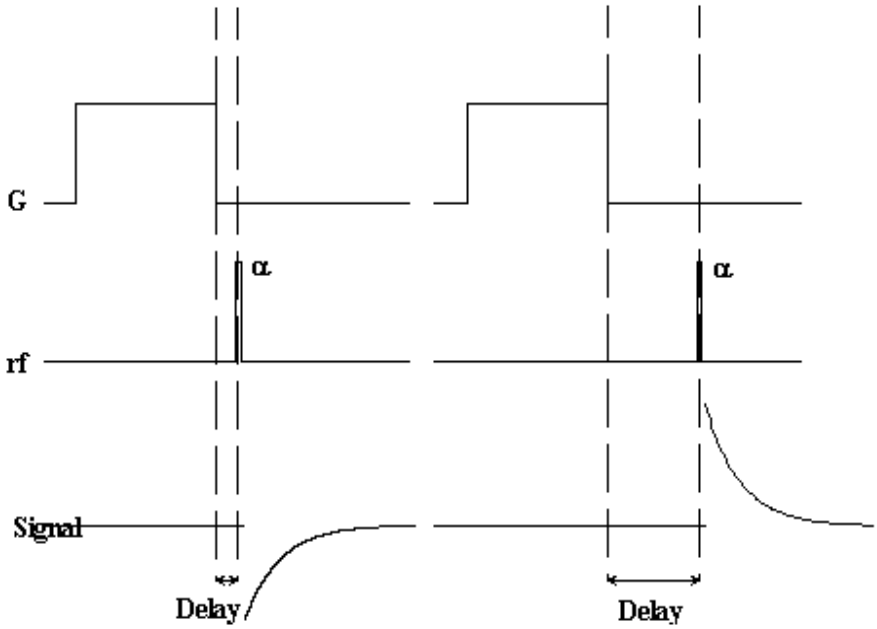
The shape of an FID or an echo, acquired with only a short delay after gradient pulses, may be distorted by shifts of the Bo field caused by gradient switching. Such field shifts can be lessened by applying compensation pulses to the sweep coil of the magnet. In order to do this, three exponential functions with amplitude and time constants are available.

The amplitudes and time constants are set in a control window and are stored for individual gradient systems. This is described as follows:

The Bo shift compensation is adjusted by observing fids *on resonance* at different times after a gradient pulse. Typical times after gradient switching are in the range between 100 µs and 1 sec, depending on the type of gradient system. The pulse program is the same as in the case of the pre-emphasis adjustment.

Note: The pre-emphasis adjustment must always be completed before the Bo shift adjustment (as described in the previous chapter).

Figure 10.10.Bo Shift Adjustment Program



Menu for the Bo shift parameters

The parameters for Bo shift compensation are in the same menu as the pre-emphasis parameters. The menu is activated as described in the previous chapter.

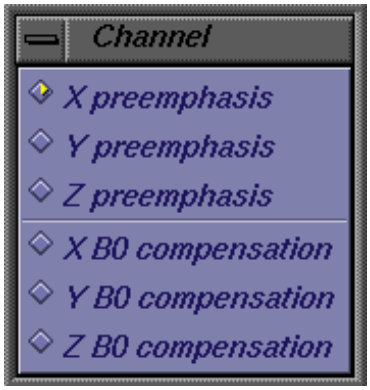
Note: The external address advance data acquisition is used for the pre-emphasis adjustment. Therefore the wiring for external address advance must exist.

Note: The hardware for the Bo shift composition consisting of an additional amplifier and a switching box, must be installed as described in the chapter ***"Installation of the Bo Shift Compensation Unit" on page 34***.

Bo Shift Adjustment

- Select the same data set, which was used for the pre-emphasis adjustment and clone this data set.
- Perform the same steps as for the pre-emphasis adjustment, but select now the Bo compenzation mode instead the pre-emphasis adjustment mode.
- Take care, that the spectrometer frequency is **on resonance**.

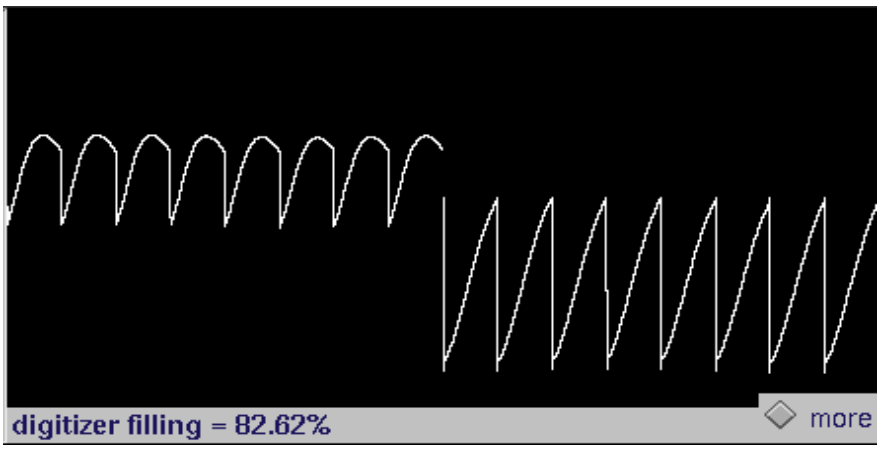
The parameters X B0 compenzation, Y B0 compenzation, Z B0 compenzation from the ***Channel*** menu are used to select the Bo compensation parameters for the x, y, or z gradient respectively.



- Select one gradient in the PVM menu to start with the adjustment (x, y or z) in the PVM menu.
- Check the excitation pulse angle and the repetition time for the experiment so that no saturation effects show up. Saturation would make the signals look different in the same style as caused eddy curents. But this difference would not be caused by eddy currents and thus lead to a complete confusion during the

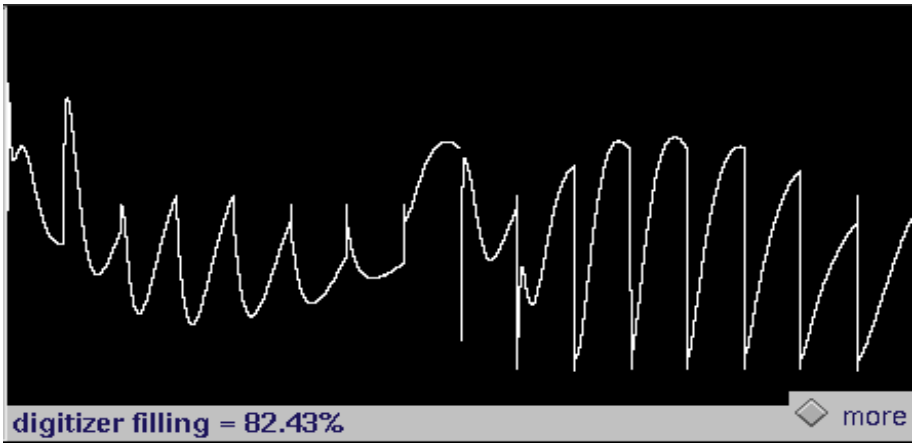
correction precedure. Therefore ***set the gradient amplitude to zero*** for the first run in order to adjust the excitation pulse angle. The excitation pulse angle should be short enough to avoid saturation effects, which can show up in this method, when the pulse angle is too large and when the repetition time is too short.

- Click ***GSP*** in the ***Spectrometer Control Tool*** menu to start the setup of the acquisition. 8 FIDs are visible in the acqDisplay and the 8 corresponding Fourier transformed spectra are visible in the recoDisplay windows, when the parameters from the previous table are used for the acquisition parameters. The O1 frequency should be on resonance.
- Adjust the excitation pulse (e.g. increase the pulse attenuation by the ***TX Attenuator 0*** slider) and the receiver gain (by the ***Receiver Gain*** slider) in the ***Spectrometer Control Tool*** menu. 8 FIDs should be visible in the acqDisplay and the Fourier transformed spectrum in the recoDisplay. All signals must look the same as shown in the following figure. Click ***STOP*** when the parameters are adjusted.



- Set the amplitude for the x gradient to 20% in the PVM menu and start the acquisition by ***GSP***.

The screen might now look like the figure below.

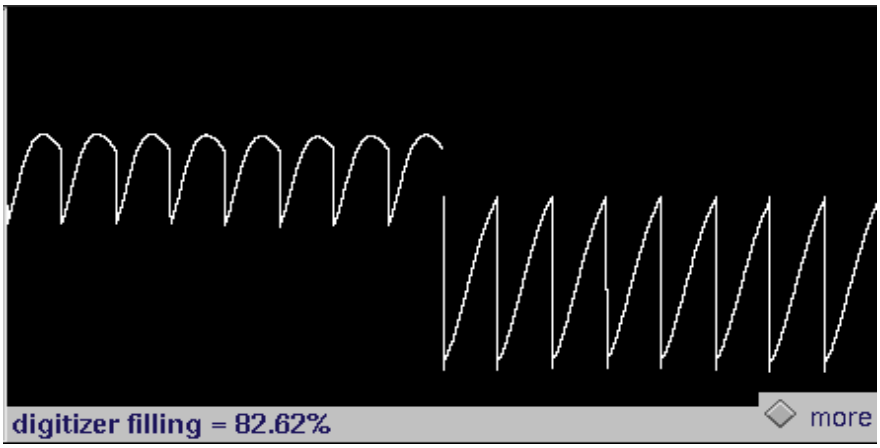


- Activate in the ***Spectrometer Control Tool*** the pre-emphasis menu by the button ***Tools*** and ***Adjust Pre-emphasis Values.*** Select the same gradient under ***Channel*** in this tool menu, that is selected in the PVM menue for the pre-emphasis adjustment.
- Modify the correction pulse shape by changing the ***time and gain parameters*** in the ***pre-emphasis menu*** until all fids are identical. The FIDon the right side is used as a reference, since the delay between gradient switching and start of data acquisition is the longest for this FID. It is assumed that all eddy currents are gone for the last fid.

During the adjustment it is recommended that you start with the long time constants and continue with the middle and short time constants afterwards. This procedure corrects the shape of the fids from right to the left.

- Set the amplitude for the x gradient to higher values in the PVM menu and continue with the adjustments.

After the correction the fids should look as shown in the figure below.



- Store the adjustment parameters with the command under the **File** pull down menu in the pre-emphasis adjustment menu.
- ***Close*** **the pre-emphasis tool menue**[1] **!!!.**
- ***Stop*** the acquisition. Select the next gradient in the PVM menu and repeat the procedure for the y and z gradients.

1. ftbp

Gradient Calibration (m_msme) *10.8*

A number of imaging and diffusion probes are available with gradient systems of different senstivities (G/cm/A or mT/m/A), as described in the chapter ***"Probes and Gradients" on page 51***.

In order to provide images with the correct field of view (FOV), correct slice thickness (SLTH) and slice position or correct gradient pulses for diffusion experiments, the program needs information about the gradient sensitivity and the maximum current, supplied by the gradient amplifiers. Other parameters for correctly scaled images are the relative gradient sensitivities between the x,y and z-gradients, caused by differences in design and production.

A calibration needs to be performed only when the probe and gradient amplifiers are first used, or when e.g. a gradient system or a gradient amplifier is exchanged.

The calibration parameters are stored for each gradient system type during the calibration procedure on disk e.g. in the file

XWINNMRHOME/exp/stan/nmr/parx/preemp/S***/default

It is possible to calibrate different gradients and store the parameters in different S*** directories.

The default parameters for the gradient system, which is selected in the ***Config*** menu, are loaded automatically every time before a new acquisition is started in ParaVision.

The calibration values are determined by special calibration phantoms, called **„GC5“** and **„GC25“** ***"Gradient Calibration Samples" on page 47***. The „microcal“ and „minical“ samples are not produced anymore, but they may still be available in some laboratories.

The gradient calibration is performed in three steps.

1. Images are acquired from three orthogonal planes of the test samples. Typical dimensions from the test sample images are extracted.
2. The dimensions from the images are compared with the dimensions of the real samples, calibration parameters are calculated and stored.
3. Control images are acquired in order to check the correct calibration of the gradients.

- Mount the gradient into the magnet and mount a 1H resonator on the probe base as described in ***"Probes and Gradients" on page 51***
- Load the gradient calibration sample „GC5“ for the Micro5 or „GC25“ for the Micro2.5, Mini0.5 or Mini0.36 probes ***"Gradient Calibration Samples" on page 47***.
- Tune and match the probe.
- Shim the sample.

Three experiments are made and the dimensions of the gradient calibration samples in the images are compared with the dimensions of the real objects. Note, that only the dimensions along the phase encoding direction are precise, because they are not affected by a non perfect shim, as it is along the read direction.

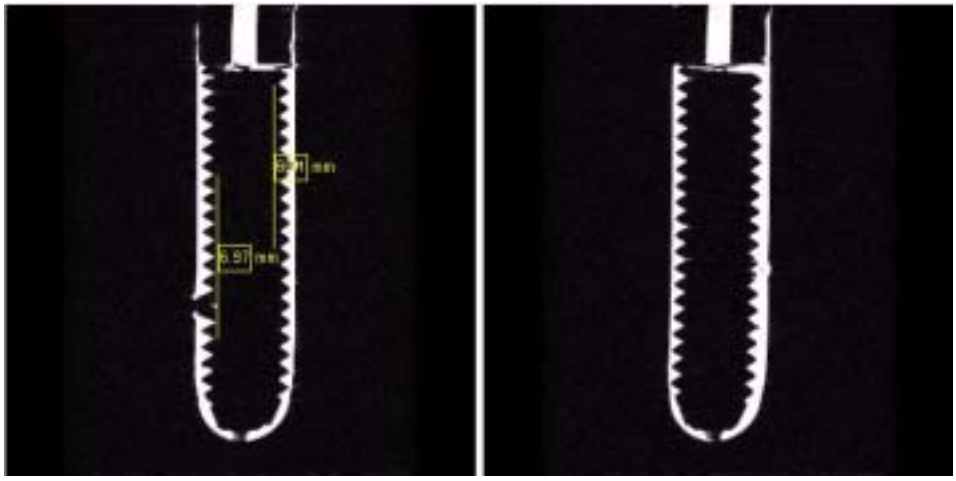
Details for the different calibration samples are described in the following.

Calibration with the GC5 sample

- Create a new data set as described in ***10.1***, ***"Creation of a new data set"***. Load the protocol ***m_gradcalib_gc5_z*** if the GC5 sample is used. It sets the parameters for two longitudinal image acquisitions (yz and xz) with phase encoding direction along z.
- Optimise the 90° and 180° pulse attenuations by the ***GSP*** command.
- Run the experiment by the ***GOP*** command.
- Transfer the image to ***XTIP*** and compare the dimensions along the phase encoding direction z (vertical axis in the image). Click the icon for geometrical image analysis in xtip

f

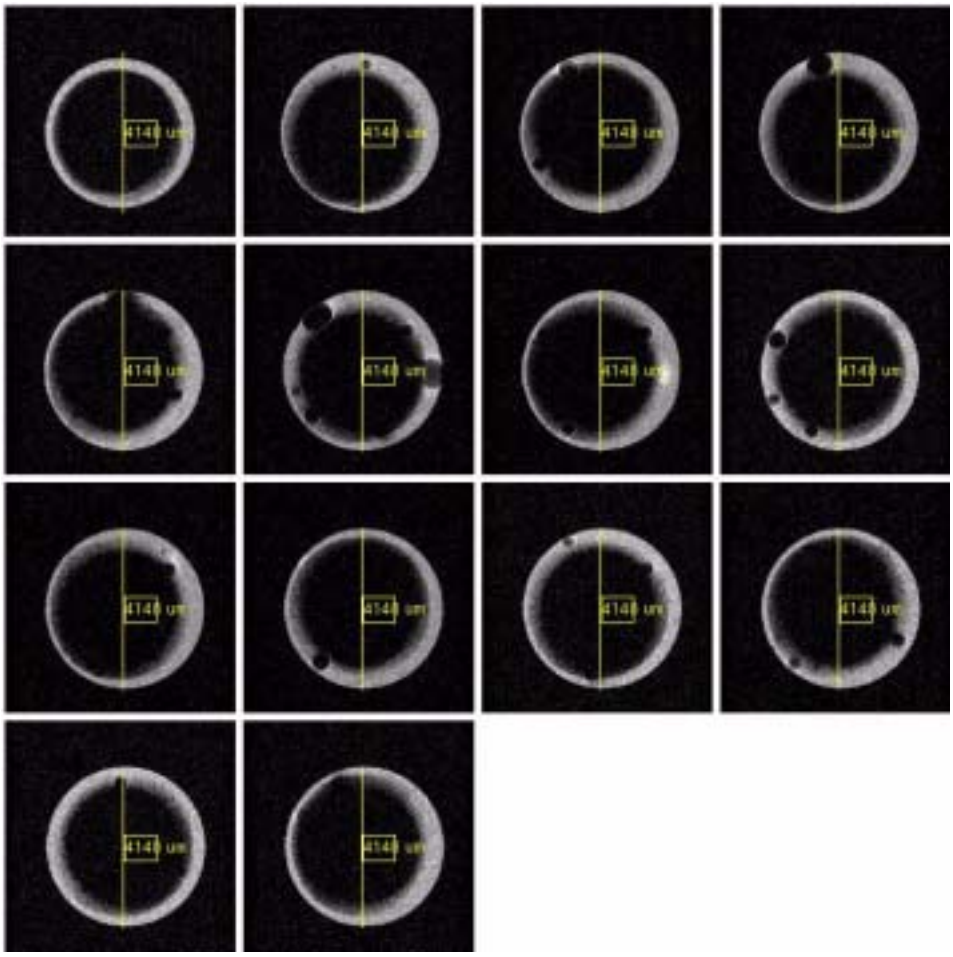
Figure 10.11.YZ and XZ Images of GC5 Sample.



The artefacts in the image are caused by small air bubbles. The slightly warped shape of the nmr tube is caused by a non perfect shim. The distance between 11 tips is exactly 7.5 mm, if the gradients are perfectly calibrated.

- Create a ***New Scan*** in the ***Scan Control menu***.
- Load the protocol ***m_gradcalib_gc5_y*** if the GC5 sample is used. It sets the parameters for some transverse image acquisitions (xy) with phase encoding direction along y.

Figure 10.12.XY Images of GC5 Sample.

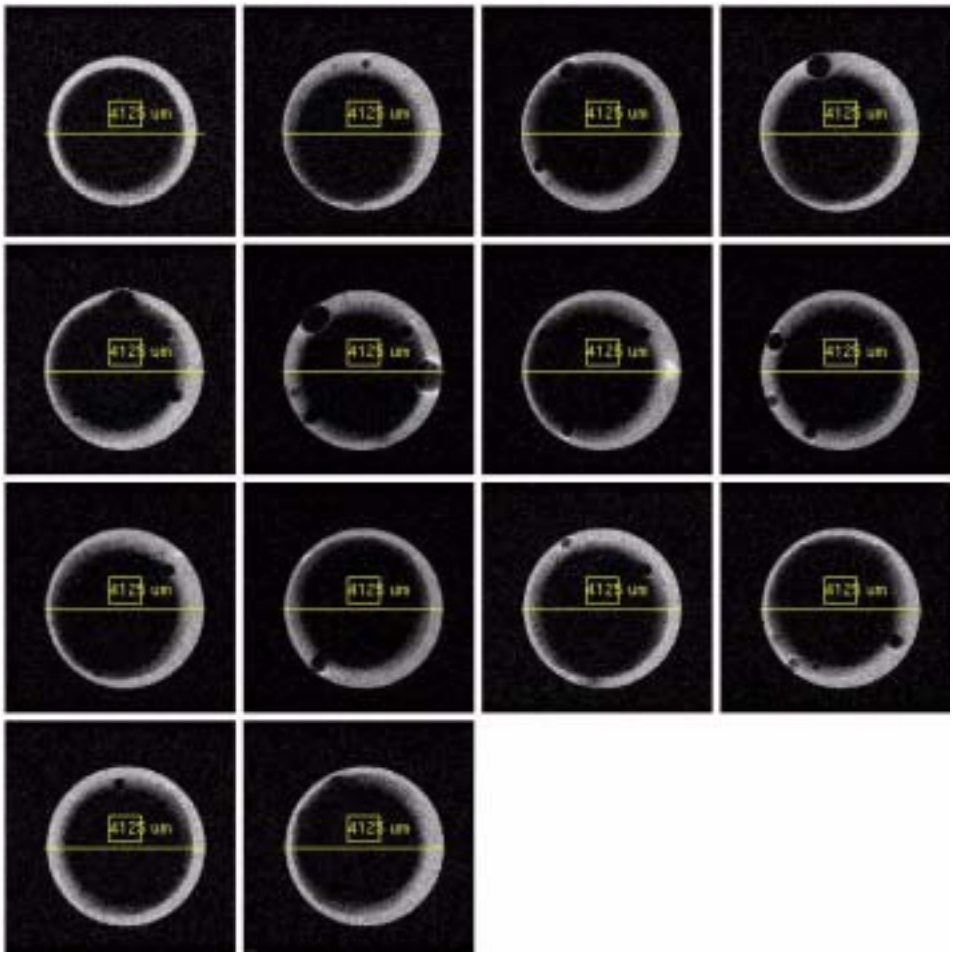


The artefacts in the image are caused by small air bubbles.

The inner diameter along the phase encoding direction (vertical direction in the images) of the 5 mm nmr tube is 4.1 mm, if the gradients are perfectly calibrated.

- Create a ***New Scan*** in the ***Scan Control menu***.
- Load the protocol ***m_gradcalib_gc5_x*** if the GC5 sample is used. It sets the parameters for some transverse image acquisitions (yx) with phase encoding direction along x.

Figure 10.13.YX Images of GC5 Sample.



The artefacts in the image are caused by small air bubbles.

The inner diameter along the phase encoding direction (horizontall direction in the images) of the 5 mm nmr tube is 4.1 mm, if the gradients are perfectly calibrated.

Extract the following dimensions from the images as shown in the previous figures:

Table 10.8. Gradient Calibration Sample GC5

GC5	From Images	From Real Sample
Inner nmr tube diameter along x		4.1 mm
Inner nmr tube diameter along y		4.1 mm
Distance between 10 tips of thread		7.5 mm

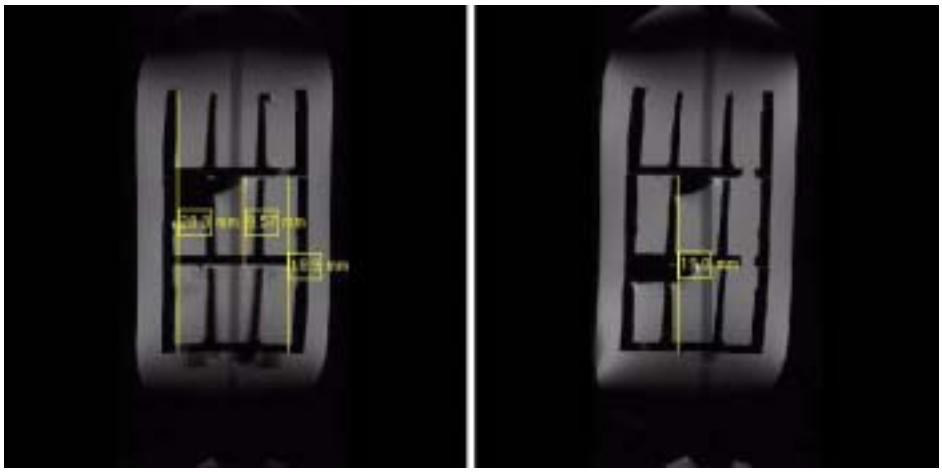
Calibration with the GC25 sample

Create a new data set and run a m_gefi_ortho experiment to ensure, that the legos are aligned as shown in the following figures. The axes of the legos must be parrallel to the x, y, z gradient directions.

- Create a new data set as described in ***10.1***, ***"Creation of a new data set"***. Load the protocol ***m_gradcalib_GC25_z*** if the GC25 sample is used. It sets the parameters for two longitudinal image acquisitions (yz and xz) with phase encoding direction along z.
- Optimise the 90° and 180° pulse attenuations by the ***GSP*** command.
- Run the experiment by the ***GOP*** command.
- Transfer the image to ***XTIP*** and compare the dimensions along the phase encoding direction z (vertical axis in the image). Click the icon for geometrical image analysis in xtip

f

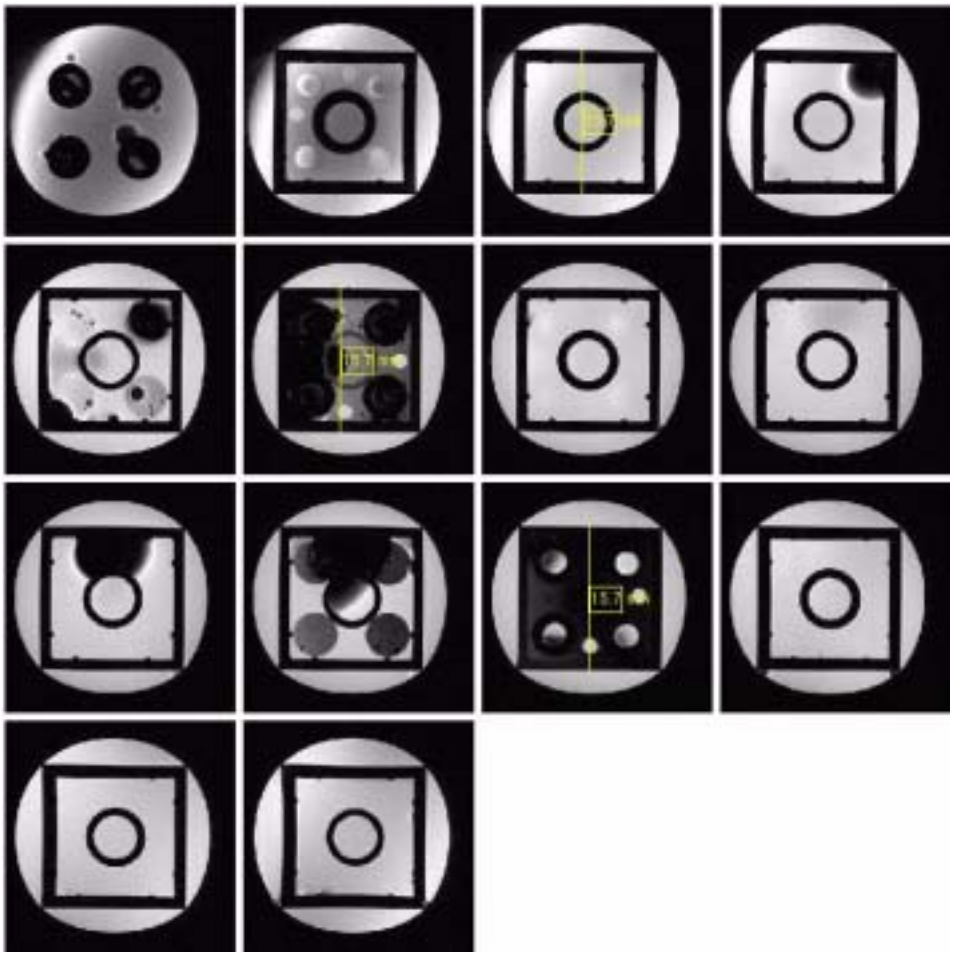
Figure 10.14.YZ and XZ Images of GC25 Sample.



The artefacts in the image are caused by small air bubbles. The slightly warped shape of the nmr tube is caused by a non perfect shim. The height of a single lego block is exactly 9.55 mm, if the gradients are perfectly calibrated.

- Create a ***New Scan*** in the ***Scan Control menu***.
- Load the protocol ***m_gradcalib_GC25_y*** if the GC25 sample is used. It sets the parameters for some transverse image acquisitions (xy) with phase encoding direction along y.

Figure 10.15.XY Images of GC25 Sample.

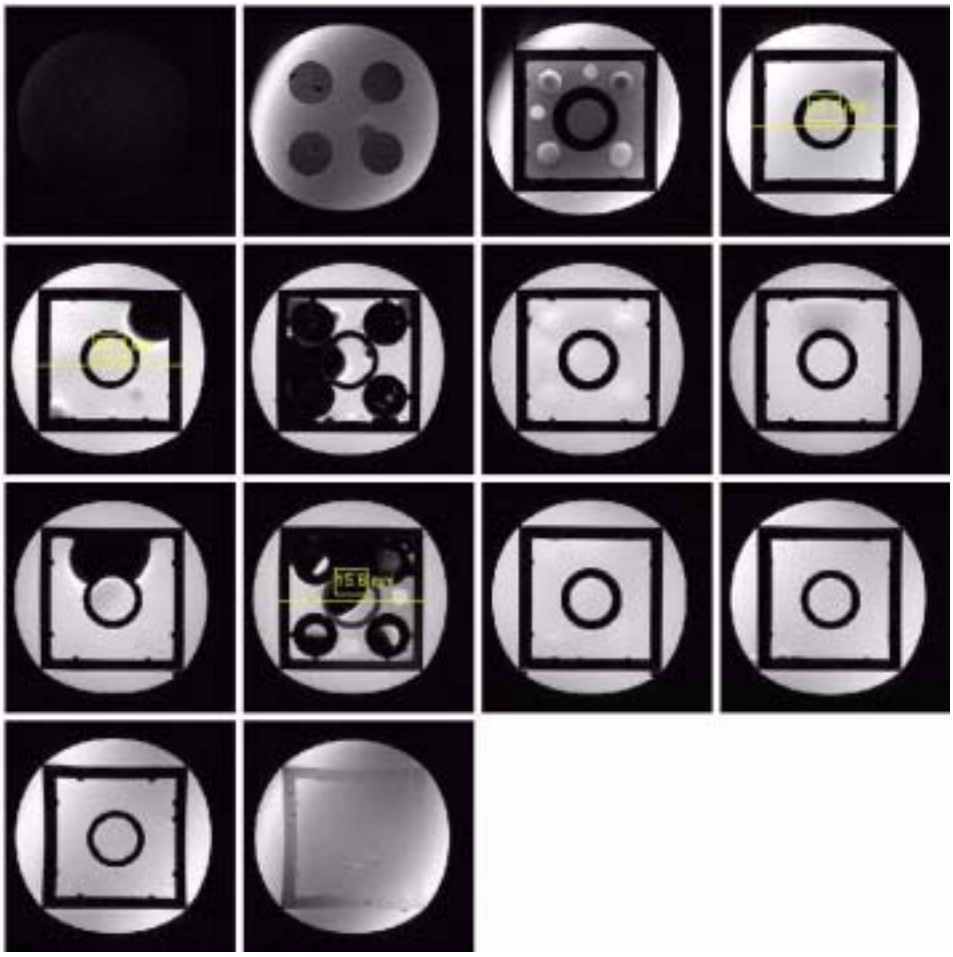


The artefacts in the image are caused by small air bubbles.

The outer width of the lego block along the phase encoding direction (vertical direction in the images) is 15.8 mm, if the gradients are perfectly calibrated.

- Create a ***New Scan*** in the ***Scan Control menu***.
- Load the protocol ***m_gradcalib_GC25_x*** if the GC25 sample is used. It sets the parameters for some transverse image acquisitions (yx) with phase encoding direction along x.

Figure 10.16.YX Images of GC25 Sample.



The artefacts in the image are caused by small air bubbles.

The outer width of the lego block along the phase encoding direction (horizontal direction in the images) is 15.8 mm, if the gradients are perfectly calibrated.

Extract the following dimensions from the images:

Table 10.9. Gradient Calibration Sample GC5

GC25	From Images	From Real Sample
Outer width of the lego block		15.8 mm
Height of a single lego block		9.55 mm

Automatic Calculation of the Calibration Parameters *10.8.2*

- Create a ***New Scan*** in the ***Scan Control*** menu and load the method ***m_gradcalc***.
- Enter the dimensions of real object (***REAL***) and the corresponding dimensions, extracted in Xtip from the images along the phase encoding dimensions (***MEASURE***) .
- Set the parameter ***Save Calc Data*** to ***Save_Now***.
- Exit from the menu.

The new scalings can be checked by creating a New Scan and acquiring some new images.

Clone Scan will not activate the new scalings.

Manual Calculation of the Calibration Parameters *10.8.3*

This part can be skipes, if the ***10.8.2 "Automatic Calculation of the Calibration Parameters"***has been made before. It describes the procedure for a manual calculation of the gradient calibration parameters. The method ***m_gradcalc*** performs these steps automatically.

The default gradient calibration parameters for 40 A amplifiers are shown in the following table.

Table 10.10. Gradient Calibration Start Values with 40 A Amplifiers

		Micro5	**Micro2.5**	**Mini0.5**	**Mini0.5S**	**Mini0.36**
Gradient calibration constant, [Hz/cm] for 40 A maximum current	GCC	850000	425700	85000	85000	61000
Gradient scaling factors	Sx Sy Sz	1.0 for X 1.0 for Y 1.0 for Z	1.0 for X 1.0 for Y 1.0 for Z	1.0 for X 1.0 for Y 0.7 for Z	1.0 for X 1.0 for Y 1.0 for Z	1.0 for X 1.0 for Y 1.0 for Z
Gradient ramp mode		Constant time	Constant time	Constant time	Constant time	Constant time
Gradient ramp time [us]		100	100	100	100	150
Gradient rise time		180	180	180	180	230

The manual calibration is made by acquiring three orthogonal images with such default parameters. Then the dimensions of the structures in the images are compared with the dimensions of the real objects. The following steps describe the calculations for the corrected calibration values.

- Microcal: Determine the inner diameters of the nmr tube ***dx*** and ***dy*** in the xy plane and the length ***dz*** of the plexi-cylinder in the zx or zy planes as shown in the previous images. The units must be mm!
- Minical: Determine the inner diameters ***dx*** and ***dy*** in the xy plane and the length ***dz*** of the cylinder in the zx or zy planes as shown in the previous images. The units must be mm!
- LEGO: Detrmine the dimesions of the LEGO from thr nmr images.
- Look into the following table for Dx, Dy, Dz and calculate the ratios

  Rx = dx / Dx

  Ry = dy / Dy

  Rz = dz / Dz

Table 10.11. Geometry Parameters of Calibration Samples

Gradient	Micro5, Micro2.5	Mini0.5, Mini0.5S, Mini0.36
Sample	GC5	minical
Dx	4.1 mm inner diameter of nmr tube	30 mm
Dy	4.1 mm inner diameter of nmr tube	30 mm
Dz	7.5 mm distance between 10 tips of longitudinal thread image	25 mm

- Calculate the new relative scaling values for the x,y and z gradients according to the following formula:

  Sx = minimum of (Rx,Ry,Rz) / Rx

  Sy = minimum of (Rx,Ry,Rz) / Ry

  Sz = minimum of (Rx,Ry,Rz) / Rz

- Calculate the new Gradient Calibration Constant GCC according to the following formula:

  GCC_{new} = GCC_{old} x minimum of (Rx,Ry,Rz)

- Load the ***Pre-emphasis Tools*** menu as described before, enter the new values Sx, Sy, Sz and GCC_{new} and store them.
- Create a new scan, acquire new images and check, if the new scaling values are correct.

Verification of the Gradient Calibration Parameters *10.8.4*

Acquire the same images again as described in ***10.8.1 "Acquisition of test images"***, after the calibration parameters are stored. Now the dimensions in the measured images should be the same as from the real samples.

Signal to Noise Determination from Images *10.9*

A quick check for the performance of the imaging system, including all components (spectrometer, imaging rack, gradient system and RF-probe) is e.g. a multi-slice experiment with a standard sample and with standard parameters. The Singnal to Noise Ratio (SNR) from the images is calculated and stored. These values can be used at later tests as a base for comparisons of the system performance.

A convenient and easy to produce sample is 20% H_2O, 80% D_2O and 1g/l $CuSO_4$ in a sample tube, that filles the resonator as good as possible. D_2O is added in order to avoid radiation damping effects at higher fields and with large diameter resonators.

Protocols for the experiments are available for the different resonator sizes. The important parameters are the repetition time of 1s, the echo time of 7 ms and the bandwiths of the excitation and refocusing pulses of 3000 Hz. The number of slices has to be adapted to the size of the resonator along the resonator axis. The protocols are stored during the installation of the micro-imaging patch CD and are activated as described in the following.

The calculation of the SNR per mm3 is made by the macro m_SNR_Calculation. The results are stored in the directory of the processed data as

DataFileName_SNR.txt.

This file can be imported e.g. into excel for convenient documentation.

SNR Determination Procedure

- Mount the probe with the 1H resonator of interest in the magnet as described in ***"Probes and Gradients" on page 51***
- Put a sample of 20% H_2O, 80% D_2O and 1g/l $CuSO_4$ in a sample tube, that filles the volume of the resonator as good as possible (largest possible diameter).
- Tune and match the probe.
- Shim the sample.
- Create a new data set as described in ***"Creation of a new data set" on page 89***. Load the protocol ***m_msme_snr_nn*** from the location ***m_installation***. nn denotes the diameter of the resonator. It sets the parameters for a xy spin echo multi slice experiment.
- Adapt the ***number of slices*** by ***Edit Method*** (in the Spectrometer Control menu) to the length of the resonator and verify, that the echo time is 7 ms and

the repetition time is 1 s. Optimise the 90° and 180° pulse attenuations and the receiver gain by the ***GSP*** command.

- Start the experiment by the ***GOP*** command.
- Transfer the images to ***XTIP*** .
- Start the macro ***m_SNR_Calculation*** by clicking the button for the macro manager in the ParaVision System Control menu and selecting the macro in the Bruker category.

The macro creates two predefined regions if interest (ROI). One ROI covers the signal intensity in 80% of the resonators diameter. The other ROI covers some noise area in the image.

The SNR is calculated for each slice individually from the data of two predefined regions of interest.

SNR = MeanSignalIntensity from ROI_{signal} / StandardDeviation from ROI_{noise}.

The results of the SNR calculation are stored as ***DataFileName_SNR.txt*** in the directory of the processed data:

- Print the file ***DataFileName_SNR.txt*** or store it as a reference for future comparisons.
- It is possible to import the ***DataFileName_SNR.txt*** file e.g. into EXCEL to make to look nicer.

Example:

FrameNr	Signal	MeanSignal	Noise	Std.DevNoise	SNR	SNRpermm3
1	Roi_Signal	33130	Roi_Noise	1094	30.27	2204.15
2	Roi_Signal	42411	Roi_Noise	1104	38.40	2796.15
3	Roi_Signal	46171	Roi_Noise	1137	40.60	2956.15
4	Roi_Signal	47324	Roi_Noise	1136	41.67	3034.22
5	Roi_Signal	47349	Roi_Noise	1110	42.66	3106.71
6	Roi_Signal	47102	Roi_Noise	1104	42.66	3106.08
7	Roi_Signal	46791	Roi_Noise	1031	45.39	3305.50
8	Roi_Signal	46222	Roi_Noise	1125	41.09	2991.77
9	Roi_Signal	45980	Roi_Noise	1116	41.19	2999.20
10	Roi_Signal	45360	Roi_Noise	1067	42.51	3095.35
11	Roi_Signal	44751	Roi_Noise	1122	39.89	2904.36
12	Roi_Signal	44115	Roi_Noise	1136	38.84	2827.93
13	Roi_Signal	42789	Roi_Noise	1094	39.11	2847.64
14	Roi_Signal	40551	Roi_Noise	1136	35.71	2600.49
15	Roi_Signal	35743	Roi_Noise	1166	30.67	2233.01
16	Roi_Signal	26703	Roi_Noise	1079	24.76	1802.84

Table 10.12. System Check Parameters

Spectrometer	
Date / Operator	
Probe and Resonator	
Rf Amplifier	
Sample	
Linewidth at 50% amplitude **Linewidth at 5% amplitude**	
90° hard pulse duration **90° hard pulse attenuation**	
90° softpulse shape **90° softpulse duration** **90° softpulse attenuation**	
180° softpulse type **180° softpulse duration** **180° softpulse attenuation**	

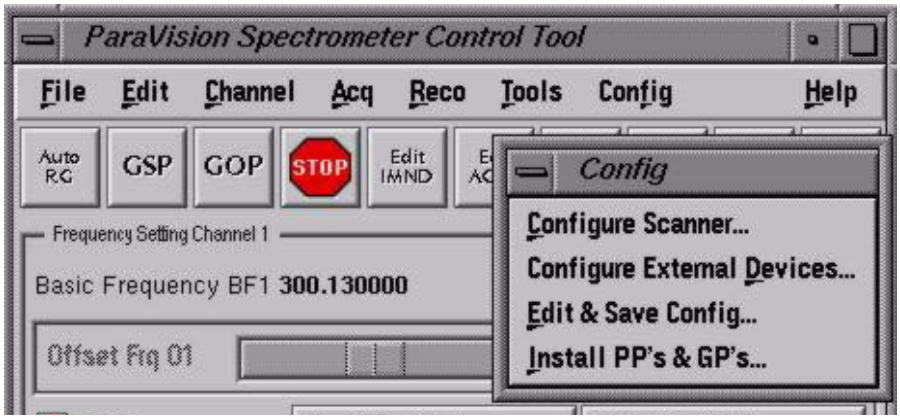
Table 10.12. System Check Parameters

Average SNR in how many slices along how many mm in Z	
Notes:	

Re-Configuration of the System *10.10*

A re-configuration of the system is mandatory, when the hardware of the spectrometer or of the imaging accessory or a imaging probe/gradient is changed. The following steps have to be performed:

- Create a new data set as described in ***10.1***, ***"Creation of a new data set"***and load the protocol ***onepulse*** in step 7.
- Click in the ParaVision Scan Control window the button with the ***hammer and screw driver*** to enter the ParaVision Spectrometer Control Tool.
- Click the button ***Config*** and activate ***Configure Scanner*** and answer the questions.



- Click the button ***Config*** and activate ***Edit & Save Config*** and answer the questions.

Some recommended parameters are the following:

Table 10.13. Parameters for Edit & Config

Parameter Name	Parameter Value
Institution name	e.g. Bruker
Instrument/Station Name	spect
Instrument Type	AVANCE
Reco scratch directory	none
Type of magnet	Cryogenic
Type of shim unit	BSMS
Autotuning available	no
Powertuning available	no
Type of tuning	_Reference

Table 10.13. Parameters for Edit & Config

Parameter Name	Parameter Value
Rf supervisor connected	no
FGSV connected	no
GPSCU connected	no
User Type	Research
Size of buffer for xfer of acq data	512 KWords
Basic spectrometer frequency	e.g. 300.13
Standard digitizer	select a available digitizer
20 MHz FADC Digitizer available	yes or no
Default mode of digitizer	digital_mode
Default acquisition mode	qsim
Firmware used for digital filtering	DSP_medium
default FCUCHAN	enter 0 now, correct value will be set later by a macro
default RSEL	enter 0 now, correct value will be set later by a macro
default SWIBOX	enter 0 now, correct value will be set later by a macro
default PRECHAN	enter 0 now, correct value will be set later by a macro
Prefered RF-pulse	Shaped_Pulse
Length of Transmitter Enable	5 µsecs
System status	select S019 for Micro5 select S040 for Micro2.5 select S057 for Mini0.5 or Mini0.5S select S085 for Mini0.36
Type of pre-emphasis	BGU_II
Probe encoding installed	no
Dual DDS installed	no or DDS_3_4_MHz

Setup Sequences for Imaging Methods 11

In many imaging methods the same parameters e.g. for the correct object positioning, attenuations for slice selective or chemical shift selective RF-pulses, receiver gain etc. are used. It is convenient to have a few setup routines available to adjust such parameters. The same setup programs can be used for various imaging methods. They are described in the following section and are referenced in the chapters on imaging methods.

m_onepulse acquires a high resolution spectrum of the sample. The method can be used for shimming, frequency adjustments, pulse angle adjustments, etc. It is described in detail in ***"Spectrum Acquisition (m_onepulse)" on page 98***.

m_profile acquires 1D spatially resolved profiles along the X, Y, Z axis of the gradient system. The method can be used to check the position of the sample relative to the gradient system.

m_rfprofile acquires profiles of the rf pulse shapes. The method is used to study and optimize the profiles of shaped RF-pulses, e.g. for slice excitation, refocusing or inversion.

m_suppress acquires a high resolution spectrum after three selective RF-pulses followed by spoiler gradient pulses were applied to the sample. The method is used to check the parameters for the suppression of unwanted spectral contributions in a spectrum or a image, (e.g. for fat or water suppression).

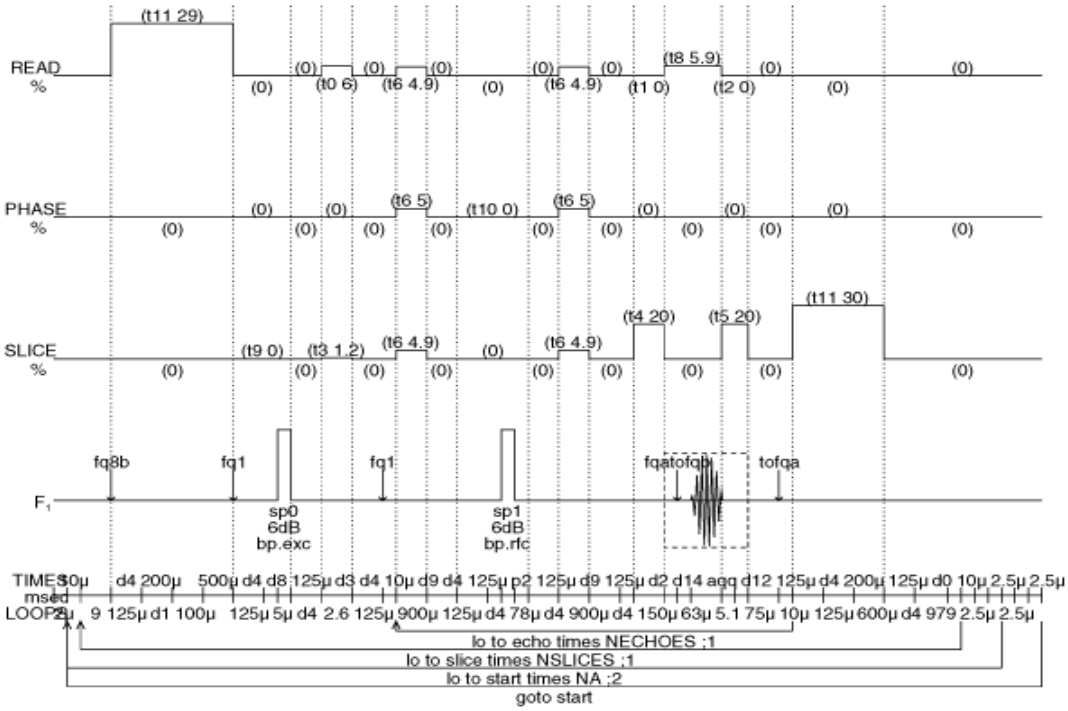
1D Profiles (m_profile) 11.1

One dimensional (1D) profiles can be obtained from the entire sample or from slabs through an object. In the first case non selective RF-pulses are used to excite the magnetization from the whole object. This is explained in the following.

In the second case a stick is excited from the whole sample by applying selective RF-pulses together with slice gradients. This style can be used to study e.g. the penetration of a liquid into porous media or the penetration of labeled compounds into tissue. The method parameters for such applications are described in ***"1D Profiles from sticks (m_profile)" on page 207***.

The 1D profiles along the x, y, or z gradient axes are used e.g. in order to check the **correct positioning of the sample**. A 1D profile from the complete sample is obtained by applying a 90°-180°-AQ non selective spin echo sequence with a read gradient as shown in the figure below.

Figure 11.1. m_profile Method with Two Non-selective RF-pulses



- Create a new data set as described in ***"Creation of a new data set" on page 89***. Select the protocol ***m_profile*** as described in step 7. This is a protocol for the acquisition of profiles. If this protocol is not available, then exit from the menu with cancel and set the parameters as described in the following steps.
- Click in the ParaVision Scan Control window the button with the ***hammer and screw driver*** to enter the ParaVision Spectrometer Control Tool.
- Check the correct Basic Frequency ***BF1*** value in the ***Spectrometer Control Tool .***

- Enter the PVM menu for the optimization of the acquisition parameters. Some usefull parameters are:

Table 11.1. m_profile Parameters with Non-selective Selective RF-pulses

Parameter	Value
Measuring Method	m_profile
Matrix Size	0-0 indicates a 1D experiment e.g. 256 pixels
Read Orientation	x_dir or y_dir or z_dir
Effective Spectral Bandwidth	50000 Hz
Echo Time Mode	Min_EchoTime for short echo times or Read_Dephase_aq_2 for longer echo times or User_def_EchoTime
Echo Time	e.g. 10 ms for User_def_EchoTime
Repetition Time	e.g. 1000 ms
Number of Averages	e.g. 2
Estimated total scan time	Is set by ParaVision
Excitation Pulse	Expand
Select Excitation Pulse Shape	bp for a rectangular pulse shape
Excitation Pulse Length	Duration of 90° pulse
Excitation Pulse Gain	e.g. 6.0, this value can be adjusted under slider control during GSP
Excitation Pulse Attributes	Are set by ParaVision
Refocusing Pulse	Expand
Select Refocusing Pulse Shape	bp for a rectangular pulse shape
Refocusing Pulse Length	Duration of 180° pulse
Refocusing Pulse Gain	e.g. 6.0, this value can be adjusted under slider control during GSP
Refocusing Pulse Attributes	Are set by ParaVision
Refocus Spoiler	Expand
Ref Spoiler Amplitude	e.g. 5%
Ref Spoiler Length	e.g. 1 ms
Geometry	expand
Patient Position	Is defined during creation of a new data set, e.g. by New Patiant or New Study etc. or any value is ok here

Table 11.1. m_profile Parameters with Non-selective Selective RF-pulses

Parameter	Value
Field of View	Field of View according to the size of the subject
Spatial Resolution	Is callculated according to FOV and Matrix Size, but can be changed here
Number of slice packages	1
Anti Aliasing Factor	1
Volume Geometry	Expand
Read Orientation	X_dir, or Y_dir or Z_dir for a profle along the x,y or z direction (this is the same parameter, shown already before)
Echo Customization	Expand
Number of Echoes	1 as default.
Number of echo images	1 as default. An image (echo profile) is reconstructed from each individual echo, when this parameter is the same as the number of echoes. Some echoes can be added to result in the same image, when this parameter smaller than the number of echoes.
Scan list	Defines, how many echoes are summarized to the individual profiles.
Method Customization	Expand
Nucleus	e.g. _1H for protons
bf1	Basic frequency, e.g. 300.13
Number of Dummy Scans	0 as default. Number of Dummy Scans before the data acquisition starts.
ConfigTiming	Expand
SliceRephaseTime	Is set by PVM, according to the read dephase time
ReadDephaseTime	Is set by PVM, except, when EchoTImeMode is set to User_def_echo_time
Slice Spoil Time	e.g. 1 ms for the spoiler gradient duration
Match Pulse Bandwidth	No as default.
Derive Pulse Gains	Yes, when the pulse gains should automatically be set, according to the set up information, gathered by using the traffic light of by using Auto_RFGain in the Acq menue. No, when the pulses should be adjusted under slider control during GSP.
Config Gradients	Expand

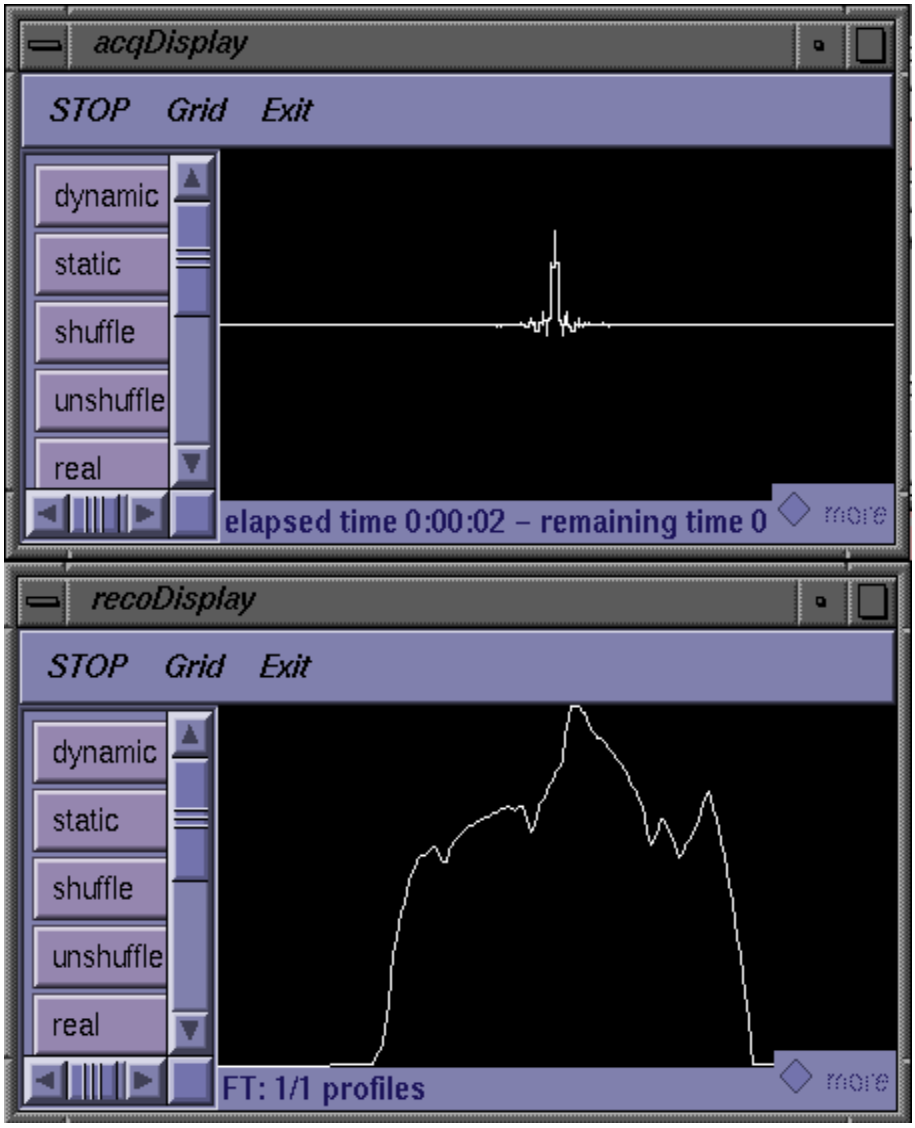
Table 11.1. m_profile Parameters with Non-selective Selective RF-pulses

Parameter	Value
R, P and S Gradient Limit Mode	Fixed Limit in percent, when a limit for the gradient amplitude should be used Fixed Single Oblique, (square root of 2), when the image geometry must not be distorted in oblique image orientations. Fixed Double Oblique, (square root of 3), when the image geometry must not be distorted in double oblique image orientations.
R, P and S Gradient Limits	Gradient Limits with the maximum gradient values, when Fixed Limit mode is selected. 100, 100, 100 as default
Image spoiler amplitude	e.g. 10% amplitude of the spoiler gradient
Modules	Expand
ECG	For ECG trigger parameters
Image gradient spoiling	For spoiler gradients before and after the scans. no as default
Info	Is set by ParaVision

- Check the correct parameter setting by clicking the ***Pulse Program Tool*** in the ***Tools*** menu from ***Spectrometer Control Tool .*** The pulse program display should look as ***Figure 11.1.***
- Start the acquisition by ***GSP*** for the pulse and receiver gain adjustments or ***GOP*** for the profile acquisition.

The spin echo and the profile after Fourier transformation should look as shown in the following figures.

Figure 11.2. Spin Echo and 1D Profile

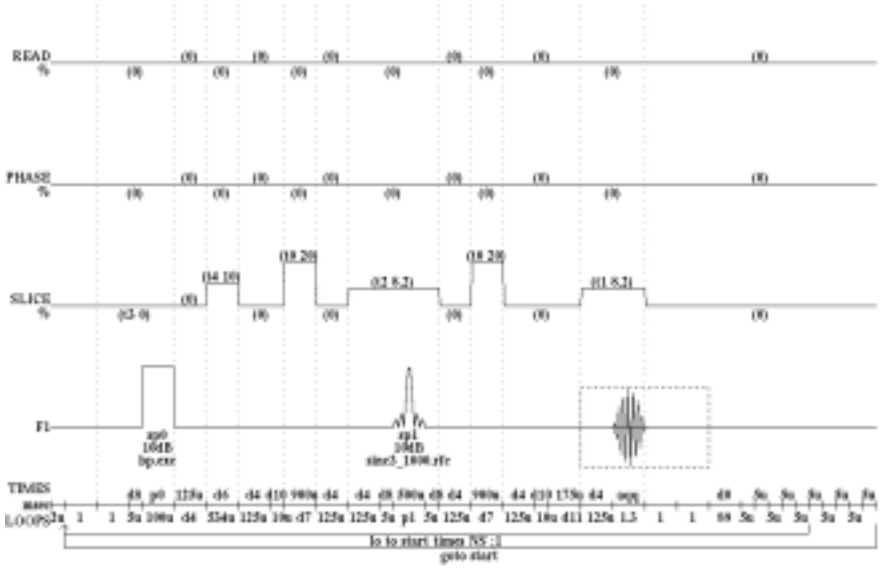


Slice selective pulse adjustment (m_rfprofile) *11.2*

Selective RF-pulses for the excitation and refocusing or inversion of magnetization in slices from the samples are used in many imaging experiments. In this example a slice selective 180 degree pulse is adjusted. Then the applicaton of this method for 90 degree excitation and 180 degree inversion pulses is explaned.

A spin echo is produced by a 90° hard rf pulse, that excites the entire sample, followed by a 180° selective pulse together with a gradient. The selective pulse refocuses only the magnetization of a slice, perpendicular to the gradient direction. The largest echo amplitude is obtained when the flip angle of the selective rf pulse is equal to 180°.

Figure 11.3. Slice Selective 180° Pulse Adjustment



- Create a new data set as described in ***"Creation of a new data set" on page 89***. Select the protocol ***m_rfprofile*** as described in step 7. This is a protocol for the acquisition of profiles. If this protocol is not available, then exit from the menu with cancel and set the parameters as described in the following steps.
- Click in the ParaVision Scan Control window the button with the ***hammer and screw driver*** to enter the ParaVision Spectrometer Control Tool.
- Check the correct Basic Frequency ***BF1*** value in the ***Spectrometer Control Tool .***
- Enter the PVM menu for the optimization of the acquisition parameters. Some usefull parameters are:

Table 11.2. m_rfprofile Parameters with non-Selective Selective RF-pulses

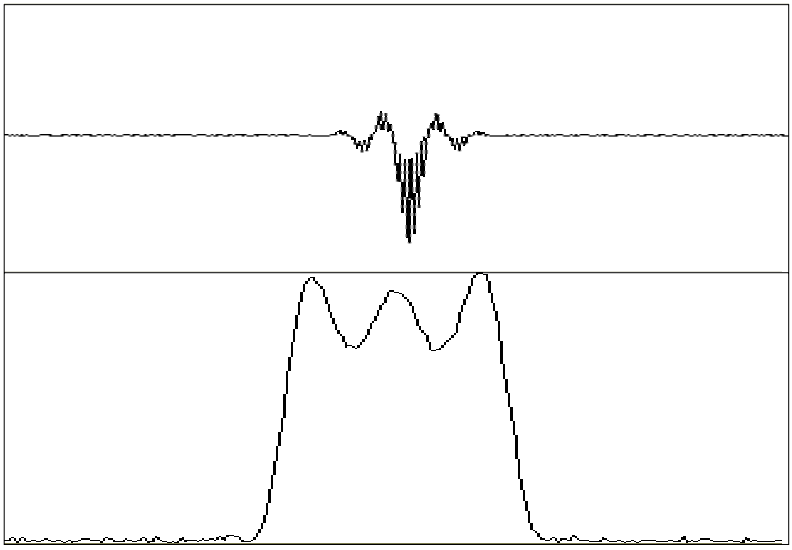
Parameter	Value
Measuring Method	m_rfprofile
Matrix Size	0-0 indicates a 1D experiment e.g. 256 pixels
Profile mode	Select Refocusing_prof for the 180 degree refocusing pulse
Effective Spectral Bandwidth	50000 Hz
Echo Time Mode	Min_EchoTime for short echo times or Read_Dephase_aq_2 for longer echo times or User_def_EchoTime
Echo Time	e.g. 10 ms for User_def_EchoTime
Repetition Time	e.g. 1000 ms
Number of Averages	e.g. 2
Estimated total scan time	Is set by ParaVision
Excitation Pulse	Expand
Select Excitation Pulse Shape	bp for a rectangular pulse shape
Excitation Pulse Length	Duration of 90° pulse
Excitation Pulse Gain	e.g. 6.0, this value can be adjusted under slider control during GSP to match a 90 degree pulse
Excitation Pulse Attributes	Are set by ParaVision
Refocusing Pulse	Expand
Select Refocusing Pulse Shape	e.g. sinc3 for a selective pulse shape
Refocusing Pulse Length	Duration of 180° pulse
Refocusing Pulse Gain	e.g. 6.0, this value can be adjusted under slider control during GSP
Refocusing Pulse Attributes	Are set by ParaVision
Geometry	Expand
Patient Position	Is defined during creation of a new data set, e.g. by New Patiant or New Study etc. or any value is ok here
Field of View	Field of View according to the size of the subject
Spatial Resolution	Is callculated according to FOV and Matrix Size
Anti Aliasing Factor	1
Method Customization	Expand

Table 11.2. m_rfprofile Parameters with non-Selective Selective RF-pulses

Parameter	Value
Nucleus	e.g. _1H for protons
bf1	Basic frequency, e.g. 300.13
ConfigTiming	Expand
ReadDephaseTime	Is set by PVM, except, when EchoTImeMode is set to User_def_echo_time
Ref. Spoil Time	e.g. 1 ms for the spoiler gradient duration
Match Pulse Bandwidth	No as default.
Derive Pulse Gains	Yes, when the pulse gains should automatically be set, according to the set up information, gathered by using the traffic light of by using Auto_RFGain in the Acq menue. No, when the pulses should be adjusted under slider control during GSP.
Config Gradients	Expand
R, P and S Gradient Limit Mode	Fixed Limit in percent, when a limit for the gradient amplitude should be used Fixed Single Oblique, (square root of 2), when the image geometry must not be distorted in oblique image orientations. Fixed Double Oblique, (square root of 3), when the image geometry must not be distorted in double oblique image orientations.
R, P and S Gradient Limits	Gradient Limits with the maximum gradient values, when Fixed Limit mode is selected. 100, 100, 100 as default
Info	Is set by ParaVision

- Check the correct parameter setting by clicking the ***Pulse Program Tool*** in the ***Tools*** menu from ***Spectrometer Control Tool .*** The pulse program display should look as shown in the figure ***Figure 11.3.***.
- Start the acquisition by ***GSP*** for the pulse and receiver gain adjustments or ***GOP*** for the profile acquisition.
- Adjust the pulse power under slider control in the ***Spectrometer Control Tool*** until the echo and profile show the maximum amplitude as shown in the following figure.

Figure 11.4. Spin Echo and Slice Profile Created with a sinc RF-pulse.



- Stop the acquisition.

The same method is used:

- for the calibration of selective 90 degree pulses,
- for the simultaneous calibration of selective 90 and 180 degree pulses,
- for the calibration of 180 degree inversion pulses.

This is controlled by the parameter ***Profile mode***, mentioned in the previous parameter table.

Table 11.3. Selective RF-pulse Adjustments

Profile mode	Excitation_prof Refocusing_prof Spinecho_prof Inversion_prof

The pulse programs for these cases look as shown in the following figures.

Figure 11.5. Slice Selective Excitation Pulse Adjustment

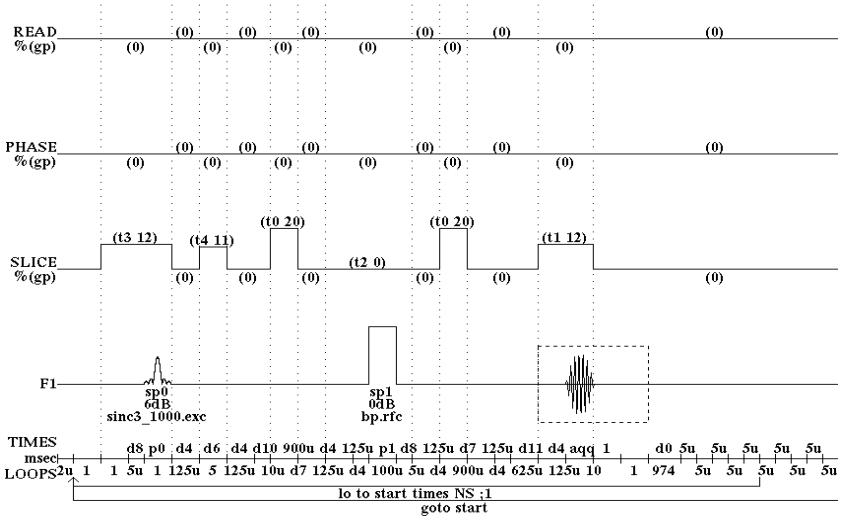


Figure 11.6. Slice Selective Excitation and Refocusing Pulse Adjustment

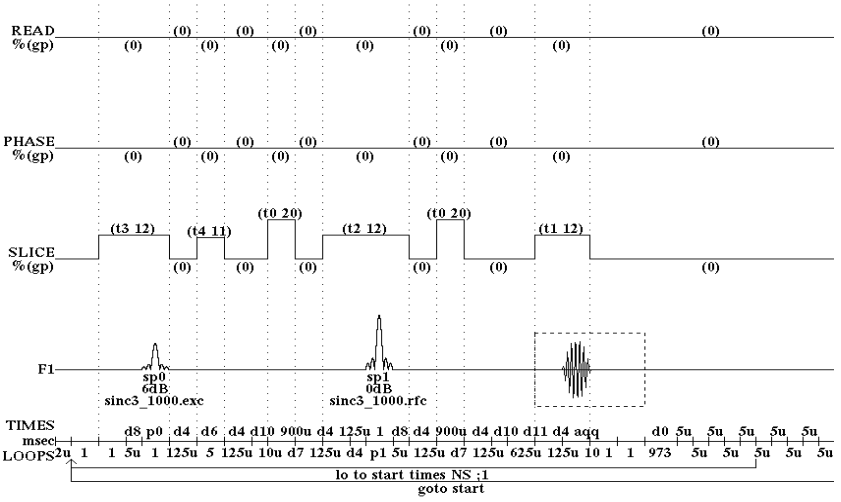
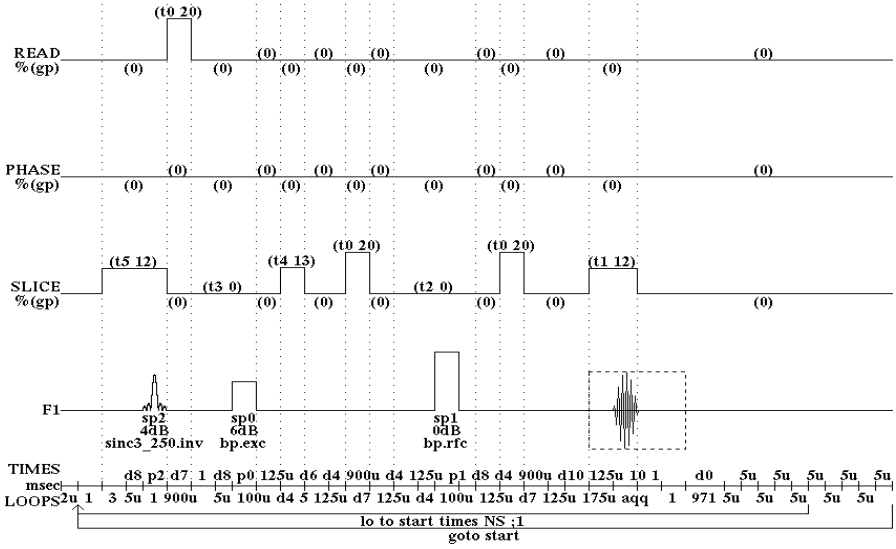


Figure 11.7. Inversion Pulse Adjustment



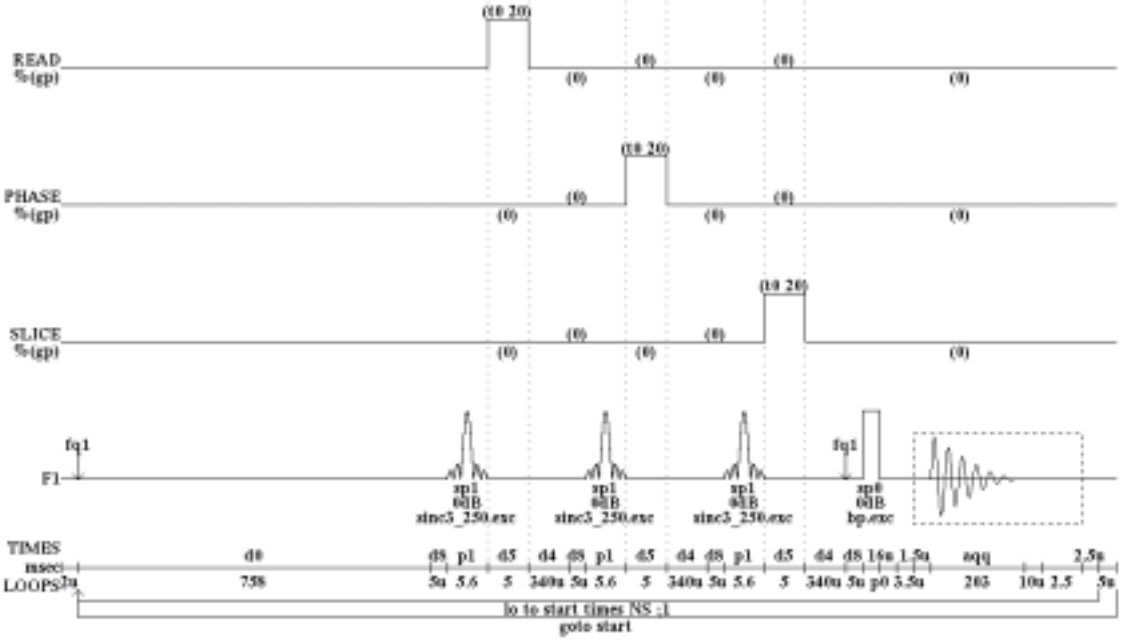
Water, Fat or Solvent Suppression (m_suppress) *11.3*

This method is used to adjust selective RF-pulses and spoiler gradient pulses for the suppression of unwanted spectral components, e.g. water or fat signals.

The unwanted signal is excited by three selective 90 degree RF-pulses, followed by spoiler gradients in order to dephase its transverse magnetization. Then the remaining magnetization is acquired after a non selective 90 degree pulse and shown as a spectrum. The resulting parameters can be used in other imaging or spectroscopy experiments.

This pulse and gradient program is shown in the figure below.

Figure 11.8. m_suppress Method



- Create a new data set as described in ***"Creation of a new data set" on page 89***. Select the protocol ***m_suppress*** as described in step 7. This is a protocol for the acquisition of a spectrum after the suppression of unwanted signals. If this protocol is not available, then exit from the menu with cancel and set the parameters as described in the following steps.
- Click in the ParaVision Scan Control window the button with the ***hammer and screw driver*** to enter the ParaVision Spectrometer Control Tool.
- Check the correct Basic Frequency ***BF1*** value in the ***Spectrometer Control Tool .***
- Enter the PVM menu for the optimization of the acquisition parameters. Some usefull parameters are:

Table 11.4. m_suppress Parameters

Parameter	Value
Measuring Method	m_suppress
Effective Spectral Bandwidth	e.g. 10000 Hz
Acquisition Size	e.g. 4096
Repetition Time	e.g. 1000 ms
Number of Averages	e.g. 1
Spoiler Length	Duration of spoiler gradient pulse e.g. 5 ms
Spoiler Amplitude	strEngth of spoiler gradient in percent, e.g. 10 %

Table 11.4. m_suppress Parameters

Parameter	Value
Estimated total scan time	Is calculated by ParaVision
rfPulse	Expand
RF-pulse Shape for Excitation	Select the rf pulse shape, e.g. bp
RF-Excitation Pulse Shape File	Expand
.filename	Pulse shape file name e.g. bp.exc
.length	Duration of 90° rf pulse in ms
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision
.attenuation	Attenuation for 90° pulse, can be modified under slider control
.flipangle	e.g. is applied only, if derive pulse gains is activated
.properties	Contains information about pulse properties
Suppression Pulse Offset	Offset frequency of the suppression pulse
RF-pulse Shape for Suppression	Select the rf pulse shape, e.g. gauss100
RF-Suppression Pulse Shape File	Expand
.filename	Pulse shape file name e.g. gauss100.exc
.length	Duration of 90° rf pulse in ms
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision
.attenuation	Attenuation for 90° pulse, can be modified under slider control
.flipangle	e.g. is applied only, if derive pulse gains is activated
.properties	Contains information about pulse properties
Method Customization	Expand
Nucleus	e.g. _1H for protons
bf1	Basic frequency, e.g. 300.13
Derive Pulse Gains	Yes, when the pulse gains should automatically be set, according to the set up information, gathered by using the traffic light of by using Auto_RFGain in the Acq menue. No, when the pulses should be adjusted under slider control during GSP.
Modules	Expand
ECG	For ECG trigger parameters
Info	Is set by ParaVision

- Check the correct parameter setting by clicking the ***Pulse Program Tool*** in the ***Tools*** menu from ***Spectrometer Control Tool .*** The pulse program display should look as ***Figure 11.8.***
- Start the acquisition by ***GSP*** for the pulse and receiver gain adjustments and optimize the RF-pulse gains under slider control. Start with the highest possible attenuation for the suppression pulse. Observe the spectrum and reduce the attenuation until the unwanted resonances are reduced to a minimum. The duration and amplitude of the spoiler gradient pulses can be optimized in the parameter menu.
- **Stop** the acquisition, when the best parameters are adjusted.

The spectrum should look as shown in the following figures.

No suppression is applied, when the attenuation of the suppression RF-pulses is very high. This means, that there is no rf excitation of the unwanted signal. Then the following non selective 90° rf pulse acquires the complete spectrum of the sample.

The water signal or the oil signal is suppressed by setting the suppression pulse offset frequency in the menu to the appropriate values.

Figure 11.9. Spectrum from an Oil/water Sample,without the Supression Pulse

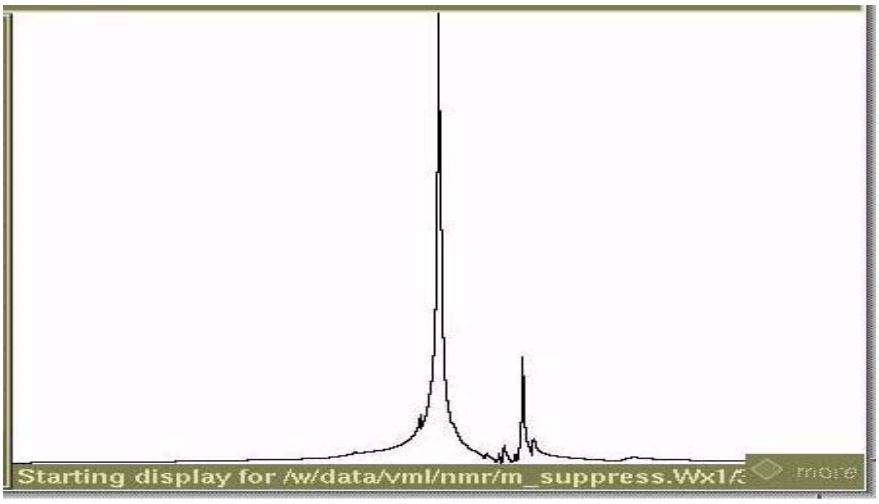


Figure 11.10.Spectrum from an Oil/water Sample,with Water Supression

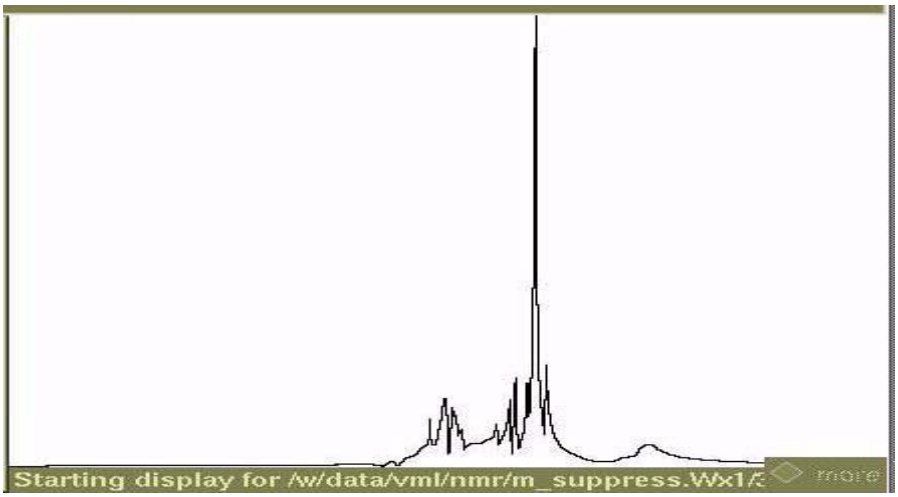
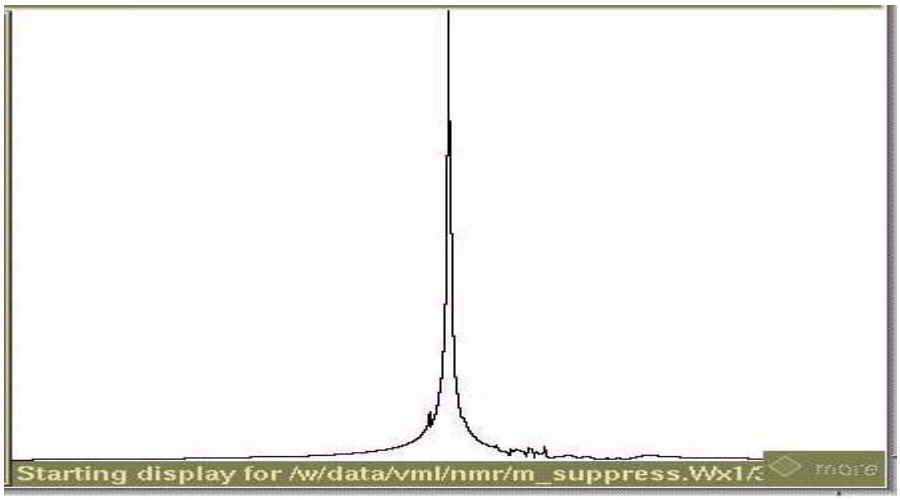


Figure 11.11.Spectrum from an Oil/water sample,with Oil Supression



Methods 12

Overview 12.1

The first part of this chapter ***12.1.1***, ***"Methods Under PVM Control"*** contains a list of the methods, which are available under PVM control. Additional methods might be available, which are not yet mentioned here, because they might be brand new. Ask the micro-imaging application group for more information, if you need a special method.

The second part ***12.1.2*** ***"Activation of Methods Under PVM Control"*** describes the steps, that are involved in using the individual methods. Most of such steps are always the same, independent of the selected method, e.g. creation of a new data set, parameter editing, parameter optimization and data acquisition.

The individual methods are described in detail from chapter ***12.4*** on.

Methods Under PVM Control 12.1.1

m_gefi acquires gradient echo recalled 2D data sets. The method is used for fast experiments using small flip angle excitations. This allows fast imaging acquisitions without running into saturation problems, but it is sensitive to local susceptibility changes in the sample.

m_ge3d acquires gradient echo recalled 3D data sets. The method is used for fast experiments using small flip angle excitations. This allows fast imaging acquisitions without running into saturation problems, but it is sensitive to local susceptibility changes in the sample.

m_msme acquires 2D single or multi-slice, multi-echo, and 3D spin echo images. The method is used for high contrast or highest resolution images on samples with a T2 relaxation time down to a few milliseconds. A fast repetition causes saturation but may result in good T1 contrast.

m_msmevtr acquires 2D multi-slice images with different echo times and repetition times in one experiment. The method is used to check the parameters for the best image contrast.

m_chess acquires 2D and 3D images, where only one spectral component is selectively excited. The method is used for chemical shift selective imaging studies, e.g. pure fat or pure water images.

m_se3d acquires 3D spin echo images. The method is used for highest resolution images on samples with a T2 relaxation time down to a few milliseconds. A fast repetition causes saturation but may result in good T1 contrast.

m_rare acquires 2D or 3D spin echo images, where more than one echoes are individually phase encoded. The methods results in T2 weighted images and the acquisition time gets shortened compared to standard spin echo methods.

m_spi acquires 2D and 3D images from samples with very short T2 or T2* relaxation times (approximately 50 μs to 1 ms). The method is known as Single Point

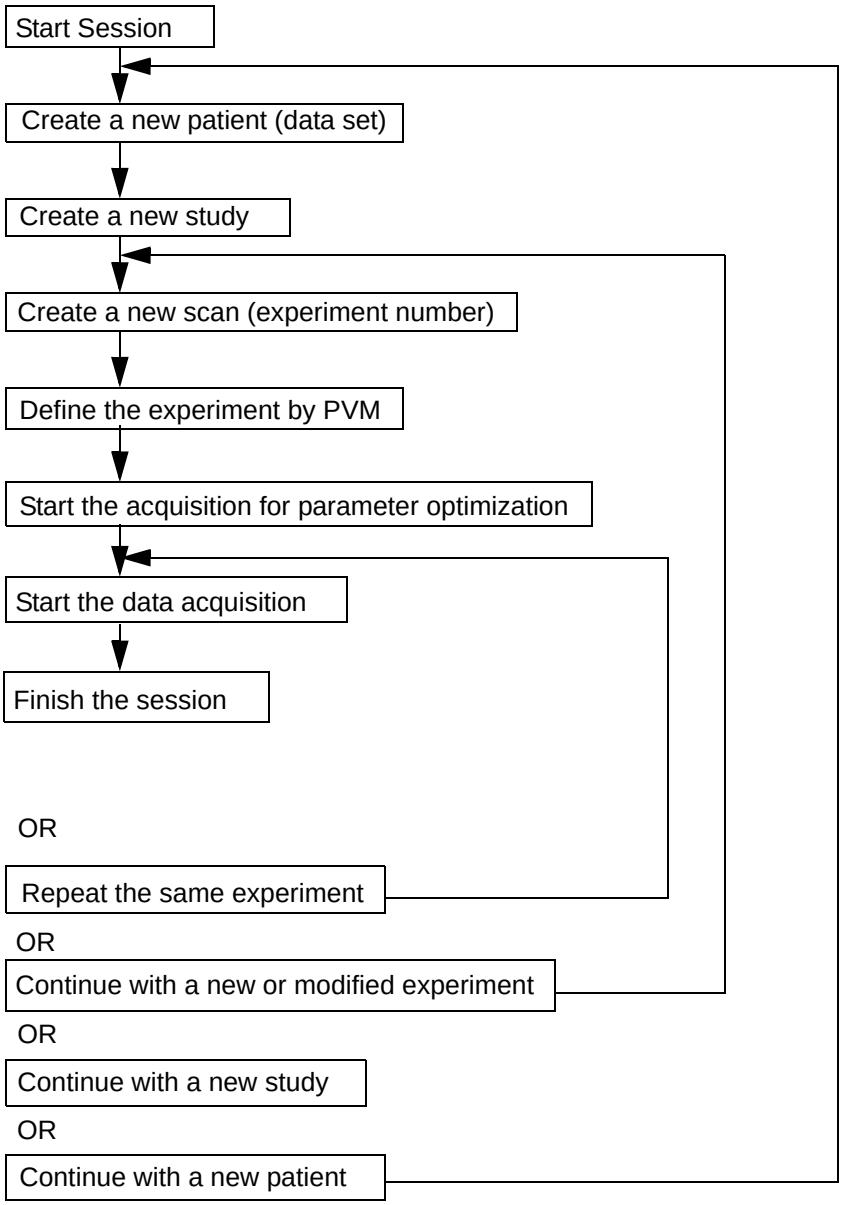
Imaging or Constant Time Imaging. Each complex time domain data point is collected after a individual excitation (external address advance mode). Therefore the experiment time is very long.

m_profile acquires intensity profiles from the entire object or profiles of higher precision, where only a stick from the sample is excited by applying selective RF-pulses together with slice gradients.

m_vselse acquires spectra from localized volumes in an object. The method uses a 90° - 180° - 180° rf pulse sequence.

Activation of Methods Under PVM Control *12.1.2*

Whenever a single experiment or a series of experiments is performed, a data set name has to be defined. Study numbers, experiment numbers and processing numbers must be created for the storage of the experimental parameters and data. Then the method is loaded, the method parameters are edited and some parameters are optimized in a set up acquisition mode (GSP). Finally the experiment is started (GOP). Further experiments can follow as shown in the flow chart below.



The individual steps are described in the following section:

Note: ParaVision considers all objects as patients. They might have a sex, a weight, head and feet, even when they are stones, wood, polymers, plants or liquids.

- Create a new patient.

  Click ***New Patient*** in the ***ParaVisionScanControl*** window and enter a Name (e.g. Jumping Jack) and a Registration (e.g. Jack). Quit the menu with ***Accept***.

  Enter in the now appearing Study Editor window a Study (e.g. brainpower) and quit the menu by ***Accept***.

  Select a PVM protocol in the now appearing Protocols window or quit the now appearing window by ***Cancel*** and load the PVM method later.

  A data set with the name Jack, Jumping 1:1:1 is created and visible as new entry in the ***ParaVisionScanControl*** list.

  Continue with „Define the experiment by PVM“.

- Create a new study.

  Click ***New Study*** in the ***ParaVisionScanControl*** window and enter a Study (e.g. leg) and quit the menu by ***Accept***.

  Select a PVM protocol in the now appearing Protocols window or quit the now appearing window by ***Cancel*** and load the PVM method later.

  A data set e.g. with the name Jack, Jumping 2:1:1 is created and visible as new entry in the ***ParaVisionScanControl*** list. The first number e.g. 2 indicates study number 2.

  Continue with „Define the experiment by PVM“.

- Create a new scan (experiment).

  Click ***New Scan*** in the ***ParaVisionScanControl*** window. Select a PVM protocol in the now appearing Protocols window or quit the now appearing window by ***Cancel*** and load the PVM method later.

  A data set e.g. with the name Jack, Jumping 2:2:1 is created and visible as new entry in the ***ParaVisionScanControl*** list. The second number e.g. 2 indicates experiment number 2.

- Define the experiment by PVM.

  Click the ***EditPVM button*** (see also), load the method and set the parameters to the appropriate values as described in the following chapters for the individual methods.

  Check the methods parameters by the ***PulseProgramTool*** in ***Tools*** of the ***ParaVisionSpectrometerControlTool*** window.

- Start the acquisition for parameter optimization.

  Click the GSP Button in the ***ParaVisionSpectrometerControlTool*** and optimize some acquisition parameters under slider control, e.g. ***Receiver Gain***, rf pulse attenuations (***TX Attenuator 0, TX Attenuator 1***,...). Observe the time and frequency domain FID’s, echoes, spectra or profiles in the now appearing AcqDisplay and RecoDisplay windows. Stop the acquisition by the ***STOP*** button in the ***ParaVisionSpectrometerControlTool*** window.

The most important parameters for the acqDisplay and recoDispay windows are set by clicking the ***Edit GS*** button in the ***SpectrometerControlTool*** window. Some recommended values are shown in the following table.

Parameter	Value
Set up dimension	1
Update of display	Each PE step
Steady state adjustment	Yes
Online reconstruction	Yes
Reco display	Yes
Output image type	Magnitude image
Calculate receiver offset	Yes
Calculate digitizer filling factor	Yes
Calculate normalized area	Of raw data

Then the FID's or echoes and the corresponding profiles e.g. for the individual slices are shown in the Display windows.

- Start the data acquisition.

  Click the GoP Button in the ***ParaVisionSpectrometerControlTool*** to start with the data acquisition.

- Finish the session.

  Wait until the acquisition is finished or stop the acquisition by the ***STOP*** button in the ***ParaVisionSpectrometerControlTool*** window, when the acquisition should be aborted.

- Repeat the same experiment.

  The experiment with exactly the same parameters can be repeated under a new experiment (scan) number. Select the experiment by moving the mouse cursor to the line of the current data set in the ***ParaVisionScanControl*** window and by clicking the ***left*** mouse button. Then the line gets highlighted. Click now the ***right*** mouse button and select ***Clone Scan***. A new experiment (scan) number is created. Continue with ***GOP***.

- Continue with a new or modified experiment.

  A new experiment with similar parameters can be repeated or with a completely new method can be made under a new experiment (scan) number. Select the experiment by moving the mouse cursor to the line of the current data set in the ***ParaVisionScanControl*** window and by clicking the ***left*** mouse button. Then the line gets highlighted. Click now the ***right*** mouse button and select ***Clone Scan***. A new experiment (scan) number is created. Continue as described under „Define the experiment by PVM".

- Continue with a new study.

  A new study can be created, when another method is applied or when other regions of the object are studied. Continue as described under „Create a new study“.

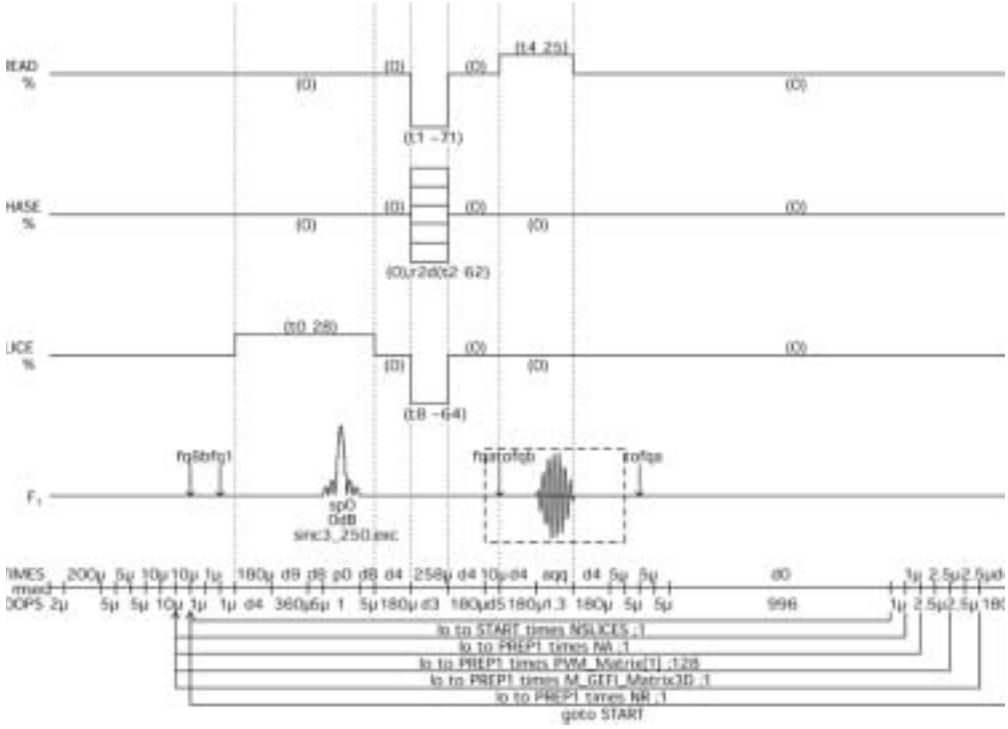
- Continue with a new patient.

  A new data set can be created, if a new object or sample is investigated. Continue as described under „Create a new patient“.

Gradient echo fast imaging (m_gefi) *12.2*

m_gefi acquires gradient echo recalled 2D single or multi-slice images. The method is used for fast experiments using small flip angle excitations. This allows fast imaging acquisitions without running into saturation problems. Larger flip angles may result in improved T1 contrast on heterogeneous objects. The method is sensitive to local susceptibility changes in the sample, which can reduce image resolution.

Figure 12.1. m_gefi method



Typical parameters are described in the following table.

Table 12.1. Typical Gradient Echo Fast Imaging Parameters

Parameter	Value
Measuring Method	m_gefi.
Acquisition Dimension	_2D.
Matrix Isotropy	Matrix_Isotropic.
Matrix Size	e.g.128 x 128.
Effective Spectral Bandwidth	e.g. 100000 Hz.
Echo Time Mode	Min_EchoTime for short echo times, or Read_Dephase_aq_2 for longer echo times, or User_def_EchoTime.
Echo Time	e.g. 10 ms for User_def_EchoTime.
Repetition Time	e.g. 100 ms.
Number of Averages	e.g. 2.
Estimated total scan time	Is set by ParaVision.
rfPulse	Expand.
RF-pulse Shape for Excitation	Select the rf pulse shape, e.g. sinc3_250.
RF-Excitation Pulse Shape File	Expand.
.filename	Pulse shape file name e.g.sinc3_250.exc.
.length	Duration of excitation rf pulse, e.g. 1 ms.
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision.
.attenuation	Attenuation for rf pulse, can be modified under slider control.
.flipangle	e.g. is applied only, if derive pulse gains is activated.
.properties	Contains information about pulse properties.
Geometry	Expand.
Geo Isotropy	FOV_Isotropic for isotropic Field of View, or Res_Isotropic for isotropic resolution, or Non_Isotropic_Geo when FOV and Resolution should be set independently.
Patient Position	Is defined during creation of a new data set, e.g. by new patient or new study etc.
Field of View	Field of View according to the size of the subject.
Spatial Resolution	Is set by PVM.
Slice Thickness	Slice thickness e.g. 1 mm.

Table 12.1. Typical Gradient Echo Fast Imaging Parameters

Parameter	Value
Number of Slice Packages	One or more individual slice pack-ages can be defined, where each package has its own number of slices and slice orientation.
Object ordering mode	Sequential or Reverse_sequential, when one after the other neighboring slices are excited starting from the first or last slice respectively. Interlaced or Reverse_interlaced when first the odd and then the even numbered slices are excited starting from the first or last slice respectively. User_defined when slices are excited according to a user defined sequence.
Anti Aliasing Factor	When more than the specified data points have to be acquired for later processing. It should be 1 as default value.
Slice Package Properties	Expand (only available if a selective excitation pulse is used)
Which Slice Package	Specify the one for the following parameter set up (only available if a selective excitation pulse is used)
Package orientation	Axial, sagittal or coronal.
Package Read Orientation	L_R for left right. A_P for anterior posterior. H_F for head foot.
Slice Angle LH Slice Angle AH Read Angle Package Read Offset Package Phase1Offset Package Phase2Offset	These parameters should be set by the Pilot Scan User Interface, when selective pulses are used instead of the default non selective pulses. They can be set to zero as default.
Method Customization	Expand.
Nucleus	e.g. _1H for protons.
bf1	Basic frequency, e.g. 300.13.
Rewind phase gradient	Yes, if a phase unwind gradient should be applied.
Number of Dummy Scans	Number of Dummy Scans before the data acquisition starts.
Phase encoding mode	Read for the read gradient (dimension 1). Linear for the phase encoding Gradient, where the ramp starts at -1. Centered for the phase encoding gradient. where the ramp starts at 0. User_defined_encoding for a user defined phase encoding gradient list.
Phase encoding start	Start of the phase encoding gradient ramps (-1 to 1).
ConfigTiming	Expand.

Table 12.1. Typical Gradient Echo Fast Imaging Parameters

Parameter	Value
SliceRephaseTime	Is set by PVM, according to the read dephase time.
ReadDephaseTime	Is set by PVM, except, when EchoTImeMode is set to User_def_echo_time.
PhaseEncodingTime	Is set by PVM, according to the read dephase time.
Match Pulse Bandwidth	Yes, when the duration of the RF-pulses should be modified, so that the bandwidth is exactly the same for all RF-pulses. No as default. Then the gradient amplitudes e.g. for the slice gradients are matched according to the RF-pulse bandwidth.
Derive Pulse Gains	Yes, when the pulse gains should automatically be set, according to the set up information, gathered by using the traffic light of by using Auto_RFGain in the Acq menu. No, when the pulses should be adjusted under slider control during GSP.
Config Gradients	Expand.
R, P and S Gradient Limit Mode	Fixed Limit in percent, when a limit for the gradient amplitude should be used. Fixed Single Oblique, (square root of 2), when the image geometry must not be distorted in oblique image orientations. Fixed Double Oblique, (square root of 3), when the image geometry must not be distorted in double oblique image orientations.
R, P and S Gradient Limits	Gradient Limits with the maximum gradient values, when Fixed Limit mode is selected.
Image spoiler	Expand for spoiler gradients before and after the 180° pulse.
Image spoiler direction	Various directions and combinations for the spoiler gradient.
Image spoiler length	Duration of the spoiler gradient.
Image spoiler amplitude	Amplitude of the spoiler gradient.
Modules	Expand.
ECG	For ECG trigger parameters.
Image gradient spoiling	For spoiler gradients before and after the scans.
Info	Is set by ParaVision.

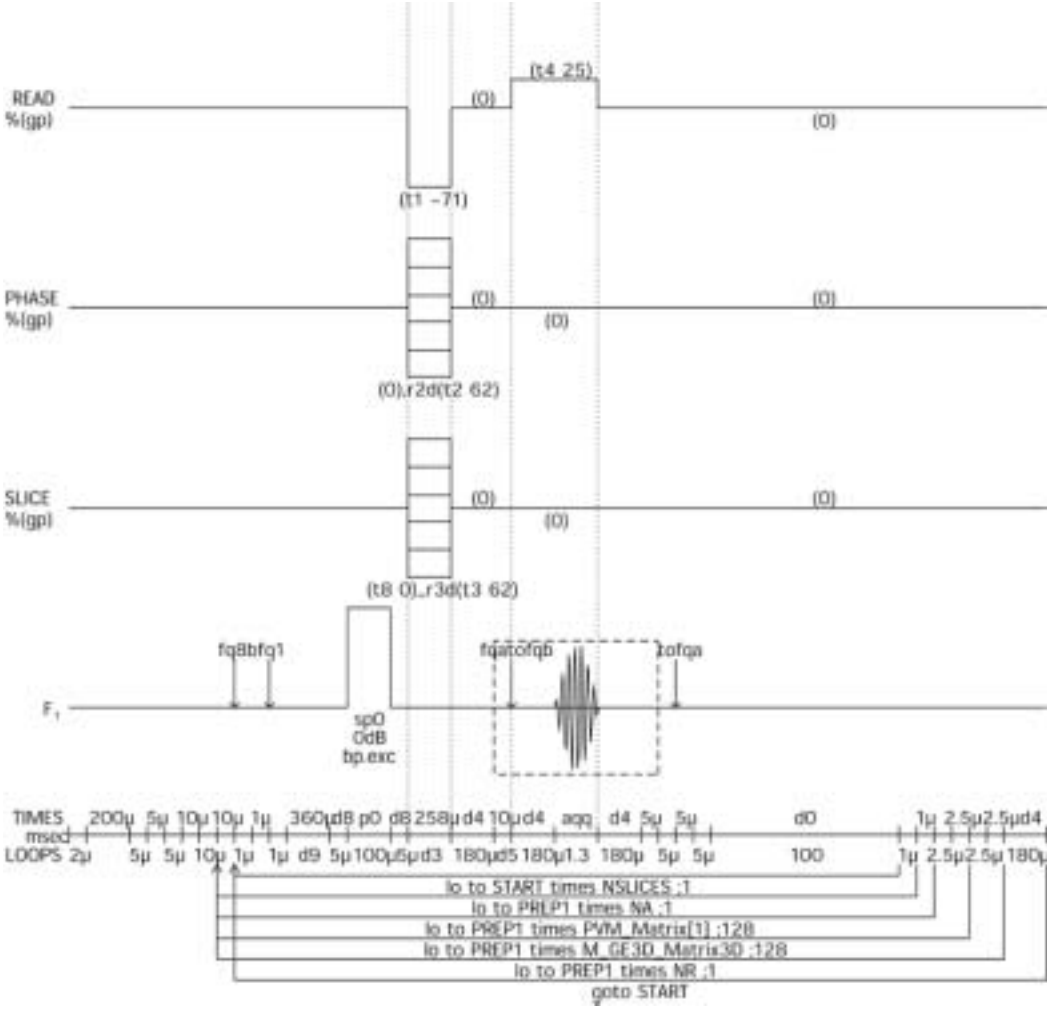
Start the acquisition with ***GSP*** to optimize the RF-pulse attenuations (Tx Attenuator 0) and Receiver Gain.

Start the image acquisition with ***GOP***.

Gradient Echo 3D Imaging (m_ge3d) *12.3*

m_ge3d acquires gradient echo recalled 3D data sets. The method is used for fast experiments using small flip angle excitations. This allows fast imaging acquisitions without running into saturation problems. Larger flip angles may result in improved T1 contrast on heterogeneous objects. The method is sensitive to local susceptibility changes in the sample, which can reduce image resolution.

Figure 12.2. m_gefi method m_ge3d.ppg.eps



Typical parameters are described in the following table.

Table 12.2. Typical Gradient Echo 3D Imaging Parameters

Parameter	Value
Measuring Method	m_gefi.
Acquisition Dimension	_3D.
Matrix Isotropy	Matrix_Isotropic.
Matrix Size	e.g.128 x 128 x 128.
Effective Spectral Bandwidth	e.g. 100000 Hz.
Echo Time Mode	Min_EchoTime for short echo times, or Read_Dephase_aq_2 for longer echo times, or User_def_EchoTime.
Echo Time	e.g. 5 ms for User_def_EchoTime.
Repetition Time	e.g. 100 ms.
Number of Averages	e.g. 2.
Estimated total scan time	Is set by ParaVision.
rfPulse	Expand.
RF-pulse Shape for Excitation	Select the rf pulse shape, e.g. bp.
RF-Excitation Pulse Shape File	Expand.
.filename	Pulse shape file name e.g. bp.exc.
.length	Duration of excitation rf pulse, e.g. 0.01 ms.
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision
.attenuation	Attenuation for rf pulse, can be modified under slider control.
.flipangle	e.g. is applied only, if derive pulse gains is activated.
.properties	Contains information about pulse properties.
Geometry	Expand.
Geo Isotropy	FOV_Isotropic for isotropic Field of View, or Res_Isotropic for isotropic resolution, or Non_Isotropic_Geo when FOV and Resolution should be set independently.
Patient Position	Is defined during creation of a new data set, e.g. by new patient or new study etc.
Field of View	Field of View according to the size of the subject.
Spatial Resolution	Is set by PVM.
Anti Aliasing Factor	When more than the specified data points have to be acquired for later processing. It should be 1 as default value.

Table 12.2. Typical Gradient Echo 3D Imaging Parameters

Parameter	Value
Slice Package Properties	Expand (only available if a selective excitation pulse is used).
Which Slice Package	Specify the one for the following parameter set up (only available if a selective excitation pulse is used).
Package orientation	Axial, sagittal or coronal.
Package Read Orientation	L_R for left right. A_P for anterior posterior. H_F for head foot.
Method Customization	Expand.
Nucleus	e.g. _1H for protons.
bf1	Basic frequency, e.g. 300.13.
Rewind phase gradient	Yes, if a phase unwind gradient should be applied.
Number of Dummy Scans	Number of Dummy Scans before the data acquisition starts.
Phase encoding mode	Read for the read gradient (dimension 1). Linear for the phase encoding Gradient, where the ramp starts at -1. Centered for the phase encoding gradient, where the ramp starts at 0. User_defined_encoding for a user defined phase encoding gradient list.
Phase encoding start	Start of the phase encoding gradient ramps (-1 to 1).
ConfigTiming	Expand
SliceRephaseTime	Is set by PVM, according to the read dephase time.
ReadDephaseTime	Is set by PVM, except, when EchoTImeMode is set to User_def_echo_time.
PhaseEncodingTime	Is set by PVM, according to the read dephase time.
Match Pulse Bandwidth	Yes, when the duration of the RF-pulses should be modified, so that the bandwidth is exactly the same for all RF-pulses. No as default. Then the gradient amplitudes e.g. for the slice gradients are matched according to the RF-pulse bandwidth.
Derive Pulse Gains	Yes, when the pulse gains should automatically be set, according to the set up information, gathered by using the traffic light of by using Auto_RFGain in the Acq menu. No, when the pulses should be adjusted under slider control during GSP.
Config Gradients	Expand.

Table 12.2. Typical Gradient Echo 3D Imaging Parameters

Parameter	Value
R, P and S Gradient Limit Mode	Fixed Limit in percent, when a limit for the gradient amplitude should be used. Fixed Single Oblique, (square root of 2), when the image geometry must not be distorted in oblique image orientations. Fixed Double Oblique, (square root of 3), when the image geometry must not be distorted in double oblique image orientations.
R, P and S Gradient Limits	Gradient Limits with the maximum gradient values, when Fixed Limit mode is selected.
Image spoiler	Expand for spoiler gradients before and after the 180° pulse.
Image spoiler direction	Various directions and combinations for the spoiler gradient.
Image spoiler length	Duration of the spoiler gradient.
Image spoiler amplitude	Amplitude of the spoiler gradient.
Modules	Expand.
ECG	For ECG trigger parameters.
Image gradient spoiling	For spoiler gradients before and after the scans.
Info	Is set by ParaVision.

Start the acquisition with ***GSP*** to optimize the RF-pulse attenuations (Tx Attenuator 0) and Receiver Gain.

Start the image acquisition with ***GOP***.

Multi-slice Multi-echo (m_msme) *12.4*

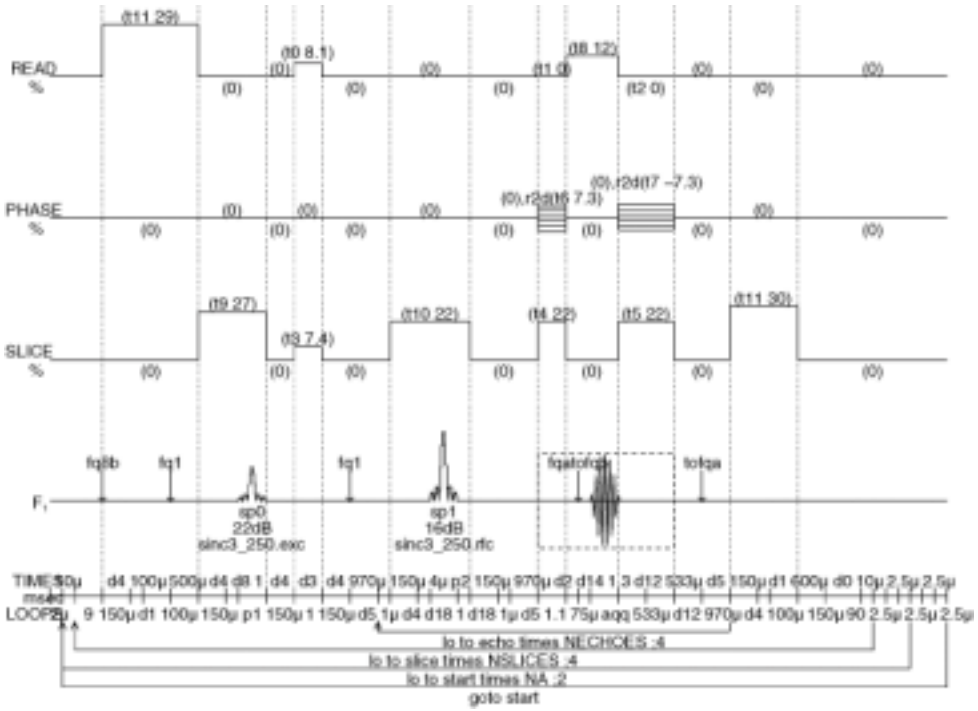
m_msme acquires 2D single or multi-slice, multi-echo and 3D spin echo images. The method is used for high contrast or highest resolution images on samples with a T2 relaxation time down to a few milliseconds. A fast repetition causes saturation but may result in good T1 contrast. Selective (shaped) or rectangular (hard) RF-pulses can be used for excitation and refocusing. The magnetization of the individual slices is excited by 90 degree RF-pulses and refocused by 180 degree RF-pulses. More than one echo can be obtained, when several 180 pulses are applied after the 90 degree pulse.

The different possibilities are described in the following section.

Multi-slice Multi-echo Images with Selective RF-Pulses *12.4.1*

The magnetization of the individual slices is excited by selective 90 degree RF-pulses and refocused by selective 180 RF-pulses. More than one echo can be obtained, when several 180 pulses are applied after the 90 degree pulse.

Figure 12.3. m_msme Method with Selective Excitation & Refocusing RF-pulses



Typical parameters are described in the following table.

Table 12.3. m_msme Parameters (selective RF-pulses)

Parameter	Value
Measuring Method	m_msme.
Acquisition Dimension	_2D.
Matrix Isotropy	Matrix_Isotropic.
Matrix Size	128.
Effective Spectral Bandwidth	100000 Hz.
Echo Time Mode	Min_EchoTime for short echo times, or Read_Dephase_aq_2 for longer echo times, or User_def_EchoTime
Echo Time	e.g. 10 ms for User_def_EchoTime.
Repetition Time	e.g. 1000 ms.

Table 12.3. m_msme Parameters (selective RF-pulses)

Parameter	Value
Number of Averages	e.g. 2.
Estimated total scan time	Is set by ParaVision.
RF-pulse	Expand.
Match pulse bandwidth	No.
RF-pulse Shape for Excitation	Select the RF-pulse shape, e.g. sinc3_250.
RF-Excitation Pulse Shape File	Expand.
.filename	Pulse shape file name e.g. sinc3_250.exc.
.length	Duration of 90° rf pulse in ms.
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision.
.attenuation	Attenuation for 90° pulse, can be modified under slider control.
.flipangle	e.g. is applied only, if derive pulse gains is activated.
.properties	Contains information about pulse properties.
RF-pulse Shape for refocusing	Select the rf pulse shape, e.g. sinc3_250.rfc.
RF-Refocusing Pulse Shape File	Expand.
.filename	Pulse shape file name e.g. sinc3_250.rfc.
.length	Duration of 180° rf pulse in ms.
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision.
.attenuation	Attenuation for 180° pulse, can be modified under slider control.
.flipangle	e.g. is applied only, if derive pulse gains is activated.
.properties	Contains information about pulse properties.
Geometry	Expand.
Geo Isotropy	FOV_Isotropic for isotropic Field of View, or Res_Isotropic for isotropic resolution, or Non_Isotropic_Geo when FOV and resolution should be set independently
Patient Position	Is defined during creation of a new data set, e.g. by a new patient or a new study, etc.
Field of View	Field of View according to the size of the subject.
Spatial Resolution	Is set by PVM.
Slice Thickness	Slice thickness.

Table 12.3. m_msme Parameters (selective RF-pulses)

Parameter	Value
Number of Slice Packages	One or more individual slice pack-ages can be defined, where each package has its own number of slices and slice orientation.
Object ordering mode	Sequential or Reverse_sequential, when one after the other neighboring slices are excited starting from the first or last slice respectively. Interlaced or Reverse_interlaced when first the odd and then the even numbered slices are excited starting from the first or last slice respectively. User_defined when slices are excited according to a user defined sequence.
Anti Aliasing Factor	When more than the specified data points have to be acquired for later processing. It should be 1 as default value.
Slice Package Properties	Expand.
Which Slice Package	Specify the one for the following parameter set up.
Number of Slices in Package	Number of slices.
Package orientation	Axial, sagittal or coronal.
Package Read Orientation	L_R for left right. A_P for anterior posterior. H_F for head foot.
Slice Angle LH Slice Angle AH Read Angle Package Slice Offset Package Read Offset Package Phase1 Offset	These parameters should be set by the Pilot Scan User Interface. They can be set to zero as default.
Echo Customization	Expand
Number of Echoes	Number of Echoes
Number of echo images	An image is reconstructed from each individual echo, when this parameter is the same as the number of echoes. Some echoes can be added to result in the same image, when this parameter smaller than the number of echoes.
Scan list	Defines, how many echoes are summarized to the individual images.
Method Customization	Expand
Nucleus	e.g. _1H for protons
bf1	Basic frequency, e.g. 300.13
Flip-back enable	Yes, when a 180° and a 90° RF-pulse should be applied after the acquisition of each scan.
Number of Dummy Scans	Number of Dummy Scans before the data acquisition starts.

Table 12.3. m_msme Parameters (selective RF-pulses)

Parameter	Value
Phase encoding mode	Read for the read gradient (dimension 1). Linear for the phase encoding Gradient, where the ramp starts at -1. Centred for the phase encoding gradient, where the ramp starts at 0. User_defined_encoding for a user defined phase encoding gradient list.
Phase encoding start	Start of the phase encoding gradient ramps (-1 to 1).
ConfigTiming	Expand
SliceRephaseTime	Is set by PVM, according to the read dephase time
ReadDephaseTime	Is set by PVM, except, when EchoTImeMode is set to User_def_echo_time
PhaseEncodingTime	Is set by PVM, according to the read dephase time
Match Pulse Bandwidth	Yes, when the duration of the RF-pulses should be modified, so that the bandwidth is exactly the same for all RF-pulses. No as default. Then the gradient amplitudes e.g. for the slice gradients are matched according to the RF-pulse bandwidths.
Derive Pulse Gains	Yes, when the pulse gains should automatically be set, according to the set up information, gathered by using the traffic light of by using Auto_RFGain in the Acq menu. No, when the pulses should be adjusted under slider control during GSP.
Config Gradients	Expand
R, P and S Gradient Limit Mode	Fixed Limit in percent, when a limit for the gradient amplitude should be used. Fixed Single Oblique, (square root of 2), when the image geometry must not be distorted in oblique image orientations. Fixed Double Oblique, (square root of 3), when the image geometry must not be distorted in double oblique image orientations.
R, P and S Gradient Limits	Gradient Limits with the maximum gradient values, when Fixed Limit mode is selected.
Image spoiler	Expand for spoiler gradients before and after the 180° pulse.
Image spoiler direction	Various directions and combinations for the spoiler gradient.
Image spoiler length	Duration of the spoiler gradient.
Image spoiler amplitude	Amplitude of the spoiler gradient.
Modules	Expand.
ECG	For ECG trigger parameters.

Table 12.3. m_msme Parameters (selective RF-pulses)

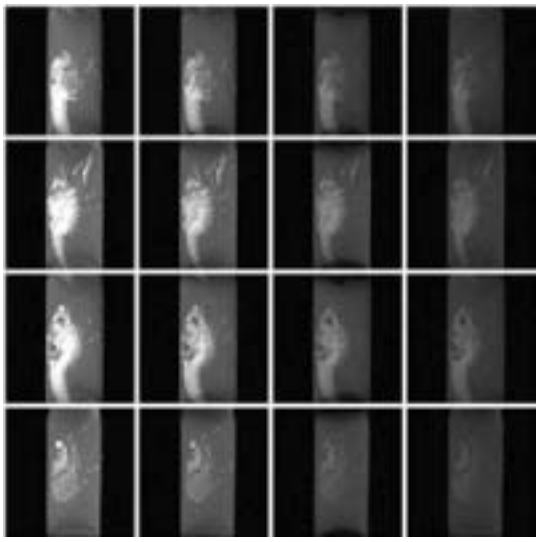
Parameter	Value
Image gradient spoiling	For spoiler gradients before and after the scans.
Info	Is set by ParaVision.

These parameters produce a image data set of 4 slices and 4 echoes respectively as shown in the following figure.

Start the acquisition with ***GSP*** to optimize the RF-pulse attenuations (Tx Attenuator 0, Tx Attenuator1) and Receiver Gain.

Start the image acquisition with ***GOP***.

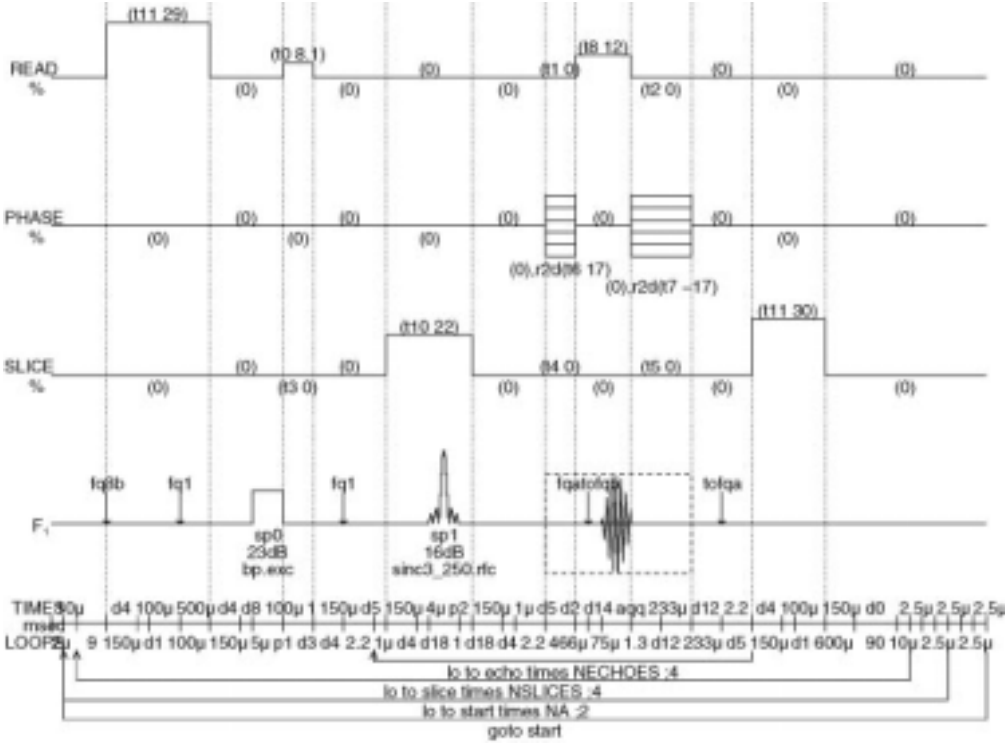
Figure 12.4. Multi-slice, Multi-echo Images from a Prawn.



Images with Selective and Non-selective RF-pulses *12.4.2*

For some applications with short T2 samples is it useful to acquire images with the shortest possible echo times. Such experiments are possible just by replacing one of the selective 90° and 180° RF-pulses in the m_msme method a non selective RF-pulse and by setting the number of slices to one.

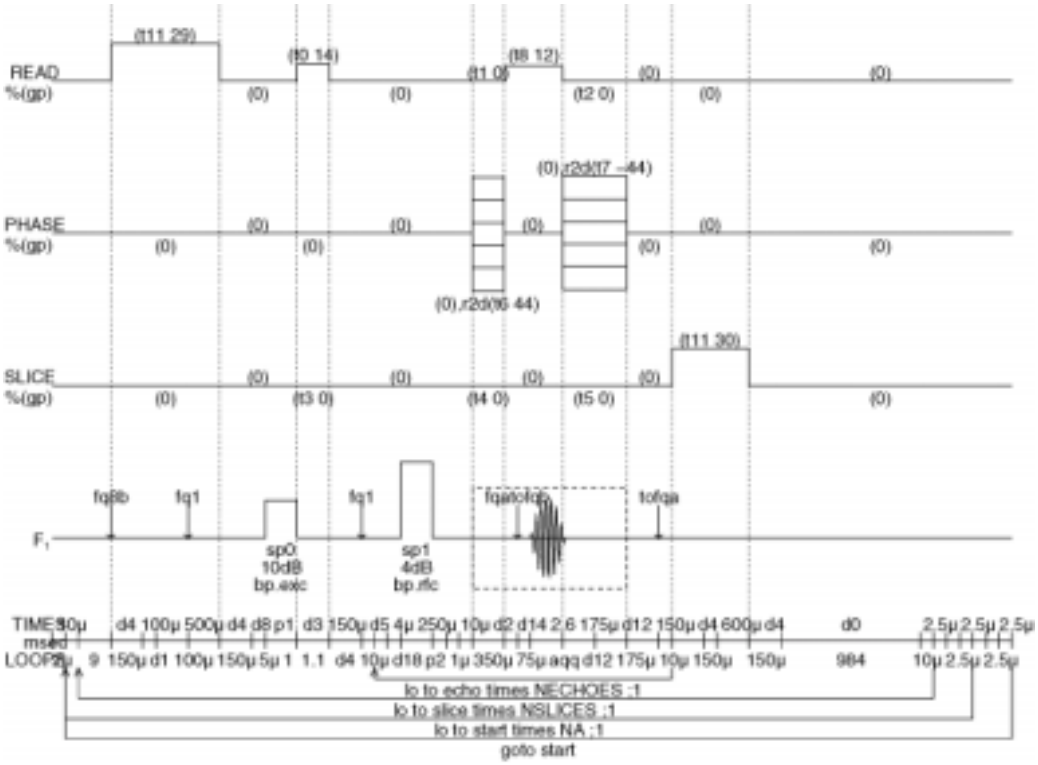
Figure 12.5. m_msme, Non-selective Excitation & Selective Refocusing Rf Pulses



Two Dimensional Images without Slice Selection *12.4.3*

For some applications is it useful to acquire images without slice selection (or with infinite slice thickness). Such experiments are possible just by replacing the selective 90° and 180° RF-pulses in the m_msme method by non selective RF-pulses and by setting the number of slices to one.

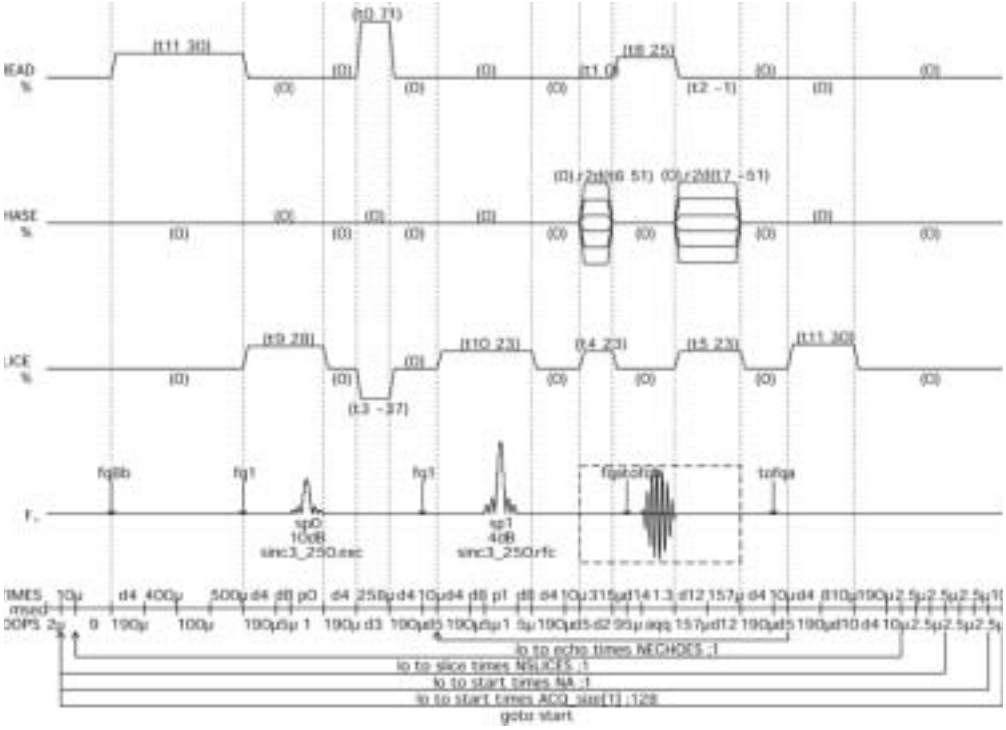
Figure 12.6. m_msme method without slice selection



Multi-slice, Multi-echo, Variable TR (m_msmevtr) *12.5*

m_msmevtr acquires 2D single or multi-slice spin echo images with different echo times and different repetition times in one series of experiments. The method is used to determine the parameters (TE, TR) for the best image contrast. It is recommended to use e.g. a series of a single slice, 8 different repetition times and 8 echoes per repetition time. This results in 8 x 8 images. The number of images and the range of TE and TR depends of course on the magnetic field strength and the properties of the sample.

Figure 12.7. m_msmevtr Method m_msmevtr.ppg.eps



Typical parameters are described in the following table.

Table 12.4. m_msme parameters (selective RF-pulses)

Parameter	Value
Measuring Method	m_msmevtr.
Matrix Isotropy	Matrix_Isotropic.
Matrix Size	128 x 128.
Effective Spectral Bandwidth	100000 Hz.
Echo Time Mode	Min_EchoTime for short echo times, or Read_Dephase_aq_2 for longer echo times, or User_def_EchoTime
Echo Time	e.g. 10 ms for User_def_EchoTime.
Number of RepDelays	Number of the experiments with different repetition times, e.g. 8.
TR list	Repetition times for the individual experiments in ms, e.g. 100, 200, 300, 400, 500, 700, 1000, 2000.
Number of Averages	e.g. 2.
GS Info	Displays the value of TR, that is used for the set up mode (GSP).
Estimated total scan time	Is set by ParaVision.
RF-Pulse	Expand.
Match pulse bandwidth	No.

Table 12.4. m_msme parameters (selective RF-pulses)

Parameter	Value
RF-pulse Shape for Excitation	Select the RF-pulse shape, e.g. sinc3_250.
RF-Excitation Pulse Shape File	Expand.
.filename	Pulse shape file name e.g. sinc3_250.exc.
.length	Duration of 90° rf pulse in ms.
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision.
.attenuation	Attenuation for 90° pulse, can be modified under slider control.
.flipangle	e.g. is applied only, if derive pulse gains is activated.
.properties	Contains information about pulse properties.
RF-pulse Shape for refocusing	Select the rf pulse shape, e.g. sinc3_250.rfc.
RF-Refocusing Pulse Shape File	Expand.
.filename	Pulse shape file name e.g. sinc3_250.rfc.
.length	Duration of 180° rf pulse in ms.
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision
.attenuation	Attenuation for 180° pulse, can be modified under slider control.
.flipangle	e.g. is applied only, if derive pulse gains is activated.
.properties	Contains information about pulse properties.
Geometry	Expand.
Geo Isotropy	FOV_Isotropic for isotropic Field of View, or Res_Isotropic for isotropic resolution, or Non_Isotropic_Geo when FOV and resolution should be set independently.
Patient Position	Is defined during creation of a new data set, e.g. by new patient or new study etc.
Field of View	Field of View according to the size of the subject.
Spatial Resolution	Is set by PVM.
Slice Thickness	Slice thickness.
Number of Slice Packages	One or more individual slice pack-ages can be defined, where each package has its own number of slices and slice orientation.

Table 12.4. m_msme parameters (selective RF-pulses)

Parameter	Value
Object ordering mode	Sequential or Reverse_sequential, when one after the other neighboring slices are excited starting from the first or last slice respectively. Interlaced or Reverse_interlaced when first the odd and then the even numbered slices are excited starting from the first or last slice respectively. User_defined when slices are excited according to a user defined sequence.
Anti Aliasing Factor	When more than the specified data points have to be acquired for later processing. It should be 1 as default value.
Slice Package Properties	Expand.
Which Slice Package	Specify the one for the following parameter set up.
Number of Slices in Package	Number of slices, e.g. 1.
Package orientation	Axial, sagittal or coronal.
Package Read Orientation	L_R for left right. A_P for anterior posterior. H_F for head foot.
Slice Angle LH Slice Angle AH Read Angle Package Slice Offset Package Read Offset Package Phase1 Offset	These parameters should be set by the Pilot Scan User Interface. They can be set to zero as default.
Echo Customization	Expand.
Number of Echoes	Number of Echoes, e.g. 8.
Number of echo images	An image is reconstructed from each individual echo, when this parameter is the same as the number of echoes. Some echoes can be added to result in the same image, when this parameter smaller than the number of echoes.
Scan list	Defines, how many echoes are summarized to the individual images.
Method Customization	Expand.
Nucleus	e.g. _1H for protons
bf1	Basic frequency, e.g. 300.13.
Flip-back enable	Yes, when a 180° and a 90° RF-pulse should be applied after the acquisition of each scan.
Number of Dummy Scans	Number of Dummy Scans before the data acquisition starts.

Table 12.4. m_msme parameters (selective RF-pulses)

Parameter	Value
Phase encoding mode	Read for the read gradient (dimension 1). Linear for the phase encoding Gradient, where the ramp starts at -1. Centred for the phase encoding gradient, where the ramp starts at 0. User_defined_encoding for a user defined phase encoding gradient list.
Phase encoding start	Start of the phase encoding gradient ramps (-1 to 1).
ConfigTiming	Expand.
SliceRephaseTime	Is set by PVM, according to the read dephase time
ReadDephaseTime	Is set by PVM, except, when EchoTImeMode is set to User_def_echo_time
PhaseEncodingTime	Is set by PVM, according to the read dephase time
Match Pulse Bandwidth	Yes, when the duration of the RF-pulses should be modified, so that the bandwidth is exactly the same for all RF-pulses. No as default. Then the gradient amplitudes e.g. for the slice gradients are matched according to the RF-pulse bandwidths.
Derive Pulse Gains	Yes, when the pulse gains should automatically be set, according to the set up information, gathered by using the traffic light of by using Auto_RFGain in the Acq menu. No, when the pulses should be adjusted under slider control during GSP.
Config Gradients	Expand.
R, P and S Gradient Limit Mode	Fixed Limit in percent, when a limit for the gradient amplitude should be used. Fixed Single Oblique, (square root of 2), when the image geometry must not be distorted in oblique image orientations. Fixed Double Oblique, (square root of 3), when the image geometry must not be distorted in double oblique image orientations.
R, P and S Gradient Limits	Gradient Limits with the maximum gradient values, when Fixed Limit mode is selected.
Image spoiler	Expand for spoiler gradients before and after the 180° pulse.
Image spoiler direction	Various directions and combinations for the spoiler gradient.
Image spoiler length	Duration of the spoiler gradient.
Image spoiler amplitude	Amplitude of the spoiler gradient.
Modules	Expand.
ECG	For ECG trigger parameters.

Table 12.4. m_msme parameters (selective RF-pulses)

Parameter	Value
Image gradient spoiling	For spoiler gradients before and after the scans.
Info	Is set by ParaVision.

These parameters produce 8 x 8 images of the same slice, but with different repetition times and 8 echoes for each repetition time.

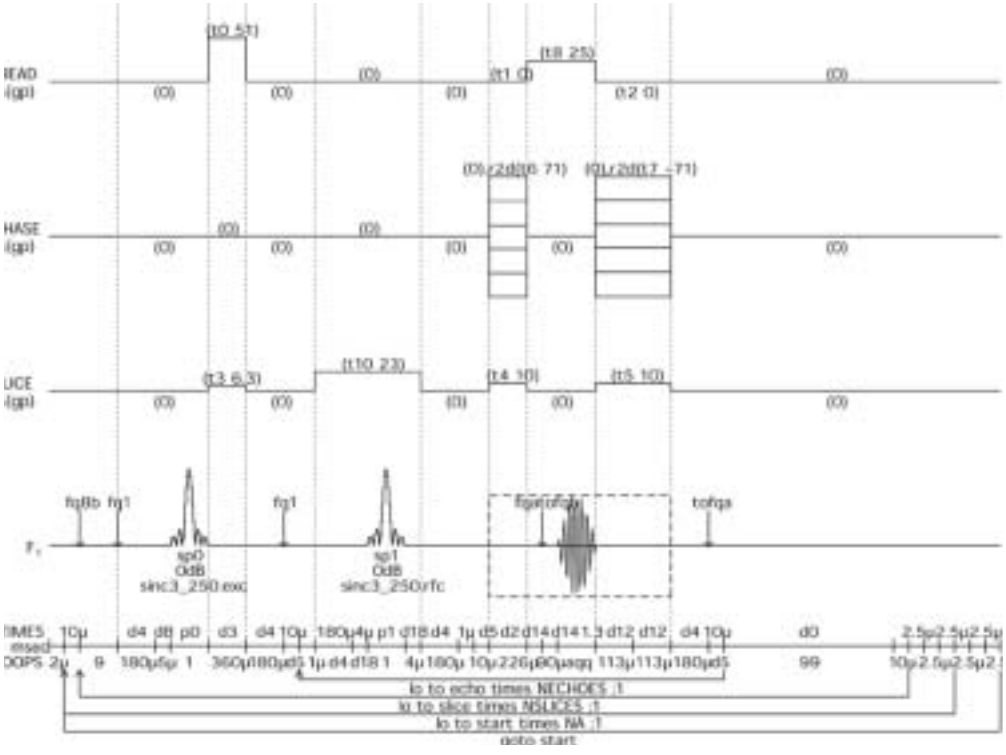
Start the acquisition with ***GSP*** to optimize the RF-pulse attenuations (Tx Attenuator 0, Tx Attenuator1) and Receiver Gain.

Start the image acquisition with ***GOP***.

Multi-slice, Multi-echo, Chemical Shift Selective (m_chess) 12.6

m_chess acquires 2D and 3D spin echo images, where only one spectral component (one resonance line) is selectively excited. The method is used for chemical shift selective imaging studies, e.g. pure fat or pure water images.

Figure 12.8. m_chess method m_chess.ppg



Typical parameters are described in the following table.

Table 12.5. m_chess Parameters (selective RF-pulses)

Parameter	Value
Measuring Method	m_chess.
Acquisition Dimension	_2D.
Matrix Isotropy	Matrix_Isotropic.
Matrix Size	128 x 128.
Effective Spectral Bandwidth	100000 Hz.
Echo Time Mode	Min_EchoTime for short echo times, or Read_Dephase_aq_2 for longer echo times, or User_def_EchoTime.
Echo Time	e.g. 10 ms for User_def_EchoTime.
Repetition Time	e.g. 1000 ms.
Number of Averages	e.g. 2.
Estimated total scan time	Is set by ParaVision.
rfPulse	Expand
Match pulse bandwidth	No.
RF-pulse Shape for Excitation	Select the rf pulse shape, e.g. sinc3_250.
RF-Excitation Pulse Shape File	Expand
.filename	Pulse shape file name e.g. sinc3_250.exc
.length	Duration of 90° rf pulse in ms
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision
.attenuation	Attenuation for 90° pulse, can be modified under slider control.
.flipangle	e.g. is applied only, if derive pulse gains is activated.
.properties	Contains information about pulse properties.
Excitation pulse offset	Frequency offset for the excitation RF-pulse, should be set e.g. to the resonance offset of the water or fat signal.
RF-pulse Shape for refocusing	Select the rf pulse shape, e.g. sinc3_250.rfc.
RF-Refocusing Pulse Shape File	Expand.
.filename	Pulse shape file name e.g. sinc3_250.rfc.
.length	Duration of 180° rf pulse in ms.
.bandwidth	is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision

Table 12.5. m_chess Parameters (selective RF-pulses)

Parameter	Value
.attenuation	Attenuation for 180° pulse, can be modified under slider control.
.flipangle	e.g. is applied only, if derive pulse gains is activated.
.properties	Contains information about pulse properties.
Geometry	Expand.
Geo Isotropy	FOV_Isotropic for isotropic Field of View, or Res_Isotropic for isotropic resolution, or Non_Isotropic_Geo when FOV and Resolution should be set independently.
Patient Position	Is defined during creation of a new data set, e.g. by new patient or new study etc.
Field of View	Field of View according to the size of the subject.
Spatial Resolution	Is set by PVM.
Slice Thickness	Slice thickness.
Number of Slice Packages	One or more individual slice pack-ages can be defined, where each package has its own number of slices and slice orientation.
Object ordering mode	Sequential or Reverse_sequential, when one after the other neighboring slices are excited starting from the first or last slice respectively. Interlaced or Reverse_interlaced when first the odd and then the even numbered slices are excited starting from the first or last slice respectively. User_defined when slices are excited according to a user defined sequence.
Anti Aliasing Factor	When more than the specified data points have to be acquired for later processing. It should be 1 as default value.
Slice Package Properties	Expand.
Which Slice Package	Specify the one for the following parameter set up.
Number of Slices in Package	Number of slices.
Package orientation	Axial, sagittal or coronal.
Package Read Orientation	L_R for left right. A_P for anterior posterior. H_F for head foot.
Slice Angle LH Slice Angle AH Read Angle Package Slice Offset Package Read Offset Package Phase1 Offset	These parameters should be set by the Pilot Scan User Interface. They can be set to zero as default.

Table 12.5. m_chess Parameters (selective RF-pulses)

Parameter	Value
Echo Customization	Expand.
Number of Echoes	Number of Echoes.
Number of echo images	An image is reconstructed from each individual echo, when this parameter is the same as the number of echoes. Some echoes can be added to result in the same image, when this parameter smaller than the number of echoes.
Scan list	Defines, how many echoes are summarized to the individual images.
Method customization	Expand.
Nucleus	e.g. _1H for protons.
bf1	Basic frequency, e.g. 300.13.
Flip-back enable	Yes, when a 180° and a 90° RF-pulse should be applied after the acquisition of each scan.
Number of Dummy Scans	Number of Dummy Scans before the data acquisition starts.
Phase encoding mode	Read for the read gradient (dimension 1). Linear for the phase encoding Gradient, where the ramp starts at -1. Centered for the phase encoding gradient, where the ramp starts at 0. User_defined_encoding for a user defined phase encoding gradient list.
Phase encoding start	Start of the phase encoding gradient ramps (-1 to 1).
ConfigTiming	Expand.
SliceRephaseTime	Is set by PVM, according to the read dephase time.
ReadDephaseTime	Is set by PVM, except, when EchoTImeMode is set to User_def_echo_time.
PhaseEncodingTime	Is set by PVM, according to the read dephase time.
Match Pulse Bandwidth	Yes, when the duration of the RF-pulses should be modified, so that the bandwidth is exactly the same for all RF-pulses. No as default. Then the gradient amplitudes e.g. for the slice gradients are matched according to the RF-pulse bandwidths.
Derive Pulse Gains	Yes, when the pulse gains should automatically be set, according to the set up information, gathered by using the traffic light of by using Auto_RFGain in the Acq menu. No, when the pulses should be adjusted under slider control during GSP.
Config Gradients	Expand

Table 12.5. m_chess Parameters (selective RF-pulses)

Parameter	Value
R, P and S Gradient Limit Mode	Fixed Limit in percent, when a limit for the gradient amplitude should be used Fixed Single Oblique, (square root of 2), when the image geometry must not be distorted in oblique image orientations. Fixed Double Oblique, (square root of 3), when the image geometry must not be distorted in double oblique image orientations.
R, P and S Gradient Limits	Gradient Limits with the maximum gradient values, when Fixed Limit mode is selected.
Image spoiler	Expand for spoiler gradients before and after the 180° pulse.
Image spoiler direction	Various directions and combinations for the spoiler gradient.
Image spoiler length	Duration of the spoiler gradient.
Image spoiler amplitude	Amplitude of the spoiler gradient.
Modules	Expand.
ECG	For ECG trigger parameters.
Image gradient spoiling	For spoiler gradients before and after the scans.
Info	Is set by ParaVision.

Start the acquisition with ***GSP*** to optimize the RF-pulse attenuations (Tx Attenuator 0, Tx Attenuator1) and Receiver Gain.

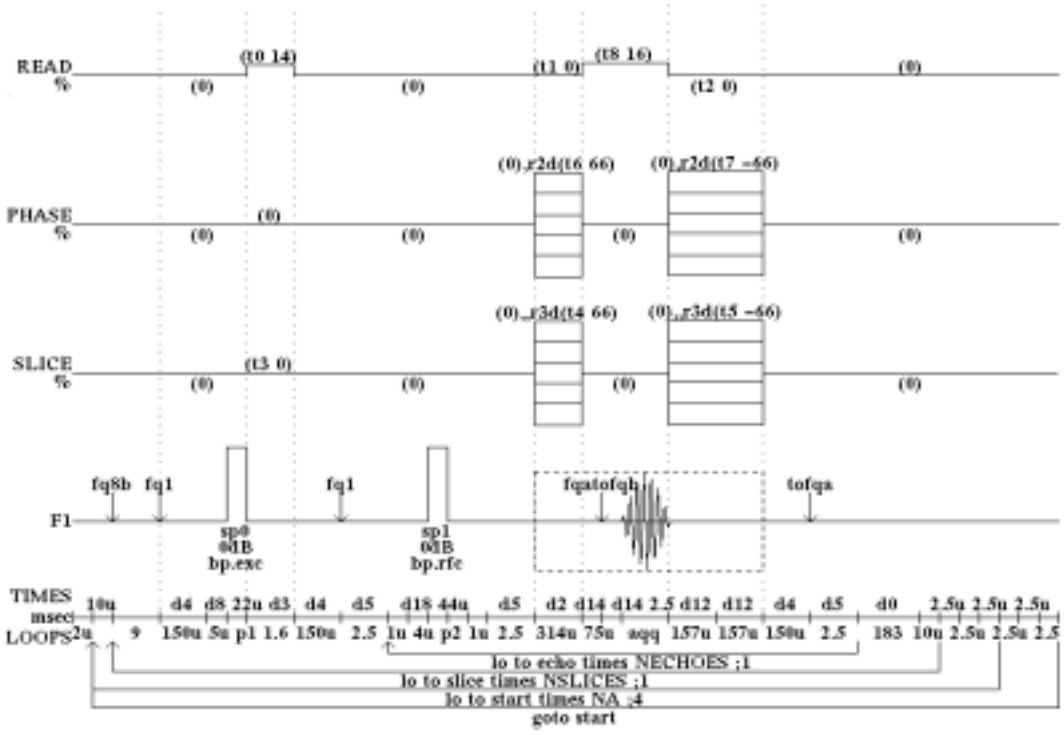
Start the image acquisition with ***GOP***.

Spin echo 3d (m_se3d) *12.7*

m_se3d acquires 3D spin echo images. The method is used for highest resolution images on samples with a T2 relaxation time down to a few milliseconds.

In a three dimensional spin echo experiment data sets are usually acquired from the entire subject volume, which is covered by the RF-coil. Typical data sets are 128x128x128 or 256x256x256. Isotropic voxels can be created. The entire magnetization inside the RF-coil is excited by a 90° RF-pulse and refocused by a 180° RF-pulse. This method is recommended for samples with strong internal in-homogeneities and susceptibility changes. The 180° pulse refocuses at least to a certain extend the distortions, caused by such in homogeneities. The images often are T1 weighted, when the recovery time is shorter than 5x T1, because the 90° and the 180° pulse, acting on the complete sample result in saturation effects, when TR is rather short. This effect can be used for contrast enhancements for convenient subjects.

Figure 12.9. m_se3d Method



Typical parameters are described in the following table.

Table 12.6. m_se3d parameters

Parameter	Value
Measuring Method	m_se3d.
Acquisition Dimension	_3D.
Matrix Isotropy	Matrix_Isotropic.
Matrix Size	e.g.128 x 128 x 128.
Effective Spectral Bandwidth	e.g. 100000 Hz.
Echo Time Mode	Min_EchoTime for short echo times, or Read_Dephase_aq_2 for longer echo times, or User_def_EchoTime.
Echo Time	e.g. 10 ms for User_def_EchoTime.
Repetition Time	e.g. 200 ms.
Number of Averages	e.g. 2.
Estimated total scan time	Is set by ParaVision.
rfPulse	Expand.
Match pulse bandwidth	No.
RF-pulse Shape for Excitation	Select the rf pulse shape, e.g. bp.
RF-Excitation Pulse Shape File	Expand.
.filename	Pulse shape file name e.g. bp.exc.
.length	Duration of 90° rf pulse in ms.
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision.
.attenuation	Attenuation for 90° pulse, can be modified under slider control.
.flipangle	e.g. is applied only, if derive pulse gains is activated.
.properties	Contains information about pulse properties.
RF-pulse Shape for refocusing	Select the rf pulse shape, e.g. bp.rfc.
RF-Refocusing Pulse Shape File	Expand.
.filename	Pulse shape file name e.g. bp.rfc.
.length	Duration of 180° rf pulse in ms.
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision.
.attenuation	Attenuation for 180° pulse, can be modified under slider control.
.flipangle	e.g. is applied only, if derive pulse gains is activated.

Table 12.6. m_se3d parameters

Parameter	Value
.properties	Contains information about pulse properties.
Geometry	Expand.
Geo Isotropy	FOV_Isotropic for isotropic Field of View or Res_Isotropic for isotropic resolution or Non_Isotropic_Geo when FOV and Resolution should be set independently.
Patient Position	Is defined during creation of a new data set, e.g. by new patient or new study etc.
Field of View	Field of View according to the size of the subject.
Spatial Resolution	Is set by PVM.
Anti Aliasing Factor	When more than the specified data points have to be acquired for later processing. It should be 1 as default value.
Slice Package Properties	Expand (only available if a selective excitation pulse is used).
Which Slice Package	Specify the one for the following parameter set up (only available if a selective excitation pulse is used).
Package Orientation	Axial, sagittal or coronal.
Package Read Orientation	L_R for left right. A_P for anterior posterior. H_F for head foot.
Slice Angle LH Slice Angle AH Read Angle Package Read Offset Package Phase1Offset Package Phase2Offset	These parameters should be set by the Pilot Scan User Interface, when selective pulses are used instead of the default non selective pulses. They can be set to zero as default.
Echo Customization	Expand.
Number of Echoes	Number of Echoes. Complete 3D data sets can be acquired for different echo times, when the value is not equal to 1. Note, that this will use a lot of disk space.
Number of echo images	An 3D data set is reconstructed from each individual echo, when this parameter is the same as the number of echoes. Some echoes can be added to result in the same 3D data set, when this parameter smaller than the number of echoes.
Scan list	Defines, how many echoes are summarized to the individual images.
Method Customization	Expand.
Nucleus	e.g. _1H for protons.
bf1	Basic frequency, e.g. 300.13.

Table 12.6. m_se3d parameters

Parameter	Value
Flipback enable	Yes, when a 180° and a 90° RF-pulse should be applied after the acquisition of each scan.
Number of Dummy Scans	Number of Dummy Scans before the data acquisition starts.
Phase encoding mode	Read for the read gradient (dimension 1). Linear for the phase encoding Gradient, where the ramp starts at -1. Centered for the phase encoding gradient, where the ramp starts at 0. User_defined_encoding for a user defined phase encoding gradient list.
Phase encoding start	Start of the phase encoding gradient ramps (-1 to 1).
ConfigTiming	Expand
SliceRephaseTime	Is set by PVM, according to the read dephase time
ReadDephaseTime	Is set by PVM, except, when EchoTImeMode is set to User_def_echo_time
PhaseEncodingTime	Is set by PVM, according to the read dephase time
Match Pulse Bandwidth	Yes, when the duration of the RF-pulses should be modified, so that the bandwidth is exactly the same for all RF-pulses. No as default. Then the gradient amplitudes e.g. for the slice gradients are matched according to the RF-pulse bandwidth.
Derive Pulse Gains	Yes, when the pulse gains should automatically be set, according to the set up information, gathered by using the traffic light of by using Auto_RFGain in the Acq men. No, when the pulses should be adjusted under slider control during GSP.
Config Gradients	Expand
R, P and S Gradient Limit Mode	Fixed Limit in percent, when a limit for the gradient amplitude should be used. Fixed Single Oblique, (square root of 2), when the image geometry must not be distorted in oblique image orientations. Fixed Double Oblique, (square root of 3), when the image geometry must not be distorted in double oblique image orientations.
R, P and S Gradient Limits	Gradient Limits with the maximum gradient values, when Fixed Limit mode is selected.
Image spoiler	Expand for spoiler gradients before and after the 180° pulse.
Image spoiler direction	Various directions and combinations for the spoiler gradient.
Image spoiler length	Duration of the spoiler gradient.

Table 12.6. m_se3d parameters

Parameter	Value
Image spoiler amplitude	Amplitude of the spoiler gradient.
Modules	Expand.
ECG	For ECG trigger parameters.
Image gradient spoiling	For spoiler gradients before and after the scans.
Info	Is set by ParaVision.

Start the acquisition with ***GSP*** to optimize the RF-pulse attenuations (Tx Attenuator 0,) and Receiver Gain.

Start the image acquisition with ***GOP***.

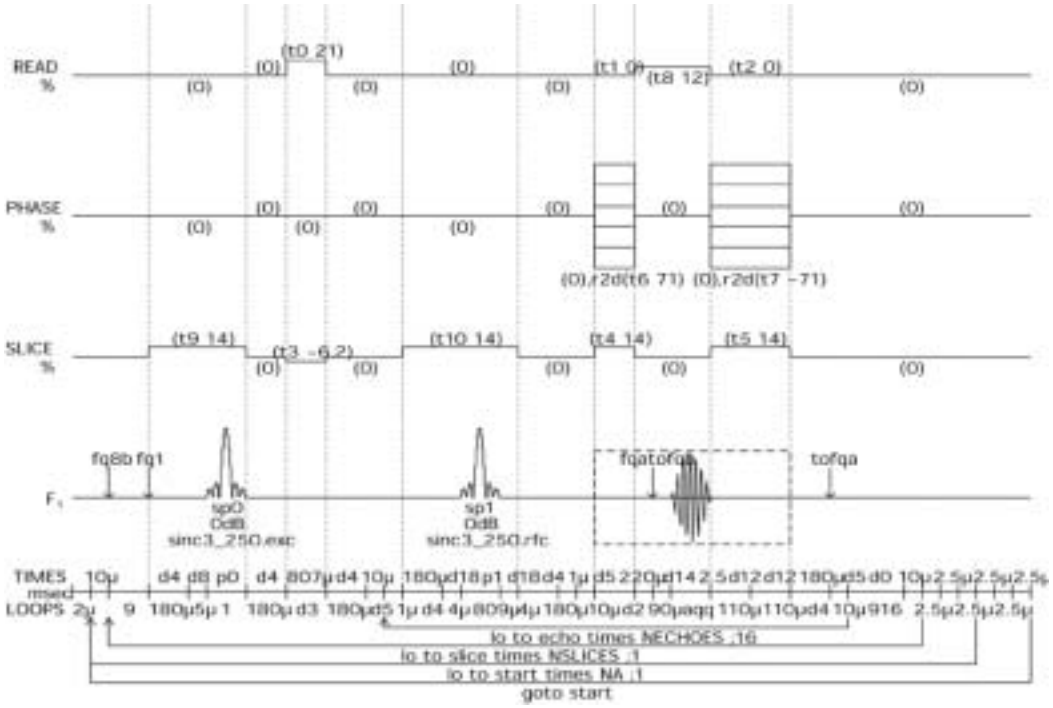
Three dimensions surface reconstructions or multi-planar data analyses can be performed after the data acquisition and 3D Fourier transformation. More information is collected in ***"Image Processing" on page 213***.

Rare 2D (m_rare) *12.1*

m_rare acquires 2D multiple spin echo images, where each of the echoes is individually phase encoded by a different phase encoding gradient. The number of the echoes, created after one excitation pulse, is called the RARE factor. The method results in T2 weighted images. The higher the RARE factor, the stronger is the T2 weighing in the image and the shorter is the time per image acquisition.

A complete image may be acquired with one excitation and e.g. 128 phase encoded spin echoes from objects with a sufficient long T2 relaxation time. It is recommended to use rather long repetition times TR, if the entire image is acquired with more than one excitation (RARE factor < number of all phase encoding steps for the complete image).

Figure 12.10.m_rare for 2D images



Typical parameters are described in the following table.

Table 12.7. m_rare Parameters

Parameter	Value
Measuring Method	m_rare.
Spatial Acquisition Dimension	_2D.
Matrix Isotropy	Matrix_Isotropic.
Matrix Size	0-1. 256 256.
Effective Spectral Bandwidth	100000 Hz.
Echo Time Mode	Min_EchoTime.
Echo Time	Calculated by PVM.
Rare factor	The highest possible number of echoes, that give sufficient signal. The more echoes, the better the T2 weighting of the image.
Repetition Time	e.g. 3000 ms.
Number of Averages	e.g. 2.
Estimated total scan time	Is set by PVM.
RF-Pulse	Expand.
Match pulse bandwidth	Yes, when the duration of the RF-pulses should be modified, so that the bandwidth is exactly the same for all RF-pulses.
RF-pulse Shape for Excitation	Select the rf pulse shape, e.g. sinc3_250.
RF-Excitation Pulse Shape File	Expand.
.filename	Pulse shape file name e.g. sinc3_250.exc.
.length	Duration of 90° rf pulse in ms, e.g. 1.
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision.
.attenuation	Attenuation for 90° pulse, can be modified later under slider control.
.flipangle	e.g. is applied only, if derive pulse gains is activated.
.properties	Contains information about pulse properties.
RF-pulse Shape for refocusing	Select the rf pulse shape, e.g. sinc3_250.rfc.
RF-Refocusing Pulse Shape File	Expand.
.filename	Is set by PVM, if „Match pulse bandwidth“ parameter is „yes“.
.length	Is set by PVM, if „Match pulse bandwidth“ parameter is „yes“.

Table 12.7. m_rare Parameters

Parameter	Value
.bandwidth	Is set by PVM, if „Match pulse bandwidth“ parameter is „yes“.
.attenuation	Is set by PVM, if „Match pulse bandwidth“ parameter is „yes“.
.flipangle	Is set by PVM, if „Match pulse bandwidth“ parameter is „yes“.
.properties	Is set by PVM, if „Match pulse bandwidth“ parameter is „yes“.
Geometry	Expand
Geo Isotropy	FOV_Isotropic for isotropic Field of View, or Res_Isotropic for isotropic resolution, or Non_Isotropic_Geo when FOV and Resolution should be set i.dependently
Patient Position	Is defined during creation of a new data set, e.g. by new patient or new study etc.
Field of View	Field of View according to the size of the subject.
Spatial Resolution	Is set by PVM.
Slice Thickness	Slice thickness.
Number of Slice Packages	One or more individual slice pack-ages can be defined, where each package has its own number of slices and slice orientation.
Object ordering mode	Sequential or Reverse_sequential, when one after the other neighboring slices are excited starting from the first or last slice respectively. Interlaced or Reverse_interlaced when first the odd and then the even numbered slices are excited starting from the first or last slice respectively. User_defined when slices are excited according to a user defined sequence.
Anti Aliasing Factor	When more than the specified data points have to be acquired for later processing. It should be 1 as default value.
Slice Package Properties	Expand
Which Slice Package	Specify the one for the following parameter set up.
Number of Slices in Package	Number of slices.
Package orientation	Axial, sagittal or coronal.
Package Read Orientation	L_R for left right. A_P for anterior posterior. H_F for head foot.

Table 12.7. m_rare Parameters

Parameter	Value
Slice Angle LH Slice Angle AH Read Angle Package Slice Offset Package Read Offset Package Phase1 Offset	These parameters should be set by the Pilot Scan User Interface. They can be set to zero as default.
Method Customization	Expand.
Nucleus	e.g. _1H for protons.
bf1	Basic frequency, e.g. 300.13.
Flipback enable	No.
Number of Dummy Scans	Number of Dummy Scans before the data acquisition starts, e.g. 2.
Phase encoding mode	0-1. Read Rare.
Phase encoding start	0-1. 0.00 -0.87.
ConfigTiming	Expand.
SliceRephaseTime	Is set by PVM, according to the read dephase time.
ReadDephaseTime	Is set by PVM, except, when EchoTImeMode is set to User_def_echo_time.
PhaseEncodingTime	Is set by PVM, according to the read dephase time.
Derive Pulse Gains	Yes, when the pulse gains should automatically be set, according to the set up information, gathered by using the traffic light of by using Auto_RFGain in the Acq menu. No, when the pulses should be adjusted under slider control during GSP.
Config Gradients	Expand
R, P and S Gradient Limit Mode	Fixed Limit in percent, when a limit for the gradient amplitude should be used. Fixed Single Oblique, (square root of 2), when the image geometry must not be distorted in oblique image orientations. Fixed Double Oblique, (square root of 3), when the image geometry must not be distorted in double oblique image orientations.
R, P and S Gradient Limits	Gradient Limits with the maximum gradient values, when Fixed Limit mode is selected.
Image spoiler	e.g. No_spoiler.
Image spoiler length	0.

Table 12.7. m_rare Parameters

Parameter	Value
Image spoiler amplitude	Amplitude of the spoiler gradient.
Modules	Expand.
ECG	For ECG trigger parameters.
Image gradient spoiling	For spoiler gradients before and after the scans.
Info	Is set by ParaVision.

These parameters produce a 256 x 256 image e.g. with 16 echoes after each ecitation.

Start the acquisition with ***GSP*** to optimize the RF-pulse attenuations (Tx Attenuator 0, Tx Attenuator1) and Receiver Gain. Check the amplitude of the echoes in the ***acqDisplay***. Increase or decrease the number of echoes according to the amplitude of the last echo by changing the ***Rare factor*** in the PVM parameter menu.

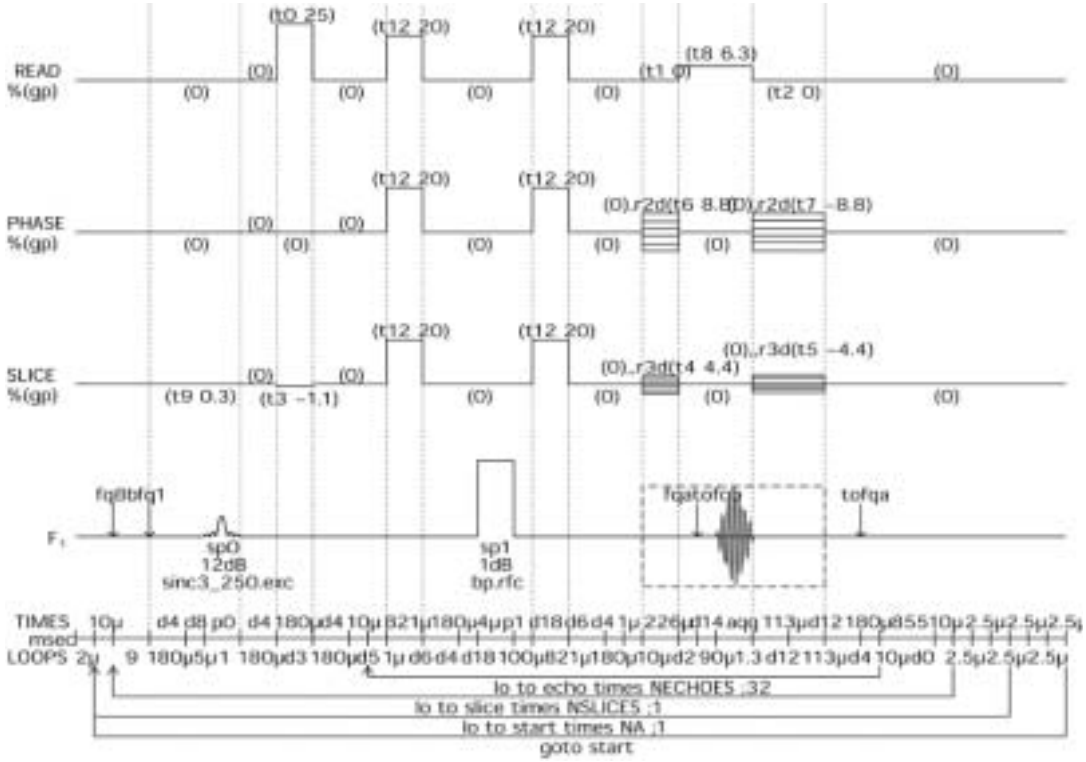
Start the image acquisition with ***GOP***.

m_rare3d acquires 3D multiple spin echo images, where each of the echoes is individually phase encoded by a different phase encoding gradient. The number of the echoes, created after one excitation pulse, is called the RARE factor. The method results in T2 weighted images. The higher the RARE factor, the stronger is the T2 weighing in the image and the shorter is the time per image acquisition.

The second dimension of the experiment is phase encoded in the RARE style, while the third dimension is handled in the same way as in the conventional 3D spin echo or gradient echo methods.

It is recommended to used rather long repetition times TR, if the entire image is acquired with more than one excitation (RARE factor < number of all phase encoding steps for the second dimension of the image).

Figure 12.11.m_rare3d



Typical parameters are described in the following table.

Table 12.8. m_rare Parameters

Parameter	Value
Measuring Method	m_rare.
Acquisition Dimension	_3D.
Matrix Isotropy	Matrix_Isotropic.
Matrix Size	e.g.128 x 128 x 128.
Effective Spectral Bandwidth	e.g. 100000 Hz.
Echo Time Mode	Min_EchoTime for short echo times.
Echo Time	Set by PVM.
Rare Factor	Number of echoes e.g. 32.
Repetition Time	e.g. 1000 ms.
Number of Averages	e.g. 2.
Estimated total scan time	Is set by ParaVision.
rfPulse	Expand.
Match Pulse Bandwidth	No, (not useful in this experiment because a bp-pulse is used for refocusing).
RF-pulse Shape for Excitation	Select the rf pulse shape, e.g. bp.
RF-Excitation Pulse Shape File	Expand.
.filename	Pulse shape file name e.g. bp.exc.
.length	Duration of 90° rf pulse in ms.
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision.
.attenuation	Attenuation for 90° pulse, can be modified under slider control.
.flipangle	e.g. is applied only, if derive pulse gains is activated.
.properties	Contains information about pulse properties.
RF-pulse Shape for refocusing	Select the rf pulse shape, bp.rfc.
RF-Refocusing Pulse Shape File	Expand.
.filename	Pulse shape file name e.g. bp.rfc.
.length	Duration of 180° rf pulse in ms.
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision.
.attenuation	Attenuation for 180° pulse, can be modified under slider control.

Table 12.8. m_rare Parameters

Parameter	Value
.flipangle	e.g. is applied only, if derive pulse gains is activated.
.properties	Contains information about pulse properties.
Geometry	Expand.
Geo Isotropy	FOV_Isotropic for isotropic Field of View, or Res_Isotropic for isotropic resolution, or Non_Isotropic_Geo when FOV and Resolution should be set independently.
Patient Position	Is defined during creation of a new data set, e.g. by new patient or new study etc.
Field of View	Field of View according to the size of the subject.
Spatial Resolution	Is set by PVM.
Slice Thickness	Only available, when shaped pulses are used for excitation.
Anti Aliasing Factor	When more than the specified data points have to be acquired for later processing. It should be 1 as default value.
Slice Package Properties	Expand (only available if a selective excitation pulse is used).
Which Slice Package	1 (only available if a selective excitation pulse is used).
Package orientation	Axial, sagittal or coronal.
Package Read Orientation	L_R for left right. A_P for anterior posterior. H_F for head foot.
Slice Angle LH Slice Angle AH Read Angle Package Read Offset Package Phase1Offset Package Phase2Offset	These parameters should be set by the Pilot Scan User Interface, when selective pulses are used instead of the default non selective pulses. They can be set to zero as default.
Method Customization	Expand.
Nucleus	e.g. _1H for protons.
bf1	Basic frequency, e.g. 300.13.
Flipback enable	Yes, if a 180° and a 90° RF-pulse should be applied after the acquisition of each scan.
Number of Dummy Scans	Number of Dummy Scans before the data acquisition starts, e.g. 2.
Phase encoding mode	0-2. Read Rare Linear.
Phase encoding start	0-2. 0 -0.87 -1.
ConfigTiming	Expand.

Table 12.8. m_rare Parameters

Parameter	Value
SliceRephaseTime	Is set by PVM, according to the read dephase time.
ReadDephaseTime	Is set by PVM, except, when EchoTImeMode is set to User_def_echo_time.
PhaseEncodingTime	is set by PVM, according to the read dephase time.
Derive Pulse Gains	Yes, when the pulse gains should automatically be set, according to the set up information, gathered by using the traffic light of by using Auto_RFGain in the Acq menu. No, when the pulses should be adjusted under slider control during GSP.
Config Gradients	Expand.
R, P and S Gradient Limit Mode	Fixed Limit in percent, when a limit for the gradient amplitude should be used. Fixed Single Oblique, (square root of 2), when the image geometry must not be distorted in oblique image orientations. Fixed Double Oblique, (square root of 3), when the image geometry must not be distorted in double oblique image orientations.
R, P and S Gradient Limits	Gradient Limits with the maximum gradient values, when Fixed Limit mode is selected.
Image spoiler	Expand for spoiler gradients before and after the 180° pulse.
Image spoiler direction	Various directions and combinations for the spoiler gradient.
Image spoiler length	Duration of the spoiler gradient, e.g. 1 ms.
Image spoiler amplitude	Amplitude of the spoiler gradient, e.g. 10%.
Modules	Expand.
ECG	For ECG trigger parameters.
Image gradient spoiling	For spoiler gradients before and after the scans.
Info	Is set by ParaVision.

Start the acquisition with ***GSP*** to optimize the RF-pulse attenuations (Tx Attenuator 0, Tx Attenuator1) and Receiver Gain. Check the amplitude of the echoes in the ***acqDisplay***. Increase or decrease the number of echoes according to the amplitude of the last echo by changing the ***Rare factor*** in the PVM parameter menu.

Start the image acquisition with ***GOP***.

Three dimensions surface reconstructions or multi-planar data analyses can be performed after the data acquisition and 3D Fourier transformation. More information is collected in ***"Image Processing" on page 213***.

m_spi acquires 1D, 2D and 3D images from samples with very short T2 or T2* relaxation times (approximately 50 µs to 1 ms). The method is known as **Single Point Imaging (SPI)** or **Constant Time Imaging (CTI)**.

Each single complex time domain data point is collected after a individual excitation (external address advance mode). The time between excitation and detection is constant for each data point. The method is therefore not sensitive to chemical shift evolution, field in homogeneity and local susceptibility changes in the object. These properties will reduce signal intensity, but they do not create image artefacts.

The spatial encoding is achieved by using phase encoding gradients for each spatial dimension.

Note, that the experimental time can become very long for large data matrices.

Figure 12.12.m_spi pulse program for a 3D experiment with dummy pulses.

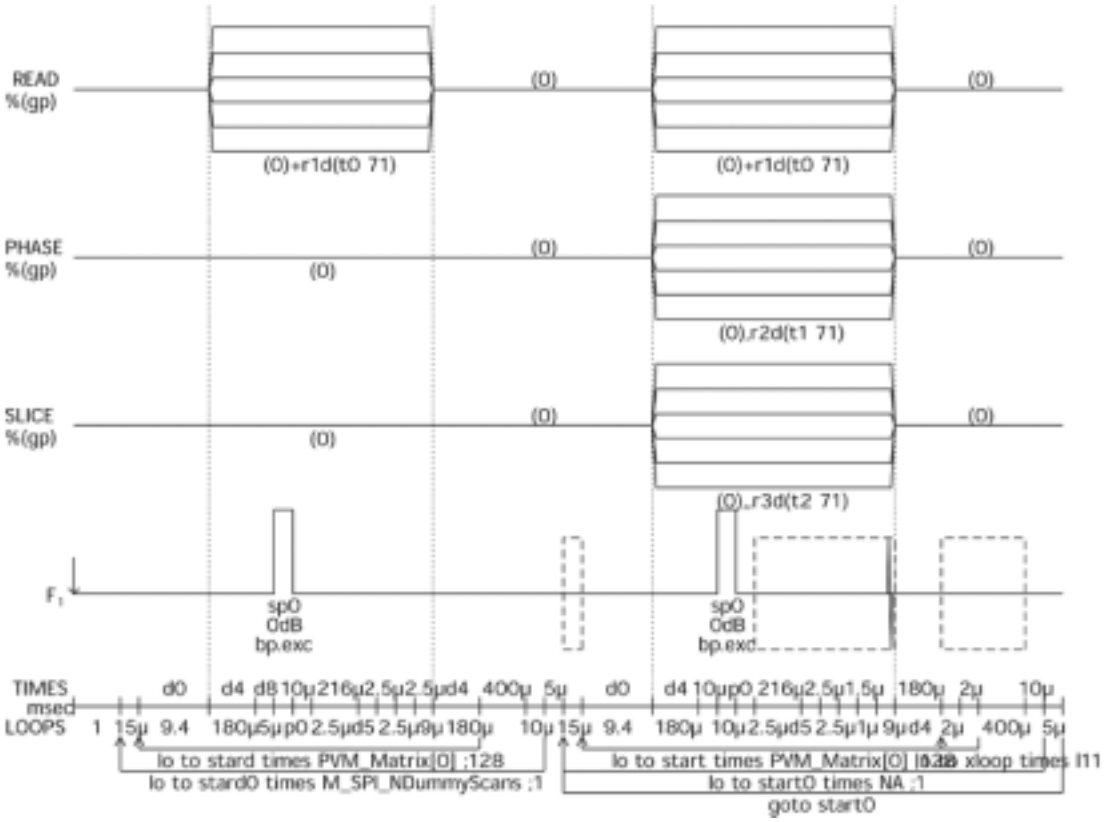


Table 12.9. m_spi Parameters

Parameter	Value
Measuring Method	m_spi.
Acquisition Dimension	_3D.
Matrix Isotropy	Matrix_Isotropic.
Matrix Size	0-2. e.g.128 128 128.
Filter width	e.g. 125000 Hz.
Dephase Time Mode	Min_DephTime for shortest dephase times. Note that this time depends on the selected FOV, which is defined later. or, User_def_DephTime for user defined dephase time.
Dephase Time	Set by PVM, if Min_DephTime, or set by user, e.g. 0.1 ms.
Repetition Time	e.g. 10 ms.
Number of Averages	e.g. 2.
Estimated total scan time	Is set by ParaVision.
rfPulse	Expand.
RF-pulse Shape for Excitation	Select the rectangular rf pulse shape: bp.
Optimize BW and FW	Yes to calculate the optimum bandwidths of the rf pulse and the filter bandwidth. The previous parameter filter width is overwritten in this case.
RF-Excitation Pulse Shape File	Expand.
.filename	Pulse shape file name e.g. bp.exc.
.length	Duration of e.g. 10° rf pulse in ms.
.bandwidth	Is calculated by ParaVision, or can be set, then the pulse length will be set by ParaVision.
.attenuation	Attenuation for 10° pulse, can be modified under slider control.
.flipangle	E.g. is applied only, if derive pulse gains is activated.
.properties	Contains information about pulse properties.
Geometry	Expand.
Geo Isotropy	FOV_Isotropic for isotropic Field of View, or Res_Isotropic for isotropic resolution, or Non_Isotropic_Geo when FOV and Resolution should be set independently.
Patient Position	Is defined during creation of a new data set, e.g. by new patient or new study etc.

Table 12.9. m_spi Parameters

Parameter	Value
Field of View	Field of View according to the size of the subject.
Spatial Resolution	Is set by PVM.
Anti Aliasing Factor	When more than the specified data points have to be acquired for later processing. It should be 1 as default value.
Slice Package Properties	Expand (only available if a selective excitation pulse is used).
Package orientation	Axial, sagittal or coronal.
Package Read Orientation	L_R for left right. A_P for anterior posterior. H_F for head foot.
Method Customization	Expand.
Nucleus	e.g. _1H for protons.
bf1	Basic frequency, e.g. 300.13.
Number of Dummy Scans	Number of Dummy Scans before the data acquisition starts, e.g. 2.
Phase encoding mode	0-2. Linear Linear Linear.
Phase encoding start	0-2. -1 -1 -1.
Derive Pulse Gains	Yes, when the pulse gains should automatically be set, according to the set up information, gathered by using the traffic light of by using Auto_RFGain in the Acq menu. No, when the pulses should be adjusted under slider control during GSP.
Config Gradients	Expand.
R, P and S Gradient Limit Mode	Fixed Limit in percent, when a limit for the gradient amplitude should be used. Fixed Single Oblique, (square root of 2), when the image geometry must not be distorted in oblique image orientations. Fixed Double Oblique, (square root of 3), when the image geometry must not be distorted in double oblique image orientations.
R, P and S Gradient Limits	Gradient Limits with the maximum gradient values, when Fixed Limit mode is selected.
Spoiler	Expand for spoiler gradients before and after the acquisition of each data point.
Spoiler direction	Various directions and combinations for the spoiler gradient.
Spoiler length	Duration of the spoiler gradient, e.g. 1 ms.

Table 12.9. m_spi Parameters

Parameter	Value
Spoiler amplitude	Amplitude of the spoiler gradient, e.g. 10%.
Info	Is set by ParaVision.

Start the acquisition with ***GSP*** to optimize the RF-pulse attenuations (Tx Attenuator 0, Tx Attenuator1) and Receiver Gain. Check the amplitude of the echoes in the ***acqDisplay***. Start the image acquisition with ***GOP***.

Three dimensions surface reconstructions or multi-planar data analyses can be performed after the data acquisition and 3D Fourier transformation. More information is collected in ***"Image Processing" on page 213***.

1D Profiles from sticks (m_profile) *12.4*

One dimensional (1D) profiles can be obtained from the entire sample when non selective RF-pulses are used to excite the magnetization from the whole object. This is explained in ***"1D Profiles (m_profile)" on page 146***.

Intensity profile of higher precision are obtained, when only a stick from the sample is excited by applying selective RF-pulses together with slice gradients. This style can be used to study e.g. the penetration of a liquid into porous media or the penetration of labeled compounds into tissue. The method parameters for such applications is described in the following.

Figure 12.13.m_profile method

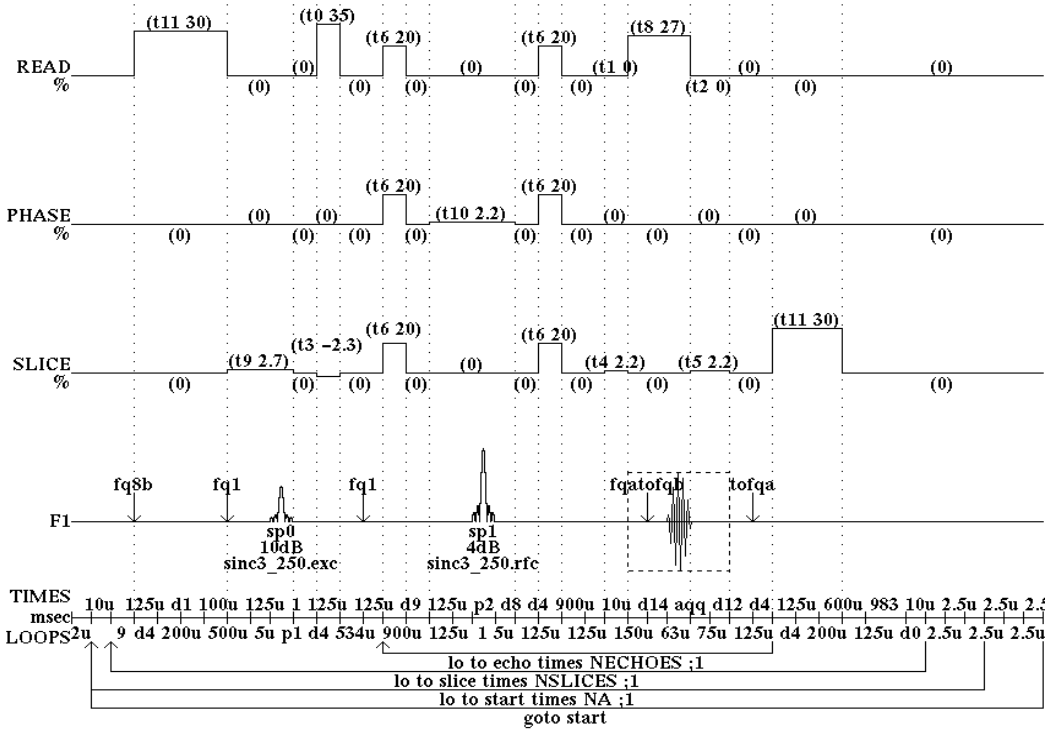


Table 12.10. m_profile Parameters

Parameter	Value
Measuring Method	m_profile
Protocol name	Name of a loaded protocol
Matrix Size	e.g.128
Read Orientation	X_dir or Y_dir or Z_dir (for more specific information see GEOMETRY->VolumeGeometry)
Effective Spectral Bandwidth	e.g. 100000 Hz
Echo Time Mode	Min_EchoTime for short echo times, or Read_Dephase_aq_2 for longer echo times, or User_def_EchoTime
Echo Time	e.g. 10 ms for User_def_EchoTime
Repetition Time	e.g. 1000 ms
Number of Averages	e.g. 2
Estimated total scan time	Is set by ParaVision
Excitation Pulse	Expand
Select Excitation Pulse Shape	Is bp for unselectable excitation or any selective pulse for a volume selective profile

Table 12.10. m_profile Parameters

Parameter	Value
Excitation Pulse Length	e.g. 0.1 ms.
Excitation Pulse Gain	To be adjusted under slider control during GSP.
Excitation Pulse Attributes	Are set by ParaVision.
Refocusing Pulse	Expand.
Select Refocusing Pulse Shape	Is bp for unselectable refocusing or any selective pulse for a volume selective profile.
Refocusing Pulse Length	e.g. 0.1 ms.
Refocusing Pulse Gain	To be adjusted under slider control during GSP.
Refocusing Pulse Attributes	Are set by ParaVision.
RefocusSpoiler	Expand for spoiler gradient attributes before and after the 180° pulse.
Ref. Spoiler Amplitude	Amplitude of the spoiler gradient.
Ref. Spoiler Length	Duration of the spoiler gradient.
Geometry	Expand.
Patient Position	Is defined during creation of a new data set, e.g. by new patient or new study etc.
Field of View	Field of View according to the size of the subject
Spatial Resolution	Is set by PVM
Anti Aliasing Factor	When more than the specified data points have to be acquired for later processing. It should be 1 as default value.
VolumeGeometry	Expand (only available if a selective excitation pulse is used).
Read Orientation	X_dir or Y_dir or Z_dir.
Volume Thickness Volume Depth XZ-Angle YZ-Angle Read-Angle Volume Offset in Plane Volume Offset in Depth Read Offset	These parameters should be set by the Pilot Scan User Interface. They can be set to zero as default.
Echo Customization	Expand.
Number of Echoes	Number of Echoes.
Number of echo images	An image is reconstructed from each individual echo, when this parameter is the same as the number of echoes. Some echoes can be added to result in the same image, when this parameter smaller than the number of echoes.
Scan list	Defines, how many echoes are summarized to the individual images.

Table 12.10. m_profile Parameters

Parameter	Value
Method Customization	Expand.
Nucleus	e.g. _1H for protons.
bf1	Basic frequency, e.g. 300.13.
Number of Dummy Scans	Number of Dummy Scans before the data acquisition starts.
ConfigTiming	Expand.
SliceRephaseTime	Is set by PVM, according to the read dephase time.
ReadDephaseTime	Is set by PVM, except, when EchoTImeMode is set to User_def_echo_time.
PhaseEncodingTime	Is set by PVM, according to the read dephase time.
Match Pulse Bandwidth	Yes, when the duration of the RF-pulses should be modified, so that the bandwidth is exactly the same for all RF-pulses. No as default. Then the gradient amplitudes e.g. for the slice gradients are matched according to the RF-pulse bandwidths.
Derive Pulse Gains	Yes, when the pulse gains should automatically be set, according to the set up information, gathered by using the traffic light of by using Auto_RFGain in the Acq menu. No, when the pulses should be adjusted under slider control during GSP.
Config Gradients	Expand.
R, P and S Gradient Limit Mode	Fixed Limit in percent, when a limit for the gradient amplitude should be used. Fixed Single Oblique, (square root of 2), when the image geometry must not be distorted in oblique image orientations. Fixed Double Oblique, (square root of 3), when the image geometry must not be distorted in double oblique image orientations.
R, P and S Gradient Limits	Gradient Limits with the maximum gradient values, when Fixed Limit mode is selected.
Modules	Expand.
ECG	For ECG trigger parameters.
Image gradient spoiling	For spoiler gradients before and after the scans.
Info	Is set by ParaVision.

Start the acquisition with ***GSP*** to optimize the RF-pulse attenuations (Tx Attenuator 0, Tx Attenuator 1) and Receiver Gain.

Start the image acquisition with ***GOP***.

Localized Spectroscopy with Spin Echoes (m_vselse) *12.5*

m_vselse acquires spectra from localized volumes in an object. The method uses a 90° - 180° - 180° rf pulse sequence with appropriate gradients for the localization of voxels.

The position and size of the voxel can be defined in the **vselse** parameter menu, but it is much easier to select the voxel in the pilot scan style. A 2D image should be acquired the reference image. Clicking the pilot scan bottom displays then the pilot image and a voxel. The position and size of this voxel can be modified under mouse control.

Figure 12.14.m_vselse Localized Spectroscopy

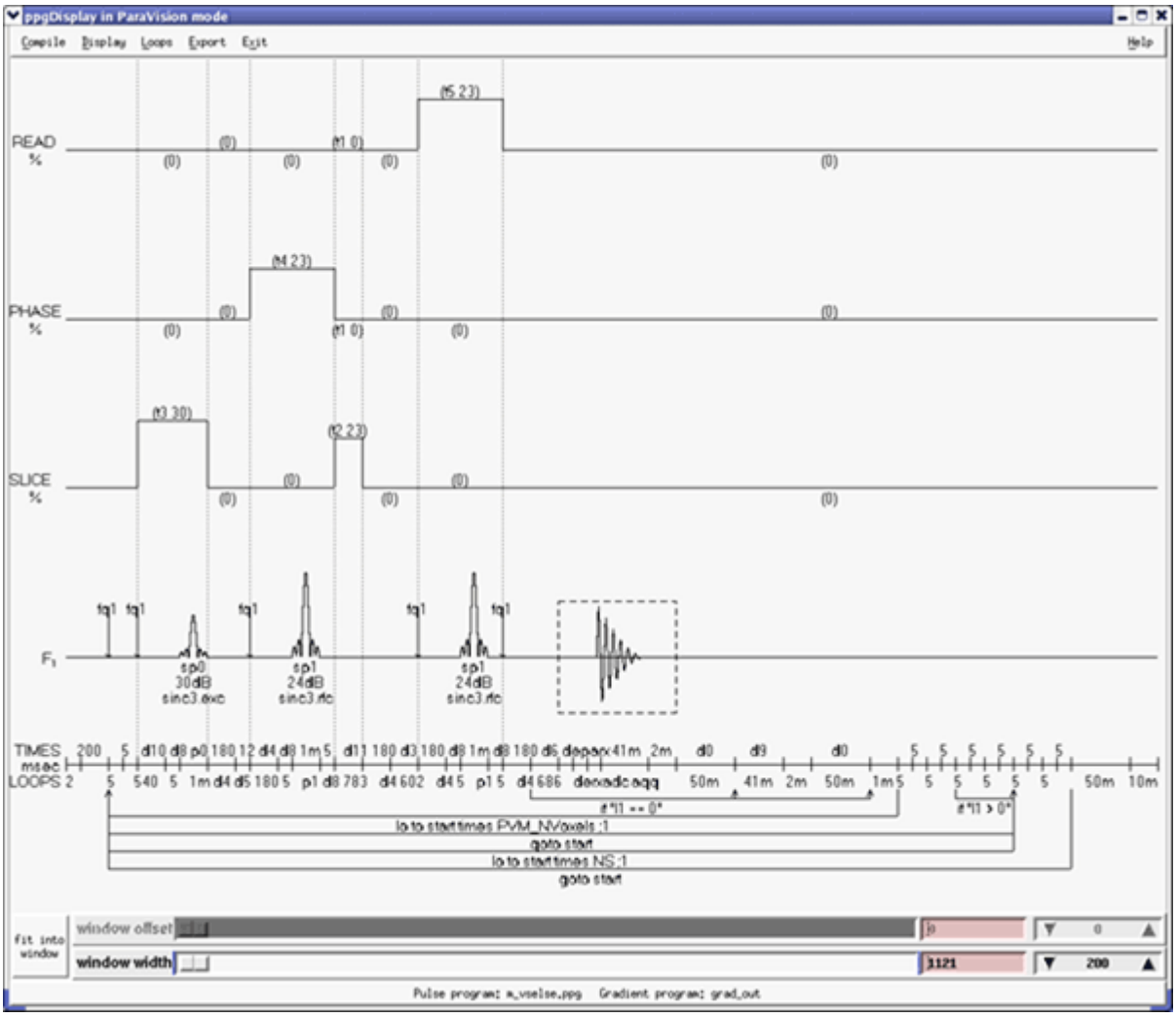


Image Processing 13

All images, acquired in the high resolution part of XWIN-NMR and in ParaVision are processed in the xtip part from ParaVision. The image processing is described in detail in the separate ParaVision manual:

Part Number: T6553 SWM_PVR1SGI Man

Some processing procedures are described in the following sections.

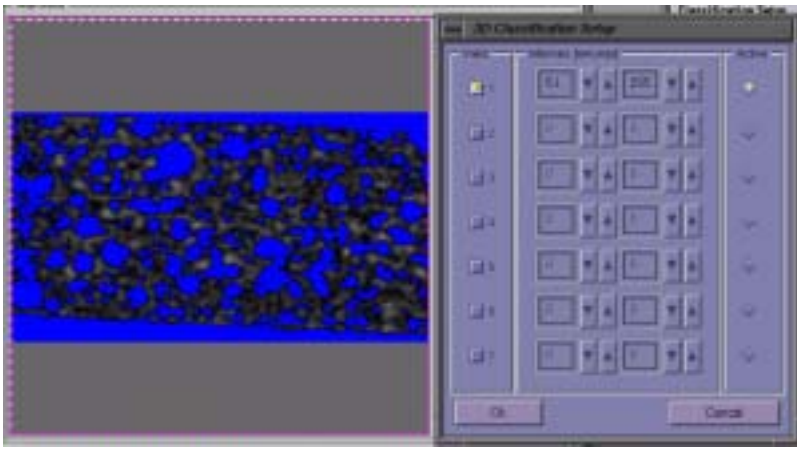
3D Surface Rendering - A Step-by-step Guide 13.1

After obtaining a 3D data set with a matrix size from 64x64x64 to 256x256x256 a surface rending can be started.

The first step is the classification of the threshold levels.

To do this select in the menu **View => 3D => Classification Setup**.

The following display will appear:



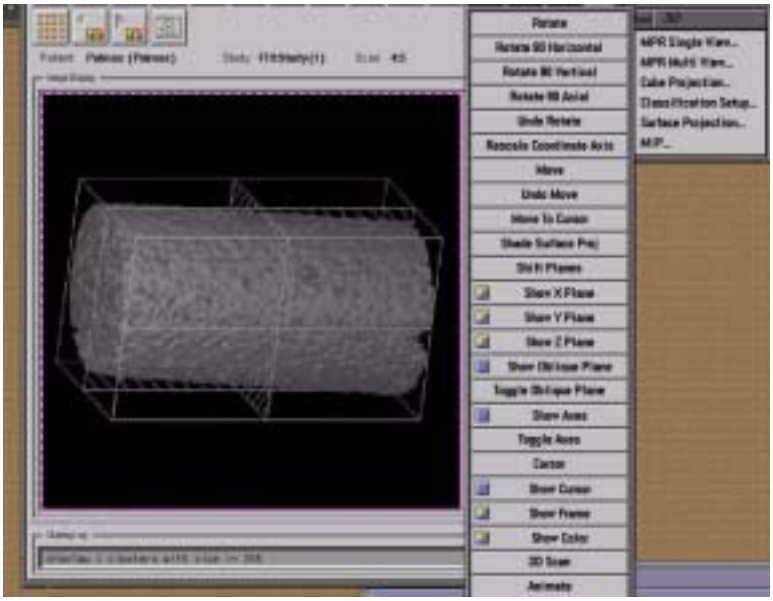
Select a cluster class by clicking the corresponding radio button for **Valid (1 - 7)** and activate it with the **Active** button.

Select a suitable minimum and maximum threshold. This threshold range should specify the part of the data which you want to render.The selected area will be displayed in black and white. The part of the data with the intensity below the minimum level is displayed in blue. The part of the data with the intensity above the maximum level is displayed in red.

To finish this setup exit the routine by clicking the **OK** button.

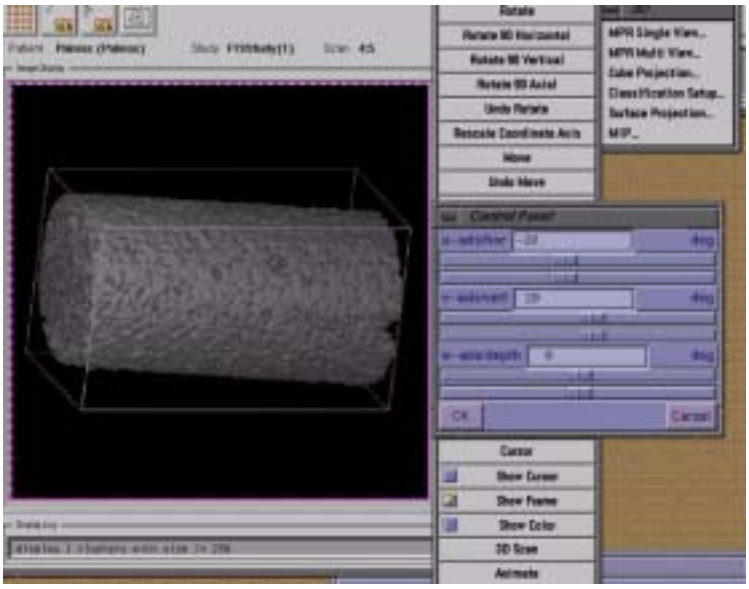
The next step is to start the surface rendering.

Click **View => 3D => Surface Projection**
The actual status of the rendering is displayed in the Display Log below the image window:

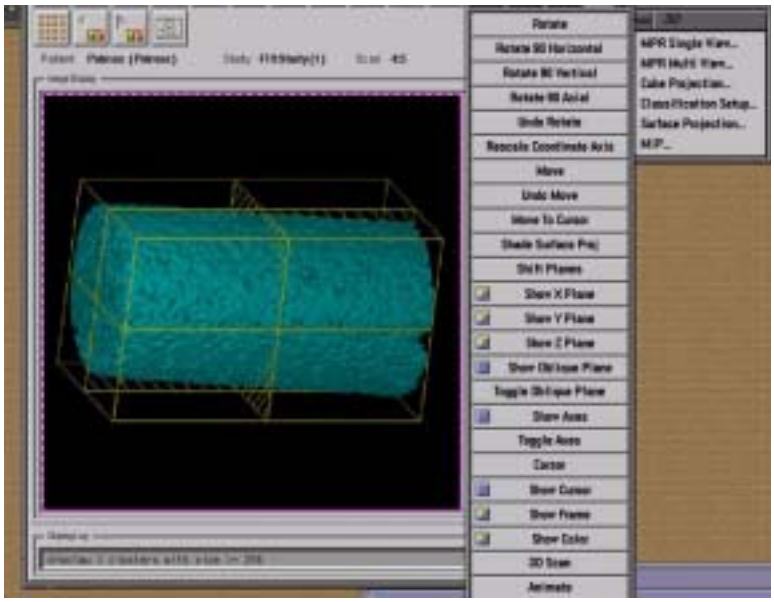


The surface of the rendered object appears in black and white. A rendering menu pops up.

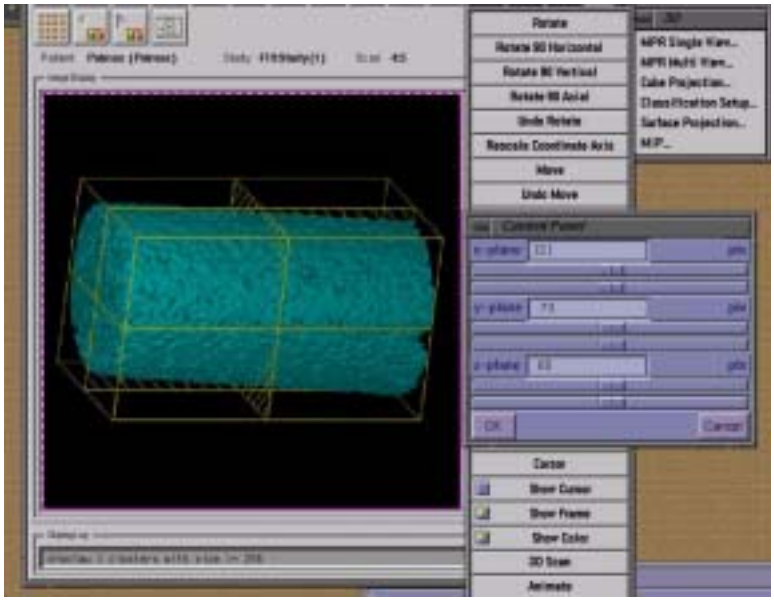
Now you can rotate the 3D object by using the menu **Rotate**.



Rotate the object e.g. so that you can see the part which you want to cut off later.

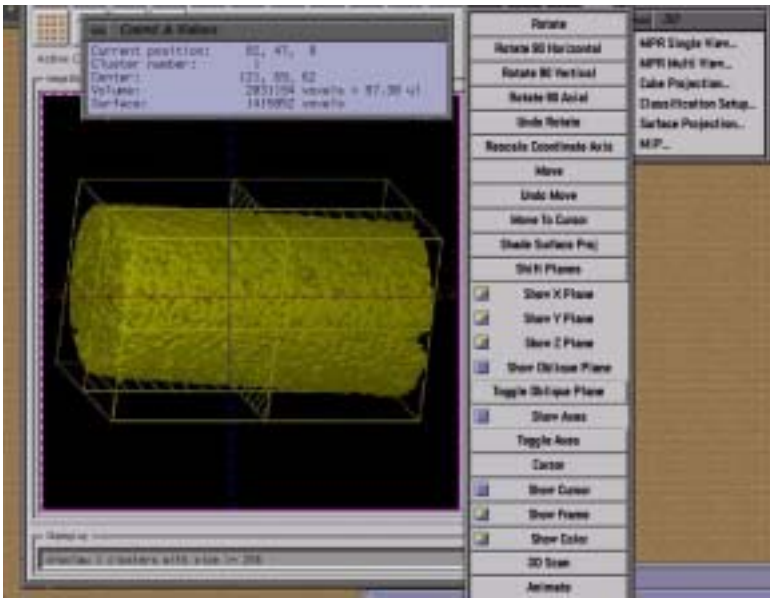


You can activate up to three orthogonal planes by clicking at **Show X Plane** and/ or **Show Y Plane** etc.



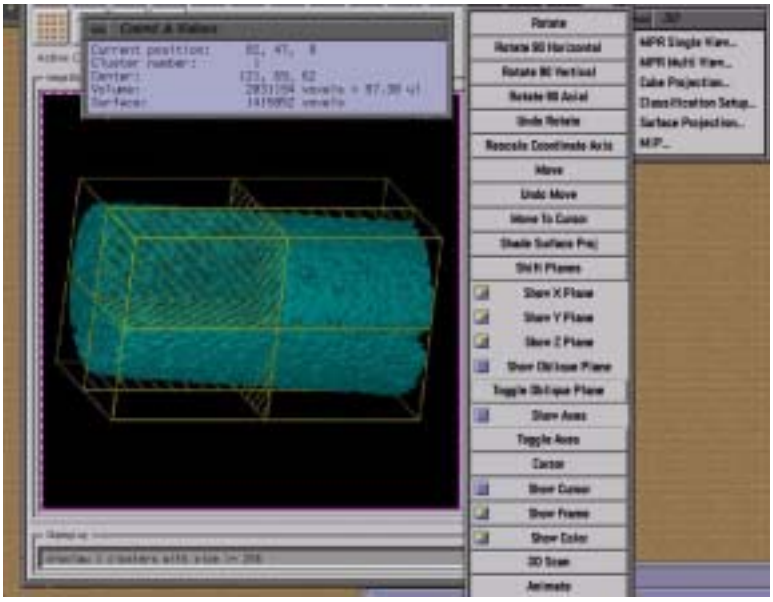
Shift the planes by activating the menu **Shift Planes**.
Select with this planes the part of the object which you want to cut off.

To cut off a part of the object click the button 3D Scan.

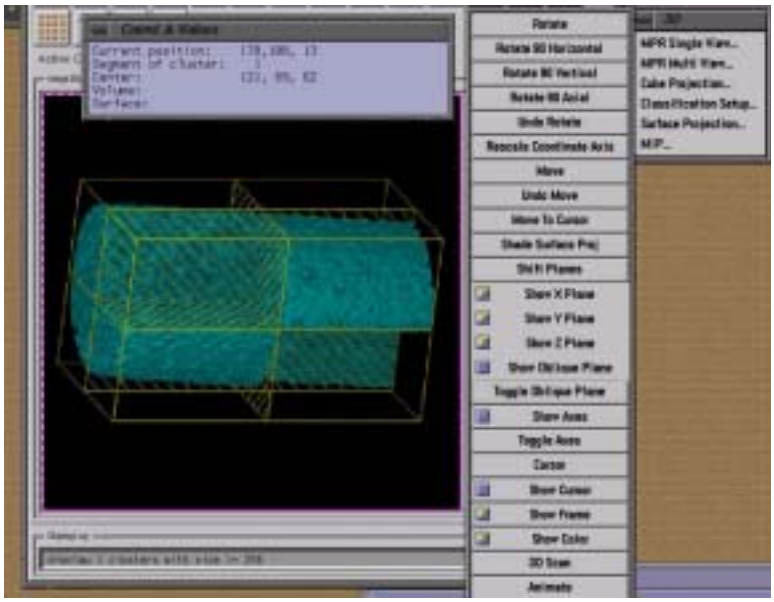


A cross-hair appears. Click with the left mouse button on the part you want to hide. The color of the selected part changes.

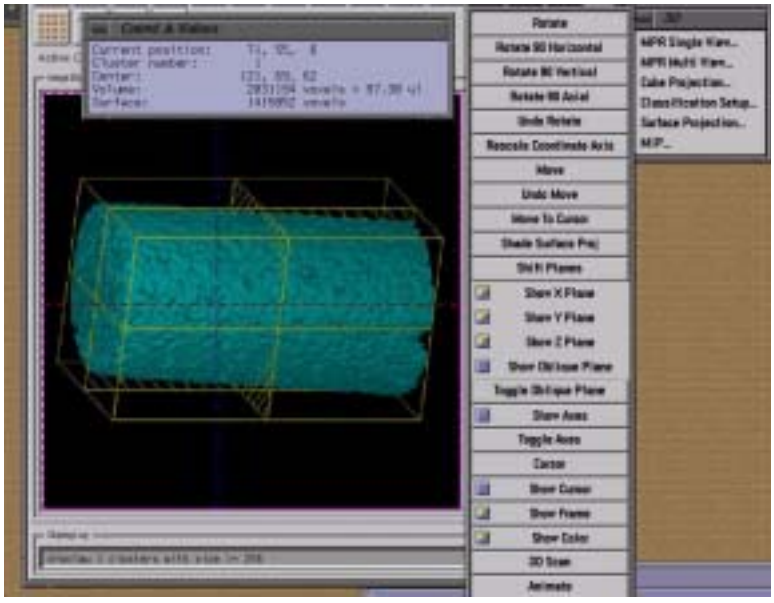
Now click ***h*** at the keyboard to hide your selection.



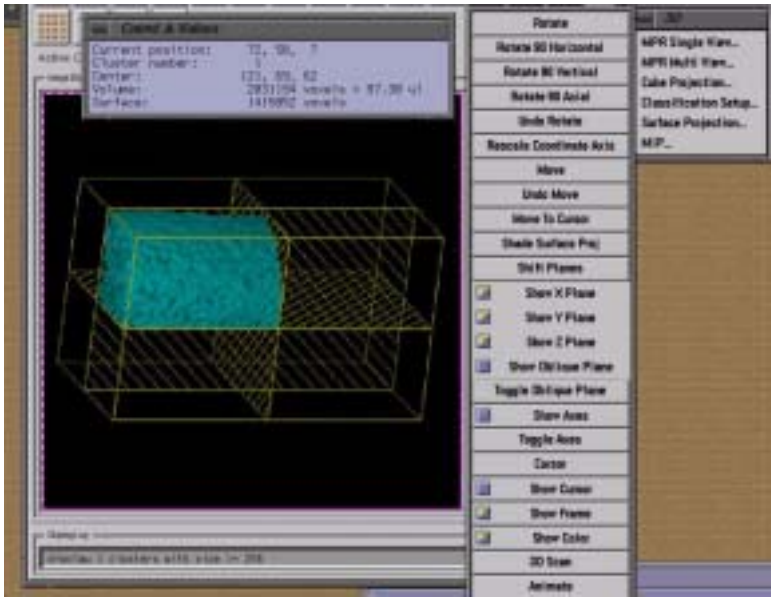
You can repeat this procedure several times.



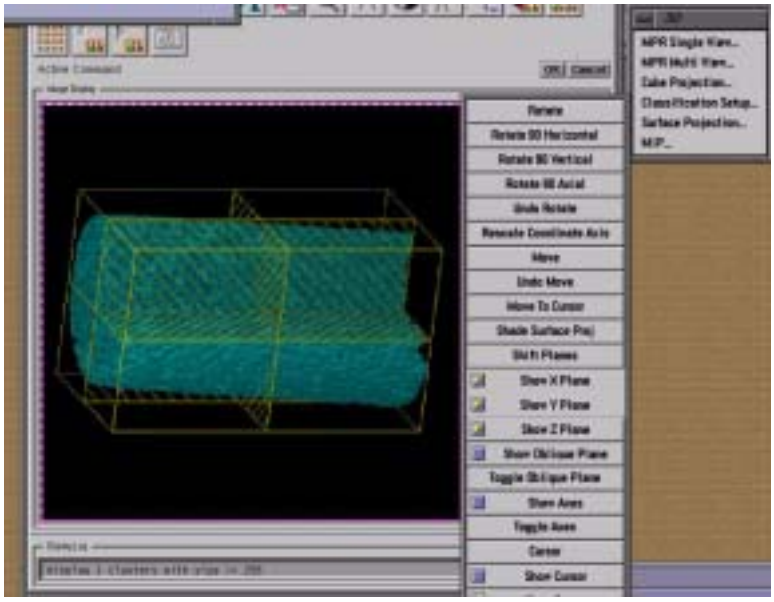
If you like to see the whole object again press ***a.***



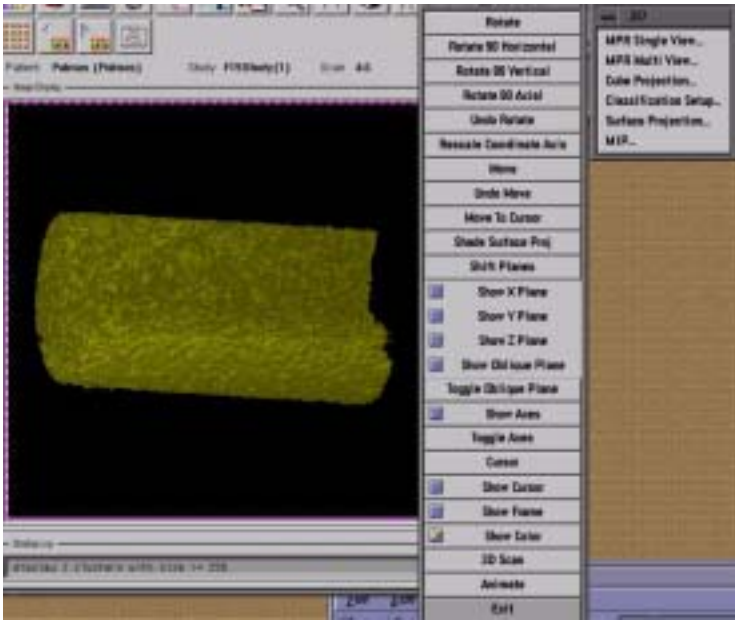
You can also invert the selection by clicking **shift I**.



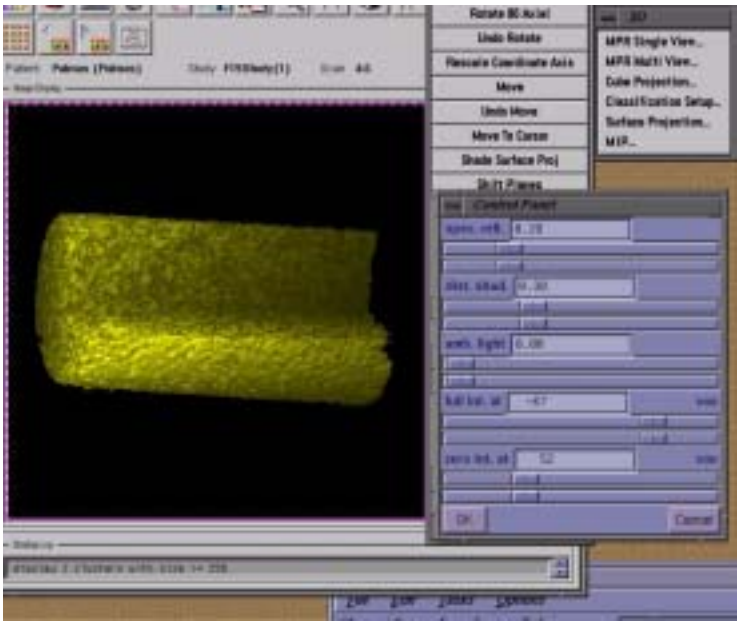
If you want to keep the result, exit the 3D Scan menu by clicking **ok**.
The ok button is at the upper right corner of the xtip window.



You can hide the planes and the wire frame by clicking the corresponding radio buttons at the 3D menu.

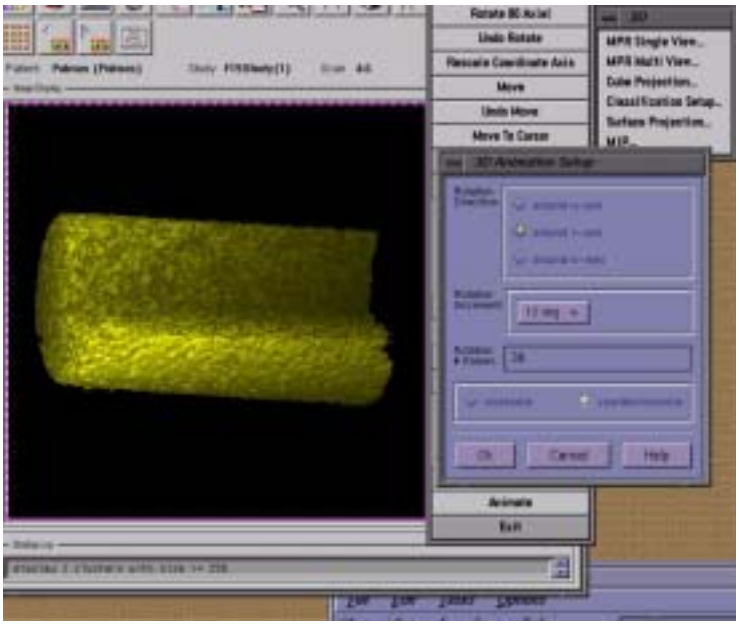


You can now adjust the illumination parameter by activating the menu **Shade Surface Proj.**

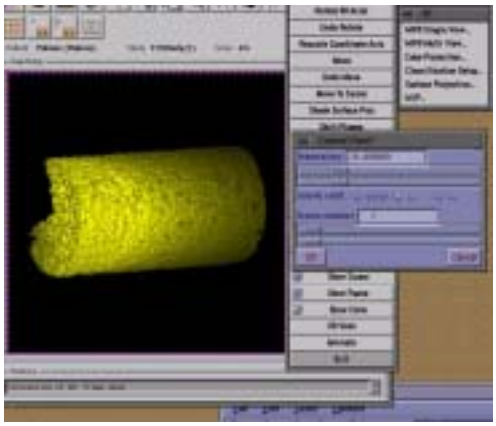


Especially the parameter **full int. at** (this is the plane in front of the object where the light intensity is 100%.) and the parameter **zero int. at** (this is the plane behind the object where the light intensity is 0.) helps to find the right shading parameters to show the object with a high contrast.

To create an animation of your selected object, click the button **Animate** and specify the rotation axis, the rotation angle increment and the number of increments for the movie.



You can store the movie after the calculation is finished. Click **ok**, the a window appears where the next unused processing number is suggested.



To run the movie exit the 3D surface rendering menu and load the movie processing number with the scan editor into xtip. By clicking the camera icon at the xtip icon list you can run the movie.

Conversion of a 2D Image to ASCII Format *13.2*

2dseq files from 2D images, which are processed in xtip can be converted into ASCII format for further usage in other programs, e.g. WORD or EXCEL.

The automation program m_2dseqtxt reads the 2dseq file from the active xtip frame, converts the data to ascii and stores them as 2dseq.txt in the same directory where the 2dseq file is stored. m_2dseqtxt should be stored in /DU/exp/stan/nmr/au/src.

The m_2dseqtxt handles only 2D single image data sets. Such 2D single image file scan be created or cut out from e.g. multi slice or 3D data sets by the image algebra tool.

The following example describes the individual steps:

Load any data set into xtip.

Select the frame with the data for the conversion to ascii.

Activate the image algebra tool by selecting ***Xtip / Processing / Algebra***

Click ***Edit***

Create a new function: y = x(1)*1 with output scaling NO.

Click ***Store*** to store the new function

Click ***Select*** to select the new function for execution.

Click ***Execute*** to execute the function.

Click on the selected frame of the input data and on another frame for the output data.

The new 2D data set is now in a frame of xtip.

Note the result is stored e.g. in */DU/data/.userid_0.0/nmr/xtip/expno/pdata/procno*

Click ***Xtip/View/Show Viewport Info*** to visualize this data path.

Drag this data set by mousing from Xtip into the ParaVision Scan Control Window.

Click ***ParaVision Spectrometer Control Tool / Edit / EditAUs*** and select ***m_2dseqtxt***.

Compile the Au program

Click ***ParaVision Spectrometer Control Tool/Edit/Execute AUs*** and select ***m_2dseqtxt***.

The new file ***2dseq.txt*** is created in:

e.g. */DU/data/.userid_0.0/nmr/xtip/expno/pdata/procno*

Creation of a 2dseq Test Data Set 13.3

A 2dseq file can be created with artificial values for testing image processing features etc.

The automation program ***m_make2dseq*** creates such a file. m_make2dseq reads the parameters of the existing 2dseq file (number of pixels etc.) and creates a new file 2dseq.test. The values start at 1 for the first pixel and are incremented by one for each next pixel.

The m_make2dseq can be used as an example for other test files.

Visualization of Fitted Values from ISA Images 13.4

The Image Sequence Analysis Tool (ISA) from Xtip can create parameter maps e.g. T1, T2 or diffusion value maps. These maps can be further interactively analyzed by the Coord. & Values tool from Xtip. But it may happen, that the displayed values from the pixels at the cursor position are not the real T1, T2 or Diffusion constant parameters, because the image display function uses a scaling, optimized for good image intensity display, but not for the true parameter values. The image has to be rescaled in this case.

The following example describes the individual steps for the rescaling:

Load a parameter image into a frame of Xtip.

Start ***Xtip / Processing / Image Sequence Analysis***.

Click ***ImageSequenceAnalysis Tool / Parameters / Edit ISA Parameter Class***.

Click ***Function Parameters*** and ***expand***.

Get the ***.par_scale*** value for the parameter, related to the selected image,

e.g. scaling of „T2 relaxation time“ in the case of the T2 map.

Exit from ISA tool.

Activate the image algebra tool by selecting ***Xtip / Processing / Algebra***

Click ***Edit***

Create a new function: y = x(1) * (value of .par_scale) from ISA with output scaling NO.

Click ***Store*** to store the new function

Click ***Select*** to select the new function for execution.

Click ***Execute*** to execute the function.

Click on the selected frame of the input data and on another frame for the output data.

Activate the Coord. & Values tool from Xtip and use the cursor for the data presentation.

This data set can be converted into ASCII format ***"Conversion of a 2D Image to ASCII Format" on page 221*** and exported in WORD or EXCEL programs.

Implementation of New Methods 14

A new method consists in principle of a **new pulse program** and a **new gradient program**. When these two programs exist, the method can already be used, but all the parameters of the new method must be calculated and set by hand. For a more comfortable and safer usage of the new method it is recommended, to create a **new user interface**, containing all method specific parameters and the relations between the parameters. The new method is then controlled in a user friendly interface. The creation of such a new user interface and of the relations is described in this chapter.

ParaVision Methods Manager PVM *14.1*

The Methods Manager is a new parameter handling concept with which the measuring methods can be implemented so that the different methods are both physically (in terms of source code) and logically separate. What the user will see of the Methods Manager is a special parameter overlay, named '**methManag**', and a collection of individual binary files, referred to as 'methods'. Each method contains the complete definition of a single measuring method.

In principle, a method consists of the pulse program, the gradient program, and base level parameters such as delays, rf pulse shapes amplitudes, phases and durations, gradient amplitudes and durations. Up to this level the parameters used in the pulse and gradient programs are set using a menu based editor referring to the ACQP class. Some parameters like the gradient trim values or delays used in the pulse and/or gradient programs can then be adjusted interactively while a gsp pipeline is running.

Once a measuring sequence is established on this base level, it is recommended to integrate it into a more intuitive environment. Our goal in introducing the ParaVision Method Manager is to make the implementation of such new methods as much easy and reliable as possible:

- Within the ParaVision Method Manager environment different methods are both physically and logically independent, which means that any method consists of a unique binary file, which will be linked at runtime of ParaVision. Methods can be installed on any Bruker system running ParaVision Method Manager simply by copying the binary method file from one system to another.
- Linking binary methods at runtime makes it possible for cooperation partners to exchange methods without having to provide the source code, thus providing better protection of intellectual property.
- Means are provided to include the pulse and gradient programs in the method under control of the method manager. This integrates all of the components of a measurement method in one component in one place and puts it all under the control of the person developing the method.

- The Methods Manager supports two different classifications of methods. There are those methods which have been developed by Bruker and are guaranteed to be tested and reliable and there are those which have been developed by users or which are in a prototype state. When a method is selected the method name will show whether or not this is a Bruker-guaranteed method.
- The access to library functions, covering commonly needed operations, provides a versatile means to avoid redundancy. Even though different methods are independent of each other, many basic operations will remain the same for many methods. A Bruker toolkit is provided with a number of library functions for commonly needed operations. In addition the means are also provided to locally create a User Toolkit, providing user defined basic functions which can also be used in different methods.
- Unrestricted (high-level) parameter definition is provided which are more intuitive from a user's point of view than base level parameters might be. This allows sequences to be run in a routine way by even less experienced users.
- For every parameter declaration a subroutine may be defined containing the relations of that parameter. The subroutines are written using the C programming language. Every time the parameter's value is changed (e.g. from within an editor) its relation subroutine is called. Within these subroutines a complete and consistent set of base level parameters must be setup at least.
- High-level parameter definitions are provided already by Bruker, which can be used in any new method. For some parameters relational subroutines are defined which will be run by default.
- The 'Method Class' contains a complete set of parameters describing a method. These are the parameters which will be presented in the ParaVision user interface when the user edits a protocol using this method. Putting this under user control makes it possible for a method to define this class to truly include only the parameters which are relevant to the method. The Methods Manager also makes it possible to include any of the parameters provided by Bruker in the Method Class, which means that base level parameter may also be directly included as part of the protocol for a user defined method. It also helps to eliminate redundancy since base level parameters need never be mirrored within a method, they can be included directly.
- Parameters contained in the 'Method Class' can be assigned to subclasses, which form the layout of the parameters in the editor (menu). The visibility and edit ability status of each parameter is designed to be user controlled.
- When including a base level parameter in the Method Class, it is often desirable to be able to redefine the relations associated with that parameter. This makes it possible for a base level parameter to interact with parameters which you have defined within your method. This capability is of course also supported. At the same time, the default relations of the parameter are still available and can be used when needed.
- Finally, the Methods Manager supports licensing. A method can be marked as requiring a license without which it will not work.

Setup of the environment for PVM *14.2*

The following discussion will describe the recommended procedure to setup the system environment in order to compile and subsequently run measuring methods with PVM. All the settings can be done automatically at system startup by placing them into your login script, which is `$HOME/.bash` or `$HOME/.profile` for the Bourne shell and `$HOME/.cshrc` for the **cshell** or any equivalent. Then every user needs to follow the procedure described below only once on each system as this same procedure can be used for any of the methods for which source code has been provided.

Define a shell variable which points to the directory under which ParaVision was installed. For the Bourne shell add the command following commands to your start script:

PvHome=‘xwinnmr -p‘

export PvHome

For the C shell, add the following line to the start script:

setenv PvHome ‘xwinnmr -p‘

This variable will be used in several of the steps described later.

Create a 'methods' directory in your `$HOME` directory within which the source code may be held for all the methods you will be developing. Enter the commands:

mkdir -p $HOME/methods/src/<method name>

For the first time, you may simply examine the example source code for the method *onepulse*. Create the directory using ’`mkdir -p $HOME/methods/src/onepulse`’ and copy the onepulse source, provided by Bruker, to:

cp $PvHome/prog/parx/src/onepulse/* $HOME/methods/src/onepulse

Now define the search path for your private methods. When the source code is compiled, the resulting binary method file should be copied to the directory `$HOME/methods/bin`. Specify this path in the environment, so that ParaVision knows where to look for methods. This must be done by setting the environment variable `ParxMethodSearchPath`:

For the bash (in ~/.bash):

ParxMethodSearchPath = “$HOME/methods/bin“

export ParxMethodSearchPath

For the **cshell**, enter the command (in ~/.cshrc):

setenv ParxMethodSearchPath “$HOME/methods/bin“

ParaVision will search for methods in all paths specified in this variable. This means, more than one path can be specified to search for private methods. So it is possible to add the method path of a colleague to test or use his private methods.

Additionally ParaVision search in the standard directories for public accessible methods, `$PvHome/prog/parx/pub` and `$PvHome/prog/parx/methods`. If a new method is finished and tested, simply copy the binary to this directory and every ParaVision user can access it.

The ParxMethodSearchPath may contain as many directories as one wishes, but please don't put extra white spaces in. The directories in the ParxMethodSearchPath are searched in the order in which they are named. When assembling the list of available methods, the directories named in ParxMethodSearchPath are searched first, then $PvHome/prog/parx/pub is searched and finally $PvHome/prog/parx/methods is searched. If two methods are found which have the same name (for example, two different versions of onepulse) the first one found will be used.

The private directory, in which a binary method will be copied must be defined within the Makefile of each method (the Makefile is located in the source directory of your method). Search for the definition of the METHODS_DIR macro in the Makefile and modify it for your needs. If you want to make your method public, enter:

```
DISKUNIT = $(PvHome)
METHODS_DIR = $(DISKUNIT)/prog/parx/pub
```

To keep it private enter

```
DISKUNIT = $(PvHome)
METHODS_DIR = $(HOME)/methods/bin
```

Now setup the compiler to be used to compile your source code. The compiler used in ParaVision is called '**parcomp**' and uses a GNU-compiler delivered with ParaVision. But take care that the correct GNU-Compiler is used to compile the method. Therefore it is the easiest way, to redefine the environment search path as follows. The example is valid for ParaVision 2.0, but it should be the same path structure in the following releases. To add the correct compiler path to the search path add the following line to your start script:

For the Bourne shell the PATH variable is extended by:

```
PATH="$PvHome/gnu/bin:$PATH"
export PATH
```

For the **cshell** or equivalent by:

```
setenv PATH "$PvHome/gnu/bin:$PATH"
```

Activate your changes by typing 'rehash' and check with 'which gcc', wether the correct compiler is used (the result should be $PvHome/gnu/bin/gcc).

Compilation of the First Method *14.2.1*

Compilation of the first method checks, if all settings are correct. Please use the *onepulse* example, which has been copied to $HOME/methods/src/onepulse in the previous chapter.

Change to this directory and edit the Makefile. Check the paths especially change the SRCDIR line from:

```
SRCDIR = $(PROGDIR)/parx/src/$(OVERLAY)
```

To:

```
SRCDIR = $(HOME)/methods/src/$(OVERLAY)
```

This will specify the source directory, where $OVERLAY is the method name.

If that's done, compile the *onepulse* method by entering:

`make clean` -> remove previously compiled files

`make cproto` -> create prototypes

`make depend` -> create dependencies

`make install`-> compile and install the new method

Or in a single line:

make clean && make cproto && make depend && make install

Control the compiling process on the screen. If everything works fine, (no error messages) the resulting binary methods file is copied to `$HOME/methods/bin/onepulse`. Please check this! Now start ParaVision and use the self-compiled *onepulse* method to setup parameters and acquire data. It is the one with the lowercase start letter. If this method should be used on another spectrometer, simply copy this binary file to the second computer, and setup the environment as described above.

Test the compiled Method *14.2.2*

If your compiled methods exists (whether in your private or the public folder), it is time to test it. Start ParaVision and create a new patient or select a existing one from the Scan Control window. Now open the Spectrometer Control window (with the hammer & screwdriver button) and select the **EditClass** button. Scroll down the appearing class list and choose the class 'MethodClass'. Click on the Button behind 'Measuring Method' and search for your own method. If a method is released by Bruker, the method name will start with a capitalized letter. All methods that aren't released by Bruker will start with a lowercase letter. After your selection, you will get a graphical user interface (GUI) with the parameters defined in `parsLayout.h` (will be described later in this chapter). Now you are free to change any existing parameter, setup a parameter set and start the sequence with `GSP` or `GOP` or simply check your settings in the menu point 'Tools -> Pulse Program Tool' in the Spectrometer Control Tool.

Add a Button for EditPVM to the Tool chest Menu 14.2.3

If you want to add an EditPVM button to you Tool chest menu, you have to add the following lines to the file `~/.auxchestrc`. After restart, you get an button which is called EditPVM, with which you can open the PVM-GUI-editor. The string `<PvHome>` must be replaced by the installation path of your Paravision, e.g. `/v/pv201`.

```
# Top Level Menu Description
Menu ToolChest
{
no-label f.separator
"EditPVM" f.checkexec "<PvHome>/prog/bin/scripts/pvcmd
pvScan pvEditPars MethodClass"
```

Relations and Toolboxes 14.3

For each image acquisition or spectroscopy **method**, created in PVM exists a individual **GUI**, where the acquisition and/or processing parameters are handled. The creation of such menus is described later. Two powerful features exist to make the creation of new methods easier. The first one, **relations**, describe the connections between the parameters and their reactions, caused by a parameter change (e.g. a change of the spectral width parameter changes the dwell time parameter).

The other feature is the possibility to work with libraries, which we will refer to as **toolboxes**. Bruker delivers a toolbox which provide much functionality and make programming much easier because a lot of basic calculations are handled there (e.g. calculations of read, phase encoding or slice gradient amplitudes depending on the requested field of view or slice thickness). Toolbox functions are used optionally. It is also possible to do all the work without toolbox functions or to create your own toolbox functions.

Relations 14.3.1

A relation defines how the current parameter is connected to other parameters and/or which action has to be performed, whenever this parameter is edited by the user.

Every change of a parameter inside ParaVision is followed by the execution of a relation!

Such an execution is called whenever a parameter in a PVM menu for a selected method is modified. The parameter handling is not in a style where the complete

parameter set is computed at once after values are given to all parameters of a menu.

If any parameter value is modified by the user, an **event** for the modified parameter is released automatically. PVM has to catch this event and execute the code provided for the parameter which created the event. This code is defined in the relation of the parameter. (For programmers who haven't worked in a graphical user interface yet, it might be a bit difficult to understand, but it is quite similar to any graphical window programming.)

The program then waits for the next action as long as there is no change of any value. If a new parameter value is entered in any field of the menu, the relation for the new parameter will be called, and after finishing, the program wait again for the next change. Therefore parameter changes (e.g. in the methods menu) can be checked immediately in any other ParaVision-Window (e.g. where the base level parameters are displayed or the pulse program display).

ParaVision internally works with a lot of different parameters to adjust everything possible within the NMR. Parameters exist for the acquisition (ACQ parameters), for the reconstruction of images and spectra (RECO parameters), for the pre-emphasis adjustment (PREEMP parameters) and lots more. The lowest level of all parameters are the so called **base level parameters** (e.g. NA, NI, NS, NECHOES...). Other parameter groups are so called **ParaVision parameters, PVM-Parameters** or **user defined parameters**.

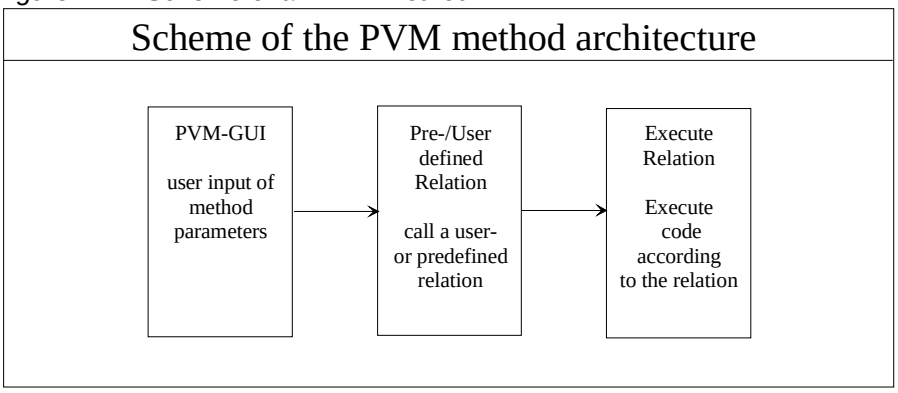
When e.g. the number of data points in read direction is changed in a method, it is necessary to recalculate several parameters, so that the correct number of data points will be acquired and displayed in the resulting image. For example the parameters `ACQ_size` and `RECO_size` depend on the number of data points, as well as the gradient amplitude and gradient duration for the read gradient and for the phase encoding gradient. The programmer of a new method is forced to take care of all parameters, so that they are set correctly.

This seems to be an enormous amount of work for the implementation of a new method. In order to reduce this, **ParaVision has a lot of build in relations** for parameters, which are common to many imaging or spectroscopy experiments. When a ParaVision parameter is changed, ParaVision often has the functionality to set all the related parameters to be changed automatically. This saves a lot of work for the programmer. On the other hand, the programmer has to know, which parameters are set automatically, an which one he has to set himself.

When new parameters are created within PVM, the programmer has:

- To define the corresponding relations.
- To check the parameter value, entered by the user in the menu, and decide whether it is in a valid range.
- To calculate related parameter values.
- To (often) call some predefined ParaVision relations to make sure that all parameters are set consistently.

Figure 14.1. Scheme of an PVM method



There are two types of relations: **predefined relations** and **user defined relations**. The predefined relations are supplied by the Method Manager program code. With PVM the user can create own, user defined parameters. This means, the user has to create a parameter, build the relation and map the relation to a user defined function.

User defined Relations

User defined relations are the way to **combine own method parameters with any requested functionality.** Within the relation any function can be called, build in relations can be activated or simply a single value can be calculated. The definition for such an user defined relation is quite simple. Here is an example.

```
relations myFov myFovFunction;
```

What's the function of this line?

There is a user defined, method specific parameter called `myFov`. This parameter appears in the PVM-GUI. If the user change the parameter inside the GUI, the relation for this parameter, defined in the above line, is called. This simply means, the function `myFovFunction()` is called, and the code inside is executed.

Predefined Relations

Bruker delivers some toolbox functions for the basic functionality of PVM (described later in this chapter). The library support a lot of basic parameters in PVM, which are common in most methods, such as the RF-pulse, field of view and number of slices. For these parameters exist predefined relations. Such relations are called automatically by changing the corresponding parameter. When e.g. the RF-pulse shape is changed, the corresponding relation will be automatically executed without any programming work to be made by the user. Of course, only functionality common to any method is included in the predefined 'pulsesphape' subroutine. In addition it is possible to change the predefined relations.

You have two possibilities to work with the predefined relations. You can continue it with your own functionality or replace it completely by your own one.

1. Using the predefined relation mostly needs the completion by a method specific function. When a predefined parameter relation is called, a parameter specific relation is called, to give the possibility, to add a user functionality. For the parameter PVM_Fov (or any geometric parameter), the relation for the parameter `PVM_GeometryFn` is executed. To accomplish this, a subroutine must be

mapped to the parameter PVM_GeometryFn. This can simply be done by entering the following line in parsRels.h:

relations PVM_GeometryFn myAddFovRelation;

Now, the predefined relation for the parameter PVM_Fov is called first. After passing this relation, the function myAddFovRelation() is executed subsequently.

2. Replacing the predefined relation and using your own instead. This can simply be done by a redefinition of the parameter's relation.

   relations PVM_Fov myFovRelation;

   If the line above is included in the method code, the predefined relation for PVM_Fov is overwritten, and the relation to the function myFovRelation() is called instead.

Toolboxes *14.3.2*

A set of toolbox functions is delivered with ParaVision from Bruker. The other possibility is to create an user toolbox with own definitions of any functions.

THE BRUKER TOOLKIT

The Bruker toolkit, methTools, may be found in the directory $PvHome/prog/shlib/methTools. Any source file which uses a procedure from this toolkit should contain the include reference:

```
#include "methTools.h"
```

This toolkit provides a lot of functions to calculate most parameters for the methods. It contains e.g. calculations of gradient strengths, phase encoding time, pulse parameters, slice thickness and much more. All functions that are defined inside this Bruker toolkit use the prefix 'PVR_'. Therefore these functions can be easily identified in a method code.

Creating and using functions of the user's toolkit

A template for the creation of a user toolkit may be found under $PvHome/prog/parx/src/usrTools. This can be compiled using exactly the same procedure that was used to compile the Bruker supplied methods, which is described in 'Compiling a method'. If you want to add new source files to this library, you must edit the Makefile and change the definition of the RELOBJS macro.

Example: The C source file named myToolFuncs.c should be part of the user's toolbox. Edit the Makefile and extend the RELOBJS macro by "myToolFuncs.o" to look somewhat like

```
RELOBJS         =  myToolFuncs.o \
                   otherToolFuncs. o
```

This is the same as adding new source files containing procedures of a method. If you want to create a **usrToolKit** library located and named different than the default name 'usrTools' copy the template found under $PvHome/prog/parx/src/usrTools to e.g. $PvHome/prog/parx/src/myToolKit. Then look in the Makefile for the line containing the definition of the OVERLAY macro, which in fact is identical to the **usrTool** overlay. Change it to 'myToolKit' by typing:

```
OVERLAY    =    myToolKit
```

Look for the line containing the definition of the SRCDIR macro, indicating the source directory of your new user toolbox. Check it to be:

```
SRCDIR    =    $(PROGDIR)/parx/src/$(OVERLAY)
```

Look for the line containing the definition of the PARX_TOOLKIT_DIR macro, indicating the location of your new binary library. Check it to be:

```
PARX_TOOLKIT_DIR    =    $(SHLIBDIR)
```

Creation of a New Method *14.4*

A new method can of course be **created from the scratch**, where nothing exists at the beginning. But it is much easier and faster, to **modify an existing method**, which is similar to the one, that should be created as the new method. Following this way saves time and makes it much easier to explain and understand the procedure of the method creation.

Before starting to make changes to an existing method, create a new one by copying in order to keep the old method alive.

In ***"Compilation of the First Method" on page 226*** is described how to compile a method, whose source code is available. This step must have been made successfully, before the following method creation can be used.

The simplest way to create a new method is to modify an existing one. Therefore Bruker delivers a **script called CopyMethod**. It typically resides in $HOME/bin and is a simple script which asks for an existing source method to be copied to a new method. The script automatically copies all files from the source method into the destination directory and converts all strings with the name of the source method to the name of the new method (e.g. if the new method is called two pulse the function **onepulse_setGain** is renamed to **twopulse_setGain**). After copying, the method is compiled and the new method with the new methods name is available, at the moment still functionally identical to the source method.

This new created method is the starting point for the new method.

Now the modifications have to be made in the program code according to the requests of the new method. A number of standard changes are described below. But for the first time, is looks extremely hard to get an overview over the file structures. Therefore the structure of an existing method is described next.

A multi-slice, multi-echo method is used as an example instead of the one-pulse method, because one-pulse does not contain any gradients.

The Structure of a PVM Method *14.5*

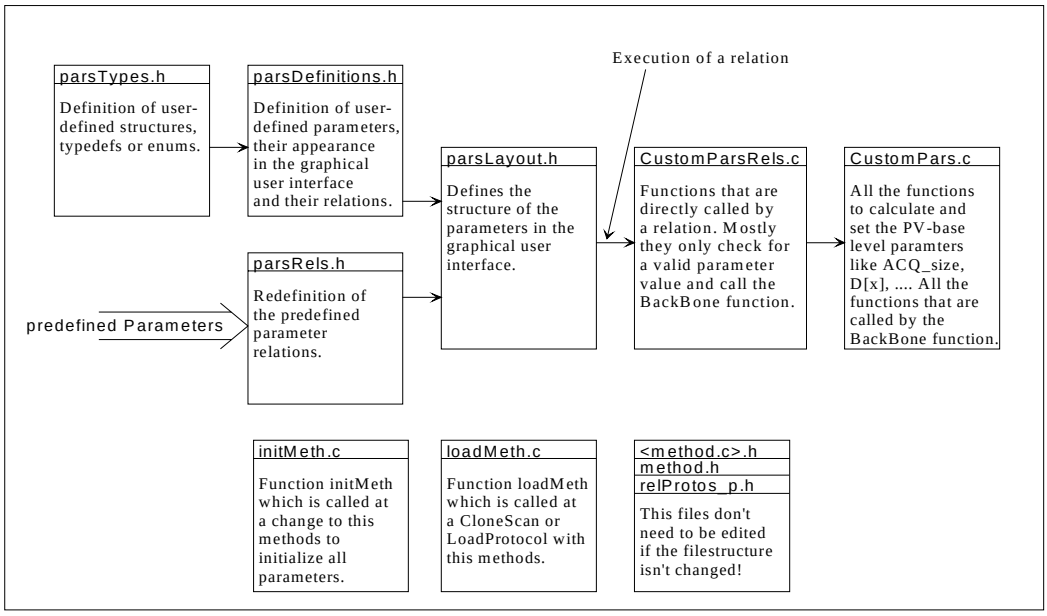
There are two different requirements for the methods manager which have an influence on the structure of the PVM methods.

From the users view, the parameter setup of a method should be made with a **simple, intuitive graphical user interface** where a minimum number of parameters should be involved. On the other hand, every parameter possible should be accessible in order to **handle every special case** of a method. After the data acquisition the acquired images should be ready for analyzing with a minimum amount of work and usually no care should be taken to control a default reconstruction process.

From the programmers view, a good **structure** has to be found to create the **interface between the users needs and the ParaVision environment**. The structure should be simple but expandable to any possible new method requests. The same architecture should be used all time and there should be no need to redefine definitions depended on the method. Therefore a good structured interface between the users parameter input and the different types of parameters used inside ParaVision has to be defined. ParaVision supports a lot of functions to simplify this interface, called **`Parx`**.

Files for a PVM-method *14.5.1*

The examples provided by Bruker always use the same file structure. It is possible to create own file structures, but the Bruker file structure is evaluated and should be an easy way to setup the own methods. The methods directory contains a lot of different header-files and c-files. The following table gives an overview of the functionality of these files. It is not necessary to understand every file description now. It will get much clearer, when you read the next chapters, where the examples will be done.



method.h: Linking of some necessary header files from the compiler library, ParaVision and own methods.

relProtos_p.h: This file contain all prototypes of the methods. It is created automatically by `make cproto`. Don't edit this file!

parsLayout.h: Definition of the method Class. All parameters appearing in the PVM method GUI are combined in this file. This file defines the structure of the menu in **methManag** (the GUI), whether a parameter exits at the main level for input or in a submenu,...

parsTypes.h: Here are the user parameters defined, no matter if they are single `int/double` values, `typedef`-structures or something else.

parsRels.h: Definition of all relations. This file includes the definitions for the change or the completion of predefined relations.

initMeth.c: The procedure **`initMeth`**`()`, which is defined in the file '`initMeth.c`' will be automatically called when the method is selected. This procedure is expected to provide a reasonable initialization for any method specific parameters (which are defined in `methPars.h`, as described above) and is also expected to ensure that the parameters are all consistently set. The goal here must be to always provide a valid starting state.

loadMeth.c: When a method protocol is loaded the method must first be initialized by calling the '**`initMeth`**`()`' procedure (as described above). Then the values of the method parameters are read from the method file. Finally the procedure '**`loadMeth`**`()`' is called to derive the correct values of the base level parameters. This forces the methods programmer to explicitly decide which derivations are to be performed and the order in which they are to be done. Since the final results are dependent on the order in which the derivations are performed, which can have significant effects, the decision was made to make the solution explicit and visible.

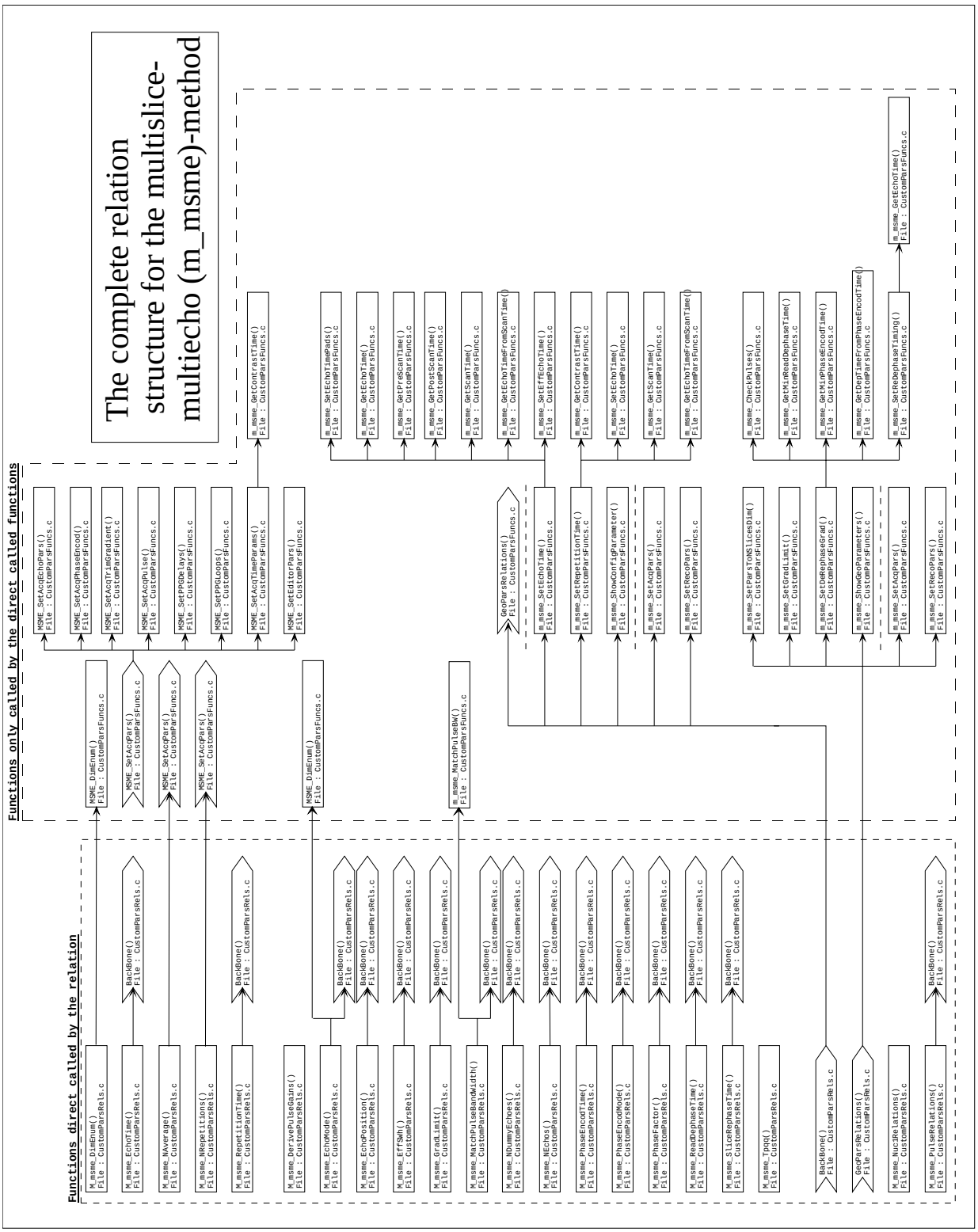
CustomParsRels.c: Here are the functions, which are directly called by a relation. Most of them only check, if the input parameter is within an acceptable range

and call then an other function or relations common to other parameter subroutines.

CustomPars.c: Functions which are called from within a relation. This file includes all functions, which change anything at ParaVision- or base level-parameters (like NI, NA, ACQ_size, ACQ_ns_list, RECO_...) and sets all pulse program and gradient program parameters.

On the next page, the **complete file structure of the multi-slice, multi-echo method** (MSME) is printed. It looks a little bit complex, but piece by piece is explained in order to show the functionality step by step.

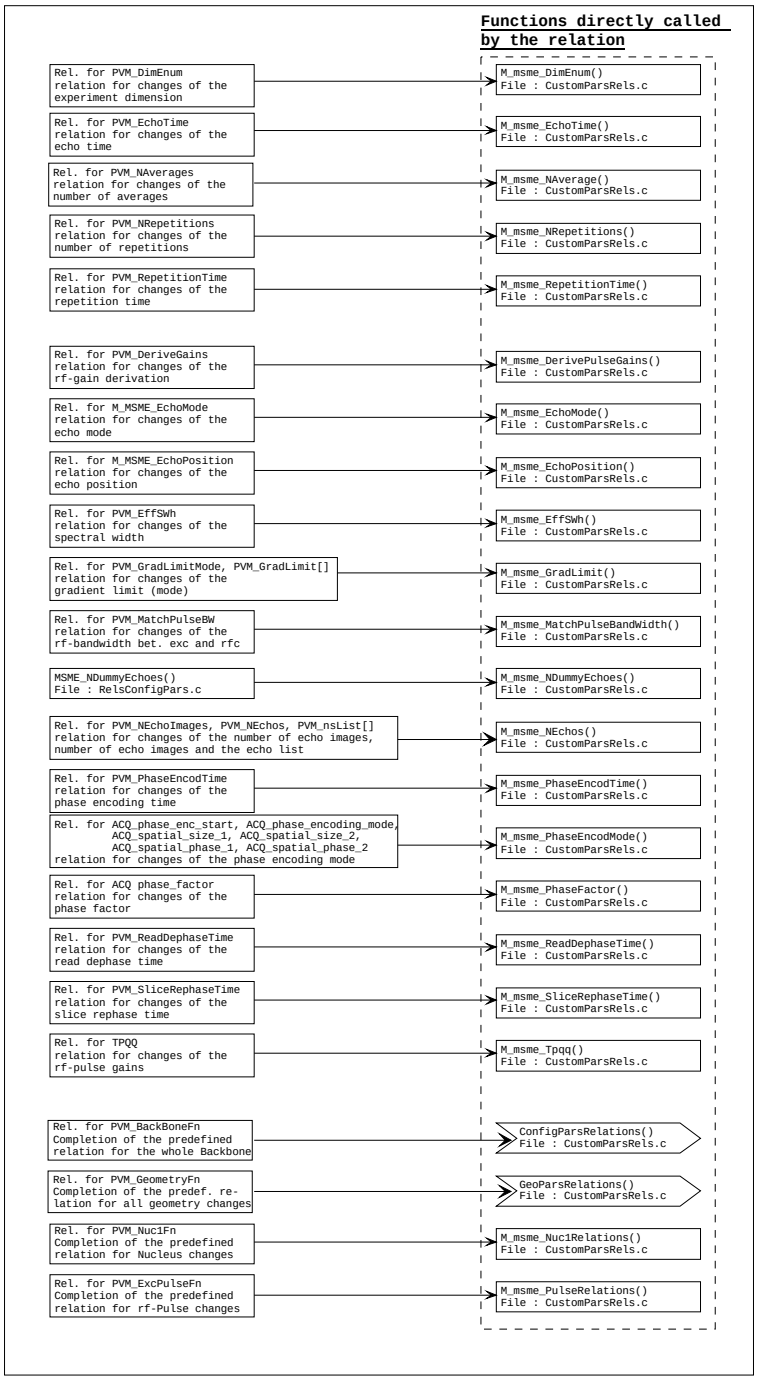
Figure 14.2. Overview of the MSME-relations



Relations for a MSME PVM Method *14.5.2*

The previous diagram shows all functions of the m_msme method, which involve relations. But **which relation is activated by which parameter call**? All the functions in the first column of diagram ***"Mapped relations of the MSME-method" on page 237*** are called directly by a relation. The following diagram shows, which of these functions are called by changes of the individual method parameters.

Figure 14.3. Mapped relations of the MSME-method



Examples and Conventions 14.6

Before you start to program new methods it is important, that you know the conventions used in PVM. You don't have to use all the conventions for your private methods, but it will make your work much easier. After you have be informed about that, you can start to examine the m_msme method and right after that there is an example in which you can modify the m_onepulse method, to create a suppression method.

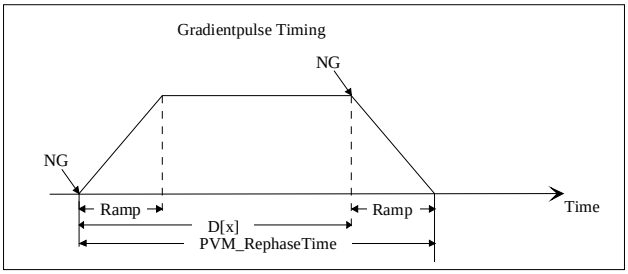
Conventions 14.6.1

There are a few conventions you have to know, when you want to setup a new method. They mainly affect the timing and a few other things.

1. As you may notice in the above figures, there's a **convention about the parameter names**. When a parameter, used inside the method Class (the GUI), is defined from ParaVision, the parameter keeps its original name (ex.: ACQ_phase_mode). Predefined Method Manager parameters use the prefix 'PVM_'. When a parameter is user defined, the parameter gets the prefix 'METHODNAME_' (e.g. M_MSME_). All relations of a method use the prefix '<Methodname>_', in our example 'M_msme_' to mark them as method specific. The functions of a method use the prefix '<methodname>_', in our example 'm_msme_' to mark them. The base level parameters of ParaVision can be included directly in PVM and keep their original name.
2. You must define the filename of your **pulse program** and your **gradientprogram**. This is done by copying the filename into the char arrays 'GRDPROG' and PULPROG. The filenames must have the appendix.r (gradient program) and .ppg (pulse program) but you have to take care of the char arrays. The PULPROG array must contain the complete name of the pulse program file (i.e. PVM_msme2D.ppg) whereas the GRDPROG array must contain the gradient file name without the appendix (i.e. PVM_msme2D).
   Example:
   ```
   strcpy(PULPROG, "PVM_msme2D.ppg");
   strcpy(GRDPROG, "PVM_msme2D");
   ```
3. **All timings used in the PVM source code are calculated in milliseconds**, no matter whether it is a RF-pulse-, gradient- or echo time. If you set the timing parameters in the pulse program, you have to be very careful. The definition for delays (named D[x]) must be in seconds. This means, you have to multiply your calculated timing parameter (in msec) by the factor 1e-3 to get the timing in seconds.
   Example: `D[0] = 1e-3 * PVM_RepetitionTime;`
   The definitions of the pulse length must be in microseconds, so you have to multiply your calculated pulse length by the factor 1e3.
   Example: `P[0] = 1e3 * PVM_ExcPulseLength;`
4. **The calculated timings in the PVM source code contain both ramps of the gradient pulses**, if possible. For example the rephase time. After the slice selection gradient, the spins, dephased during the selective excitation RF-pulse, must be refocused by a gradient pulse. This gradient pulse will be ramped to its maximum value, stay a this value and ramp down to zero. The rephase time is the sum of all these three sections. But if you define the delay parameter (D[x]) for the pulse program, be careful to subtract one ramp time because the next gradient command (NG) must be set like shown in figure ***"Timing of a***

Gradient Pulse" on page 239. If a toolbox function needs a time as input parameter, it is the complete time with both ramps (i.e. `PVM_RephaseTime`).

Figure 14.4. Timing of a Gradient Pulse



5. All calculated **gradient values** in the PVM source code are **in percent** of the maximum gradient strength.
6. All parameters for **spatial resolution** are calculated in **millimeters**.
7. There is a **basic function** in every method called **`BackBone()`**. It refreshes nearly all parameters of a method, no matter if it is necessary or not. It takes only a very short time, to recalculate all parameters, but it is very difficult, do decide which single parameters must be recalculated for each parameter change. So all parameters are recalculated for nearly every parameter change.

Following a Relation *14.6.2*

Now you can observe the way of parameter change followed by a user defined relation. Please take the ***"Overview of the MSME-relations" on page 236***. First, the parameter must be defined in `parsDefinitions.h` and included in the GUI (defined in `parsLayout.h`). It will be described in a following chapter, how this could be done. At this time please accept, that we change a parameter, that appears in the GUI.

The functionality of the PVM_ReadDephaseTime Relation

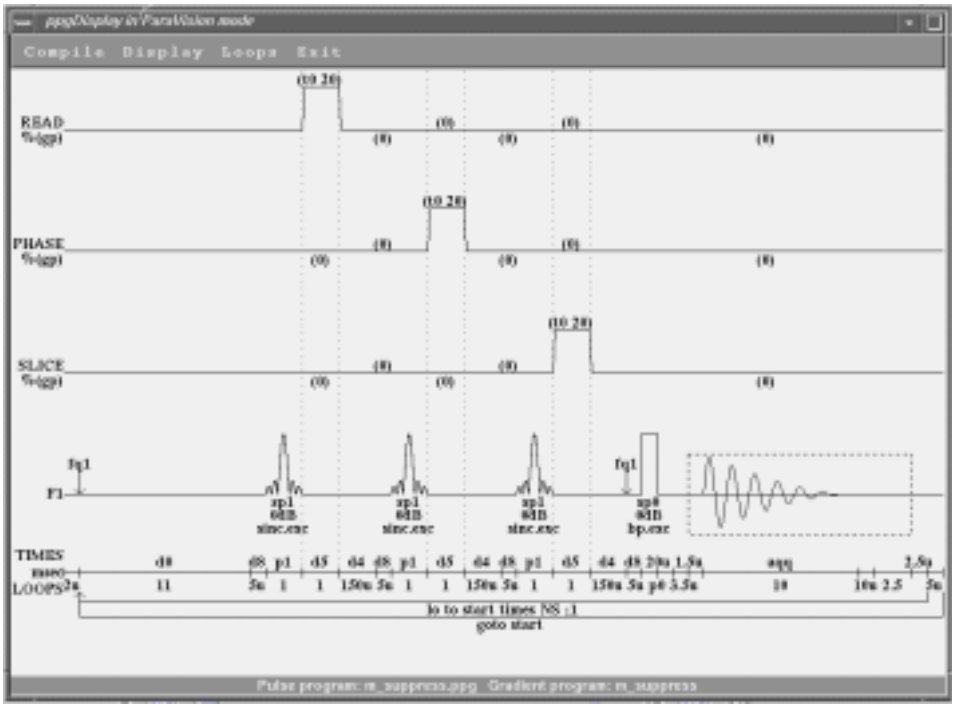
The parameter `PVM_ReadDephaseTime` can be found in the GUI of the m_msme method. Referring to ***"Mapped relations of the MSME-method" on page 237*** the relation of the `PVM_ReadDephaseTime` parameter call the function `M_msme_ReadDephaseTime()`. You will find this function again at ***"Overview of the MSME-relations" on page 236***. This function only checks, whether the time is in a valid range and calls the function `BackBone()`. You can see, that at first all slice parameters are set again (`m_msme_SetParsToNSlicesDim()`) and the gradient limit is recalculated (`m_msme_SetGradLimit()`). This is not necessary but results in an easier file structure. Then the first parameter dependent on `PVM_ReadDephaseTime` is calculated, the rephase gradient strength (`m_msme_SetDeRephaseGrad()`). The function calculates the new rephase gradient, dependent on the rephase time you entered in the GUI. This is followed by some other recalculations that don't depend on the rephase time. The next changes will be in `m_msme_SetEchoTime()`. Because the echo time depends on the rephase time, it will change to a new value. The same happens with the repetition time (`m_msme_SetRepetitionTime()`), because it is a function of the echo

time. Finally the new calculated parameters are set into the gradient trim value matrix (`m_msme_SetAcqTrimGradient()`) and the pulse program delays are set. Between these functions which calculate new parameters dependent on `PVM_SliceRephaseTime` are a lot of functions which recalculate values that don't depend on `PVM_SliceRephaseTime`, as described above, so it is not necessary to call them, but it results in a much easier structure and require only a minimum of time.

Create a Suppression Method *14.6.3*

We can create a simple suppression method with the `m_onepulse` method as base. The suppression method is a simple onepulse with the ability to suppress a part of the NMR-spectrum. First a bandwidth limited selective RF-pulse is applied to the sample, and the excited transverse magnetization is dephased by a gradient pulse spoiler. After the suppression of a spectrum part, the standard onepulse will excite only the remaining spins. So it is possible, to hide a single resonance line of the sample in the NMR-spectrum m_suppress (e.g.: fat, water, etc.).

Figure 14.5. Pulse sequence of the `m_suppress` method



Because all parameters should be edited in a menu, we have to design a simple menu structure, which is shown in the following picture.

Figure 14.6. Menu of the `m_suppress` method

The following steps describe, how to modify the `m_onepulse` method, to create the new `m_suppress` method.

1. First copy the existing `m_onepulse`-method to a new method, `m_suppress` using the `~/bin/CopyMethod` script. Enter the created `m_suppress` directory. All the name conversions where done by the CopyMethod-script, meaning all strings '`m_onepulse`' where changed to '`m_suppress`'. You can check this with the command '`grep m_onepulse *`'.

2. You need an additional RF-pulse which will be called the suppression pulse. It should be independent on the excitation pulse. Thereforem_suppress it is necessary to use a new pulse. A pulse, that can be used for this purpose is should be called `M_SUPPRESS_SatPulse`, and it should be defined as an excitation pulse, whose functionality is identical to the `ExcPulse`. To add the `SatPulse` define its parameter in the file `parsDefinition.h`

   ```
   PV_PULSE parameter
   {
   display_name "RF-SatPulse Shape";
   relations M_suppress_SatPulse;
   } M_SUPPRESS_SatPulse;

   PV_PULSE_LIST parameter
   {
   display_name "Saturation Pulse Shape";
   relations M_suppress_SatPulse;
   } M_SUPPRESS_SatPulseEnum;
   ```

   To display the pulse in the GUI-Editor add the following lines

```
M_SUPPRESS_SatPulseEnum;
M_SUPPRESS_SatPulse;
```

to the GUI layout definition file `parsLayout.h`. This can be done in the class `MethodClass`. The pulse can be added to the `rfPulse` class so simply expand this class by adding the two lines above.

3. Next the `M_SUPPRESS_SatPulse` must be initialized. Open the file `initMeth.c` and initialize the `SatPulse` with the following lines (this can be done right after the initialization of the `M_SUPPRESS_ExcPulse`:

```
PVR_InitRFPulse(
!ParxRelsParHasValue("M_SUPPRESS_SatPulse"),
Excitation,
"gauss100.exc",
3.0,
30.,
PVM_DeriveGains,
90.,
1,
1,
&M_SUPPRESS_SatPulse);


PVR_RFPulseFileNameToEnum(
"M_SUPPRESS_SatPulseEnum",
&M_SUPPRESS_SatPulseEnum,
M_SUPPRESS_SatPulse.filename,
Excitation);
```

4. All you have done now, is to define a new pulse, put it to the GUI and initialize it with some parameters. You can compile the method, and you will see, you have all the functionality you expect from a pulse in your GUI. But you must create the relations which are called by any parameter changes of the `SatPulse`. Therefore open the file `CustomPars.c` and add the two functions, which are called by the SatPulse relations:

```
void M_suppress_SatPulse()
{
PVR_RFPulse(&M_SUPPRESS_SatPulse,
Excitation,
PVM_DeriveGains,
1,
1);


PVR_RFPulseFileNameToEnum(
"M_SUPPRESS_SatPulseEnum",
&M_SUPPRESS_SatPulseEnum,
M_SUPPRESS_SatPulse.filename,
Excitation);

BackBone();
}
```

```
void M_suppress_SatPulseEnum()
{
PVR_RFPulseEnumToFileName("M_SUPPRESSSatPulseEnum",
&M_SUPPRESS_SatPulseEnum,
M_SUPPRESS_SatPulse.filename,
Excitation);

ParxRelsParRelations("M_SUPPRESS_SatPulse.filename", No);

}
```

5. Now you have created the whole functionality for the new suppression pulse! The next thing you have to do, is adding the pulse to the pulse program, to decide, when the pulse must be applied. Therefore edit the pulse program file `m_suppress.ppg` in the following way

```
...
Start, d0 fq1:f1
suppress, d8
p1:sp1           ph0
20u
lo to suppress times 3
...
```

These 4 lines (from `suppress`, to `times 3`) will put out the `SatPulse`, followed by a delay of 20 µsec. This is done 3 times. The pulse program file should be copied to `$(PvHome)/exp/stan/nmr/lists/pp`.
To use this pulse program within your method, you must define it in `initmeth.c` (this should be done automatically by the `CopyMethod` script, but please check it).

```
strcpy(PULPROG, "m_suppress.ppg");
strcpy(GRDPROG, "\0");
```

Now it is time, to add some gradients.

6. Now you have created the method with a new RF-pulse! The next you have to do, is adding some spoiler gradients, to dephase the magnetization created by each `SatPulse`. Edit the pulse program file `m_suppress.ppg` in the following way

```
...
Start, d0 fq1:f1; this line already exists
suppress, d8; this line already exists
p1:sp1           ph0; this line already exists
d5:ngrad
d4:ngrad
lo to suppress times 3; this line already exists
...
```

Now, in each loop a gradient is active after the RF-pulse. It is switched on at the line `d5:ngrad` with a duration of `d5`, and switched of at `d4:ngrad` with a pause of `d4`. Because you use some gradients (spoilers) and `m_onepulse` doesn't, we have to create a gradient program. This is called `m_suppress.r`, and exist of the following lines:

```
 {(t0)   | (0)   | (0) }
```

```
{(0)    | (0)   | (0) }
{(0)    | (t0) | (0) }
{(0)    | (0)   | (0) }
{(0)    | (0)   | (t0)}
{(0)    | (0)   | (0) }
```

This file has the following functionality. At the first `ngrad` in the pulse program it outputs the value of `ACQ_trim[0]` to the read gradient. The second `ngrad` reset all gradients to zero, the third `ngrad` outputs the value of `ACQ_trim[0]` to the phase gradient, the next make a reset, five outputs the value of `ACQ_trim[0]` to the slice gradient and the last resets the gradients again.
The new pulse program file should be copied to `$(PvHome)/exp/stan/nmr/lists/pp` and the gradient program to `$(PvHome)/exp/stan/nmr/lists/gp`.
To use these pulse- and gradient program within your method, you must define them in `initmeth.c`

```
strcpy(PULPROG, "m_suppress.ppg");
strcpy(GRDPROG, "m_suppress");
```

7. As noticeable, we have added two new parameters to the pulse program (`d4, d5`) and one new parameter (`ACQ_trim[0]`) to the gradient program. These parameters must be filled with useful values. `d4` is the gradient ramp time, therefore it is predefined in PVM. So open the file `parsDefinitions.h` and add the definition of the new parameters.

```
double parameter
{
display_name "SpoilerLength";
relations M_suppress_SpoilerLength;
units "ms";
} M_SUPPRESS_SpoilerLength;

int parameter
{
display_name "SpoilerAmplitude";
relations M_suppress_SpoilerAmplitude;
units "%";
} M_SUPPRESS_SpoilerAmplitude;

double parameter
{
display_name "Grad Delay";
units "ms";
} M_SUPPRESS_GradDelay;
```

`M_SUPPRESS_GradDelay` is a value, which defines an additional delay to the gradient ramp time in the pulse program. After this is done, the parameters can be added to the class `MethodClass` in `parsLayout.h`.

```
M_SUPPRESS_SpoilerLength;
M_SUPPRESS_SpoilerAmplitude;
```

Before they can be used, they should be initialized by a useful value in `initMeth.c`

```
PVM_RampTime = PVR_GetGradientRampTime();

M_SUPPRESS_GradDelay    =
(PVR_GetGradientRiseTime() - PVM_RampTime)/2.0;

Set(M_SUPPRESS_MinDelay, 0.01, 100000, 0.01);

if (M_SUPPRESS_GradDelay < M_SUPPRESS_MinDelay)
M_SUPPRESS_GradDelay = M_SUPPRESS_MinDelay;

Set(M_SUPPRESS_SpoilerAmplitude, -100.0, 100.0, 20);
Set(M_SUPPRESS_SpoilerLength, 2 * (PVM_RampTime +
M_SUPPRESS_GradDelay), 1e6, 5.0);
```

When you compile your work, you should see the two parameters correctly initialized in the PVM-GUI, but the functionality of the new parameters must be defined first. Therefore, the PulseProgramTool will not work now, because the new parameters must be copied to d4, d5 and ACQ_trim[0], which are defined in the gradient- and pulse program.

8. The next thing to do, is to create the functions, which are called by the relations of the user defined parameters. The definition of these functions is located in `CustomParsRels.c`. Please open this file and add the two functions for the new parameters, which are called by the relation:

```
void M_suppress_SpoilerLength()
{
M_SUPPRESS_SpoilerLength =
MAX_OF(M_SUPPRESS_SpoilerLength,  2.0  *  (PVM_RampTime  +
M_SUPPRESS_GradDelay));
M_SUPPRESS_SpoilerLength =
MIN_OF(M_SUPPRESS_SpoilerLength, 100.0);

BackBone();
}

/************************/

void M_suppress_SpoilerAmplitude()
{
M_SUPPRESS_SpoilerAmplitude =
MAX_OF(M_SUPPRESS_SpoilerAmplitude, -100.0);
M_SUPPRESS_SpoilerAmplitude =
MIN_OF(M_SUPPRESS_SpoilerAmplitude, 100.0);

BackBone();
}
```

Both functions simply check, whether the parameter is in a valid range and call the function `BackBone()`. The `BackBone()` function itself calls all functions to recalculate the methods parameter. Therefore we need to complete some functions which are called by the `BackBone()` for the new parameters or add some new one.

9. Now it is time to set the gradient and pulse program parameters. The pulse program parameters can simply be set by adding the new parameters to the

function m_suppress_SetPPGDelays() in CustomPars.c. This function already contains the settings necessary for the m_onepulse method. Complete the function simply by adding the following lines:

```
D[4] = 1e-3 * (PVM_RampTime+M_SUPPRESS_GradDelay);
D[5] = 1e-3 * (M_SUPPRESS_SpoilerLength) - D[4];
```

For the setting of the gradient value it is useful, to create a new function, because the m_onepulse function doesn't contain any gradient settings. For the overview it is much easier, to separate this functionality from the other. So add a new function called m_suppress_SetGradAmp ().

```
void m_suppress_SetGradAmp ()
{
double XYZGradScale[3];
XYZGradScale[0] = 1.0;
XYZGradScale[1] = 1.0;
XYZGradScale[2] = 1.0;

ACQ_n_trim = 1;
PARX_call_rels("ACQ_n_trim");

/* Spoiler */
(void) PVR_SetAcqTrim(M_SUPPRESS_SpoilerAmplitude,
XYZGradScale,0);
}
```

Now you have to take care, that these functions is called by the BackBone() function. m_suppress_SetAcqPars() in the file CustomPars.c is the head function, which calls all functions, that are related to ACQ parameters. So simply add the function call m_suppress_SetGradAmp (); to this function, to guarantee that it is called correctly.
Now you can check, whether all changes are done correctly. Compile your method, open the PVM-GUI and check your settings in the PulseProgramTool. At this time, you have entered 3 RF-pulses and 3 gradient pulses before the original m_onepulse method.

10. Next, we have to implement, that the suppression pulse can have another frequency than the excitation pulse. Because we want to edit the frequency offset, we have to create a new parameter, display it in the GUI and create a relation. First define the parameter in parsDefinitions.h

```
double parameter
{
display_name "SuppressionOffset";
relations M_suppress_SuppressionOffset;
units "Hz";
} M_SUPPRESS_SuppressionOffset;
```

and define a initialization value in initMeth.c

```
Set(M_SUPPRESS_SuppressionOffset, -1e7, 1e7, 1000.0);
/* offset in Hz */
```

After that is done, add the parameter to the GUI. Simply do this by adding the

following line in parsLayout.h

```
M_SUPPRESS_SuppressionOffset;
```

Then add the function, which is called directly by the relation. This function must be inserted in CustomParsRels.c

```
void M_suppress_SuppressionOffset()
{
M_SUPPRESS_SuppressionOffset =
MAX_OF(M_SUPPRESS_SuppressionOffset,   -(BF1   *   1e6   *
0.001));
M_SUPPRESS_SuppressionOffset =
MIN_OF(M_SUPPRESS_SuppressionOffset,(BF1 * 1e6 * 0.001));

BackBone();
}
```

Now be careful, that the correct ACQ parameters are set by a call of the BackBone() function. Therefore the ParaVision parameter ACQ_O1_list must be 'filled' with the offset values. In the file CustomPars.c exist a function which is called m_suppress_SetAcqFreqList(). The function is build in as default but includes no code. Simply add the ACQ parameters to this function by entering the following lines.

```
ACQ_O1_list_size = 2;
PARX_change_dims("ACQ_O1_list",ACQ_O1_list_size);
ACQ_O1_list[0] = M_SUPPRESS_SuppressionOffset;
ACQ_O1_list[1] = 0.0;
```

These lines create a ACQ_O1_list with 2 entries and fill them with the offset for the suppression pulse (ACQ_O1_list[0]) and the resonance frequency (ACQ_O1_list[1]) for the excitation pulse.

11. Last you have to do is to guarantee, that the repetition time is set correctly. You've simply add some pulses and gradients to the pulse program, but the delay between two scans must be recalculated. Therefore, please open the fil CustomPars.c and search for the function m_suppress_GetScanTime(). This function calculates the time, needed from the first gradient/pulse to the last of one scan. Because you added three gradients and RF-pulses, this scan time will increase in time. For the calculation, you have to add the new time consuming components.
    Add or complete the following lines:
    ```
    ...
    double p0, p1, d0, d4, d5, d8;
    ...
    d4 = PVM_RampTime;
    d5 = M_SUPPRESS_SpoilerLength;
    p1 = M_SUPPRESS_SatPulse.length;
    methTime = (d8 + p1 + d5 + d4) * 3.0;
    methTime +=...
    ```

Now the suppression method is complete. Compile the function and start it within PVM. You can try to use a water-fat sample and suppress one of the resonance lines. Therefore change the suppression pulse in bandwidth and offset and try to minimize one of the lines.

Further PVM-Features 14.7

Adding Debug Messages to Your Relations 14.7.1

Often during development and testing of a new method it is desirable to have print statements present within the relations of your method both to help trace the execution and to find errors. In the examples that have been provided, you will notice that the macro 'DB_MSG' is used for this purpose. This macro is used in a very similar fashion to the normal 'printf' procedure (which you may also use should you so wish) but has the advantage that it is very easy to switch the debugging messages on/off for individual files or for the entire method.

To use the DB_MSG macro, you must first edit the Makefile and ensure that the definition of the STD_DEFINES macro *doesn't* contain the string '-DNDEBUG'. If STD_DEFINES does contain '-DNDEBUG', this will have the effect of globally suppressing, or turning off, the DB_MSG macro for the entire method. This is usually done when you are finished with development and debugging. It is the state in which Bruker source code is delivered.

The second step in using the DB_MSG macro is to select the source files from which you want to see debug messages. Edit those files and ensure that the following lines exist at or near the top of the file:

```
#define DEBUG 1
#define DB_MODULE 1
#define DB_LINE_NR 1
```

Setting the DEBUG compiler constant to 1 will cause the DB_MSG macro to be activated within that source file, setting it to 0 will cause them to be deactivated. Setting the DB_MODULE compiler constant to 1 will cause every message that is output with DB_MSG to be preceded by the path name of this source file. Setting the DB_LINE_NR compiler constant to 1 will cause every message that is output with DB_MSG to be preceded by the line number in the source file where the DB_MSG macro appears.

You will notice that the DB_MSG macro always appears with its arguments contained within two sets of parentheses. THIS IS NOT AN ERROR! It is an unfortunate necessity so that the full argument list of the DB_MSG macro can be correctly used internally as the argument list of a 'printf' procedure call. Feel free to add more DB_MSG lines anywhere you desire within the source code.

Now the method must be recompiled. After recompilation you will receive debug messages from those source files in which debug messages were enabled.

How should a method be compiled after any changes? 14.7.2

If you have made any changes in any of the '#include' statements in ANY of the files, you must enter the command:

```
make depend
```

If you have made any changes in the relations, you must enter the command:

```
make cproto
```

Then you can compile and install your method with the command:

```
make install
```

The 'make cproto' command causes the file 'relsProto_p.h' to be updated. This file contains forward function references for all of the non-static procedures in your relations files. This makes it possible for the compiler to do extra checking to ensure that you are using all of these procedures correctly.

The 'make depend' command causes the dependencies between different source files to be correctly entered in the Makefile. This makes it possible for the 'make' command to correctly compare the date and time when the different files were last changed and to only compile the files which must be compiled.

Linking the Pulse and Gradient Programs into Your Method *14.7.3*

When a method is used to perform a measurement, a pulse program and gradient program are an essential part of the overall method. If your method is used in a context in which patient safety is a factor, it is essential to guarantee that the correct pulse and gradient programs are always used in conjunction with your method. The Methods Manager provides the capability to link these programs into the method. Every time that a measurement is started, ParaVision will attempt to extract the pulse and gradient programs from the method as one of the final steps prior to starting the measurement. This will ensure that the pulse and gradient programs used in a routine situation will be exactly those that you intended.

During the development of your method you will want to ensure that your method is using pulse and gradient programs that are available on the disk as ASCII files. This will make it easier to develop these programs. To do this, simply ensure that your method will derive the values of the GRDPROG and PULPROG parameters. This is the standard procedure that is already well known to all methods developers from the past.

When you have completed the development of your pulse and gradient programs and you want them to be 'hardwired' into your method, you must do the following:

1. Enter the file initMeth.c and define the pulse- and gradient program as 'ParaVision'.
   ```
   strcpy(PULPROG, "ParaVision.ppg");
   strcpy(GRDPROG, "ParaVision");
   ```
2. Edit the Makefile for your method and make the following changes:
   - change the GRDPROG macro definition. If you don't want the gradient program 'hardwired' into your method, set this to "none". Otherwise, set this to the filename of your gradient program. Don't forget to include the '.r' suffix as part of the definition of GRDPROG.

   -change the PULPROG macro definition. If you don't want the pulse program 'hardwired' into your method, set this to "none", otherwise, set this to the filename of your pulse program. Don't forget to include the '.ppg' suffix as part of the definition of PULPROG.

   -change the PULPROG_INC macro definition. If your pulse program contains '#include' directives, and if the files which are included do not all reside in the same source directory as does your method, you may specify a (single) additional directory here which will also be searched to resolve the include ref-

erences in your pulse program. If no '#include' directives were used, or if all of the 'included' files are in the same source directory as the rest of your method, set this to "none".

When you now recompile your method and use it within ParaVision, you will notice that the GRDPROG parameter will be given the default value of "ParaVision.r" and the PULPROG parameter will be given the default value of "ParaVision.ppg". When a measurement is started, one of the final actions prior to starting the measurement will be to extract the pulse and gradient programs contained in your method. They will always be extracted using these default names.

Troubleshooting *14.8*

1. I changed my method, but when I open the PVM editor, the old functionality appears.

   - Close and open ParaVision, because all methods are linked at the start.
   - Be sure that you change to your private method (noted by a lowercase start letter)

   - The methods will be listed in the order in which they are found. When assembling the list of available methods, the directories named in ParxMethodSearchPath are searched first, then $PvHome/prog/parx/pub and finally $PvHome/prog/parx/methods is searched. If two methods are found which have the same name, only the first found will be available.

2. ParaVision tell me, that a PV-session is already running, but it isn't.

   - This may happen due to some irregular parameter settings during the method development. Edit the file $(PvHome)/prog/curdir/<user>/ParaVision/activeSessions and delete all entries to fix this problem.

3. The Scan Control window opens and close immediately, after a scan is loaded. This may happen due to some irregular parameter settings during the method development. Edit the file $(PvHome)/prog/curdir/<user>/ParaVision/pvScan/Scan Overview and delete all entries to fix this problem.

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