VnmrJ Imaging User Guide

Varian MR Systems
With VnmrJ 2.2B Software
Pub. No. 01-999344-00, Rev. A 0207

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SAFETY PRECAUTIONS

The following warning and caution notices illustrate the style used in Varian manuals for safety precaution notices and explain when each type is used:

This symbol might be used on warning labels attached to the equipment. When you see this symbol, refer to the relevant manual for the information referred to by the warning label.

WARNING: ***Warnings*** **are used when failure to observe instructions or precautions could result in injury or death to humans or animals, or significant property damage.**

CAUTION: ***Cautions*** **are used when failure to observe instructions could result in serious damage to equipment or loss of data.**

Warning Notices

Observe the following precautions during installation, operation, maintenance, and repair of the instrument. Failure to comply with these warnings, or with specific warnings elsewhere in Varian manuals, violates safety standards of design, manufacture, and intended use of the instrument. Varian assumes no liability for customer failure to comply with these precautions.

WARNING: **Persons with implanted or attached medical devices such as pacemakers and prosthetic parts must remain outside the 5-gauss perimeter from the centerline of the magnet.**

The superconducting magnet system generates strong magnetic fields that can affect operation of some cardiac pacemakers or harm implanted or attached devices such as prosthetic parts and metal blood vessel clips and clamps.

Pacemaker wearers should consult the user manual provided by the pacemaker manufacturer or contact the pacemaker manufacturer to determine the effect on a specific pacemaker. Pacemaker wearers should also always notify their physician and discuss the health risks of being in proximity to magnetic fields. Wearers of metal prosthetics and implants should contact their physician to determine if a danger exists.

Refer to the manuals supplied with the magnet for the size of a typical 5-gauss stray field. This gauss level should be checked after the magnet is installed.

WARNING: **Keep metal objects outside the 10-gauss perimeter from the centerline of the magnet.**

The strong magnetic field surrounding the magnet attracts objects containing steel, iron, or other ferromagnetic materials, which includes most ordinary tools, electronic equipment, compressed gas cylinders, steel chairs, and steel carts. Unless restrained, such objects can suddenly fly towards the magnet, causing possible personal injury and extensive damage to the probe, dewar, and superconducting solenoid. The greater the mass of the object, the more the magnet attracts the object.

Only non ferromagnetic materials—plastics, aluminum, wood, nonmagnetic stainless steel, etc.—should be used in the area around the magnet. If an object

is stuck to the magnet surface and cannot easily be removed by hand, contact Varian service for assistance.

Refer to the manuals supplied with the magnet for the size of a typical 10-gauss stray field. This gauss level should be checked after the magnet is installed.

WARNING: **Only qualified maintenance personnel shall remove equipment covers or make internal adjustments.**

Dangerous high voltages that can kill or injure exist inside the instrument. Before working inside a cabinet, turn off the main system power switch located on the back of the console.

WARNING: **Do not substitute parts or modify the instrument.**

Any unauthorized modification could injure personnel or damage equipment and potentially terminate the warranty agreements and/or service contract. Written authorization approved by a Varian, Inc. product manager is required to implement any changes to the hardware of a Varian NMR spectrometer. Maintain safety features by referring system service to a Varian service office.

WARNING: **Do not operate in the presence of flammable gases or fumes.**

Operation with flammable gases or fumes present creates the risk of injury or death from toxic fumes, explosion, or fire.

WARNING: **Leave area immediately in the event of a magnet quench.**

If the magnet should quench (sudden appearance of gasses from the top of the dewar), leave the area immediately. Sudden release of helium or nitrogen gases can rapidly displace oxygen in an enclosed space creating a possibility of asphyxiation. Helium will displace air from the top of a room and cold nitrogen can displace air from the lower levels of a room. Do not return until the oxygen level returns to normal.

WARNING: **Avoid helium or nitrogen contact with any part of the body.**

Cold gasses or liquids (helium and nitrogen) contacting the body can cause an injury similar to a burn. Never place your head over the helium and nitrogen exit tubes on top of the magnet. If cold gasses or liquids contact the body, seek immediate medical attention, especially if the skin is blistered or the eyes are affected.

WARNING: **Do not look down the upper barrel.**

Unless the probe is removed from the magnet, never look down the upper barrel. You could be injured by the sample tube as it ejects pneumatically from the probe.

WARNING: **Do not exceed the boiling or freezing point of a sample during variable temperature experiments.**

A sample tube subjected to a change in temperature can build up excessive pressure, which can break the sample tube glass and cause injury by flying glass

and toxic materials. To avoid this hazard, establish the freezing and boiling point of a sample before doing a variable temperature experiment.

WARNING: **Support the magnet and prevent it from tipping over.**

The magnet dewar has a high center of gravity and could tip over in an earthquake or after being struck by a large object, injuring personnel and causing sudden, dangerous release of nitrogen and helium gasses from the dewar. Therefore, the magnet must be supported by at least one of two methods: with ropes suspended from the ceiling or with the antivibration legs bolted to the floor. Refer to the *Installation Planning Manual* for details.

WARNING: **Do not remove the relief valves on the vent tubes.**

The relief valves prevent air from entering the nitrogen and helium vent tubes. Air that enters the magnet contains moisture that can freeze, causing blockage of the vent tubes and possibly extensive damage to the magnet. It could also cause a sudden dangerous release of nitrogen and helium gases from the dewar. Except when transferring nitrogen or helium, be certain that the relief valves are secured on the vent tubes.

WARNING: **On magnets with removable quench tubes, keep the tubes in place except during helium servicing.**

On Varian 200- and 300-MHz 54-mm magnets only, the dewar includes removable helium vent tubes. If the magnet dewar should quench (sudden appearance of gases from the top of the dewar) and the vent tubes are not in place, the helium gas would be partially vented sideways, possibly injuring the skin and eyes of personnel beside the magnet. During helium servicing, when the tubes must be removed, follow carefully the instructions and safety precautions given in the manual supplied with the magnet.

Caution Notices

Observe the following precautions during installation, operation, maintenance, and repair of the instrument. Failure to comply with these cautions, or with specific cautions elsewhere in Varian manuals, violates safety standards of design, manufacture, and intended use of the instrument. Varian assumes no liability for customer failure to comply with these precautions.

CAUTION: **Keep magnetic media, ATM and credit cards, and watches outside the 5-gauss perimeter from the centerline of the magnet.**

The strong magnetic field surrounding a superconducting magnet can erase magnetic media such as floppy disks and tapes. The field can also damage the strip of magnetic media found on credit cards, automatic teller machine (ATM) cards, and similar plastic cards. Many wrist and pocket watches are also susceptible to damage from intense magnetism.

Refer to the manuals supplied with the magnet for the size of a typical 5-gauss stray field. This gauss level should be checked after the magnet is installed.

CAUTION: **Keep the PCs, (including the LC STAR workstation) beyond the 5-gauss perimeter of the magnet.**

Avoid equipment damage or data loss by keeping PCs (including the LC workstation PC) well away from the magnet. Generally, keep the PC beyond the 5-gauss perimeter of the magnet. Refer to the *Installation Planning Guide* for magnet field plots.

CAUTION: **Check helium and nitrogen gas flow meters daily.**

Record the readings to establish the operating level. The readings will vary somewhat because of changes in barometric pressure from weather fronts. If the readings for either gas should change abruptly, contact qualified maintenance personnel. Failure to correct the cause of abnormal readings could result in extensive equipment damage.

CAUTION: **Never operate solids high-power amplifiers with liquids probes.**

On systems with solids high-power amplifiers, never operate the amplifiers with a liquids probe. The high power available from these amplifiers will destroy liquids probes. Use the appropriate high-power probe with the high-power amplifier.

CAUTION: **Take electrostatic discharge (ESD) precautions to avoid damage to sensitive electronic components.**

Wear grounded antistatic wristband or equivalent before touching any parts inside the doors and covers of the spectrometer system. Also, take ESD precautions when working near the exposed cable connectors on the back of the console.

Radio-Frequency Emission Regulations

The covers on the instrument form a barrier to radio-frequency (rf) energy. Removing any of the covers or modifying the instrument may lead to increased susceptibility to rf interference within the instrument and may increase the rf energy transmitted by the instrument in violation of regulations covering rf emissions. It is the operator's responsibility to maintain the instrument in a condition that does not violate rf emission requirements.

Introduction

This manual describes the general procedures used for imaging and localized spectroscopy experiments on Varian, Inc. NMR spectrometers using the VnmrJ 2.2B imaging interface.

- Chapter 1, “Setting Up an Imaging System,” describes the steps necessary for setting up a spectrometer for imaging experiments. Most of procedures in this chapter are done during system installation, and need not be repeated.
- Chapter 2, “Running an Imaging Study,” describes the typical steps in setting up and running a VnmrJ imaging study.
- Chapter 3, “Prescan,”describes the prescan functions, their purpose, experimental setup, and outcome.
- Chapter 4, “Protocols for Imaging,” describes some of the pulse sequences for imaging available in Varian NMR spectrometers.
- Chapter 5, “Image Viewing and Review Queue,” describes the image display and manipulation tools and the Review Queue.
- Chapter 6, “Interactive Image Planning,” describes the interactive image planning functions available in VnmrJ.
- Chapter 7, “Image Processing in VnmrJ,” describes the image processing functions available in VnmrJ.
- Chapter 8, “Math Processing,” describes the Image Math software, which is used in conjunction with the VnmrJ Math Tool.
- Chapter 10, “CSI Data Processing,” describes a tool for easy processing of chemical shift image data (CSI).
- Chapter 9, “Digital Eddy Current Compensation,” describes the digital eddy current compensation (DECC) module and decctool, the associated software interface.
- Chapter A, “VnmrJ Imaging Interface,” describes the VnmrJ imaging interface.
- Chapter B, “Locator,” describes the VnmrJ Locator.
- Chapter D, “NMR Imaging Concepts,” describes the basic concepts necessary to understand MRI experiments.
- Chapter C, “DICOM® Conformance Statements,” describes the DICOM conformance statement for VnmrJ.

Notational Conventions

The following notational conventions are used throughout all Varian NMR manuals:

- Typewriter-like characters identify VnmrJ and UNIX commands, parameters, directories, and file names in the text of the manual. For example:

  The `shutdown` command is in the `/etc` directory.

- The same type of characters show text displayed on the screen, including the text echoed on the screen as you enter commands during a procedure. For example:

  ```
  Self test completed successfully.
  ```

- Text shown between angled brackets in a syntax entry is optional. For example, if the syntax is `seqgen spuls<.c>`, entering the "`.c`" suffix is optional, and typing `seqgen spuls.c` or `seqgen spuls` is functionally the same.

- Lines of text containing command syntax, examples of statements, source code, and similar material are often too long to fit the width of the page. To show that a line of text had to be broken to fit into the manual, the line is cut at a convenient point (such as at a comma near the right edge of the column), a backslash (\) is inserted at the cut, and the line is continued as the next line of text. This notation will be familiar to C programmers. Note that the backslash is not part of the line and, except for C source code, should not be typed when entering the line.

- Because pressing the Return key is required at the end of almost every command or line of text you type on the keyboard, use of the Return key will be mentioned only in cases where it is *not* used. This convention avoids repeating the instruction "press the Return key" throughout most of this manual.

- Text with a change bar (like this paragraph) identifies material new to VnmrJ that was not in the previous version of VnmrJ. Refer to the *VnmrJ Release Notes* for a description of new features to the software.

Purpose of This Manual

This manual should instruct both new and experienced users. If you are a new user, this should be your reference for imaging and localized spectroscopy applications. Because we want to spare new users the duplication of effort required to learn both old and new, we have explicitly left out references to the older methods in most of this manual.

Chapter 1. Setting Up an Imaging System

Sections in this chapter:

This chapter describes the typical steps in setting up VnmrJ imaging system before running an imaging study.

1.1 Configuring VnmrJ for Imaging

This section describes how to configure VnmrJ for imaging:

The imaging software must be installed before configuring an NMR system for imaging. Imaging software includes macros, menus, parameters, and executable used for imaging. Selecting the option **Imaging_or_Triax** in **General options** during VnmrJ installation (see the manual *VnmrJ Installation and Administration*) installs the imaging software. **Imaging_Sequences** is a **Passworded option**. The password is provided on a certificate that is included if the Imaging_Sequences option is purchased.

Verifying Imaging Software is Installed

Open a terminal window and type the following command and verify that the imaging software was installed:

```
ls /vnmr/imaging
```

The software is loaded if the following libraries and directories are present: `decclib`, `eddylib`, `gradtables`, `shuffler`, and `templates`. If the software is not present, follow the procedure in the manual *VnmrJ Installation and Administration*, but check only **Imaging_or_Triax**. Optionally check **Imaging_Sequences** and supply the required password.

Setting Up Imaging User Accounts

Refer to the *VnmrJ Installation and Administration* manual for instructions and information on setting up all user accounts.

1.2 System Settings for Using Imaging Pulse Sequences

This section lists the necessary actions to be taken before using imaging pulse sequences.

Turning on the Air or Water Cooling Turned

Air or water cooling systems must be enabled for gradient experiments. Cooling is necessary to remove the heat buildup in the bore of the magnet caused by the use of gradient and shim coils. Gradients systems are usually equipped with protection devices to detect and shut down the amplifier in the absence of either air or water flow.

Turning on the Gradient Amplifier

The gradient amplifier must be turned on and enabled before proceeding with the initial setup procedure. Be aware that *X1*, *Y1*, and *Z1* shimming is done with the gradient coils and that the amplifiers can generate a small dc offset current that must be corrected by shimming.

Turning on the Shim Power Supply

The shim power supply must be turned on for shimming purposes during experiments. Air or water cooling is employed to remove the excess heat buildup in the bore of the magnet from high shim currents. Turn off the shim power supply if the air or water cooling is turned off or the system is not used for extensive periods.

Creating a Gradient Calibration File

Imaging systems can be equipped with either a single gradient coil or multiple gradient coils. To set up the gradient calibration file, see 1.3 "Setting the gcoil Parameter," page 21.

The gradient calibration information, or file, corresponding to each coil must exist in the `/vnmr/imaging/gradtables` directory. Calibration files for Varian supplied coils are included in this directory. Use the `creategtable` macro to create custom gradient calibration file.

Loading Eddy Current Compensation Files

Use the decctool program (open **Tools** -> **System Settings** and click on **Gradients and ECC**), described in Chapter 9, "Digital Eddy Current Compensation," to load the appropriate file on systems equipped with digital eddy current compensation (DECC).

Calibrating rf Pulse

The rf pulse calibration and `pulsecal` entry must be done as described in section 1.6 "Calibrating the Pulse Length," page 24. The rf coil must be set as described in "Selecting an RF Coil," page 22.

Imaging sequences expect the rf calibration information to be present in the `pulsecal` file. The `rfcoil` parameter must be initialized to an entry in the `pulsecal` file.

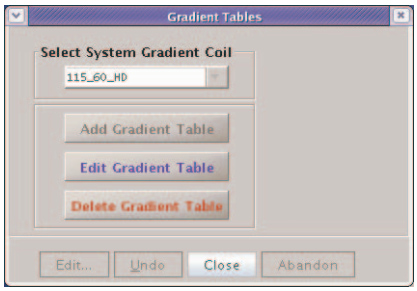
1.3 Setting the gcoil Parameter

Imaging spectrometers are often equipped with multiple interchangeable gradient sets for different sample sizes and experimental requirements. Each gradient set requires a corresponding calibration entry in the directory `/vnmr/imaging/gradtables`. A calibration file is created for each gradient set at initial system installation and is located in the `gradtables` directory.

Users with administrator privileges, such as vnmr1, have write permission to `/vnmr/imaging/gradtables` and can create a new gradient table, edit a gradient table, or delete a gradient table the macro `creategtable`, as follows:

1. Access the VnmrJ command line.
2. Enter **`creategtable`**.

   The following popup window is displayed:



3. Enter a brief description of the new gradient coil to help in identifying this `gradtables` entry in the future; for example:

   `Main Actively Shielded Gradient`
4. Click on **Close** to close the window to write the new coil name.
5. Enter **`creategtable`**.
6. Select the new coil (or an existing coil to edit).
7. Click on the **Edit Gradient Table** button or click on the **Delete Gradient Table** button to remove a gradient coil (system will not prompt for a conformation).
8. Enter the usable bore size, in cm, for this gradient set. This value is used only as an internal check for a reasonable field of view.

9. Enter the maximum gradient strength, in gauss/cm, for the gradient set.
10. Enter the rise time, in µs. Remember that Varian gradient hardware is installed with a linear slew-rate limitation that is dependent on the gradient set.
11. Click on **Close** to write the values.
12. Click on **Close** to save the results to new coil name or save the edited values to the existing coil name.

The new gradient calibration is now ready to use. Update the configuration parameter `sysgcoil` to reflect the hardware status.

1. Enter the command **`setgcoil(`*`file`*`)`**, where *`file`* is the appropriate `gradtables` file name, for example, `setgcoil('asg33')`.

   This has the effect of setting `sysgcoil` to the same file name, but in this special case, it also updates the configuration file as well.
2. As new parameter sets are retrieved, and as other experiments are joined, the system updates gradient calibration parameters to new values. To verify this, enter **`gmax?`** and **`trise?`** to see that they have the correct values for your gradient hardware.

Both `gmax` and `trise` are updated when a new parameter set is loaded or when joining a different experiment. One exception is joining an experiment that has `gcoil` parameter set to the value of `sysgcoil`. After updating the gradient calibration parameters of an existing entry in `gradtable` do one of the following:

- Manually update `gmax` and `trise` in the current experiment and others that have `gcoil` set to the `sysgcoil` value.
- Run macro `_gcoil` in each case.

1.4 Setting Parameters for Imaging Pulse Sequences

This section lists the actions that must be done before running each imaging pulse sequence.

- "Selecting an RF Coil," page 22
- "Adjusting the Receiver Gain," page 23
- "Setting Low Pulse Power," page 23

Selecting an RF Coil

This section describes how to set the RF coil.

1. Click on the **Start** Tab and select the prescan panel.
2. Select the **rf coil** from the RF coil menu in the hardware section.

The rfcoil parameter to be selected from one of the entries in the `pulsecal` file for imaging sequences.

The pulse calibration information, determined in 1.6 "Calibrating the Pulse Length," page 24, is communicated to the system through the `rfcoil` parameter. The automated pulse sequence setup routines use `rfcoil` to obtain information about probe performance from `pulsecal` and to set pulse powers (e.g., the two rf pulses in SEMS).

Adjusting the Receiver Gain

Imaging samples generally produce excessive NMR signals that often saturate the receiver. Lower the gain if the ADC overload error message is displayed. Additional attenuation might be need to further attenuate the incoming signal. Use `presig='h'` parameter (not available on human imaging systems) to set 30 dB attenuation in software. Use `presig='l'` to disable the attenuation.

Setting Low Pulse Power

Imaging spectrometers are usually equipped with high-power rf amplifiers. Make sure that the pulse power is set sufficiently low to avoid any damage to the rf coil. The maximum power that can be applied can be restricted by the system configuration settings (`config`).

1.5 Using Single-Pulse Sequence for Initial Setup

This section describes the procedure for initially setting up imaging experiments using a single-pulse sequence.

Use the initial setup procedure to ensure that the system is functioning properly and to determine the rf calibration parameters. The rf calibration parameters, such as transmitter frequency and power, can be used for subsequent imaging experiments after the initial setup has been completed. Repeating the initial setup procedure is required in some cases when the sample or coil is changed.

1. Position the sample in the center of the magnet.
2. Tune the probe.

   Different imaging samples influence the tuning of the probe depending on the size, composition, and position within the rf probe.
3. Use the single pulse sequence `spuls` to check for the NMR signal. Load the **spuls** protocol into the Study Queue, or, in the main menu, select **Scans** -> **Single Pulse**.

   The `spuls` macro can be used to load the default parameters suitable for imaging rather than for high resolution spectroscopy. Initially use a sufficiently wide spectral bandwidth to avoid aliasing of the proton signal.
4. Shim, if necessary.

   Shimming is not critical for some imaging experiments. Linewidths ranging from 50 Hz to a few hundred hertz yield good images. Typical linewidths for imaging samples such as plant and animal tissues are about 50 Hz to 150 Hz. Improved field homogeneity can produce better results. Good magnet homogeneity is critical for some experiments, such as echo planar imaging (EPI), gradient echo multislice imaging (GEMS), and spectroscopic imaging.
5. Use the **Set Frequency** button on the **Acq** page to set the transmitter frequency on resonance.

1.6 Calibrating the Pulse Length

This section describes how to initially calibrate the 90° pulse performance of a particular combination of probe and sample, and to enter that information into the `pulsecal` file.

1. Use a simple pulse-acquire sequence (e.g, spuls), set the power level to intermediate range (typically, set `tpwr` to about `50`).
2. Determine either the 90° or 180° pulse length by arraying the pulse length (e.g., `pw`). Either value works for this procedure, but a 180 is easier to determine and is less likely to produce an ADC overload condition.
3. Click on the **Start** Tab and select the **prescan** panel.
4. Select a coil from the menu in the **hardware** region.
5. Click on **Acquire**.
6. Enter the 90° pulse length, and `tpwr` in the RF Pulse region.

Example:

A180° pulse length is 800 µsec at `tpwr` of 50. Enter a name (e.g., `lic`) in the RF coil entry box, enter 400 in the Pulse length entry box and 50 in the power level entry box. The file in the system directory, `/vnmr/pulsecal`, is updated if system RF coil box is checked.

1.7 Parameters Not Normally Used for Imaging

Parameters not normally used on a horizontal bore system can lead to artifacts or inability to run imaging sequences if they are set incorrectly. Check the following parameters on horizontal bore imaging systems.

`load`	Determines how shim values are updated, i.e., if they are obtained from the software settings in the current experiment or from the actual existing hardware setting, refer to the *Command and Parameter Reference* for more information.
`solvent`	Set `solvent='none'` in all experiments, including spuls, for consistent frequency settings. Most imaging experiments are run unlocked. Failure to do this results in an incorrectly referenced `resto` parameter and possible positional errors in images.
`homo`	Set `homo= 'n'` for imaging experiments to disables time-shared homonuclear decoupling.
`lock`	`lock='n'`— the field/frequency lock must be turned off on microimaging systems
`step1`	in percent -- set to the shim step size for calibrating X, Y, and Z shims. Typically set to about 5%. Set shim step size to about 0.5-1% for high power gradients (e.g., 40 G/cm).
`step2`	in percent -- set to the shim step size for calibrating the second order shims. Typically set to about 10-20% depending on the sensitivity of the shims. Set the shim step size to about 1% for high power shims.

Chapter 2. Running an Imaging Study

Sections in this chapter:

This chapter describes the typical steps in setting up and running a VnmrJ imaging study. Sections“Making a New Protocol,” page 30 and “Making a Composite Protocol,” page 30 describe the tools used to make composite protocols and new protocols. Refer to Appendix A, “VnmrJ Imaging Interface,” for reference information about the VnmrJ imaging interface. Refer to Appendix B, “Locator,” for more information about using the Locator.

2.1 Running a New Study

A study is a collection of scans run on the same subject, generally within the same session. The currently active (open) study is shown in the Study Queue, which is below the Locator in the vertical panel on the left side of the screen.

The following procedures outline the steps needed to complete a study for the first time. Two or more stages may be required to define the image orientation and position for the area of interest. The first image is an initial scout image. It is used to accurately define the final target image.

Starting a Study

Set up new study as follows:

1. Select **Clear Study** from the **Study Options** menu at the bottom of the Study Queue, as shown in Figure 1 to clear the Study Queue.
2. Define the subject by name, weight, etc. in the fields shown in Figure 2 in the **Subject Info** page.
3. Select **Sort Protocol** in the Locator. Click on the icon and select Sort Protocol. Adjust the sort as necessary.
4. Double-click or drag-and-drop all the appropriate protocols from the Locator to the Study Queue, see Figure 1.
   - Rearrange the order of a protocol by clicking on it and dragging it higher or lower in the list in the Study Queue.
   - Remove a protocol from the Study Queue by dragging it into the trash can.
   - Copy an individual scan (child of a protocol) by holding the Control key while dragging the scan to a different place in the Study Queue.

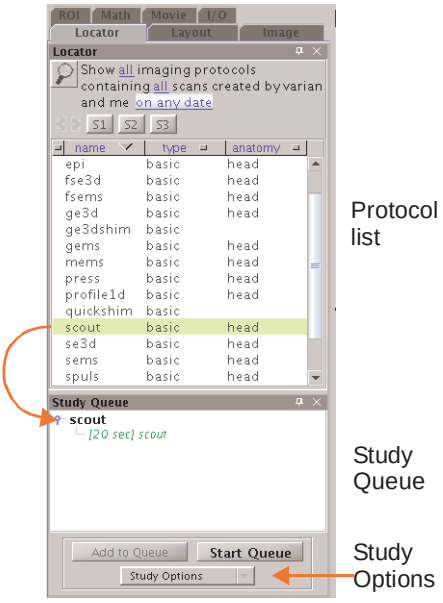


Figure 1. Study Queue

The study is now setup and ready to run.

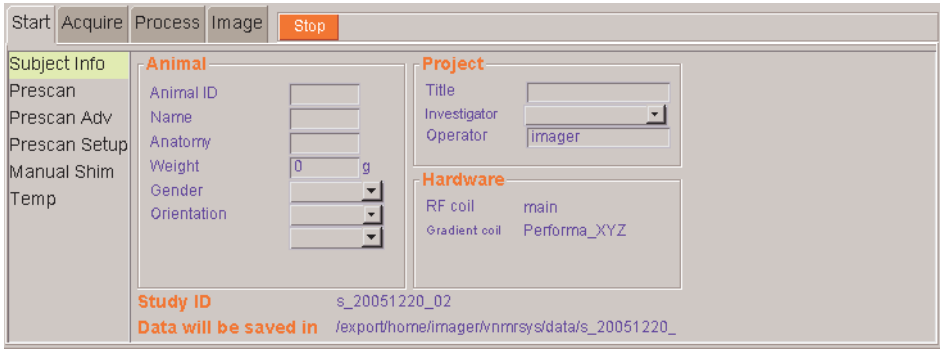


Figure 2. Study Panel

Acquire a Scout Image

Drag and drop a **scout** protocol onto the graphics canvas to accurately plan the target image.

The default scout protocol is based on a gradient echo sequence (gems) with a field-of-view (FOV) of 100 mm, slice thickness of 2 mm, matrix size of 256x128, te=10, and tr=20. The scout protocol acquires a single slice in each of the three cardinal panes in order: axial, coronal, and sagittal. The scan takes a few seconds. Any image sequence may be used.

1. Make sure the correct rf coil is selected – on the **Prescan** page of the **Start** tab.
2. Go to the **Plan** viewport.
3. Click the **Plan** button on the right side of the tool bar.

4. Make sure the **scout** protocol is in the **Study Queue**.

   Select the scout protocol in the Locator and drag it into the Study Queue if it is not in the Study Queue.

5. Load the scout scan by double-clicking it in the Study Queue or by dragging it to the Plan viewport.

6. Click on the **Acquire** tab to open the Acquire folder.

7. Enter the appropriate settings in the **Scan**, **Plan**, and **Advanced** pages, see Figure 3.

   The common parameters are on the Scan page. Image prescription and spatial control are on the Plan page. Less common parameters and acquisition control is on the Advanced page.

8. Click **Start Scan** to run the scout protocol.

9. Click on **Current** button to view the scout images as they are acquired.

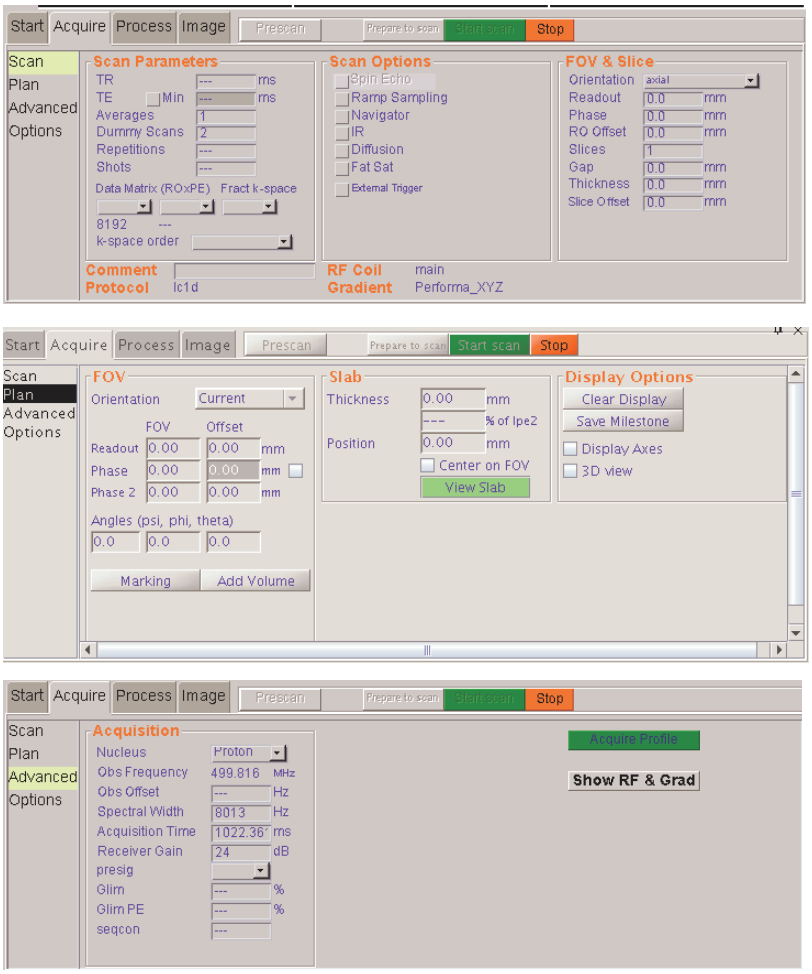


Figure 3. Setting Up to Acquire a Scot Image

Shim the system after the scout images are acquired. The scout protocol moves to the top when the acquisition is started if it was not the first protocol listed in the Study Queue.

Shimming

Global Shimming

Manual global shimming is necessary for experiments that do not use voxels (i.e., slice or volume selective, the spuls protocol).

Acquire Scans

Run other protocols:

1. Click the **Plan** button to open the Plan viewport.
2. Click the **Plan** button in the upper right area of the screen.
3. Drag the protocols from the Locator to the Study Queue.

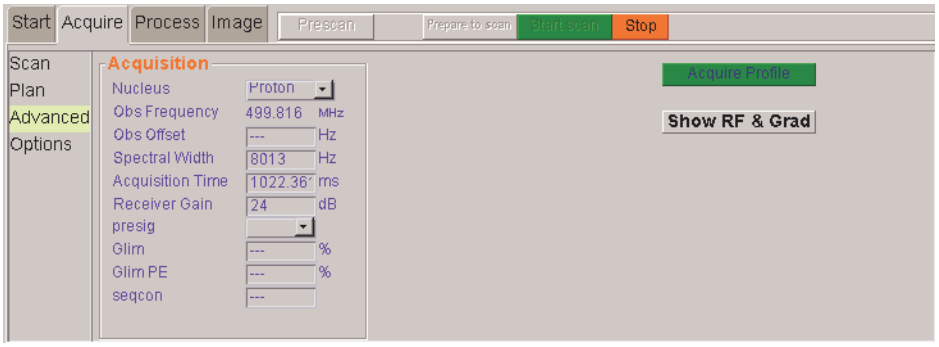
   Protocols can be acquired in any order, independent of their position in the Study Queue.
4. Verify the required protocols are listed in the Study Queue.
5. Double-click on the completed scout scan in the Study Queue or any completed imaging scans.

   Select multiple completed scans for planning:

   a. Load the first scan by double-clicking the completed scan in the Study Queue.

      This unloads any previously displayed images.

   b. Add other completed scans by dragging them into the graphics area.
6. Double-click the protocol to execute and load the parameters into the parameter page.
7. Open the **Acquire** folder.



8. Set the Scan parameters on the Scan page or set the detailed acquisition parameters on the Advanced page.
9. Plan the slices on the Plan page.

   Refer to Chapter 6, “Interactive Image Planning,” for more information on image planning.

10. Click **Acquire Profile** to see a readout projection.
11. Click **Start scan** to begin the scan.

    A delay of several seconds from clicking Start scan until the sequence begins acquiring is typical. This is due to calculations in the sequence and the downloading of the acquisition instructions. Click **Prepare to scan** begin calculations before starting the scan. Wait for completion of the calculations. Click **Start scan** and start the scan will immediately. **Start scan** *must* be clicked after clicking on **Prepare to scan**. The acquisition status field displays `Ready` when the calculations are complete and the scan is ready to start.

12. Go to the Current viewport to view the images as they are acquired.

Protocols are shuffled up in the Study Queue as they are executed; acquired scans are listed in the order of acquisition from the top of the Study Queue. Study data is saved automatically as it is acquired.

The scan time shown for each protocol in the Study Queue is only updated when you select the option Scan Time in the acquisition menu or when you click Start Scan. Scan Time also executes the calculation part of the sequence and is a convenient way to check the combination of parameters.

Continue to prepare and plan subsequent protocols in the Plan viewport while the current scan is acquired.

Queue Scans

A series of scans may be queued and run in the Study Queue.

1. Click the **Plan** button in the upper right area of the screen to open the Plan viewport.
2. Add the protocols you want to run to the Study Queue.
3. Queue scans individually.
   a. Double-click the protocol to queue.
   b. Customize any parameters.
   c. Click the **Add to Queue** button.

      Protocols are shuffled up in the Study Queue as they are queued.
4. Repeat step 3 for all scans to queue.
5. Select **Queue All** from the Study Options menu to Queue all scans in the Study Queue.
6. Remove scans from queue individually.
   a. Double-click the protocol to remove from the queue.
   b. Click the **Remove from Queue** button.
7. Select **Unqueue All** from the Study Options menu to remove all scans from the queue all scans in the Study Queue.
8. Click the **Start Queue** button.

The queued protocols are loaded one by one into the Current viewport and run in the order in the Study Queue.

9. Click the **Current** button in the upper right area of the screen to open the Current viewport and view scans as they run.
10. Follow step 1 through step 5 to queue more scans in the queue while it is running,
11. Follow step 6 and step 7 to unqueue scans from the queue while it is running,.

    Once a scan has started acquiring, it cannot be unqueued.
12. Do the following to review data while the queue is running.
    a. Click the **Review** button in the upper right area of the screen to open the Review viewport.
    b. Double-click on the completed scan of interest.

Finish the Study

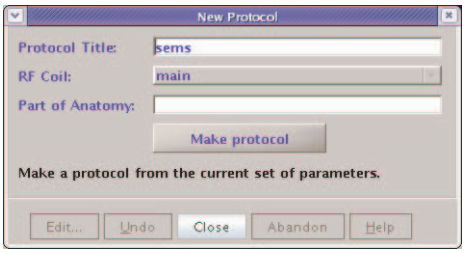
Click **Clear Study** in the **Study Options** menu and save the current study and start a new study.

2.2 Creating Protocols

Protocols are predefined parameter sets. We distinguish between a basic protocol that consists of a single parameter set (e.g., `T2wt`), and a composite protocol that is a collection of basic protocols. Refer to Chapter 4, "Protocols for Imaging," for detailed descriptions of each imaging protocol. This section describes how to make protocols.

Making a New Protocol

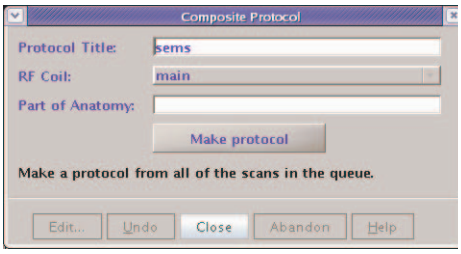
1. Load a protocol to use as a basis for the new protocol.
2. Set the parameters in the current panel.
3. Click on the **Edit** menu, select **Create Protocol**, and select **Make New Protocol**.
4. Define the protocol attributes in the New Protocol window,.
5. Click **Make protocol**. If the protocol already exists the button reads **Update protocol**.



Making a Composite Protocol

A composite protocol is a collection of basic protocols with order information, ownership, creation date, etc. A composite protocol does not create new basic protocols, but instead points to the selected basic protocols.

1. Click on the **locator**  and select **Sort Protocols**.



2. Drag one or more protocols into the Study Queue.
3. Click on the **Edit** menu, select **Create Protocol**, and select **Make a Composite Protocol**.
4. Define the protocol attributes in the Composite Protocol window.
5. Click on **Make protocol**. If the protocol already exists the button reads **Update protocol**.

2.3 Reviewing a Previous Study

A previous study can be reviewed as follows.

1. Make sure no scans are running.
2. Click the **Review** button in the upper right area of the screen to open the Review viewport.
3. Select Sort Studies in the Locator. Click on the  and select Sort Studies.Adjust the sort as necessary.
4. Drag and drop the desired study from the Locator to the Study Queue to load the study.
5. Double-click on an acquired protocol node to load and view the data.

2.4 Continuing a Previous Study

A previous study can be continued and scans added to it by loading the previous study as described above (Reviewing a Previous Study) and selecting the Continue study option in the Study Options menu at the bottom of the Study Queue.

A previous study can be continued as follows.

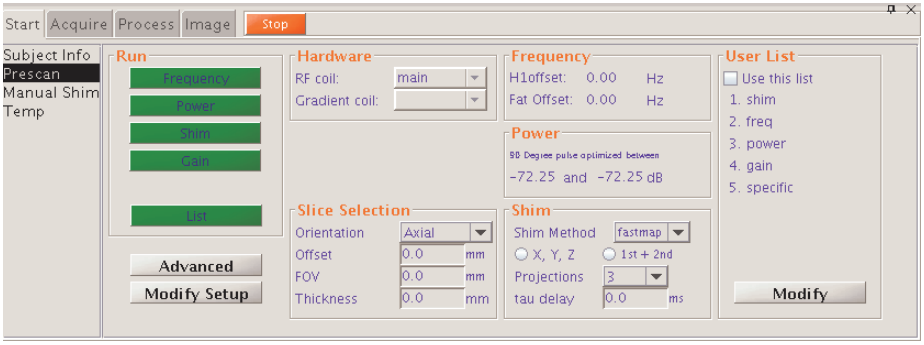
1. Make sure no scans are running.
2. Click the **Plan** button in the upper right area of the screen to open the Plan viewport.
3. Select **Sort Studies** in the Locator. Click on the  and select **Sort Studies**. Adjust the sort as necessary.
4. Drag and drop the desired study from the Locator to the Study Queue to load the study.
5. Select the **Continue Study** option in the Study Options menu at the bottom of the Study Queue.
6. Follow the procedures in “Acquire Scans,” page 28 or “Queue Scans,” page 29.

Chapter 3. Prescan

Sections in this chapter:

This chapter describes the prescan functions, their purpose, experimental setup, and outcome.

The **Start** folder initially displays the **Prescan** page of the five pages: **Subject Info, Prescan**, **Prescan Adv**, **Prescan List** and **Prescan Setup** in the **Start** folder.



3.1 Automated Prescan

Prescan is run in one of three automated modes that are selected on the Prescan pages:

- “Full Prescan,” page 34 – A standard, full prescan.
- “User List,” page 34 – You can define a list of prescan functions to execute in the specified order.
- “Single Prescan Mode,” page 34 – Execute any one of the above described prescan functions.

Prescan returns to the target sequence and restores the imaging parameters selected at the end of any of the automated prescans.

Clicking the Prescan button in the Acquire action bar runs either a full prescan or the user defined list, depending on whether the **Use this list** checkbox has been selected on the main Prescan page.

Full Prescan

A full prescan is initiated either through the Prescan button on the Acquire action bar or through the Full button on the main Prescan page.

A full prescan (default list) invokes the prescan functions in this order:

1. Center Frequency
2. Shim
3. Center Frequency (repeated after shim)
4. Power Calibration
5. Receiver Gain
6. Sequence specific prescan (if the sequence calls for it)

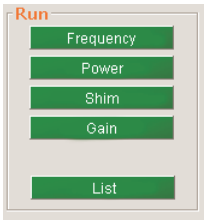
User List

1. Click **Use this list** to run **Prescan** or **Full** using a user-defined list of prescans.
2. Click **Modify** to edit the list.

   The button **Clear List** resets the list to an empty list The **Remove** Last Item button removes the last list entry. Items are added to the list by clicking the buttons under **Add** to Prescan.

The user defined prescan runs in the order specified by the user and does not provide any checks or controls to ensure a meaningful execution order.

Single Prescan Mode



Single mode prescan allows execution of individual prescan functions in an automated manner. The operator can invoke any of the prescan functions – frequency, shim, power, and gain – by clicking on the respective button in the Run group on the main Prescan page.

Initializing Parameters for Prescan

There are three types of parameters used by the prescan routines:

- Protocol parameters - saved in the `.par` file
- Coil table parameters - saved in the `Coil_Table` file
- Global parameters

The protocol related parameters can be modified in the **Acquire** page and saved in the `.par` file by clicking on the **Update params** button. Most of the `Coil_Table` parameters (related to the rf coil) appear in the **Prescan Setup** page and they are updated by clicking on the **Update** button on that page. The Global parameters are not associated with an rf or gradient coil so their values are used by the prescan routines until they are modified. Global

parameters take precedence over the other parameters. The default parameters for the prescan routines must be set correctly during installation of a new rf coil or else the prescan experiments will fail. Most of the prescan parameters appear in the **prescan setup** page. The `prescan_init` macro initializes the prescan parameters to default values. Enter a value in the entry box corresponding to **Set defaults and Pwr Limit** to execute the `prescan_init` macro. The power limit refers to the maximum power level (percent of maximum) that will be used during the prescan power calibration routine

3.2 Prescan Functions

VnmrJ provides the prescan functions, frequency, power, shimming, and gain. A default parameter set is initially loaded when running the frequency, power, or shimming prescan functions. Such coil-specific parameters defined on the **Prescan Setup** page are updated depending on the specific rf coil that is used.

A separate parameter set is not loaded when running the gain prescan function. The actual scan parameters and pulse sequence is used.

- "Center Frequency," page 35
- "Shimming," page 36
- "Power Calibration," page 38
- "Receiver Gain Adjustment," page 39

Center Frequency

Center frequency prescan is designed to locate the main resonance frequency. Typically, it is only necessary to perform this prescan once at the beginning of a study, or following any changes in the shims.

The resonance frequency depends on the local field strength. Shimming of the magnet shifts the frequency making it necessary to re-run center frequency after shimming.

Experimental Setup

The center frequency is determined using a non-selective pulse-and-acquire experiment. The default parameters are in `prescanfreq.par`, and the coil-dependent parameters that are set in the Prescan setup page are RF power, receiver gain, and a flag to specify a slice selective frequency prescan. A 4ms sinc pulse is used, in the slice selective case, to select the slice specified in the main Prescan page (orientation, offset, FOV, and thickness).

Result

The detected center frequency is stored in the global variable <tn>offset and used in all subsequent scans, where `<tn>` is the observe nucleus. For example, when observing protons, `tn='H1'` and the center frequency is stored in the parameter `H1offset`.

The frequency prescan routine also determines the frequency of fat as an offset relative to water. The fat offset is stored in the global parameter `Prescan_FatOffset`. `Prescan_FatOffset` defaults to 3.35 ppm if a fat peak is not detected.

The detection of the fat peak requires a reasonably good shim where the main (water) peak does not show any slitting (single sharp peak), and the water and fat peaks are well separated. Poor shimming can result in peak splitting and hence misinterpretation of the spectra by the center frequency prescan. A fat peak is detected if the magnitude of the fat

peak exceeds the fat threshold. The fat threshold is a percentage of the magnitude of the water peak and can be adjusted on the Prescan Setup page (typically 5-10%).

Shimming

Shimming is a process of adjusting the local magnetic field to produce a homogeneous field within the sample region. Two shimming methods implemented in VnmrJ: 3D image based method (`ge3dshim`) and FID-shim (`quickshim`). The `ge3dshim` is based on field mapping, a more advanced shimming techniques than `quickshim`, and allows a user to shim on a selected sample region. It is particularly suitable for techniques that are sensitive to field homogeneity such as localized spectroscopy and EPI. Setup procedures for `ge3Dshim` are more complicated than `quickshim` and, depending on the application and sample being used, is not usually recommended for routine (prescan) shimming operations. The quickshim protocol is limited to global shimming involving only the first order (x, y, and z) shims. It is a fast and simple method suitable for general shimming.

Shimming using 3D shim method require specification of the slice or voxel region for shimming. This is done manually using the Plan page in the Acquire folder and a scout image. Select either a voxel or a set of slices to bring up a button **Save for shimming**. Both methods acquire data over a larger region, but only attempt to optimize the shims within the specified shim region.

The 3D gradient shim method requires careful calibration of the shims, see, 3.6 “Setting Up and Calibrating 3D Gradient Shimming,” page 44. A default parameter set for shimming is first saved as described in 3.3 “Manual Prescan,” page 39. The shim parameters most often changed by the user between iterations appear on the Prescan Setup page. The shimming procedure is usually repeated multiple times with different shim parameters to improve the field homogeneity.

The procedure for shimming is more complicated than for the other prescan functions. Applications such as localized spectroscopy, CSI, EPI, etc. require different strategies for shim optimization. Run the protocol in the interactive mode, see “Autoshimming (Interactive Mode),” page 81, for these applications.

Experimental Setup for Quickshim

Shimming using either the Quickshim and 3D shim method require specification of the slice or voxel region for shimming. This is done manually using the Plan page in the Acquire folder and a scout image. Select either a voxel or a set of slices to bring up a button Save for shimming. Both methods acquire data over a larger region, but only attempt to optimize the shims within the specified shim region.

Quickshim requires calibrating the shim polarity and saving a default set of parameters for use during the shimming procedure prior to using the Prescan shim routine.

Shim Calibration

The calibration step sets the polarity of the shim coils is done automatically on VNMRS systems. Follow the "Shim Calibration" section described in the quickshim protocol for other systems.

Saving Parameters for Prescan

1. Load the quickshim protocol.
2. Set up the parameters as described in “quickshim,” page 102. Typical parameter values are:

Parameter	*Typical value*
TR	30 ms
pw	10 µsec.
flip	4 deg
Data size	256
Spectralwidth	20,000 Hz

3. Click on **Acquire Spectrum** button to obtain a spectrum and verify parameters.
4. Click on the **Save Prescan Params** button to save the current parameters to the parameter file: `~/vnmrsys/parlib/prescanquickshim.GCOIL.RFCOIL.par`. These parameters are associated with the currently selected gradient and rf coils. The parameter defining the shim step size is set in the **Prescan Setup** page during the prescan operation.

Prescan Shimming

1. Select the **Prescan** page.
1. Select the **quickshim** method for shimming.
2. Click on **Shim Settings** button.
3. Choose one or more iterations by selecting a check box.
4. Specify a shim step value (`del`) for each iteration. Typically, set it to 500 to 200 DAC units for the first iterations and 100 to 50 DAC units for the final iterations.
5. Click on the **Shim** button on the **Prescan** page to initiate Prescan shimming. Previously saved experimental parameters are read in and the data acquisition begins. The new x, y, and z shim values are determined and the hardware is updated. During each shim cycle the shim settings corresponding to the maximum signal is loaded.
6. Click on the **Shim** button to repeat the shimming procedure if necessary.

Each first order shim is arrayed and a set of spectra are collected during the quickshim procedure. The optimum shim value is determined by picking the largest peak. The shim spectra are also displayed on the screen for diagnostic purposes.

Limitations

- Shimming using the quickshim procedure is limited to first order shims.
- The quickshim protocol uses hard pulses, so the whole sample area is chosen for shimming.

Experimental Setup for 3D Shimming

1. Prior to shimming save the default experimental parameters as described in 3.6 “Setting Up and Calibrating 3D Gradient Shimming,” page 44.
2. Define the shim voxel or slices for shimming:

a. Acquire a scout image plan the voxel (for localized spectroscopy).

b. Click on the **Save Voxel for Shimming** button in the Plan page to save it.

   The region (slab) defined by the slices is used for shimming if slices are planned. This step is not needed for global shimming.

3. Choose the **3D option** in the Prescan page for 3D image based shimming.

4. Click on the **Shim Settings** button to view the shim parameters and display the Prescan Advance page.

   Set the following shimming parameters:

   - The number of iterations
   - Shim selection: 1st order (X,Y,Z), 1st and 2nd order, etc.
   - Shim region: Voxel, Slab, or Global
   - Tau (field encoding delay)

5. Click the **Shim** button to start shimming. Previously saved experimental parameters are read in, data acquisition started, and new shim values are calculated for the shim region of interest. The procedure is repeated as necessary if multiple iterations are chosen.

Result

Variation of the field the Shim region of interest is calculated after data collection. The shim currents needed to minimize the field inhomogeneity are determined and the shim settings updated using the shim calibration maps.

Power Calibration

Prescan power calibration calibrates the transmitter power for a 90 degree RF pulse.

Experimental Setup

The power calibration is determined using a profile in a slice-selective spin-echo experiment (mems with a single echo), where the coarse RF power is set to a certain level and the fine power arrayed.

The coil-specific parameters for the power prescan that are specified in the Prescan Start page are TR, coarse RF power (enter the maximum coarse power for the 180 degree pulse), and starting point, step size, and number of steps for the fine power array. Shown below the entry fields is the actual range of power levels that will be sampled for the RF pulses. The fine power array should be set up such that the profile intensity goes through both a maximum and a minimum for the processing to work optimally. Otherwise a warning message may be given.

The slice used for calibration is specified on the main Prescan page. Power prescan uses the frequency prescan receiver gain.

Result

The power prescan fits the signal intensities to a second-order polynomial and uses the maximum of this polynomial as the correct 90 degree pulse power setting.

The result of the transmitter power calibration is entered into the `pulsecal` file in the user's local vnmrsys directory.

Receiver Gain Adjustment

Receiver gain adjustment is the scaling of the receiver gain to ensure that the receiver and ADC will not be overloaded during data acquisition.

Experimental Setup

The receiver gain needs to be adjusted using the exact pulse sequence and acquisition parameters used for the target scan. There is no particular gain prescan sequence. The `execprescan` macro is invoked, prior to executing the gain prescan, if the parameter `execprescan` exists. This macro sets up the number of k-space lines acquired, steady state scans, etc., to ensure a proper signal for the gain calculation. If `execprescan` does not exist, only a single echo at the center of k-space is acquired (nv=0).

Result

Scaling is performed on the acquired FIDs collected during the execution of the selected sequence. The gain prescan is designed to handle more than one echo or FID, in which case the receiver gain is scaled to the largest echo or FID acquired.

The scaling will adjust the receiver gain in such a way that the signal is scaled to the maximum receiver resolution multiplied by a gain scaling factor that is specified on the Prescan Setup page (a typical value is 80% or 90%). A scale factor of 100% may result in receiver overflow since the sampled echo / FID can vary slightly.

3.3 Manual Prescan

Manual prescan allows manual execution of either the center frequency, shimming, or power prescan.

- “Frequency,” page 40
- “Power,” page 42
- “3D Shimming,” page 40

The parameters for manual prescan are retrieved on the **Prescan Adv** page, Figure 4, by clicking one of the buttons under **Retrieve Data/Params**.

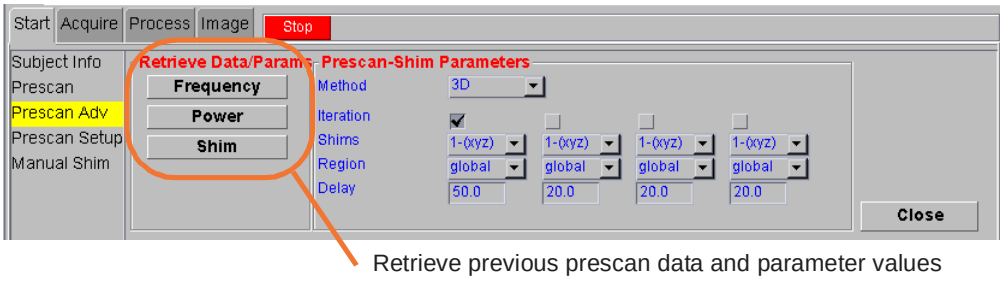


Figure 4. Prescan Adv Page

Saved data and parameters are retrieved, processed for inspection and subsequent manual execution, if the prescan of choice is run as part of an automated prescan. Only the predefined parameters are retrieved if the prescan has not previously been run.

Frequency

Running the frequency prescan in the manual mode allows modification of the following parameters on the Scan page in the Acquire folder: TR, RF pulse width, acquisition bandwidth (sw), acquisition time, number of data points, transmitter power and offset, receiver gain, and slice definition (orientation, offset, and thickness).

The Scan page, Figure 5, also contains buttons to manually Acquire and Process prescan data.

The Update params button saves the current parameter set into the user's `vnmrsys/parlib` directory, and any subsequent automated frequency prescan uses this parameter set as a starting point.

The Return to Study button restores the original scan parameters.

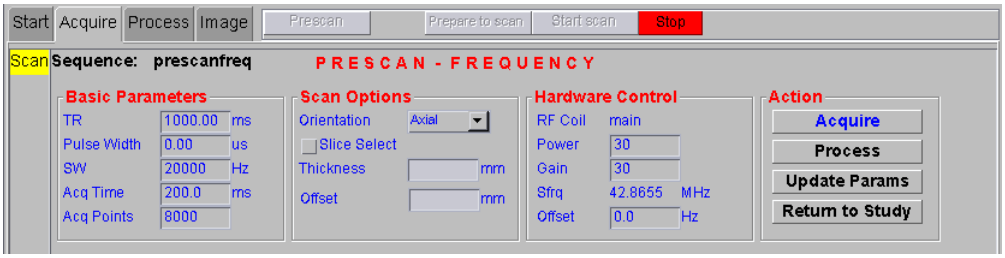


Figure 5. Frequency Prescan Acquire Page

3D Shimming

The following section describes the procedure for setting up and running the 3D shimming method interactively. The Manual Prescan mode allows the user to optimize and save a parameter set for subsequent use in Prescan shimming. The Manual Prescan mode also can be used to interactively shim the sample and to optimize parameters.

3D shimming setup and calibration are described in 3.6 “Setting Up and Calibrating 3D Gradient Shimming,” page 44. For more details on the ge3dshim protocol, refer to “ge3dshim,” page 67.

1. Plan the region of interest (ROI) for shimming.
   a. Load a scout image and Plan a voxel or slice region prior to shimming.

      The volume (slab) defined by the slice region is used for shimming if slices are planned.

   b. Click on the **Save for Shimming** button in the Plan page to save the shim ROI. This step is not required for global ROI shimming.
2. Select the 3D shimming method in the Prescan page, see Figure 6.
3. Load the 3D shimming parameters.
4. Click on the **Advanced** button to open the Prescan Adv page, Figure 7.
5. Click on the **Shim** button to load the default parameters.

   The parameters are loaded from `prescange3dshim_gcoil_rfcoil.par`.

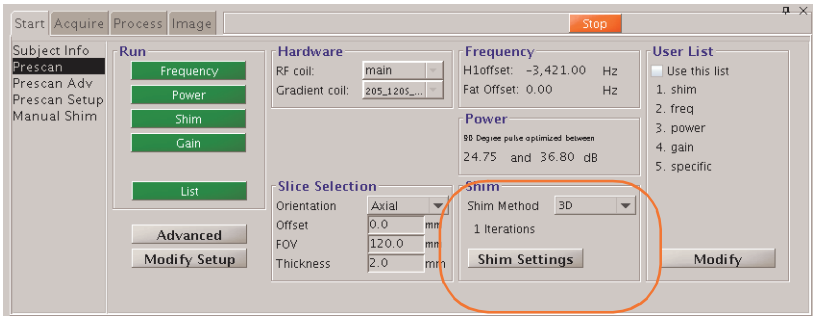


Figure 6. 3D Shimming Prescan Page

Parameters from the system file, `prescange3dshim.par` are loaded if `prescange3dshim_gcoil_rfcoil.par` does not exist.

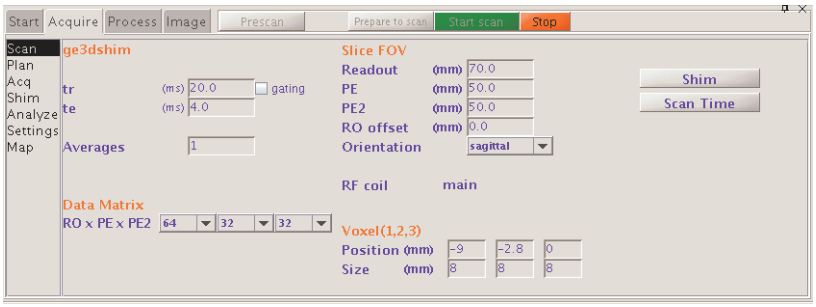


Figure 7. Prescan Acquire Page for Shimming

6. Click **Acquire Profile** to show a profile along the z-direction.

   This can be used to check the experimental parameters such as the receiver gain and SNR.

7. Check and set the parameters. Refer to "ge3dshim," page 67.

8. Set the Shim parameters.

   Choose the 1st or low order shims and use a short `del` value (field encoding delay) if the initial field inhomogeneity is poor. Set parameters for multiple iterations if necessary. A general strategy is to start with the low order shims with short `del` values. Increase `del` and include the higher order shims as the homogeneity improves.

9. Click on the **Shim** button to start acquisition.

   Do not click on the Start Scan button to initiate shimming. New shim settings will be calculated and loaded after each iteration.

10. Save (optional) the default parameters for subsequent use by the Prescan-Shim routine (see Section 2.2) by clicking on Save Params.

    Note that when shimming during the Auto Prescan mode the Shim iteration parameters mentioned in (step 8) are set from within the Prescan Advance page.

11. Optional: return to the previously loaded Study protocol by clicking on **Return to Study** or by clicking on the protocol node in the study area.

Power

Running the power prescan in the manual mode allows modification of the parameters. Course or fine power array (starting point, step size, and number of steps) can be set up.

The buttons on the Scan page have similar functionality as for the frequency prescan with the addition of a Display button that Fourier transforms the current data and displays the data array.

3.4 Coil Table

The coil table is a text file containing important acquisition parameters for each rf coil. Prescan will use the coil table to determine starting values for most of the functions and automatically update the table if small changes, < 20%, occurred. The user is queried, to accept or reject the update, if prescan detects the need for larger changes. The coil table file (`CoilTable`) is located in the vnmrsys directory.

- "Selecting a Coil," page 42
- "Adding or Modifying an RF Coil," page 42
- "Coil Setup," page 43

The coil table contains 17 entries for each rf coil defined on the system.

Selecting a Coil

Select the rf coil on the **Prescan** or **Prescan Setup** page, Figure 8.

Page	*Select coil*
Prescan	Select the coil from the **RF coil** pull-down menu in the **Hardware** field.
Prescan Setup	Select the coil from the **RF Coil** pull-down menu in the **Select Coil** field.

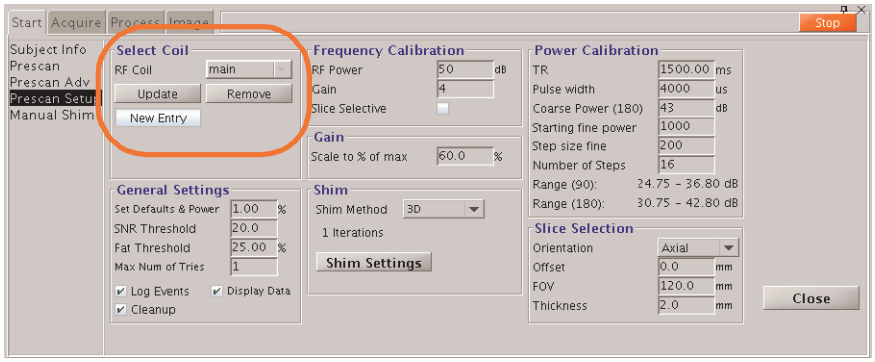


Figure 8. Selecting a Coil on Prescan Setup Page

Adding or Modifying an RF Coil

1. Click on the Start tab.
2. Select the prescan panel.
3. Click on the **Modify Setup** button.

Add an RF Coil

1. Click on the **New entry** button in the Select Coil region.
2. Enter a coil name.
3. Enter all required information in the **Prescan Setup** page fields.
4. Click on the **Save** button.

Modify an Existing RF coil

1. Select an existing coil from the drop down menu next to **RF Coil**.
2. Enter all required changes in the **Prescan Setup** page fields.
3. Click on **Update**.

Some knowledge or estimate of reasonable coil table values is required. If the coil table values are unknown, starting values can be determined by entering conservative values (i.e., low transmitter power and long TR's) and repeatedly running the prescans in the single prescan mode, until a reasonable result is obtained.

Remove an Existing RF coil

1. Select an existing coil from the drop down menu next to **RF Coil**.
2. Click on **Remove**.

Coil Setup

Obtain prescan parameters for the power calibration as follows:

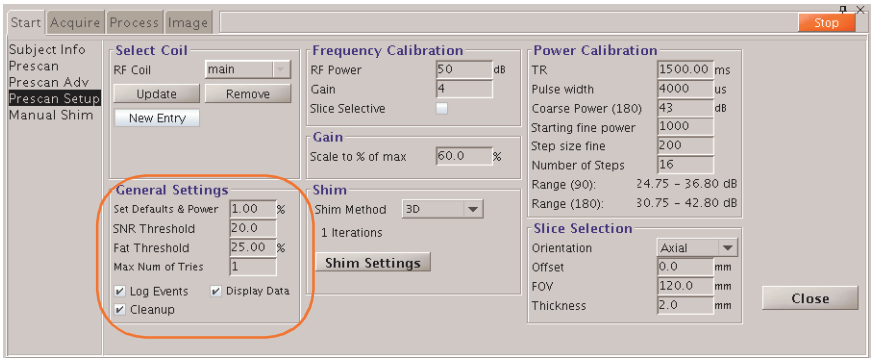
1. Use a long TR (1000-2000ms).
2. Enter the maximum power the RF-coil can handle without damage into the entry field for power coarse in the Power Setting field. If value is unknown start with a small coarse power setting (50 to 55).
3. Set the following: fine power 100; Step size 100; and Number of Steps 22 for the fine power.
4. Click **Power** on the main Prescan page.
5. Inspect the resulting spectra to ensure that there are at least three (3) points before the maximum and at least four (4) points after the minimum.

Problem	*Solution*
Too few points after the minimum	Increase the number of steps or coarse power
Too many points after the minimum	Reduce coarse power or number of steps
Too few points before the maximum	Reduce the coarse or starting fine power
Too many points before the maximum	Increase the starting fine power
Multiple maxima	Reduce the coarse power
Minima is very close to the maximum (less than four points apart)	Reduce the step size and possibly increase the number of steps

6. Click **Update**, every time parameters are changed.
7. Repeat, until the power prescan completes successfully.

3.5 Other Prescan Parameters

Other prescan parameters are set on the **Prescan Setup** page, in the **General Settings** group.



SNR Threshold	Enter an absolute value for the SNR, below which the prescan functions will return with an error. This could happen if, e.g., the RF coil is not connected correctly or the RF amplifier is not turned on.
Fat Threshold	Enter a threshold for the signal intensity of the expected fat peak relative to the size of the water peak. If no peak if found around the expected fat frequency with a sufficiently large signal, the default value of -3.5ppm is used.
Max Num of Tries	Enter a limit to the number of iterations allowed. The prescan functions will attempt to iterate until a sufficiently large SNR is obtained, by increasing the receiver gain and transmitter power.
Display Data	Check to display the frequency and power prescan data after it is processed (in the Plan viewport). Receiver gain data or sequence specific prescan data will not be displayed.
Log Events	Check to log of events during in the prescan_log file in the user's vnmrsys/prescan directory for both troubleshooting and evaluation of the system performance.
Cleanup	Check to ensure removal of temporary files created during prescan. It is highly recommended to let the Cleanup checkbox checked, unless errors occur, in which case the temporary files may explain the errors.

3.6 Setting Up and Calibrating 3D Gradient Shimming

This section describes how to set up and calibrate 3D gradient shimming. To run the 3D gradient shimming, refer to "ge3dshim," page 67. For information about running 3D gradient shimming as part of prescan, refer to "3D Shimming," page 40.

Acquiring Shim Calibration Maps

1. Place a cylindrical bottle or sphere containing doped water in the center of the magnet. The sample defines the region of interest for the autoshimming routines. The shim field maps are measured in the sample region only; it is not possible to shim outside this region.

Note: Make sure that the proper `decctool` file is loaded. The same `decctool` file must be used for subsequent shimming because the gradient and the shim scaling (gain) factors are set in decctool file. A copy of the decctool file will be saved in `$home/`

`vnmrsys/gshimdir/decc_file.GCOIL.RFCOIL` for future reference. Load the same gradient calibration file (`gcoil`) when calibrating the shims and during autoshimming.

2. Shim the sample manually using the SPULS sequence and save the result in a file named `start` (**`svs('start')`**).

   Alternatively, use the **Shim** page, Figure 9, in the **Start** folder.

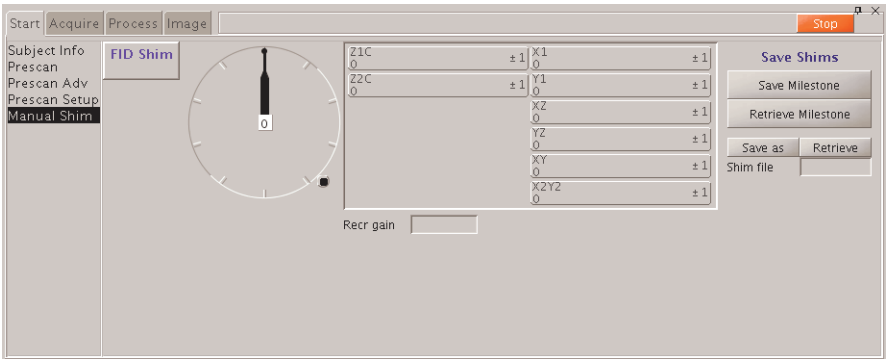


Figure 9. Manual Shim Page

3. Set the frequency on resonance.
4. Calibrate the rf power as usual.
5. Load the **ge3dshim** protocol.
6. Check and set the imaging parameters for 3D gradient shimming.

   Set up the parameters as in a regular 3D gradient echo sequence (GE3D). The TR and flip angles are chosen to maximize signal and minimize saturation effects. Sagittal orientation is selected because the sample is usually extended along the z axis. A larger FOV and size along the read dimension could be specified without sacrificing scan time. The following parameters will result in a total scan time of about 2 min. when TR is set to 50 ms. The parameters which are relevant for shimming are displayed in the Shim, Acq, and Map pages of the Acquire folder.

   Typical parameters:

`tr`	25-100 msec. `tr` must be sufficiently long to avoid the duty cycle limit on the gradient and/or RF hardware and to avoid saturation effects.
`flip`	1-10 deg.
`Matrix`	64x32x32
`orient`	sagittal
`te`	2-4 msec
`nt`	2

   The FOV (Field Of View) parameter is chosen to cover the sample used.

7. Set the parameters for mapping the shims in the Map page of the Acquire folder.

Shim selection	The shims to be mapped are selected from the shim selection menu. For example, select 1-(XYZ) for 1st order shims or 1&2 for 1st and 2nd order shims and so on. The step size for calibrating the shims are defined in percent. The step size for the 1st order shims will usually be a lower because they are driven by the high power gradient amplifiers (and not by the shim power supply unit). In the example below, 1st order shims are mapped by setting a shim DAC to a value approximately 5-10% of the maximum shim DAC value. For high-power gradients, (>40 G/cm) and shims, reduce the step size to about 1%.
Field encoding delay	del refers to the delay for encoding the residual B0 field. `delref` is chosen so that the phase change during that period is within +/-180 degrees, i.e. no phase aliasing has occurred during that period.
Intensity threshold	Threshold is the intensity threshold, in percent, used in analysis. All signals below this value will be ignored. This is useful to avoid errors caused by poor SNR. The data with the longer TE is used to determine the threshold map (or mask). Shim set sensitivity is set in DECCTOOL

Typical Parameters:

Shim change (XYZ)	5-10% (about 1% for >40 G/cm)
Shim change (2nd order)	10-20% (1-2% for shim coils < 12 cm)
del	2-5 msec
delref	0.25 to 0.3 msec
Threshold	10-20%

8. Select the shims (1&2) to be mapped:.

1-(XYZ)	1st order shims
1&2	2nd order shims
1 2&3	1st, 2nd and 3rd order shims
1&z2	x,y,z and z2 shims
all	all shims

9. Check the profile and optimize the receiver gain.
10. Collect a test image and check the image quality and SNR.
11. Click the Test image button to collect and display the images.
12. Click on the **Edit** menu.
13. Select **Create Protocol**.
14. Select **Make New Protocol**.

    The shim protocols can be recalled and used later during autoshimming.

Generating a Shimmap

1. Click **Acquire Shimmap** to acquire the shimmap data.

The shim file, start, is loaded and data acquisition begins. Three data sets are collected corresponding to `tau=0`, `delref`, and `del` for each of the shims selected. The total scan time is:

```
total_scan_time = (no_of_shims_selected+1) * 3 * scan_time
```

`scan_time` is the acquisition time for a single 3D gradient echo data set.

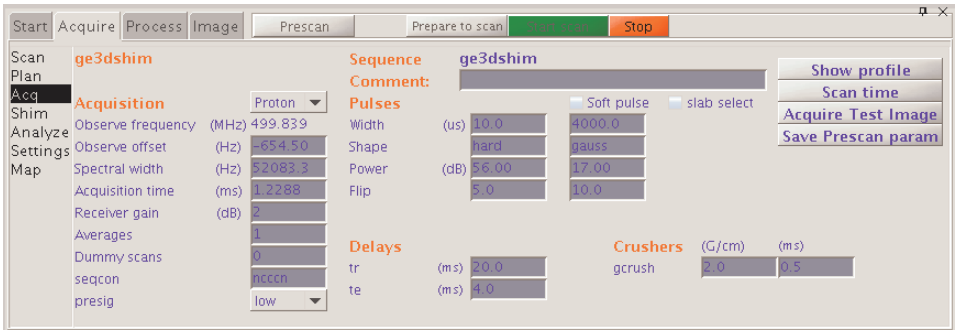
All the data files (`.fid` and `.fdf` files) are saved in the directory: `$home/vnmrsys/gshimdir/data`.

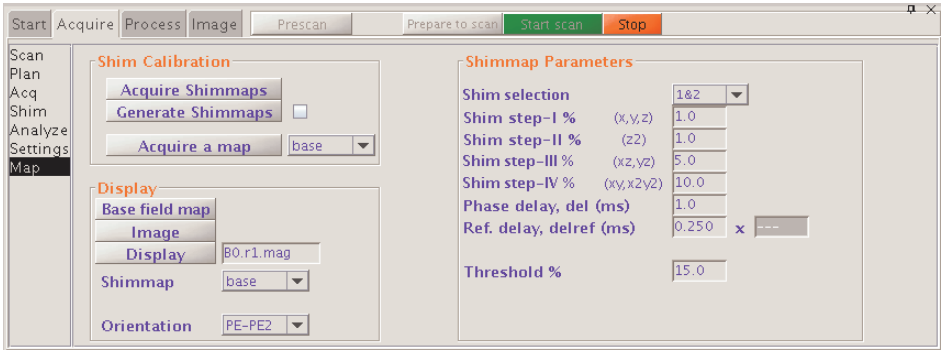
2. Click **Generate Shimmap** to generate the shim calibration file in `gshimdir/calib` directory. The shim maps are generated after data acquisition is complete if the check box is checked.

Saving the Shimmap Files

The file, `shimmap.GCOIL.<NAME>.f`, contains the shim calibration field map. The parameter file, `shimmap.GCOIL.<NAME>.param` is also generated at this stage. `<NAME>` is specified by the user to identify the shimmap files. The above files are used by the `gs_calc` macro to calculate the shim currents needed during auto shimming. The `.f` and `.param` files are created in the user's local directory, `$home/vnmrsys/gshimdir/calib`.

Copy shimmap files into the system directory `/vnmr/gshimdir/calib` if the are to be used by other users.





3.7 Troubleshooting

Turn on Display of prescan results as well as Log Events on the main Prescan page and rerun the prescan that fails. Visual inspection of the spectra will often reveal the problem.

No Water Peak Detected

The frequency prescan is usually very robust. There are only a few reasons why no water peak is detected:

- No sample in the coil
- The coil is not connected
- The RF amplifier is not turned on
- Transmitter power too small
- Pulse width too small
- The spectral width is too small.
- Defective hardware

Make sure that the equipment is turned on and that the coil is properly connected. Then run frequency prescan again.

No Fat Peak Detected

The common reasons for not detecting a fat peak:

- Poor shim, causing a poor separation and distinction between the water and fat peaks.
- Secondary (additional) peaks. Repeat shimming and check the appearance of the spectrum.

Frequency prescan does not detect the fat peak:

- Reduce the Fat Threshold. Very small fat peaks might well be below the Fat Threshold and therefore ignored by the prescan.

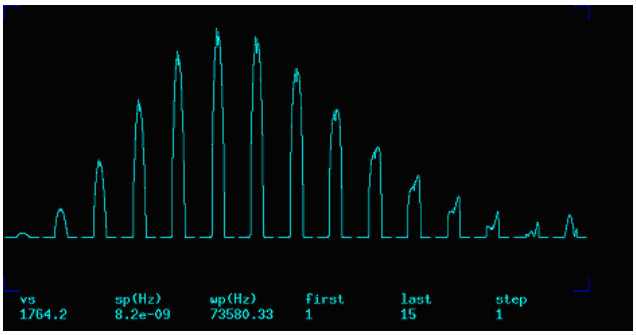
No 90 or 180 Degree Pulse Found

Generally, this is due to incorrect settings in the coil table or hardware problems. See Chapter 1, "Setting Up an Imaging System," for setting up the power calibration parameters.

No 90º pulse found:

- Improperly tuned RF coil — results in a very large power requirement for a 90º pulse.
- More power is needed. If power limit is being approached, increasing the pulse width in the default power prescan parameter set and rerun the prescan.

Odd Looking Power Calibration Curve



The envelope of the profiles is supposed to be a fairly symmetrical and smooth looking curve, as an example shows.

A very asymmetric curve could be due to saturation effects or mistuning of the coil. Try running the prescan with a much longer TR, or tune the coil. Setting the power limit to a high value can also produce strange results. Always use lower power settings when setting up for a new coil. Gradually increase the power limit.

Chapter 4. Protocols for Imaging

Sections in this chapter:

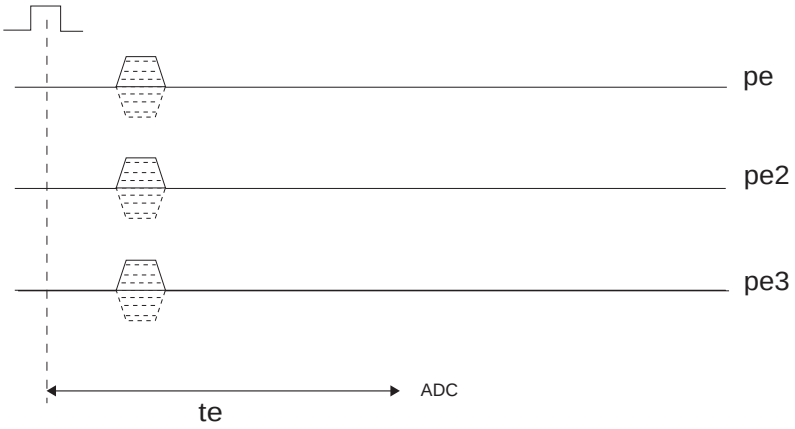
This chapter describes some pulse sequences for imaging available on Varian NMR spectrometers. Familiarity with basic spectrometer operations; such as shimming and tuning are assumed and not included in this chapter. More detailed descriptions of all commands, macros, and parameters are in the online help *VnmrJ Command and Parameter Reference*.

4.1 Imaging Protocols

ct3d

The protocol ct3d is a 3D experiment primarily used for microimaging. The ct3d experiment allows for echo times in the sub-millisecond range because it uses a non-selective excitation, followed by phase encoding in all three directions and acquisition of

only a single data point. The *ct* refers to the *constant time* between the excitation and any data point.



Advantages of ct3d

The ct3d is well suited for high resolution imaging of small samples with very short T_2, such as polymers or solids.

Limitations of ct3d

Long acquisition time. The ct3d suffers even more so from a long scan time than se3d because of the phase-encoding in all 3 directions. For example, with a tr of 100ms and a matrix size of 32x32x32, the total scan time is about 1 hour.

Running the ct3d Sequence

Use a short `tr` (10ms) and a small matrix size (32x32x32) to reduce the scan time. You can increase the image (digital) resolution by setting `fn`, `fn1`, and `fn2` to, e.g., 128x128x128. See the ge3d protocol (“ge3d,” page 65) for a description of the image orientations.

ct3d is `apptype='im3D'`.

Options for ct3d

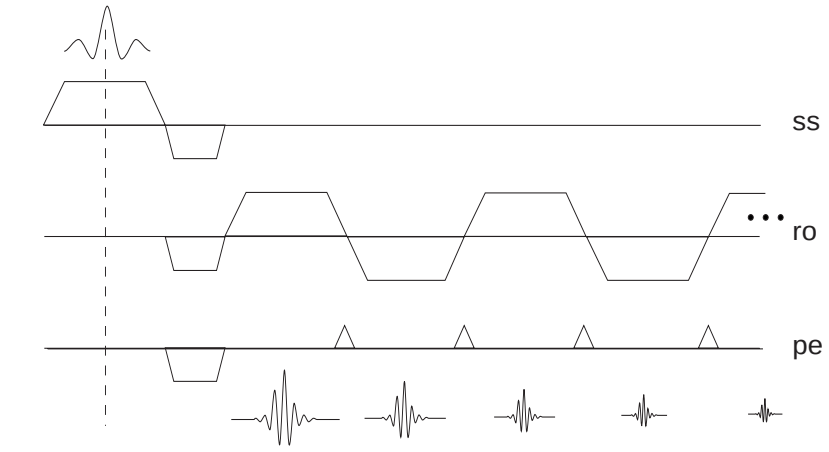
Click **Show profile** on the Acq page to obtain a profile of the object.

epi

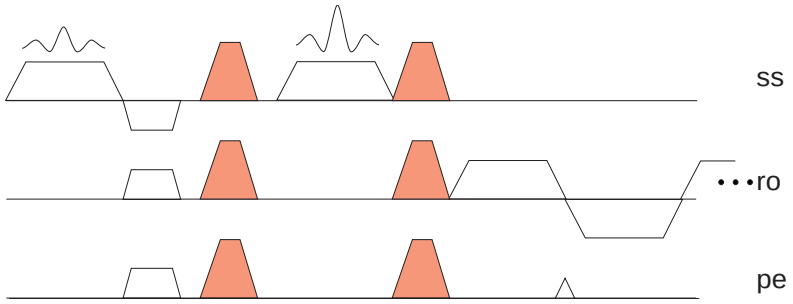
EPI (Echo Planar Imaging) is a routine imaging application for very rapid collection of imaging data and for functional MRI. EPI enables monitoring of changes occurring within

fractions of a second and is less affected by motion and flow-induced artifacts than other imaging methods.

EPI



EPI with diffusion



Advantages of EPI

- Rapid imaging data collection, typically 25-100 ms.
- EPI is less affected by motion and flow-induced artifacts than other methods.
- EPI is particularly advantageous in applications where a large number of images must be acquired in a short amount of time, or for monitoring rapid changes within fractions of a second, such as:
  - Functional MRI (fMRI)
  - Perfusion studies using bolus tracking
  - Diffusion tensor imaging
  - Time-course studies

Limitations of EPI

EPI images are prone to severe artifacts and is seldom used for routine or diagnostic work.

- “Image Distortions,” page 54
- “Low Resolution,” page 54
- “Reduced Signal-to-Noise Ratio,” page 54
- “Increased Gradient Requirements,” page 55

- "Eddy Current Compensation," page 55
- "Oblique Slices," page 55

Image Distortions

EPI echoes evolve as a function of time unlike the conventional spin-warp sequence. This evolution means that if different resonances (e.g., oil and water) are present in the sample, each of the echoes in the echo train is also chemical shift encoded.

Phase modulation caused by the chemical shift effect interferes with the phase correction routines used to correct for the echo shifts along the T_2-direction. The phase correction routine that is used to calculate the phase maps is unable to distinguish the difference between phase shift caused by incorrect alignment of echoes and phase shift caused by chemical shift. Therefore, the phase-encode dimension represents both chemical shift and spatial dimensions, which result in multiple images or ghosts corresponding to the different chemical shift components in the sample.

Magnetic field susceptibility effects are a serious limitation in EPI because they behave like chemical shift effects. Susceptibility effects are caused by either inhomogeneous fields in the main magnet or susceptibility gradients caused by the sample and other materials in the vicinity. These effects are also phase encoded and appear as frequency-shifted components in the phase-encode dimension, often leading to severe distortions in the image. Therefore, shimming is an important part of the EPI setup procedure.

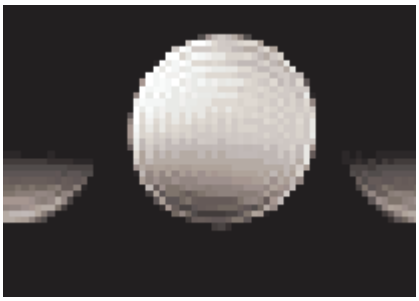


Image distortions (ghost artifact)

Shimming on the slice should give better results than the usual single-pulse method. A sequence such as **`profile1d`** can be used for shimming on the slice. When **`profile1d`** is used, the echo or FID is detected after selectively exciting the slice region.

Susceptibility artifacts due to B_0 inhomogeneity in EPI can be reduced by minimizing the effective `te` and the total readout time. Several factors can accomplish this:

- Minimum `te` option.
- Multishot (for example `nseg` = 4, 8, 16) with a long `tr` and a couple of dummy scans.
- Reduce the matrix size (`nv` and `np`).
- Increase `sw`.
- Use ramp sampling ON.
- Linear k-space encoding may be somewhat superior to centric.

Low Resolution

The matrix size for single-shot EPI is usually limited to about 64x64 or 128x128 to keep the data acquisition time short resulting in EPI images of low resolution. Higher resolution images can be obtained through multi-shot EPI at the cost of increased total acquisition time and possible artifacts.

Reduced Signal-to-Noise Ratio

Acquisition time following each excitation is typically 25 to 100 ms in an EPI experiment. This significantly longer acquisition time than for conventional imaging sequences results in images that are heavily T_2* weighted, have a significant loss of signal, and yield images with inherently lower signal-to-noise than conventional images of the same resolution.

Increased Gradient Requirements

Very strong and rapidly switching gradients are essential in EPI experiments to reduce the acquisition time. The gradient hardware (gradient coil and gradient amplifiers) must deliver high gradient strengths and short rise and fall times for the readout gradients.

Long gradient duty cycles and large gradients for relatively long periods of time (particularly during time-course experiments) are required of the gradient hardware.

Eddy Current Compensation

Eddy currents create undesirable fields in the magnet region and result in image artifacts. Actively shielded gradients and eddy current compensation hardware minimize eddy current effects. Reducing the slew rate (increasing `trise`) reduces the eddy currents at the cost of increased acquisition time and image distortions.

Oblique Slices

Oblique slices suffer from severe ghosting in EPI due to the current implementation of the readout and phase encoding gradient waveforms,.

Running the Sequence

The **`epi`** sequence is a multi-slice, multi-shot, spin/gradient Echo Planar Imaging (EPI) sequence.

Click on the **Acquire** tab and select the **Advanced** page to view or change the acquisition and receiver parameters. The Direct Digital Receiver imposes certain limitations to how closely spaced individual echoes can be acquired - error messages are generated if these limits are violated. The following are typical settings for the receiver parameters:

- Minimum echo spacing at least 100µs (spacing is automatically be increased if the minimum is larger due to duration of phase encoding blips)
- Time Correction off (primarily used for back-predicting FIDs to avoid artifacts from digital filter rampup)
- Data point size 16 bit
- Sampling Rate 5MHz (first downsampling stage)
- Filter Coefficients 5 (defines steepness of digital filters, which is typically not a limiting factor in imaging)

The **Advanced** page has the buttons **Test Scans**, for acquiring a series of data sets with the phase correction turned off (typically for debugging purposes), and **Show RF & Grad**, that open up the **RF pulses** and **Gradients** pages containing all the information about RF pulses and gradients used by epi.

The Prescan page has parameters for optimization of the sequence, described in more details below. The **`epi`** sequence is `apptype='imEPI'`.

Options

- Standard sequence options — see “Standard Sequence Options,” page 114
- “Minimum TE,” page 56
- “Multishot,” page 56
- “Phase Encoding Scheme,” page 56
- “Rampsampling,” page 57
- “Navigator,” page 57

Option	*Controlled by variable*	*Typical value*
Automatic calculation of min TE	minte	`'n' or 'y'`
Repetitions, Time series	image and images	`> 2`
Multi-shot	nseg	`1, 2, 4`
Phase encoding scheme	ky_order	`'l', 'c', 'lr' or 'cr'`
Spin echo/Gradient echo	spinecho	`'y' or 'n'`
Ramp sampling	rampsamp	`'y' or 'n'`
Navigator echo	navigator	`'n' or 'y'`
Inversion Recovery	ir	`'n' or 'y'`
Diffusion weighting	diff	`1 or 0`
Fat suppression	fatsat	`'n' or 'y'`

Minimum TE

Selecting the **TE Min** check box (`minte = 'y'`) forces the sequence to use the minimum TE possible and updates the te parameter.

Repetitions

The number of repetitions controls the number of images acquired in a series of images (for, e.g., bolus injection or fMRI). Repetitions must always be 2 or more, since the first data set is a reference scan.

Repetitions uses the parameter `images`. Setting `images>1` automatically arrays the parameter `image` and sets the parameter `image` to 0,1,1,1,.... (with as many total elements as images specify). Setting `images=1` sets `image=1`. Actual image data is acquired if `image = 1`. A reference scan (no phase encoding) is acquired if `image = 0`.

With `images>1`, the first acquired data set is not a proper image but rather a reference scan. A phasemap acquired in this way is part of the total data set and is saved with the data. Always set `images >= 2` (the only exception is with diffusion, see below). If `images = 1`, no phase correction is performed.

Manual manipulations the image array and intersperse zeros among the ones is possible using the processing function (`recon_all`) to automatically use the most recently acquired reference scan to phase correct subsequent image scans.

Multishot

The limitations of gradient strengths, resolution, and long acquisition times can be overcome by running EPI as an interleaved, multi-shot experiment, where multiple EPI echo trains are collected. Each of the echoes represents segments of k-space data and they are combined to generate the complete k-space dataset during the post processing stage. However, this type of experiment is no longer a single-shot method. The total scan time for interleaved EPI sequences is increased by TR*nseg, where nseg is the number of interleaved segments.

Phase Encoding Scheme

The order of which k-space is traversed (phase encoding direction) in multishot experiments is given by the parameter `ky_order`.

`ky_order` can be either `'l'` for linear or `'c'` for centric ordering, or `'lr'` and `'cr'` for linear and centric in the reverse directions. Linear ordering means that acquisition is started at the edge of k-space, working towards `k=0` and out to the opposite edge. With two shots, each shot samples every 2nd line in k-space, with 3 shots, every 3rd line etc. Centric ordering can only be used with an even number of shots; each shot starts at the center of k-space and works towards the edges, skipping `nseg` /2 lines if `nseg` > 2.

The sequence generates tables for phase encoding ordering on the fly. These tables are found in the user's tablib, in a file that is named using the numbers `nv`, `fract_ky`, and `nseg`, as well as `lin` for linear ordering or `cen` for centric ordering. Example, for `nv=128`, `fract_ky=64`, single shot centric ordering: `epi_nv128_f64_cen4`

The tables are used for re-ordering of data prior to Fourier Transformation.

If the parameter `pe_table` exists (integer), it will be set to an array specifying the phase encoding step ordering.

Rampsampling

Rampsampling refers to the acquisition of image data while the readout gradient is ramping up or down, although skipping acquisition during the duration of the phase encoding blips. The data is acquired in a non-linear manner, such that the dwell time between points may differ on the ramp, but the gradient integral between points remains the same to ensure constant steps in k-space.

Navigator

Check the **Navigator** check box on the Scan page to select a navigator echo. An extra echo is collected with no phase encoding prior to acquisition of the actual image data. This echo is used to correct for phase variations, typically caused by motion, throughout a series of images.

Diffusion Weighting

Checking the **Diffusion** check box on the **Scan** page to turn on **Diffusion Weighting**. Go to the **Options** page to specify the diffusion parameters see “Diffusion,” page 115.

The two diffusion gradients may be placed on either side of the 180 degree refocusing pulse, or both before the 180 pulse, depending on TE. If TE/2 is very long (relative to `tDELTA`, the separation of the diffusion gradients), they will be placed both before the 180 degree pulse. This can happen if the readout train and therefore TE is long.

Gradient Waveforms

The epi sequence uses the shaped gradient library to generate the following gradients, saved in `vnmrsys/shapelib`:

Shape	*Description*
`epiro`	The entire readout train
`epipe`	All phase encoding blips, including zeros during acquisition
`ror1`	Initial readout dephaser
`per1`	Initial phase encoding dephaser
`ss1`	Slice selective gradient for excitation
`ssr1`	Refocusing of slice selective
`ss21`	Slice selective gradient for refocusing, if spin-echo option is selected
`ssi1`	Slice selective gradient if inversion recovery option is selected

Shape	*Description*
`diff1`	Diffusion gradients, if diffusion option is selected
`crush1`	Crusher gradient if fat saturation option is selected

These shapes are overwritten every time the sequence is executed (i.e., clicking on **Scan Time** or selecting **Show pulse sequence** (dps) from the **Acquisition** main menu selection).

The displayed relative amplitudes of the shapes do not reflect their relative amplitude during acquisition, they are all scaled to full amplitude (dac value 32767).

Other acquisition parameters

Additional parameters for all of the above options are shown in the **Options** page.

Optimizing EPI

Ideally all echoes appear at the middle of the acquisition window. Nonideal behavior of gradients and spurious gradient fields (from local inhomogeneity and eddy currents, etc.) influence the amplitude and phase of odd and even signals in differently. The echo positions of the odd and even echoes shift increasingly away from the center of the acquisition window throughout the echo train causing phase shifts between the odd and even echo signals. Incorrect matching of odd and even echoes cause one of the more common and artifacts in EPI images, half FOV ghosts. Half FOV ghosts appear along the phase-encode dimension. The ghost image appears shifted from the primary image by half the FOV the images. Shown in Figure 10 is an optimized image and a ghost image.

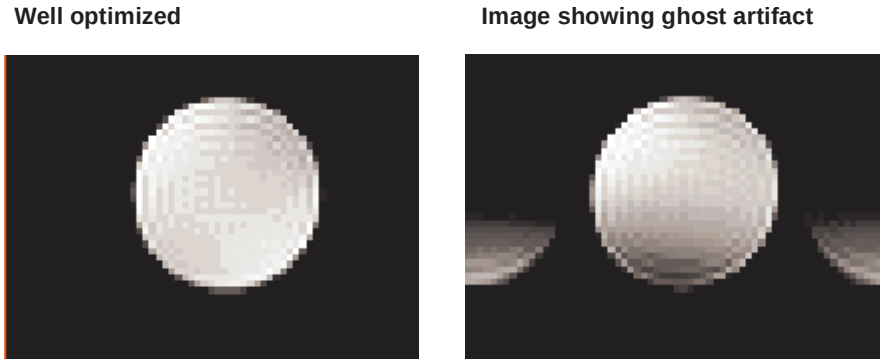


Figure 10. Effects of Optimization of the Images Produced

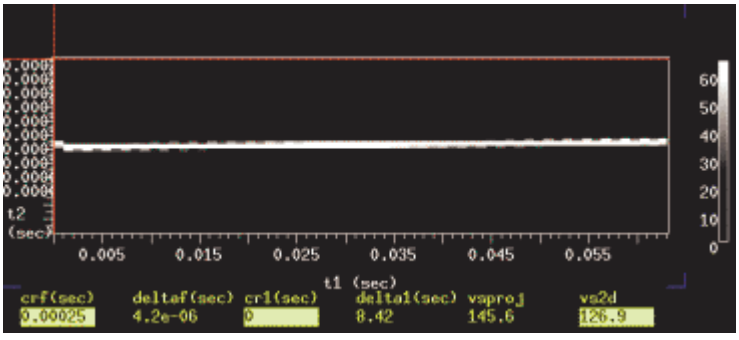


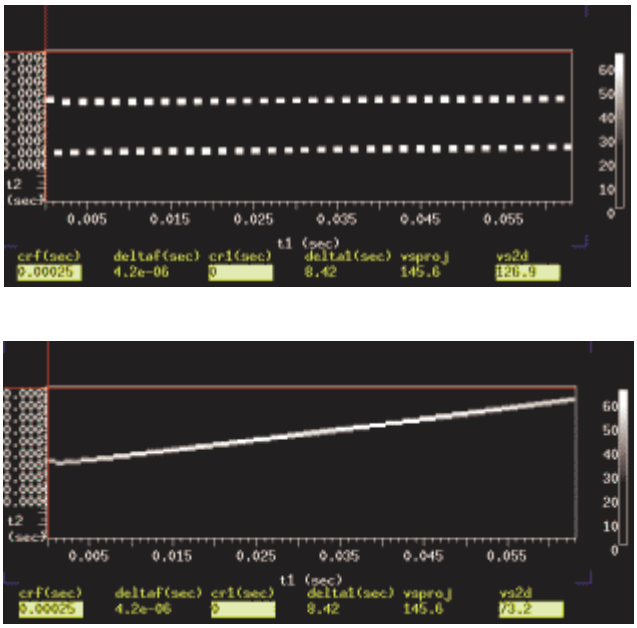
Figure 11. Well-optimized Reference

Specific EPI imaging gradients must be optimized in order to compensate for non-ideal gradients and minimize the ghosting. Gradient optimization accomplished by analyzing a reference scan, see Figure 11 for an example of a well-optimized reference scan:

A reference scan is an entire dataset, but acquired with the phase encoding gradient turned off. Thus, every single echo should in principle have the exact same phase and occur at the exact same time, but due to gradient imperfections and local inhomogeneities, this is not necessarily the case. The parameters `groa`, `grora`, and `tep` are adjusted in order to ensure this condition.

These parameters are automatically adjusted, when you click the **epi setup auto** button. Initially, the adjustment parameters are reset to all zeros, then a reference scan is done, from which values for the adjustment parameters are calculated. Subsequently, a second reference scan with new values is acquired and displayed. Several iterations of `groa` (for horizontal tilt) and `tep` (for *zipper effect*, echo shift) are needed before they are optimized. Click the buttons **adj. tilt** or **adj. shift**, respectively, to calculate new values and click epi setup manual to acquire another reference scan with the new values. The data acquired with either of these setup procedures is not saved with the study.

Examples of the reference scan and image with `tep` and `groa` incorrectly set are shown in Figure 12.



EPI reference scan with gradient delay (`tep`) incorrectly

EPI reference scan with `groa` incorrectly set

Figure 12. Improperly Set values for `tep` and `groa`

The sample reference scans, see in Figure 12, small steps are noticeable from the first to the second echo. This is primarily due to small, residual eddy currents that get into a steady state after the first couple of lobes in the readout train. In order to force this steady state before starting data acquisition, use the parameter ssepi to run a few gradient lobes identical to the other readout gradients before starting acquisition.

Use the following adjustment parameters (on **Prescan** page in the **Acquire** folder) for this EPI sequence:

Adjustment parameters:	*Functionality*	*For adjustment of*	*Typical values*
`groa`	added to `gro`, G/cm	horizontal tilt	0 to 0.05 (positive or negative)
`grora`	added to `gror`, G/cm	vertical shift	1.0 (positive or negative)
`tep`	propagation delay, µs	zipper effect	0 to 100µs
`ssepi`	dummy gradients at beginning of readout train	Step at the first one or two echoes	1 to 2

Processing of EPI Data

The standard VnmrJ processing uses the `recon_all` function (see the *Command and Parameter Reference* manual) and all settings are specified on the **Recon** page in the **Process** folder.

- "Phase Correction," page 60
- "Raw Data," page 60

Phase Correction

Even after optimization, "Optimizing EPI," page 58, phase variations throughout the data set due to local field inhomogeneities may remain causing cause severe distortion and ghosting. Use the unencoded reference scans (acquired when `image=0`) and compute a phase map that is applied to each slice of the imaging data. Estimate the phase maps using one of the following methods:

- `POINTWISE` – Directly compute the phase of each point in each echo (default).
- `PAIRWISE` – Use even and odd echo pairs of the reference scan to generate a linearly-fit phase estimate correction and applied to only the even echoes of the imaging data.
- `LINEAR` – Fit the phase of each profile (normalized by the profile of the center echo) to a linear model in a region of sufficient signal for each echo and extrapolate the model to generate a point-by-point phase map.
- `QUADRATIC` – Similar to Linear, but a second-order polynomial model is used.
- `CENTER_PAIR` – Use even and odd echo pairs occurring at the center of the train to generate 2 linearly-fit phase estimate (see Linear) correction and apply to even and odd echoes in the imaging data.

Raw Data

Click on the **Raw data** page and select to view k-space data for a particular slice and array element.

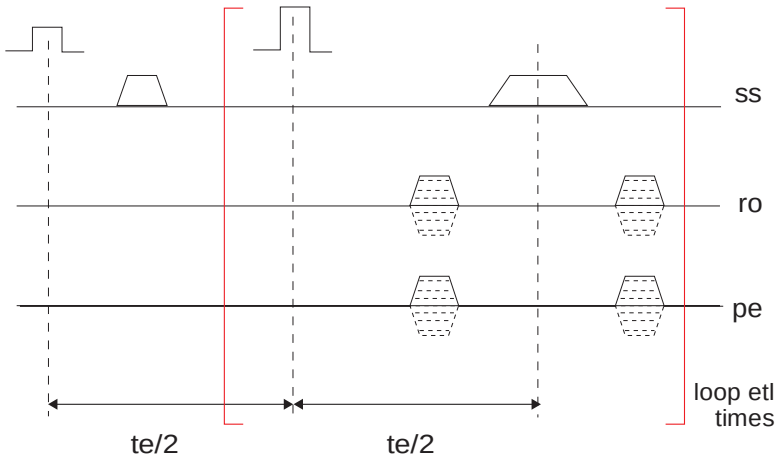
Note: Always save the data prior to running the manual preprocessing. Preprocessing (echo reversal and petable reordering) may change the data structure such that `recon_all` no longer produces correct images.

fse3d

- "Advantages of fse3d," page 61
- "Limitations of fse3d," page 61
- "Running the fse3d Sequence," page 62

- "Options for fse3d," page 62

The fse3d protocol is a 3D variation of the fsems protocol.



Advantages of fse3d

The fse3d is a good alternative to both the ge3d and the se3d experiments. It is much less prone to susceptibility artifacts than ge3d, but much faster than se3d due to the segmented data acquisition.

The fse3d is well suited for:

- High-resolution T_2-weighted images (long `te`, long `tr`)
- Imaging of regions of high susceptibility
- Scans where high signal-to-noise is critical

Limitations of fse3d

- SAR
- The fse3d experiment may be restricted by SAR limits.
- Mixed Contrast
- The contrast in an fse3d image is usually not a straight-forward T2- or T1-contrast.

Long Acquisition Time

Although the fse3d experiment is faster than the se3d, it is still a relatively lengthy experiment, due to the long `tr` – typically in the order of 3-4 seconds – necessary to allow the spins to return to equilibrium between excitations.

3D Limitations

The `fse3d` experiment suffers from the same limitations in terms of wrap-around and limited extraction capabilities as ge3d ("ge3d," page 65).

ADC Overflow

Because the fse3d sequence uses non-selective pulses with a 90° flip angle in an almost fully relaxed system, it is likely to cause ADC overflow. On animal systems, this can be avoided by setting the parameter `presig='h'`.

Running the fse3d Sequence

The parameters specific to `fse3d` are the same as for fsems ("fsems," page 62):

Parameter	*Description*	*Typical Value*
`etl`	the echo train length	4 or 8
`esp`	the echo spacing (time between echoes)	10 to 20 ms
`kzero`	the echo that shall be assigned to the center of k-space (values between 1-`etl`)	1 or 2

Preparation of the sequence results in the generation of a table for specification of the order of k-space lines (see also "gems," page 91). The name of the table is defined as: `fse<nv>_<etl>_<kzero>`

The advantage of choosing a large number of echoes (large `etl`) is the obvious reduction in scan time but at the expense of reduced signal-to-noise or image resolution. A lower `kzero` value gives spin-density weighted images, while a larger `kzero` value gives T_2-weighted images.

Additional acquisition parameters, such as the rf pulse definitions, bandwidth, acquisition time and number of dummy scans is set on the **Advanced** page. See "ge3d," page 65 for a description of the image orientations.

The sequence, fse3d, is `apptype='im3Dfse'`.

Options for fse3d

Acquire Profile

Click **Acquire profile** on the **Advanced** page to obtain a profile of the object.

This function temporarily sets the number of phase encode steps to zero (`nv=0`), which signals to the sequence to acquire a single echo under the readout gradient but without any phase encoding. This will acquire a profile for each echo in the echo train. Use cf to select which echo in the echo train you wish to view and transform it, for example: `cf=1 ft`.

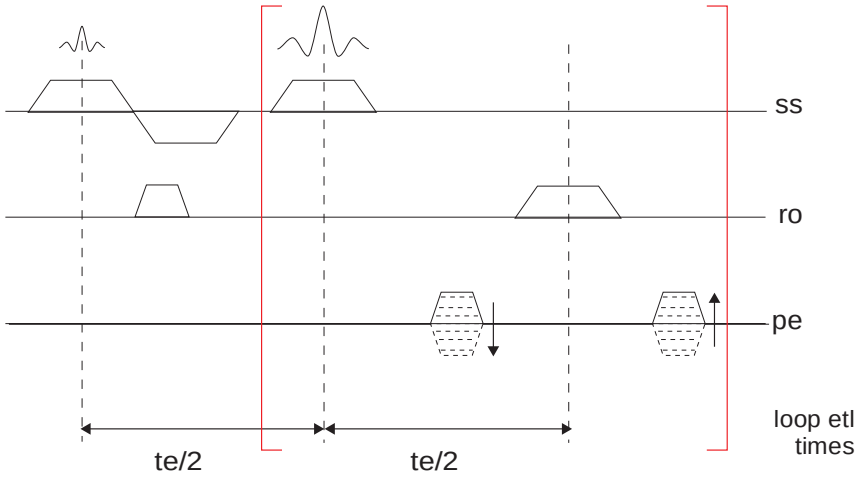
fsems

The fsems protocol is a fast spin echo multi-slice experiment where you can select the number of echoes in an echo train as well as decide which echo will be the center of k-space.

Advantages of fsems

The fast spin echo is a faster experiment than the conventional spin echo because multiple phase encode lines are acquired following each excitation.

Spin echoes are regenerated by applying multiple 180° refocusing pulses and minimizing signal loss due to T_2*.



The fast spin echo is well suited for obtaining high-resolution anatomical images in a short scan time.

Limitations of fsems

- "Specific Absorption Rate (SAR)," page 63
- "Mixed Contrast," page 63
- "Artifacts," page 63
- "Long Acquisition Time," page 64

Specific Absorption Rate (SAR)

Acquiring the data using multiple 180° pulses results in is a significant deposition of rf power. On human imaging systems the can conflict with Specific Absorption Rate (SAR) limits specified by the FDA. If the SAR limit is exceeded, the hardware will abort the acquisition with the error message `SAR limit exceeded`.

Mixed Contrast

The signal in an fsems experiment is usually a mix of the spin echo produced by the 90°-180° pulse pair and the stimulated echo caused by non-ideal 180° pulses. Consequently, the contrast in an fsems image is usually not a straightforward T_2- or T_1-contrast.

The `kzero` parameter, which specifies the echo closest to the center of k-space, can be used to change the contrast in images. For example, `kzero=1` will give a spin-density weighted image, while `kzero=etl` gives a T_2-weighted image.

Artifacts

T_2 decay creates a signal modulation that is distributed in k-space by the echo ordering scheme as multiple fsems echoes are acquired per excitation pulse. This results in edge replication, ghosting, or blurring. Another source of fsems artifact is the combination of spin echoes and stimulated echoes that can be misaligned due to imperfect gradient areas or other sources of phase variation, which can also result in edge replication, or banding.

Long Acquisition Time

Although the fsems experiment is faster than the conventional spin echo, it is still a relatively lengthy experiment. The long `tr` is typically in the order of 3-4 seconds (3-5 times T_1) and necessary to allow the spins to return to equilibrium between excitations.

Running the fsems Sequence

The parameters specific to fsems are listed in the following table:

Parameter	*Description*	*Typical Values*
`etl`	echo train length	4 or 8
`esp`	echo spacing (time between echoes)	10 to 20 ms
`kzero`	echo that shall be assigned to the center of k-space (values between 1 and `etl`)	1 or 2
`tep`	propagation delay caused by gradient hardware.	50 to 100 µs

Preparation of the sequence results in the generation of a table for specification of the order of k-space lines (refer to "gems," page 91). The name of the table is defined as: `fsems<nv>_<etl>_<kzero>`

The advantage of choosing a large number of echoes (large `etl`) is the obvious reduction in scan time but at the expense of reduced signal-to-noise or image resolution. Changing `kzero` will change the image contrast. kzero=1 gives spin density weighted images, whereas a higher `kzero` value gives T_2 weighted images

The parameter `petable` specifies which table is used for data ordering (see "gems," page 91). Additional acquisition parameters, such as the rf pulse definitions, bandwidth, acquisition time and number of dummy scans is set on the Acq page.

The `tep` parameter can be used to center the echo within the acquisition window. `tep` is the position of the echo, in microseconds, from the center.

The fsems sequence is `apptype='im2Dfse'`.

Options for fsems

- "Inversion Recovery," page 64
- "Show Profile," page 64
- "Steady-State Scans," page 65

Inversion Recovery

The spin echo sequence can be preceded by an inversion recovery (IR) pulse. The IR option is controlled through the checkbox on the Scan page; this sets the flag `ir` to `'y'` or `'n'`. When IR is activated, the inversion time (`ti`) is entered on the Scan page.

Show Profile

Obtain a profile of the object by clicking **Show profile** on the **Acq** page.

This function temporarily sets the number of phase encode steps to zero (`nv=0`), which signals to the sequence to acquire a single echo under the readout gradient but without any phase encoding. This will acquire a profile for each echo in the echo train. To view all profiles, enter `flashc ft dssh`. To view a specific profile, for example the second profile, enter `flashc ft(2)`.

Steady-State Scans

The parameter `ssc` is used to force the pulse sequence to run `ssc` number of times prior to the actual experiment.

Optimizing fsems

Readout Gradient

Optimizing the readout gradient:
The readout gradient can be optimized through the parameter `grof`. It will be multiplied onto the calculated readout dephaser and is typically within the range 0.99 to 1.01.

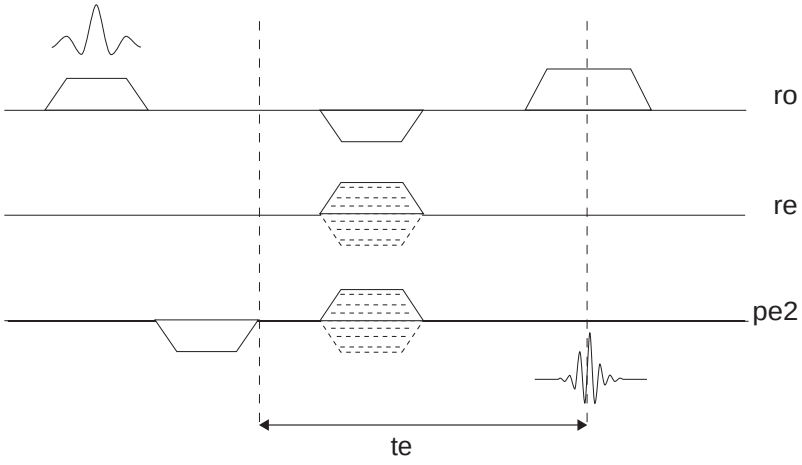
Set up an array of values and click **Show Profile** on the **Acq** page.

This acquires a set of profiles (one for each echo in the echo train) for each value of `grof`. Use `cf` to select which echo in the echo train you wish to view and do the `ft`, for example: `cf=1 ft dssh`. Select the best profile and set `grof` accordingly.

ge3d

- "Advantages of ge3d," page 65
- "Limitations of ge3d," page 66
- "Running the Sequence," page 66
- "Options for ge3d," page 67
- "Options for ge3d," page 67

The ge3d protocol is a 3D version of the gradient echo that allows you to obtain a true 3D image in a short time. ge3d uses a selective rf pulse for excitation followed by phase-encoding in two dimensions and readout in the third.



Advantages of ge3d

As is true for the 2D version, ge3d uses a single excitation pulse at a reduced pulse flip angle so a shorter repetition time (`tr`) can be used, thus reducing the time necessary for obtaining the image data.

The ge3d experiment is therefore very well suited for the following:

- High-resolution 3D images with extraction of images in any of the cardinal planes

- 3D angiography (see angio3D protocol)
- 3D contrast agent enhancement studies

Limitations of ge3d

- "Susceptibility Effects, Signal-to-Noise," page 66
- "Extraction Planes," page 66

Susceptibility Effects, Signal-to-Noise

The ge3d experiment suffers from the same limitations in regards to susceptibility effects and reduced signal-to-noise as the gems experiments (refer to "gems," page 91).

Extraction Planes

It is only possible to extract slices from the 3D data in the cardinal planes, axial, coronal, or sagittal.

Running the Sequence

Set sequence timing parameters (TE, TR, number of averages, number of dummy scans, and pulse flip angle) and the FOV/slice parameters on the **Scan** page. Typical values for te and tr are 3-5ms and 10-30ms (single-slice), while the pulse flip angle usually is in the range 5-30°. A minimum TE and TR can be applied by checking **Min TE** and **Min TR**, respectively. A minimum TR may cause a gradient duty cycle error.

The slice selective gradient is always applied in the second phase encoding direction (PE2), i.e., it limits the extent of the sample in the second phase encoding dimension. The thickness of the slice selective slab can either be given in mm or as a percent of the FOV in PE2 (on the **Plan** page). The center of the slab always coincides with the center of the FOV in PE2.

Additional acquisition parameters are set on the **Advanced** page. A page displaying the RF pulse and gradient parameters can be brought up by hitting the button **Show RF & Grad**.

Select the **Scan** page to select the orientation (orient) of the 1st extraction (ROxPE) of 2D slices from the 3D data. This orientation is automatically extracted upon completion of the data acquisition. Further extraction in any of the cardinal orientations can be done on the **Extract** page in the **Image** folder.

The following tables define which direction is assigned to readout, first and second phase encode directions; this table is essentially identical to that for 2D imaging, where the slice select direction has been replaced with a 2nd phase encode direction (see "gems," page 91):

orient	*Readout*	*Phase encode*	*Phase encode 2*
Axial	Y	X	Z
Coronal	Z	X	Y
Sagittal	Z	Y	X

Consequently, the orientations extracted depend on the value of orient:

orient	*RO x PE*	*RO x PE2*	*PE x PE2*
Axial	Axial	Sagittal	Coronal

orient	*RO x PE*	*RO x PE2*	*PE x PE2*
Coronal	Coronal	Sagittal	Axial
Sagittal	Sagittal	Coronal	Axial

The ge3d sequence is `apptype='im3D'`.

Options for ge3d

- Standard sequence options — see "Standard Sequence Options," page 114
- "Phase Encoding Rewinding," page 67
- "RF Spoiling," page 67

Phase Encoding Rewinding

Because the spins are not allowed to return to equilibrium between excitations, it may be necessary to rewind the phase introduced by the phase encoding gradient after acquisition to achieve a steady state condition. With phase encoding rewinding (PE rewind), a gradient of the same amplitude but opposite polarity of the phase encoding step is applied following data acquisition.

Phase rewinding is controlled by the variable `rewind`, which can be set to **`'y'`** or **`'n'`**.

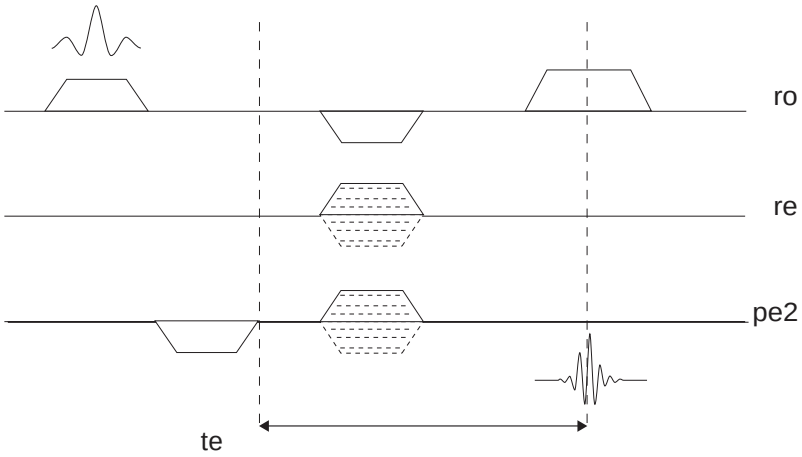
RF Spoiling

The short tr used in the gems sequence may cause image distortions due to a non-steady state condition resulting in residual transverse magnetization. To alleviate this, gradient pulses (for T1 weighting) or RF spoiling phase modulation (T2 weighting) and rf spoiler pulses (Zur, Y., Magnetic Resonance in Medicine, 21, 251, 1991) are usually employed in the pulse sequence to minimize such artifacts.

The RF spoiler is controlled by the parameter `rfspoil`, which can be set to either **`'y'`** or **`'n'`**.

ge3dshim

- "Advantages of ge3dshim," page 68
- "Limitations," page 69
- "Acquiring Shimmaps," page 69
- "Generating Shimmaps," page 70
- "Sample Effects on Shimming," page 70
- "Choosing the Field of View (FOV)," page 71
- "Setting the Optimal Data Matrix Size," page 71
- "Setting the Optimal Shim Step Size," page 71
- "Quick Procedure to Obtain Z2 Frequency Shift," page 79
- "Autoshimming (Interactive Mode)," page 81
- "Saving Parameters as a Protocol," page 84
- "Shimming for Localized Spectroscopy," page 84
- "Shimming for Imaging," page 85
- "Monitoring the Progress During Autoshimming," page 86
- "Transmitter Frequency," page 88



The GE3DSHIM method is an autoshimming method based on field mapping using a 3D gradient echo sequence. The first part of the procedure involves measuring the field produced by each of the shim coils using the GE3DSHIM protocol. The resulting field map or shim map is used to determine the optimum shim currents for shimming a sample. A any errors in the shimmap cause the shim current calculations and the shimming procedure to fail. This section, using examples, describes the steps involved in generating and analyzing the shimmaps.

The 3D gradient shimming routines are based on measuring the rate of change of phase between two 3D gradient echo images taken at two echo times, `te` and `te+del`. The echo time difference, `del`, causes a phase difference between the images as a result of residual magnetic field (B0 inhomogeneity) within the sample. The frequency or field is determined by calculating the rate of change of phase from the two images.

`phase = arctan(I/R) (radians)` [Eq. 1]

where **`R`** and **`I`** refer to the real and imaginary components in the image.

The frequency is measured by calculating the rate of change of phase:

`frequency = phase/tau (radians/sec)` [Eq. 2]

`tau` is the echo time difference between the two images.

The field, **`B`**, is directly proportional to the frequency:

`frequency = γ*B` [Eq. 3]

γ is the gyromagnetic ratio (rad/sec/T)

Advantages of ge3dshim

- GE3DSHIM is a fast and automated shimming procedure for imaging or spectroscopy.
- Multiple iterations are supported.
- Shimming over a user-defined sample region is supported.

- Easy specification of the shim region of interest when planning slices for imaging or voxels for spectroscopy.
- Robust phase unwrapping improves the reliability of field measurements.
- Works with all available shim coils.

Limitations

- The problem of phase-wrap is a serious limitation.

  A serious limitation of this approach is that the phase can only be measured from zero to ± Π. Larger phase changes, > Π, cause aliasing or phase-wrapping. Additional (phase unwrapping) routines are necessary to determine the true phase and frequency. In the current implementation an additional dataset is collected. The use of this additional field map was found to significantly improve the reliability of the field measurement.

  The phase change measured using equation (1) returns a value in the range of ± Π. Phase changes greater than ± Π. cause aliasing or phase-wrapping and cannot be directly measured from the experiment. All field mapping routines use an experimental or data processing scheme to unwrap the phase and determine the true phase or frequency. An additional dataset with an echo time set to `te+delref` is collected where `delref` is a short delay in the order of 300 µsec. The phase change during the field encoding delay, `delref`, must be less than ±Π. This is verified by viewing the corresponding field maps.
- The recommended matrix size is 64x32x32 complex points.
- The orientation of the image must be set to sagittal when acquiring data for the shim map.
- Any orthogonal orientation can be used for shimming once the shim map is obtained.
- The shims are not be updated if the shim limit exceeds 32K and the program aborts the shimming process.
- Selecting regions with poor SNR result in unreliable phase (or field) measurements. This is avoided by setting an intensity threshold.

Acquiring Shimmaps

Follow the procedures in "Acquiring Shim Calibration Maps," page 44 and acquire shimmaps. The following steps are executed by the acquisition macros:

1. Load the `start` shim file.
2. Create the shimmap parameter file, `shimmap.gcoil.param`.
3. Collect the base map datasets, `base.1.fid`, `base.A.fid` and `base.B.fid` corresponding to echo times, `te`, `te+delref`, and `te+del` respectively.

   Base map refers to the residual field within the sample.
4. Select the shim coil and set the shim offset.
5. Collect the shimmap datasets, `shim.1.fid`, `shim.A.fid` and `shim.B.fid` corresponding to echo times, `te`, `te+delref`, and `te+del` respectively. (`shim` refers to the name of the shim, for e.g. x1, y1, etc.).
6. Reset the shim value.
7. Repeat step 4 to step 6 for each of the shim coils selected.

Generating Shimmaps

Follow the procedures in "Generating a Shimmap," page 46 and acquire shimmap data. The following steps are executed by the acquisition macros:

1. Generate the phase (.p) and magnitude (.mag) images from the base datasets.

```
base.1.fid =>      base.1.p, base.1.mag
base.A.fid =>      base.A.p, base.A.mag
base.B.fid =>      base.B.p, base.B.mag
```

2. All signals (and noise) below a given threshold are ignored to improve the reliabilit.y of the field measurements. The `base.B.mag` file is used to determine the signal threshold. All signals below the threshold are set to zero and ignored in subsequent calculations.

3. Generate the phase difference images.

```
base.A.p - base.1.p =>    base.A.wf
base.B.p - base.1.p =>    base.B.wf
```

   The phase difference images may show discontinuities due to phase wrapping.

4. Determine the true phase images by unwrapping the phase.

```
base.A.wf, base.B.wf => base.f
```

5. Generate the phase (.p) and magnitude (.mag) images from each of the shim datasets.

```
shim.1.fid=>         shim.1.p, shim.1.mag
shim.A.fid=>         shim.A.p, shim.A.mag
shim.B.fid=>         shim.B.p, shim.B.mag
```

6. Generate the phase difference images.

```
shim.A.p - shim.1.p =>    shim.A.wf
shim.B.p - shim.1.p =>    shim.B.wf
```

7. Determine the true phase images by unwrapping the phase.

```
shim.A.wf, shim.B.wf =>     shim.f*
```

8. Remove the residual base field in the sample to obtain the field map generated by the shim coil .

```
shim.f* - base.f =>    shim.f
```

9. Repeat (4) - (7) for each of the shim coil selected.

10. Concatenate each of the shimmap files into a single file, `shimmap.gcoil.f`.

11. Generate FDF (`.fdf`) files for viewing purposes.

Sample Effects on Shimming

The gradient echo sequence is sensitive to field inhomogeneity. The magnetic susceptibility gradients caused by the sample leads to signal loss from T2* effects. Select a suitable sample and shim it well, using a shim method such as FID-shim or FASTMAP, prior to starting the shim calibration experiment.

Use a sphere or a long cylindrical sample for calibration experiments. A spherical sample is easier to shim than a cylindrical sample and results in a more homogeneous reference or

base field map. Sample defines the extent of the shim calibration maps and the region over which the shim calculations are performed. Regions outside this region and below a specified intensity threshold are ignored in the shim calculations. Use a spherical sample for the mapping process if the shimming is to be performed primarily for head imaging. The head must be positioned within the mapped region during the autoshimming procedure.

Use a cylindrical sample to map a larger region along the z-axis. The nature of susceptibility field gradients at the air-sample interface depend on the geometry and orientation of the sample with respect to the main field. Increasing the length of the sample minimizes the effect of susceptibility effects at ends of the sample. Large field gradients near the ends of the sample can make manual FID shimming difficult. Use a field mapping technique, if available, and shim the central part of the sample before mapping the shims.

A large water sample may cause difficulty in tuning the probe due to sample loading effects. Another limitation of large, conductive solutions, particularly at high field, is the signal variations across the sample due to dielectric effects. Under these conditions it is preferable to use a non-conductive material such as acetone. (Mineral oil is not recommended because it contains two broad CH_3 and CH_2 resonances.)

Choosing the Field of View (FOV)

Choose a FOV parameters (`lro`, `lpe` and `lpe2`) that covers the active region of the RF coil in use. The FOV along the z-direction is selected to avoid aliasing of the image from the region near or outside the ends of the RF coil. A typical RF coil extends along the z-dimension. The preferred sagittal image orientation and readout direction applied along the z-gradient allows collection of more data points to ensure sufficient digital resolution without increasing the scan time.

Samples with a wide range of sizes are typically used in imaging. Collect separate shimmaps for each range of sizes (e.g. mouse, rat, rabbit) to ensure sufficient digital resolution in the shimmaps for improved reliability and accuracy in the autoshim analysis routines.

Setting the Optimal Data Matrix Size

The optimum matrix size used for GE3DSHIM is 64 along the readout and 32 along each of the phase encoding dimensions. Increasing the phase encode dimension size increases the data acquisition time. Increasing the matrix size increases the data memory size and processing time.

Setting the Optimal Shim Step Size

During the shim calibration step, each of the shim (DAC) values is offset by a known amount and the field map (Ft) is measured. The field map includes the field produced by the shim coil (Fs) and the residual field (Fb) within the sample. To obtain the field produced by the shim coil the base field map (Fb) must be subtracted:

```
Fs = Ft - Fb                                                    [Eq. 4]
```

The shim offset values are specified through the parameters, step-I to step-IV. Step-I, for example, is the shim offset used for calibrating the `x`, `y`, and `z` shims and Step-II is the offset for the `z2` shims, etc. (The shim offsets for the 3rd and 4th order shims are specified in the macro, `gs_acqshimmap`.)A small step size will result in lower sensitivity in the field maps generated because of the small phase change induced during the phase encoding delay. A large value can contribute to signal loss in the images due to T2* effects. The step parameters must therefore be chosen based on the sensitivity of each of the shim coils. A number of factors affect the sensitivity of the shims:

- Efficiency (Gauss/cm/A) of the shim/gradient coil (refer to the manual on the shim/gradient system)
- Strength of the shim power supply driving the (higher order) shim coils
- Gradient amplifier and the gain setting for the x, y and z shims in DECCTOOL.

Experimental Example

The system, Table 1, and experimental parameters, Table 2, used for generating the shim calibration maps for this study are given below:

Table 1. System Components for the ge3dshim Example

Component	*Description*
System	4.7T (200 MHz)
Sample	58mm OD, 18 cm long plastic bottle containing doped water (T1 = 1s)
RF coil	63 mm ID birdcage coil
Gradient coil	Magnex 205/120/S, 120 mm ID, 40G/cm
Shim PSU	RRI 5 Amp
Gradient PSU	Copely Model 220, 200 Amp, 300V

Table 2. Parameters for ge3dshim Example

Parameter	*Value*
Shim gain in DECCTOOL	2%
Shim Step size for x,y,z, and z2 shims	1%
Shim Step size for xz and yz shims	2%
Shim Step size for xy and x2y2 shims	5%
Reference delay, `delref`	0.25msec
B0 field encoding delay, `del`	1msec (typical range 1 to 4 msec)
`TR`	20 msec (typical range 20 to 50 msec)
`TE`	4 msec (typical range 2 to 4 msec)
Averages	1 (typical range: 1 to 4)

A long cylindrical sample was used to map each shim coil within the entire rf coil. A scout image was used to verify the sample position in the 12 cm gradient/shim coil. The sample was shimmed manually (FID shim) using the 1st and 2nd order shims to about 25 Hz linewidth and the shim parameters saved in the `start` file for use during the shim calibration procedure.

Experimental parameters for collecting shimmaps using GE3DSHIM are shown in the Scan and Acq pages. (The voxel information is not used.) The total scan time was about 10 min. The delref and del delays were set to 250 µsec and 1 msec respectively. The x,y, and z shims, for example, were mapped by offsetting shim values by 1% of the maximum (i.e. 32K x 0.01 DAC units). The other shim step sizes used in the study are shown in the Map page.

The imaging parameters used for this study are shown in Figure 13.

Figure 13. ge3dshim Example Scan, Acq, and Map pages

Shimmap Generation

Prior to acquiring the shimmaps it is useful to acquire a test image, see Figure 14. The image can be used to identify problems associated with sample positioning, SNR, aliasing, receiver overflow, etc. and to setup and optimize the imaging parameters. Figure 14, is a test image using the GE3DSHIM routine, showing sagittal (RO-PE1) planes. The intensity variation in the images is caused by dielectric effects (high intensity near the center of the sample) and RF field inhomogeneity.

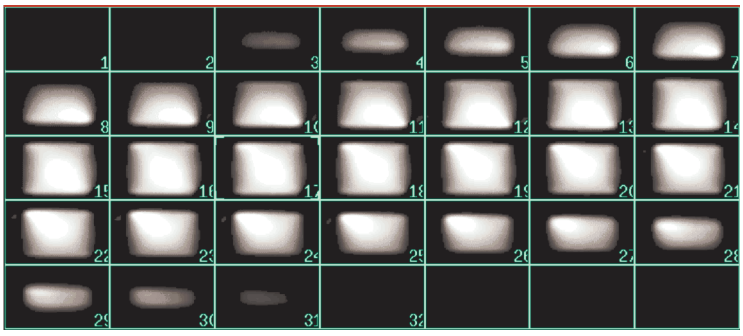


Figure 14. Sagittal (RO-PE1) planes

Shimming the sample using only the first and second order shims is sufficient for most imaging applications. The shim calibration is initiated using the **Acquire shimmaps** button in the Acquire-Map page. The field mapping routine collects two datasets with echo time values set to `te` and `te+del`. A small value of `del` (the field encoding time) causes small phase changes resulting in low sensitivity (SNR) in the field map data. A large `del` value can cause phase wraps and loss of SNR in the image due to T2* effects. In the present implementation an additional (reference) dataset with an echo time of `te+delref` is taken and used in the phase unwrapping routine to determine the true phase change. It is assumed that no phase wrapping occurs during the period `delref` and it is usually set to about 250µsec.

First the field variation within the sample is measured and is referred to as the base field map. Then each shim coil is offset by a specific shim-DAC value and the experiment repeated. The shim offset is specified using the parameters, Step-I to Step-IV. Because the sensitivity of each of the shims vary it is necessary to specify different shim offset values for each of the shims during the mapping experiment. The offsets for the x, y, and z, are determined by the Step-I parameter. Similarly, Step-II (z2), -III (zx, zy), and -IV(xy, x2y2) are used for the second order shims.

Three datasets are collected at echo times, `te`, `te+delref`, and `te+del` for each shim calibration map. If the 1st and 2nd order shims are selected for shim mapping, a total of 27 datasets are acquired - 3 base datasets, 3x3 1st order shim datasets and 5x3 2nd order shim datasets. The total data acquisition time is: 27xTRxNTxNVxNV2 (NT is the number of averages and NV and NV2 are the number of phase encoding steps).

Shimmaps are calculated after data acquisition is completed if the **Generate shimmaps** option is selected. Clicking on the **Generate shimmaps** button generates the base field map and the individual shim field maps. During the shimmap calculations the field map produced by each of the shims are generated as 3-dimensional (FDF) image files. The image files can be viewed easily using the Acquire-Map panel and can help the user to identify problems and to check the quality of the shimmaps. The base field map shows the residual field variation across the sample and is shown in Figure 15 and Figure 16.

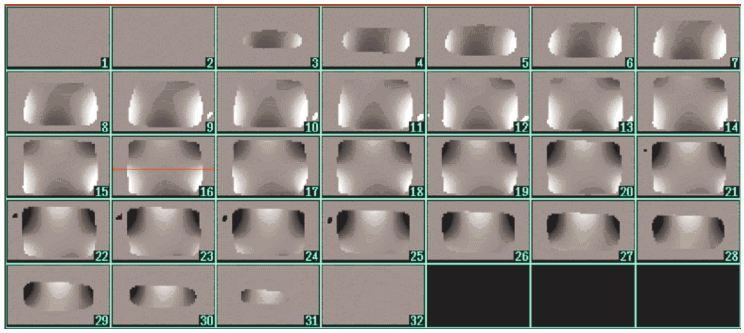


Figure 15. Sagittal planes from the (Base) Field Map

The regions near the ends of the sample show a large field variation indicating susceptibility effects in these regions or higher order field inhomogeneity in the magnet. The large field variations at the ends can cause signal loss in these regions in the resulting images. During shim calibration experiments, offsetting the shim currents can add to the base field further exaggerating the signal loss. The loss of signal at the edges will reduce the size of the resulting field map. It is therefore necessary to shim the sample well before proceeding with the calibration. The large field gradients at the ends can be minimized by using a shorter RF coil and/or by using an extended sample. A spherical sample will also help to avoid the end effect problem but it will also limit the size of the shimmaps along the z axis.

Figure 15, sagittal planes from the (base) field map produced by the sample. Darker areas correspond to negative values and the lighter areas to positive values. Signals below the threshold value are ignored and represented by zeroes (gray background). The ends of the sample show a large field variation (see also Figure 16) because the sample is extended along the z-axis making it difficult to shim well over the whole sample.

Figure 16 shows the field variation along the z-direction. A line profile was taken along one of the sagittal planes shown in Figure 15. The intensity axis corresponds to the phase difference (ΔP radians) between the two reference images taken with echo times `te` and `te+del`. The frequency is calculated from the rate of change of phase, (ΔP /`del`) radians/sec. The field is directly proportional to the frequency (Equation 3).

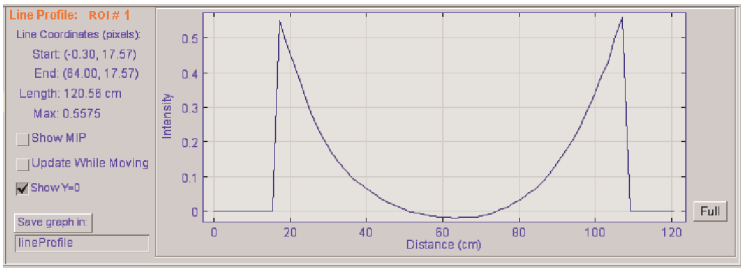


Figure 16. Field Variation in z-Direction

Figure 17 through Figure 25 show shimmaps corresponding to some of the first and second order shim coils. The shimmaps must be carefully inspected for any unusual patterns or artifacts. The field maps should show a gradually varying three dimensional function with sufficient SNR as shown in these examples. The parameters used for collecting the shimmaps are listed in Table 2.

Figure 17, the z-shimmap. Sagittal planes taken from z1c.f.fdf file showing the field variation produced by the z-shim coil.

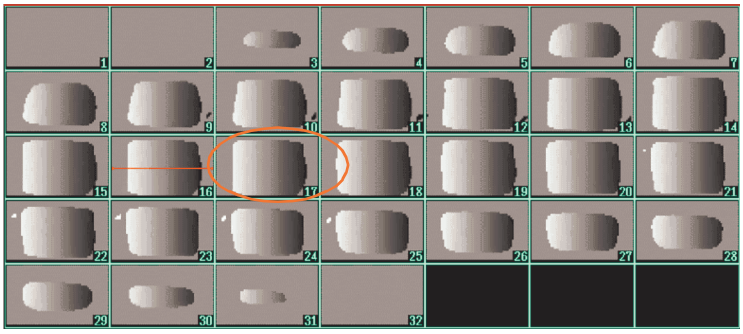


Figure 17. Sagittal Planes from z1c.f.fdf file

Figure 18, line profile, from Figure 17, along the z direction shows a linear variation of the z-shim field. The intensity axis represents the phase change (in radians) caused by the z-shim coil. The smooth profile indicates good SNR.

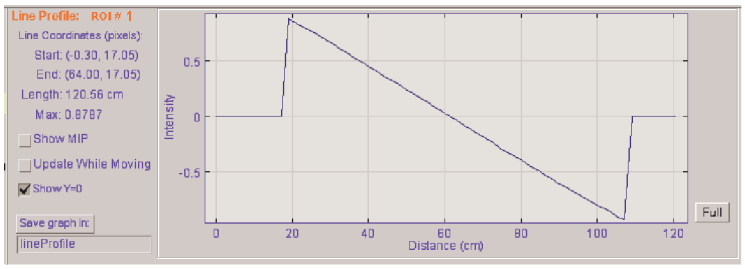


Figure 18. Line profile from Figure 17, along z-Direction

Figure 19 Shimmap (z2c.f.fdf) corresponding to the z2 shim coil.

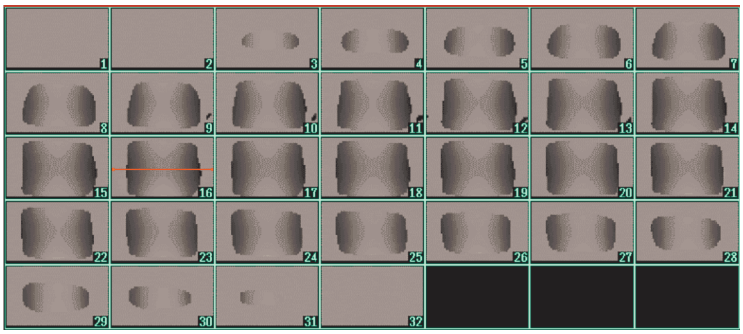


Figure 19. Shimmap (z2c.f.fdf) of the z2 Shim Coil

Figure 20 shows a line profile along the z-direction taken from Figure 19. When the z2 shim is applied during the mapping experiment a frequency (B0) shift occurs causing the profile to be offset along the vertical axis. A procedure for removing the B0 shift is described in "Field drift and B0 shift caused by Z2," page 79.

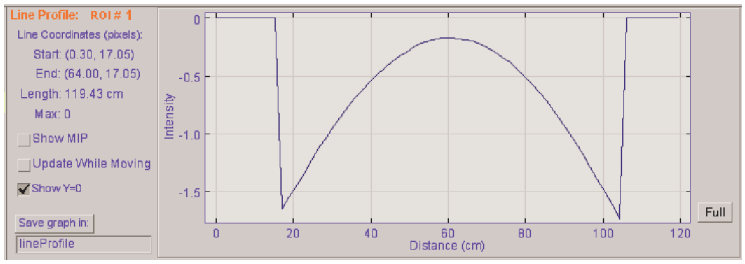


Figure 20. Line Profile Along the Z-Direction, from Figure 19

Figure 21, sagittal (RO - PE) planes taken from the 3D xz-shimmap.

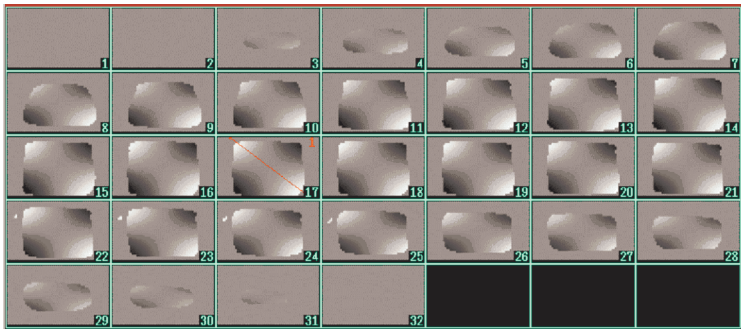


Figure 21. XZ-Shimmap, Sagittal (RO - PE) Planes

Figure 22, line profile taken from one of the planes shown in Figure 21. The profile does not appear smooth because it is not interpolated properly due to limited digital resolution and should not be interpreted as low SNR.

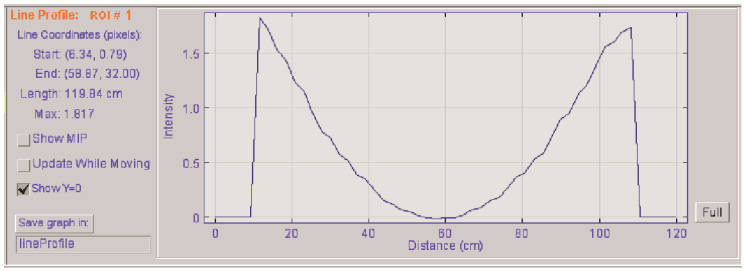


Figure 22. Line Profile From a Planes Shown in Figure 21

Figure 23, sagittal (RO-PE1) planes taken from the x2y2 shimmap.

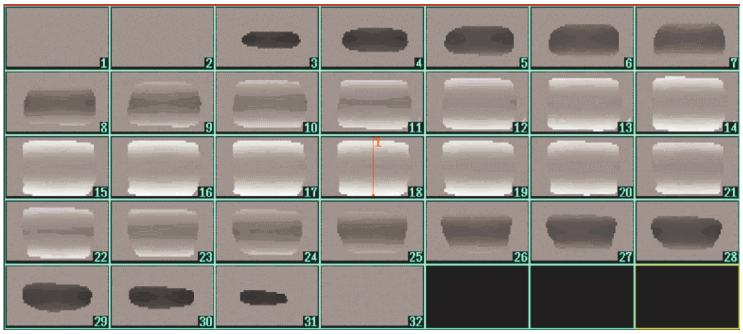


Figure 23. X2Y2 Shim Map Sagittal (RO-PE1) Planes

Figure 24, transverse (RO-PE1) planes taken from the x2y2 shimmap

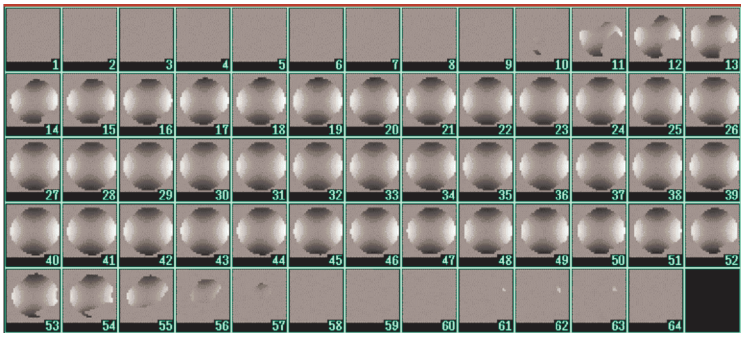


Figure 24. X2Y2 Shim Map Transverse (RO-PE1) Planes

Figure 25, a line profile taken from the image shown in Figure 23.

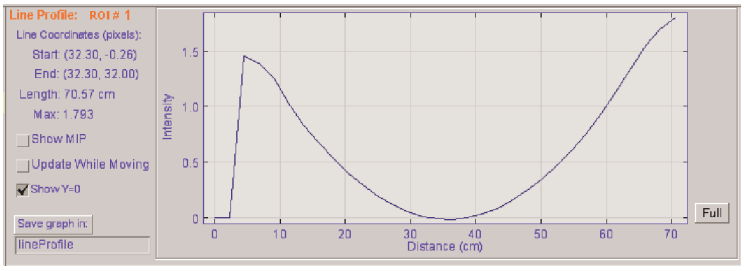


Figure 25. Line Profile From Figure 24

Figure 26, the phase difference image, yz.B.wf.fdf, showing the phase wrap problem near the ends of the coil. Notice the abrupt phase changes when the phase difference exceeds the +/- Π limit, see also Figure 27.

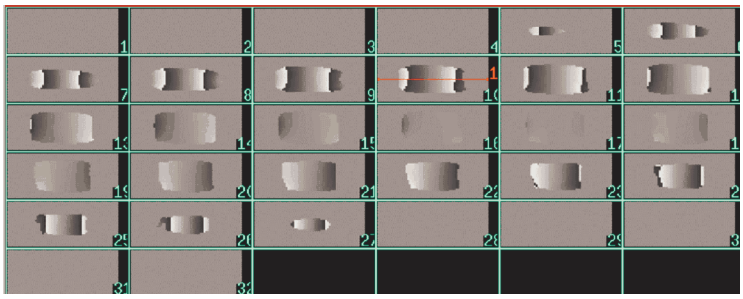


Figure 26. Phase Difference Image, yz.B.wf.fdf

Figure 27, the line profile taken from Figure 26 illustrates the phase jumps. The phase unwrapping routine, `gsphasetofield`, determines the true phase form this data.

Figure 27. Line Profile from Figure 26

Generating the Shimmaps

Clicking on **Generate shimmaps** generates the shim calibration map in the users home directory, `$home/vnmrsys/gshimdir/calib/shimmap.f.gcoil`. An additional copy of the file, `shimmap.gcoil.f.date` is also saved. Date is the date when the file was created. The `shimmap.gcoil.param` file contains the parameters which are used by the analysis routines.

Specifying an ID or name for the shimmap file in the Settings page is optional. The optional string specified by the user are contained in the `.f` (`shimmap.gcoil.ID.f`) and `.param` files.

The shimmap files are also copied to the system directory; `/vnmr/gshimdir/calib`, if the user is vnmr1 (the system hardware administrator) and provides global access to these files for shimming.

Field drift and B0 shift caused by Z2

The z2 shim offset can cause a zero order field shift (B0) resulting in a frequency shift of the water resonance. This does not pose a problem in most of the shim coils used in the animal imaging systems. The z2 induced zero order field shift can be a problem with larger shim coils such as those used in human imaging and some older shim coil designs. These coils require a few seconds or even minutes for the field to stabilize. The shim field must stabilize before proceeding with field mapping experiments.

The z2-drift and z2-field shift can be quantified using the macros `get_z2drift` and `get_z2z0` as described in the manual under the Fastmap Protocol. After running the `get_z2z0` macro the file, `z2z0.gcoil`, contains the frequency shift (Hz) per shim DAC offset. This value must be entered in the Settings page. The `get_z2drift` macro generates the file `z2drift.gcoil` showing the frequency of the water resonance at various times after setting an offset on the z2 shim. The shimmap acquisition macros, (`gs_acqshimmap` and `gs_acq1shimmap`) include a delay of 10 sec (default) whenever the z2 shim is changed for the field and shims to stabilize.

Quick Procedure to Obtain Z2 Frequency Shift

1. Shim a sample (e.g. spherical phantom used for system tests) and obtain a single pulse spectrum using the `spuls` protocol.
2. Place the cursor on the line and set the reference frequency display to zero using one of the following procedures:
   - Process => Display => Reference line, Zero
3. Save the current shim settings using one of the following procedures:
   - Start => Manual Shim => Save Milestone
4. Offset the z2 shim value by 1000 dac units in the Manual Shim page.
5. Click on **Acquire Spectrum**.
6. Move the cursor to the peak and record the cursor frequency (`cr`) displayed on the screen, this value including its sign is the frequency shift.
7. The z2 shift (Hz/DAC_unit) is given by:

```
z2z0 = frequency_shift/(z2_shim_offset)
z2z0 = cr/1000
```

8. Enter the z2z0 value in the Acquire => Settings page in the ge3dshim protocol.
9. Reset the original shims by retrieving the saved shim file:
   Start => Manual Shim =>Retrieve Milestone.

Optional Zero Filling

Selecting the **Zerofill** option on the settings page, Figure 28, doubles the digital resolution of the shimmaps by zero filling the time domain signal. The option is useful when working with small voxels because it adds more data points to the characterization of the field

variation resulting in better analysis. Select Zerofill option prior to acquiring the shimmap data. The file `shimmap.gcoil.param` is created when the shimmap is created.

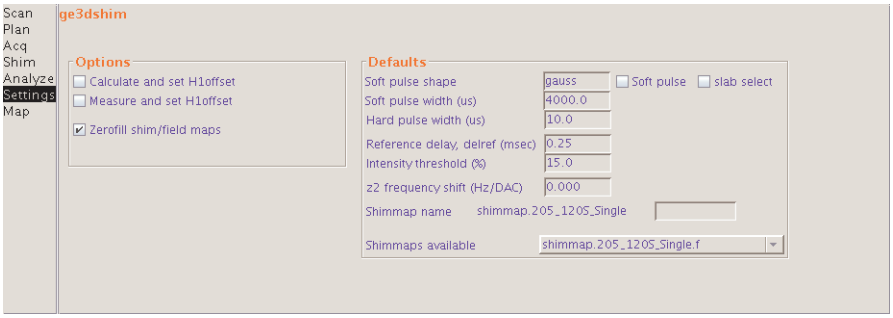


Figure 28. Selecting Zerofill Option for ge3dshim

Use the following procedure for post acquisition zero filling if zero fill flag was not set prior to data acquisition:

1. Edit the file `shimmap.gcoil.param` and change the data size
   from 64 32 32 1
   to 128 64 64 2
2. Select **Zerofill**.
3. Click on **Generate Shimmaps**.

Acquiring a single shimmap

During the shim-mapping experiment it may sometimes be necessary to repeat the measurement for a single shimmap. The following section describes the steps involved:

1. Load a parameter set that was used to collect the original shimmap dataset, for example, `base.1.fid`. The experimental parameters must be kept the same as the parameters used in the original experiment.
2. Select the map to be acquired, either the shim name or base, in the Map page.
3. Change the shim step size if necessary.

   Do not change any of the other acquisition parameters.
4. Click on **Acquire a map**.
5. Modify the `shimmap.gcoil.param` file if necessary to include the new shim offset.
6. Click on **Generate Shimmap** to regenerate the shimmap file.

Only the shim step size can be changed. Changing the shim step requires editing and editing the new value in the file, `$home/vnmrsys/gshimdir/calib/shimmap.gcoil.param`, prior to step 6. During step 2 a parameter file `shimmap_2.param` is generated for reference and this file can be copied for use in step 5 as follows:

```
% cp shimmap_2.param $home/vnmrsys/gshimdir/calib/
shimmap.gcoil.param
```

Autoshimming (Interactive Mode)

The **ge3dshim** protocol is used for 3D gradient shimming. The **Shim** page of the **Start** folder, Figure 29, contains the interface for shimming operations.

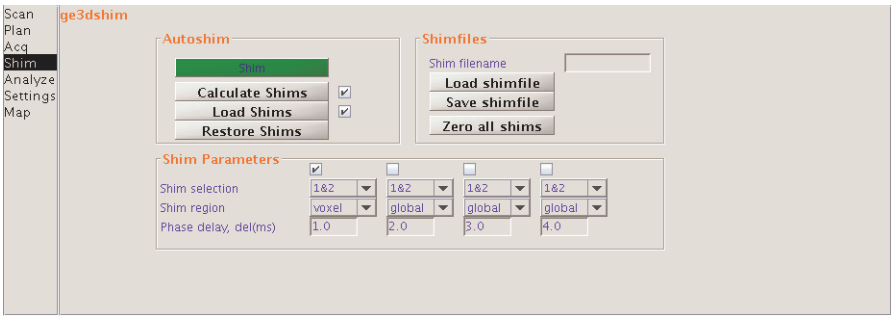


Figure 29. Interface for ge3dshim Shimming

The first step is to calibrate the shims, as described in 3.6 “Setting Up and Calibrating 3D Gradient Shimming,” page 44. The shim DAC values are changed by a particular value and the resulting 3D field map generated by each shim is calculated. During the shimming process the B0 field is measured and the shim currents (DAC values) needed to minimize the field are calculated and the shims updated.

3D autoshimming can be performed either in the Prescan mode or in the Interactive mode.

- Prescan mode default parameters are predefined and initiated by the Shim button during Prescan operations.
- The interactive mode allows the user to intervene and control the shimming procedure. The interactive mode is useful when encountering samples that are difficult to shim because a cautious and step by step procedure may be necessary for optimizing the shims.

Make sure that the DECCTOOL file and the gradient calibration files are the same ones used during the shim calibration procedure described in the previous section before proceeding with the autoshimming routines. The shim and gradient scaling (gain) are set in the DECCTOOL file.

There is no generalized, universal procedure for autoshimming because the field inhomogeneity is affected by the magnet and the sample itself. The protocol determines the size and region that is shimmed making the interactive mode preferable to the prescan option for shimming.

Multiple iterations of the autoshimming routines are sometimes requiring if the field homogeneity is poor. A general approach to shimming under those circumstances is to start shimming using the low order shims in a smaller region of interest (ROI) and then gradually include the higher order shims while increasing the shim ROI.

Autoshimming can be done by a single button action. The number of shims, the shim ROI and the number of iterations can be specified by the user. The region for shimming can be specified by the user as:

Global	The region used for shim calculation is determined by the volume defined by the field of view (i.e., `lro*lpe*lpe2`).
Voxel	The shim region is defined by the voxel parameters. This option is useful for shimming a restricted area within a sample as in localized spectroscopy. The voxel area can be specified by using the Plan routines.

Slab	The shim region is defined by the Slice parameters. In this case the volume defined by the slices is used for shimming. For slab shimming, the slices are specified by using the Plan routine.

Experimental Procedure

1. Load the **ge3dshim** protocol into the Plan Viewport.
2. Set up the parameters as in a regular 3D gradient echo sequence.

Note: The matrix size is usually set to 64 x 32 x 32, similar to the shimmap matrix size, the FOV is chosen to cover the sample of interest, and the image orientation to an orthogonal plane.

3. Check the profile by clicking on **Acquire Profile** and optimize the receiver gain.

   Set the gain lower in anticipation of an increase in the signal as the field homogeneity improves.

4. Set the transmitter frequency on the water resonance using Frequency-Prescan.

   The frequency is set based on the field map calculations or by running the frequency prescan measurement at the end of the shimming routine if one of the options to update *H1offset* is checked in the Settings page,.

5. Select the shims to be used for autoshimming. Only the shims that were mapped (see "Generating the Shimmaps," page 78) can be selected.

1-(XYZ)	1^{st} order shims
1 & 2	1^{st} and 2^{nd} order shims
1 & z2	x,y,z and z2 shims
1 2 & 3	1^{st}, 2^{nd}, and 3^{rd} order shims
all	all shims are selected

   Reduce the `del` and `delref` values if the initial magnet field homogeneity is poor. Longer `del` values can result in signal losses due to T2* effects. If in doubt collect a 3D image (using Acquire Test Image) with `te` set to `te+del` and check the image. Typical value for `del` is between 1 to 5 msec.An additional phase map is collected using a much smaller B0 encoding `delay`, `delref`. `delref` is usually set to about 0.25 to 0.5 msec and assumes the phase change during this delay is within ±180º.

6. Select the region of interest for shimming:

Global	The region of the interest is defined by the Field of view parameters, `lro*lpe*lpe2` in the above case.
Voxel	Region of interest for shimming is done by planning a voxel using a scout scan. Scout image must be axial, sagittal, coronal, or one of the other orthogonal planes. Display a scout image (by double clicking on a previously collected scout image) and use the Plan page to Add a voxel and define the voxel region of interest. Click the **Save for Shimming** button to save the voxel information for use during the shimming procedure.

Slab Defining the volume containing the slices the region for shimming when planning slices for imaging.

Planning slices while the currently loaded protocol is `ge3dshim` will modify the FOV parameters. To avoid modifying the FOV parameters, load the protocol to run, for example, GEMS or EPI. Plan the slices using the scout image and save the slice volume information by clicking **Save for Shimming**.

The shim ROI information is saved in the `userdir/prescan/` directory. It will be retrieved and used during the analysis by the `gs_calc` macro.

7. Set Threshold (typically 10-20%) to avoid low signal-to-noise regions.
8. Click **Shim** to start the autoshimming procedure.
9. Check the **Calculate Shims** and the **Load Shims** options to calculate load new shim values immediately after data acquisition without user intervention.
10. Click **Calculate Shims** to calculate the optimum shim settings.

    Calculation results are written into the file in `vnmrsys/gshimdir/data/gshim.out`. The results are also displayed Acquire-Analyze page, see Figure 30.

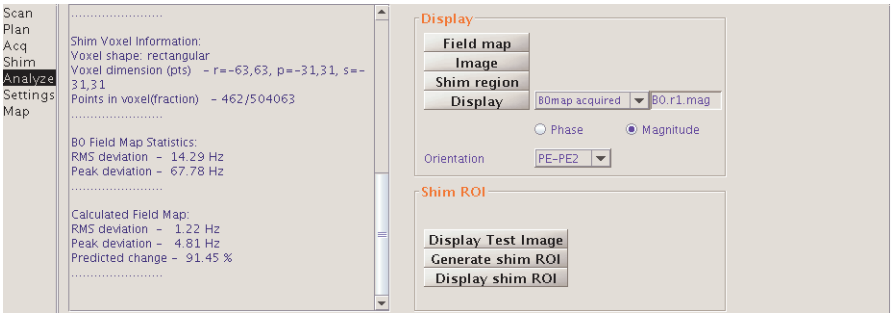


Figure 30. Shim Map Shim Calculations

11. Click **Load Shims** to update the shims.

Note: New shim values are not loaded into the hardware if any of the shim limits are exceeded. Repeat the calculation (step 8) by choosing different shims and/or shim-ROI.

12. Verify the shimming results by running the SPULS protocol (for global shim) or a localized spectroscopy sequence, e.g. PRESS, (for voxel shim). In the latter case the spectrum must be taken from the same shim-ROI. It is convenient to run in the test mode by clicking **Acquire spectrum** to collect and view the spectrum in the Plan Viewport. If a larger shim ROI is chosen, use a gradient echo image of that region to evaluate the progress in shimming.
13. Refer to "Monitoring the Progress During Autoshimming," page 86.

Repeat step 8 through step 12 for shimming different ROIs or for experimenting with different shim parameters using the data set acquired in step 7. Reduce the shim ROI and/or use lower order shims during the iteration if the shim limits are exceeded.

The **Load Shims** option loads the new, calculated, shim values. Click the **Restore Shims** button to restore the original shim values.

Setting up for Multiple Iterations

Each sample distorts the field differently. Interactively set the shim parameters and monitor the progress of the shimming as described in the previous section. Up to 3 or 4 iterations might be required to achieve optimum results. Automate the process for a given application by setting up the parameters for multiple iterations.

The numbers of iterations required typically depends on the initial shim condition and sample. Use shim settings corresponding to a spherical phantom of similar volume as a starting point when shimming with an unfamiliar sample in the magnet.

Repeating the shimming procedure for convergence is usually necessary. Convergence is experimentally verified in localized spectroscopy by checking the linewidth of the water peak as described in "Shimming for Localized Spectroscopy," page 84.

Start shimming in a small region using the 1st order shims if the initial field homogeneity is poor. Gradually increase the size of the region of interest and include the higher order shims.

Specify parameters for up to 4 iterations and press the Shim button to execute each shim iteration automatically.

Setup for multiple iterations as follows:

1. Select the shim parameters for each iteration.
2. Click the check boxes above the selection can be used to enable the parameters. For example:

Shim selection	1-(xyz)	1&2	1&2	12&3
Shim region	voxel	voxel	global	global
del (msec)	1.0	2.0	4.0	6.0

   The initial voxel shimming is done using the first order shims with the `del` value set to 1 msec. The second iteration is done using first and second order shims in the same voxel region and with `del` set to 2 msec., etc.
3. Press the **Shim** button.

Saving Parameters as a Protocol

To Save the current parameters as a protocol:

1. Click on the **Edit** menu.
2. Select **Create Protocol**.
3. Select **Make New Protocol**.
4. Save the ge3dshim protocol (or update if it already exists).

Shimming for Localized Spectroscopy

1. Setup and save the Shim parameters (Protocol) as described in the previous section. For localized spectroscopy, voxel selection should be chosen.
2. Load, for example, the PRESS protocol.
3. Setup the parameters for PRESS.
4. Load the **Scout** image and plan the voxel.
5. Save the voxel parameters (click **Save for shimming**).

During autoshimming the field inhomogeneity in the voxel region is measured and the shims set accordingly.

6. Collect a reference PRESS spectrum of water from the ROI and check its linewidth.
7. Monitor the progress of autoshimming experimentally by following the changes in linewidth of the water signal as follows.
    a. Click on the **Acquire Spectrum** button to collect a spectrum in the Plan viewport.
    b. Place the cursor line near the peak and click on **Linewidth** to obtain the width at half height.
8. Load the **ge3dshim** protocol.

    Set the parameters for autoshimming as described in the previous section on Autoshimming. The Voxel shim region must be selected.
9. Click the **Shim** button to shim the Voxel region.

    The routines will collect the field maps, calculate the new shim values, and load the shims.
10. Load the PRESS sequence from the study queue and check the linewidth of water as in step 7.
11. Repeat step 8 and step 10 as necessary.

Shim using the first order (X,Y,Z) shims if the initial shim is poor and reduce the `del` value to about 1 msec. Add the second order shims and increase the del value to about 2-5 msec when the homogeneity is improved. Automate the procedure by setting up parameters for multiple iterations.

Shimming for Imaging

Specify the slice region (slab) or the whole imaging volume (global) when shimming during imaging experiments. Define the shim ROI using voxel parameters, see "Shimming for Localized Spectroscopy," page 84.

1. Load the protocol to be run, for example, EPI, or GEMS.
2. Using the scout image plan the slices for imaging as usual.
3. Save the slice region (slab) for shimming by clicking **Save for shimming**.
4. Do not plan the slice/slab region while the `ge3dshim` protocol is loaded. The FOV. parameters will be modified if the `ge3dshim` protocol is loaded while planning the slice/slab region.
5. Defining the shimming region to be a voxel:
    a. Select a voxel regions such that regions of little interest are neglected in the shimming process.

        Avoid regions with large magnetic susceptibility effects, flow, motion, chemical shift effects (e.g. fat signals, nasal and ear cavities when doing brain imaging). These regions can lead to erroneous phase measurements.
    b. Click **Save for shimming**.
6. Image planning is not necessary if global shimming is chosen. The whole field of view region, `lro*lpe*lpe2`, in the shimming sequence (`ge3dshim`) is used as the shim-ROI.

7. Load the `ge3dshim` protocol from the study queue.
8. Check and set the shimming parameters.
9. Click the **Shim** button.

GE3DSHIM Procedure Summary

1. Acquire 3D datasets:

```
B0.1.fid,  Δte=0
B0.A.fid,  Δte=delref
B0.B.fid,  Δte=del
```

2. Fourier transform and generate the magnitude (.mag) and phase-angle (.wf) images:

```
B0.A.mag,  (Image A)
B0.B.mag,  (Image B)
B0.A.wf,   (Phase A)
B0.B.wf,   (Phase B)
```

3. Unwrap the phase using the phase-angle images to give the true phase which is proportional to the field.

```
B0.f     (Acquired field map)
```

4. Reformat (re-grid) the `B0.f` data to match the shimmap file.

```
B0.rl.f  (field map)
```

5. Use the shimmap data to calculate the shim currents needed to minimize the field deviation and save the results in the text file: `gshim.out`.
6. Load the new shim settings into the hardware.

Monitoring the Progress During Autoshimming

Shimming progress can be verified experimentally by checking the water linewidth (voxel spectroscopy) or gradient echo image quality.

During autoshimming the file, `userdir/gshimdir/data/gshim.out`, gives some useful information regarding the progress of shimming. The output can be viewed in the Analyze page of the Acquire folder. During multiple iterations, the output will be saved in the files, gshim1.out, gshim2.out, etc. A good indication of convergence is the change of shim values listed in the gshim.out file. Another parameter is the RMS deviation given in Hz. This parameter is a good indication of the NMR signal linewidth from the shim ROI.

Listing of the file gshim.out file

```
Shim     Change
.......................
z0          -43     - frequency offset (Hz)
x1         -192     - predicted change in shim (DAC) values for the X shim
y1           13
z1          417
xz          -20
yz          166
z2           27
xy         1240
x2y2       1114
.......................
B0 Field Map:
Matrix     - 64 32 32
FOV        - 25.00 16.00 16.00
Phasedelay - 8.00
Threshold - 1430601859072.0 x 10.0%  -Maximum_Intensity x Threshold
.......................
Shim Field Map:
Matrix     - 64 32 32
FOV        - 25.00 16.00 16.00
Phasedelay - 5.00                    -B0 encoding delay, del
Number of shims mapped - 8           -No. of shim field maps measured
Number of shims defined - 8          -No. of shims used in calculations
.......................
Shim Voxel Information:
Voxel shape: rectangular
Voxel dimension (pts)   - r=-31,31, p=-15,15, s=-15,15
                                     - read, phase, and slice
Points in voxel(fraction)   - 3918/60543
                                     -valid points within voxel/totalpoints
.......................
B0 Field Map Statistics:
RMS deviation -   6.67 Hz            -Measured field within the shim ROI
Peak deviation - 74.12 Hz            -Frequency range
.......................
Calculated Field Map:
RMS deviation -   5.70 Hz            -Predicted field after shimming
Peak deviation - 78.42 Hz
```

Listing of the file, shimmap.gcoil.param

The shimmap.gcoil.param file is saved in the `userdir/gshimdir/calib/` directory, when the shim calibration maps are generated. The file contains the parameters used when the shim calibration maps were generated.

The shimmap and the corresponding parameter file are named `shimmap.gcoil.ID.f` and `shimmap.gcoil.ID.parm`. The `.ID` refers to an optional user defined label for identification purposes. It is specified in the Acquire-Settings page.

The number (1) in the MAP column of each row (shim) indicates the shimmap was measured and included in the `shimmap.gcoil.f` file. A number in the ADJUST column of each row (shim) is a flag to include (1) or exclude (0) a shim during autoshimming.

```
#DATASIZE
64   32   32   1    Read, phae#1, phase #2, zerofill factor (1 or 2)
#FOV-MM
25      16      16
#DELAY-MSEC
5.0                  B0 encoding delay, del
#THRESHOLD-PERCENT
10
#REFERENCE-DELAY-MSEC
0.5
#NO-OF-SHIMS
15
#SHIM    OFFSET     UNITS   MAP   ADJUST
x1       3200       DAC     1     1
y1       3200       DAC     1     1
z1       3200       DAC     1     1
xz       8000       DAC     1     1
yz       8000       DAC     1     1
z2       3200       DAC     1     1
xy       8000       DAC     1     1
x2y2     8000       DAC     1     1
x3       8000       DAC     1     1
y3       8000       DAC     1     1
z3       8000       DAC     1     1
xz2      8000       DAC     1     1
yz2      8000       DAC     1     1
zxy      8000       DAC     1     1
zx2y2    8000       DAC     1     1
```

Transmitter Frequency

Set the transmitter on the water resonance prior to starting the shimming routine. Small frequency offsets (100Hz or less) are not going to cause a problem except when selective excitation is used, see “Fat-Water Problem,” page 88.

During the shimming process the frequency of the water resonance shifts. The shift can be significant for some systems when the Z2 and Z4 shims are adjusted. Selecting the option **Measure and Set Frequency** on the **Settings** page to start the Prescan-Frequency routine before each shim iteration and compensate for the field shift. Run the **Prescan-Frequency** routing from the Prescan page to save the parameter set as a default for the current study. Selecting the **Calculate and Set Frequency** option uses the field map information to determine the frequency shift and set the transmitter frequency (`H1offset`). The Z0 value in the `gshim.out` file refers to this frequency shift.

Eddy Current Problem

Pulsing the gradients causes eddy currents to be generated within the bore of the magnet. The residual eddy current fields after compensation are usually negligible for most practical applications but can be detected by field measurement experiment. Shimming methods cannot distinguish between static field inhomogeneity and eddy current effects erroneous shim corrections may be calculated. Eddy current effects can be cancelled by setting `nt=2`. This doubles the total scan time. A general strategy might be to set `nt=1` initially, when the field inhomogeneity is usually poor, and set it to `nt=2` during the final iterations.

Fat-Water Problem

Samples that do not include signals from fat in the shim-ROI (such as brain) do not require fat suppression.

Shimming routines measure the phase changes from two images. The phase changes from chemical shift effects in samples with two or more chemically shifted components (e.g. fat and water) obscure the phase measurements. Limiting the fat signal is necessary during autoshimming routines since water is used for mapping the field in imaging samples. Two methods of limiting the signal from fat are:

1. Selectively exciting the water signal with a soft pulse is a convenient way to limit or avoid the fat signal. Excite the water selectively in the `ge3dshim` sequence by changing the excitation pulse to a 4-10 msec. gaussian pulse and place the transmitter frequency (H1offset) exactly on the water peak. The frequency-prescan routines set the frequency on the tallest peak (typically the water peak). The longer pulse length requires an longer `te` which can result in greater T2* signal loss.
2. Select the **Fatsat** option on the **Scan** page of the **Acquire** tab.

   Selecting this option allows the use of short and hard excitation pulses resulting in shorter echo times.

Viewing Field Maps and Images

View the field maps generated by the shimming routines for debugging purposes. Field maps produced showing artifacts the shimming routines do not work. All field maps are generated in the `vnmrsys/gshimdir/data/` directory. For example, z1.f.fdf contains the field map produced by the z1 shim. Similarly, `B0.f.fdf` corresponds to the field map generated during shimming. Load and view the field maps by typing the name of the file, e.g. `B0.f`, and clicking **Display image** in the Map page or by clicking on **FieldMap**.

View the images. The 3 images collected during the fieldmap measurements are named, `B0.1.mag.fdf`, `B0.A`.mag.fdf and `B0.B.mag.fdf`, corresponding to `tau=0`, `delref`, and `del` respectively.

The field maps must appear as gradually varying functions. Any abrupt changes going from positive to negative frequency indicates a phase warp. Reduce the `del` and repeat the experiment if phase wraps appear within the shim ROI.

Low signal in the shim ROI indicates signal loss due to T_2* effects — reduce the `del`, `te`, and/or the threshold.

Click on **Shim ROI** (`B0.mask.fdf`) to view the shim ROI used in the fieldmap calculations select the image. The image corresponds to the points which are within the shim ROI and with intensities above the threshold level.

Select images using the image selection menu on the Analyze page. Phase A refers to the phase-angle image corresponding to the echo time `delref and` Phase B refers to the phase-angle image corresponding echo time `del`.The B0 field map is generated by unwrapping the Phase B image.

Use the image selection menu on the Shim page to select the magnitude and phase-angle images:

B0 map	acquired	`B0.f.fif`	`Δte=del`
Image B	Magnitude image	`B0.B.fdf`	`Δte=del`
Image A	Magnitude image	`B0.A.fdf`	`Δte=delref`
Phase B	Phase-angle image	`B0.B.wf.fdf`	`Δte=del`
Phase A	Phase-angle image	`B0.A.wf.fdf`	`Δte=delref`
Image Mask	Segmented shim-ROI		
Test Image	Magnitude image	`testimg.fdf`	

A B0 fieldmap acquired with FOV parameters that are different from the shimmap FOV parameters are reformatted to match the shimmap data. Click on the **Fieldmap** button to display the reformatted B0 map: `B0.rl.f.fdf`

Omitting Shims from Calculations

Edit the shimmap.GCOIL.param file in the `vnmrsys/gshimdir/calib` or `/vnmr/gshimdir/calib` directory to ignore specific shims from the standard shim selection option. This parameter file is generated when the shim calibration maps are acquired. The following file was collected when the shim selection was set to 1&2. To ignore the `x2y2` shim, set the MAP and ADJUST flags to 0 and click **Generate Shimmap**. Shim that are not mapped are not used in shim calculations.

Listing of the shimmap.GCOIL.FOV.param file

```
#NO-OF-SHIMS
8
#SHIM    OFFSET     UNITS   MAP   ADJUST

x1       3200       DAC       1     1
y1       3200       DAC       1     1
z1       3200       DAC       1     1
xz       6400       DAC       1     1
yz       6400       DAC       1     1
z2       3200       DAC       1     1
xy       6400       DAC       1     1
x2y2     6400       DAC       0     0
```

Shimming on an Arbitrary Shim-ROI

Define an arbitrary region by using the ROI drawing tools. Select the **roi** option on the Shim page to use the previously selected Shim-ROI for shimming.

1. Click on the **Acquire** button and acquire a test image.
2. Set the image orientation to **Sagittal** and the matrix size to `64x32x32` (the size is similar to parameters used in the shimmap).
3. Click on **Display Test Image** button on the Analyze page.
4. Select the **images** to be used to draw the ROI using the MMB.
5. Draw the region of interest using the ROI tools.

   Draw the same or different ROI's on the images selected.
6. Click on **Generate Shim ROI** to save the ROI information.
7. Select the **roi** shim region for shimming on the Shim panel.

Notes

- Eddy currents can introduce additional field gradients. This can have an undesirable effect on gradient shimming. Eddy currents are minimized by proper preemphasis adjustments. Eddy currents can also be minimized by increasing the slew time of the gradients and reducing the peak amplitude of the gradients.
- Error messages from the C programs used in autoshimming are not printed in the VnmrJ window. Select the window and enter the following to display the messages on a specific shell window:

  `% tty`

/dev/pts/6

Enter the following on the VnmrJ command line:

vnmrjcmd('tty','/dev/pts/6')

All VnmrJ related error messages, including those from the autoshim binary programs will be printed in the above shell window. This is useful when debugging.

- The `ge3dshim.log` is generated during the shim calculations and placed in the directory: `~/vnmrsys/gshimdir/data/`. Contained in the file is information on the shim parameters and the intermediate files generated during the shim calculations. The file is useful for trouble-shooting problems during autoshimming.
- A minimum of three points are required along each axis to represent the field with a proper pixel resolution. The pixel resolution in both the shimmap and B0 map must be considered.
- Reduce or start with a lower the receiver gain when doing multiple iterations. The signal strength increases as the field homogeneity improves with each shim iteration.
- The shim calculations will fail as a result of errors in the B0 field measurements arising from phase wrap during the `delref` interval.
- The shimming routine will fail if the SNR is not sufficient for accurate B0 field measurements.
- Collect individual shim maps for each sample size that will be used to insure sufficient data points are used to represent the field changes over the shim ROI.
- Set the transmitter frequency on the water resonance prior to running the gradient shimming routine.
- Check and set the transmitter frequency after loading a new set of shims. Z2 and Z4 shims tend to introduce a large B0 field component causing the resonance frequency to be shifted.

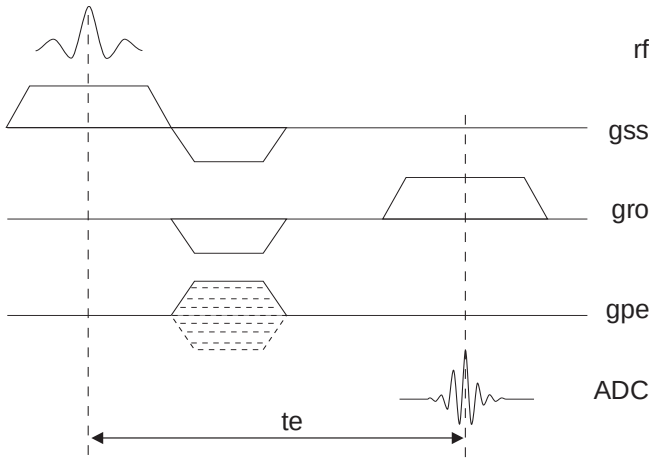
References

P.Webb and A.Macovski, *Magn. Reson. Med.* **20**, p113 (1991).
P.C.M. van Zijl, S.Sukumar, M.O.Johnson, P.Webb, and R.E.Hurd, *J. Magn. Reson. Ser. A*, **111**, p203 (1994).

gems

The protocol gems is a gradient echo 2D multi-slice acquisition technique. Common variants of gems include FLASH™ (phase incoherent, T_1 weighted) and GRASS™ (phase coherent, T_2* weighted). The gems protocol allows relatively fast acquisitions (less than 10 seconds per image) and short echo time (about 3 to 5 ms).

This protocol is provided as part of the *Imaging _Sequences* software accessory that requires separately purchased license and password. If it doesn't appear in the Locator when sorting protocols, install the *Imaging_Sequences* from the VnmrJ CD.



Advantages of gems

A single excitation pulse is used in the gradient echo sequence and allows the use of a reduced pulse flip angle and a shorter repetition time (`tr`). The data is acquired in less time and high resolution images are obtained in a few seconds.

The gradient echo is therefore very well suited for the following:

- scout scan
- angiography (see angio protocol)
- contrast agent enhancement studies

Limitations of gems

- "Susceptibility Effects," page 92
- "Reduced Signal-to-Noise Ratio," page 92
- "Nonsteady-State Artifacts," page 92

Susceptibility Effects

During the `te` delay, the spins are influenced not only by T2, but also susceptibility effects resulting in rapid loss of phase coherence of spins in inhomogeneous regions (T2*). Consequently, gems may suffer from signal loss and possibly image distortions in regions of large susceptibility gradients. This is especially true at high fields.

T2* effects can be minimized by shimming or by reducing the `te` delay. Alternatively, the susceptibility effects can be reduced by reducing the slice thickness and/or the pixel size (i.e., increasing the matrix size or decreasing the FOV), since the loss of phase coherence is directly related to phase variations within a pixel.

Reduced Signal-to-Noise Ratio

The use of a smaller rf flip angle and short `tr` in a gradient echo experiment results a lower signal-to-noise than that of a spin echo experiment with similar experimental conditions (see "sems," page 105).

Nonsteady-State Artifacts

The short `tr` used in the gems sequence tends to cause a non-steady state condition resulting in some residual transverse magnetization. Subsequent rf and gradient pulses can

generate stimulated echoes or other spurious signals that can severely distort the resulting images. Crusher pulses (`gspoil`) and ro rf spoilers are used to minimize these artifacts.

Running the sequence

Set sequence timing parameters (te, tr, number of averages, number of dummy scans, and pulse flip angle) and the FOV/slice parameters on the Scan page. Typical values for te and tr are 10ms and 30ms (single-slice or 50-200ms for multi-slice), while the pulse flip angle usually is in the range 5-30°. A minimum TE and TR can be applied by checking Min TE and Min TR, respectively; however, be aware that minimum TR may cause a gradient duty cycle error.

Additional acquisition parameters, such as the RF pulse parameters, receiver gain, and crusher gradient amplitudes are set on the Acq page.

The correlation between image orientation and direction of gradients and the corresponding Vnmr parameters psi, phi and theta is defined by the following matrix:

	Readout	*Phase encode*	*Slice select*	*(psi,phi,theta)*
Axial	Y	X	Z	(0,0,0)
Coronal	Z	X	Y	(0,0,90)
Sagittal	Z	Y	X	(90,0,90)

In 2D image display, the readout direction is always vertical, while the phase encoding direction is horizontal.

Notice, that if the gradient coil has a low duty cycle, you may need to reduce the maximum gradient allowed for refocusing and readout gradient by entering a smaller number for Glim, typically in the range 30-75% (of maximum). In addition, you can reduce the spoiler gradient by checking the Gspoil checkbox, thereby forcing it to use the value you can enter.

The gems sequence is `apptype im2D`.

Options for gems

- Standard sequence options — “Standard Sequence Options,” page 114
- “Flow Compensation,” page 93
- “Phase Encoding Rewinding,” page 93
- “RF Spoiling,” page 94
- “Gradient Limitation,” page 94
- “Spoiler Gradient,” page 94
- “Table-Ordered Data,” page 94
- “Show Profile,” page 94

Flow Compensation

Selecting Flow Compensation applies flow compensating gradients along both the readout and slice select directions. This may increase the minimum TE.

Phase Encoding Rewinding

Because the spins are not allowed to return to equilibrium between excitations, it may be necessary to rewind the phase introduced by the phase encoding gradient after acquisition to achieve a steady state condition. With phase encoding rewinding (PE rewind), a gradient

of the same amplitude but opposite polarity of the phase encoding step is applied following data acquisition.

Phase rewinding is controlled by the variable rewind, which can be set to 'y' or 'n'.

RF Spoiling

The brief tr used in the gems sequence may cause image distortions due to a non-steady state condition resulting in residual transverse magnetization. To alleviate this, gradient pulses (for T1 weighting) or RF spoiling phase modulation (T2 weighting) and rf spoiler pulses (Zur, Y., Magnetic Resonance in Medicine, 21, 251, 1991) are usually employed in the pulse sequence to minimize such artifacts.

The RF spoiler is controlled using the parameter rfspoil, which can be set to either 'y' or 'n'.

Gradient Limitation

Glim is a scaling factor on the maximum system gradient strength, which is applied to refocusing, spoiler, and readout gradients. If the gradient coil has a low duty cycle, you may need to reduce glim.

Spoiler Gradient

A spoiler gradient is always applied at the end of the sequence. Checking or unchecking Gspoil does not disable this spoiler gradient, but rather enables user control of the spoiler gradient amplitude. If Gspoil is unchecked, the maximum allowed gradient is applied. The duration of the gradient, `tspoil`, is unaffected by the checkbox.

Table-Ordered Data

It is possible to acquire data from gems in nonmonotonic order by using an external AP table to control the order. The table is selected through the parameter petable. If petable is the blank string or the letter 'n' or 'N', no table is used and the data is acquired in monotonic order. If `petable` is a non-empty string, e.g., `petable='gems128'`, the sequence will use the table in the file gems128.

The table file must include the table t1 which much contain as many integers as there are phase encode steps in the protocol, ranging from -nv/2 to nv/2, however in arbitrary order. The integers determine the order of the phase encoding steps.

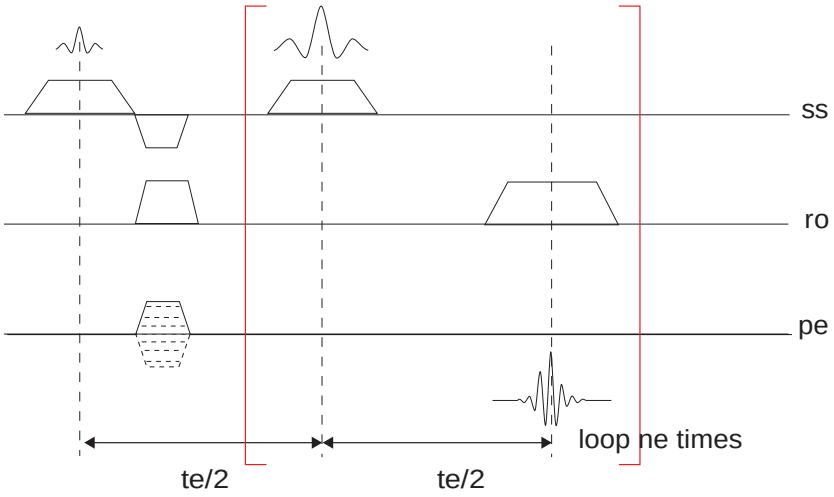
Using a table allows you to play out the phase encode gradients starting from the center of k-space (centric ordering) or specify partial k-space acquisition.

Show Profile

A profile of the object can be obtained by clicking the button [Acquire profile] on the Acq page. This function temporarily sets the number of phase encode steps to zero (nv=0), which signals to the sequence to acquire a single echo under the readout gradient but without any phase encoding. The above matrix defines which axis to acquire the profile along (readout). For example, to obtain a profile along Y, select axial, for a profile along Z, select coronal. Since none of the predefined orientations have readout along X, you must select axial and manually set phi=90 (on the Plan page) in order to get a profile along X.

mems

The mems protocol is a multi-echo experiment, where a series of spin echoes are acquired following a single excitation. Each echo is acquired following a 180° pulse, resulting in a series of images with increasing echo time that can be used for quantitative T_2 measurements.



Advantages of mems

The mems sequence allows you to sample a number of echoes with increasing echo time following a single rf excitation. The data is subsequently sorted such that all phase encoding lines acquired at a certain echo time are used to produce an image with a certain effective `te`.

The mems sequence is primarily used to obtain multiple images with increasing `te` for quantitative measurement of T_2 in a relatively short time.

Limitations of mems

Long Acquisition Time

The primary limitation of the mems (and sems) sequence is the long scan time.The spins must return completely to equilibrium in order to maintain the T_2-weighted contrast and avoid ghosting. A typical `tr` in the order of 3-4 seconds results in a total acquisition time in the order of minutes for high resolution images.

Artifacts

Artifacts caused by the interference of the spin-echo and stimulated echoes affect the mems sequence. Crusher pulses are usually applied to eliminate the spurious signals.

Running the Sequence

Set **TR** on the **Scan** page, typically in the order of 3000 ms, or select **Min TR** for calculation of the minimum TR value.

The echo times can either be set manually or automatically to the minimum possible. The **Min TE** checkbox sets the first echo time, TE, to the minimum. The **Min ESP** checkbox calculates the minimum spacing between the first and second echo, and sets the second echo time, TE2. If the EQ-ESP checkbox is checked, the echo spacing between echoes two and three, three and four, etc, are automatically set equal to the spacing between echoes one and two. Notice, that the first echo time, TE, is not the same as the echo spacing. The first echo time is the Vnmr parameter te, whereas subsequent echo times are defined as an arrayed parameter, te2.

An unfortunate side-effect: When manually defining echo times, it is possible to get into a situation where the minimum echo time reported by the sequence appears to get longer and longer, every time you enter a new value. This is related to a re-calculation of the acquisition bandwidth and thus acquisition time, based on the minimum TE.

Specify a **thk/thk2** ratio when defining the FOV and slice parameters. **thk/thk2** it the ratio of the thickness of the excitation (90º) pulse to the subsequent refocusing (180º) pulses.

Additional acquisition parameters, such as the rf pulse definitions, bandwidth, acquisition time and number of dummy scans are set on the **Acq** page.

The mems sequence is apptype im2D.

Options for mems

- Standard sequence options — see “Standard Sequence Options,” page 114
- “Flow Compensation,” page 96
- “Gradient Limitations,” page 96
- “Show Profile,” page 96

Flow Compensation

Selecting Flow Compensation applies flow compensating gradients along either the readout or the slice select direction, or both. Notice, that this in turn may increase the minimum TE.

Gradient Limitations

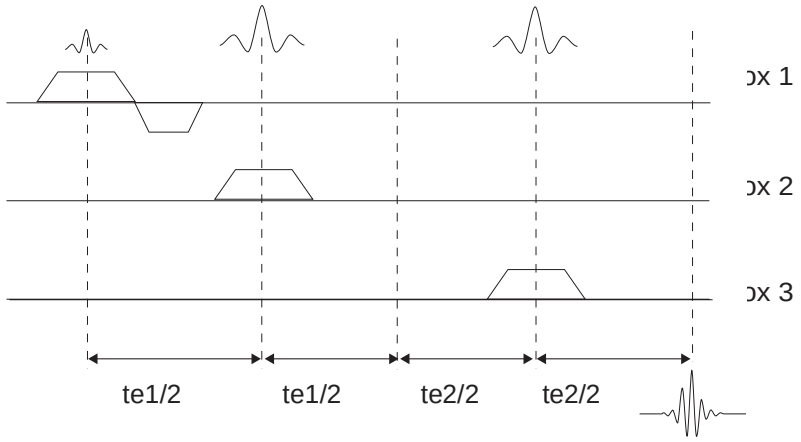
Glim is a scaling factor on the maximum system gradient strength applied to refocusing, spoiler, and readout gradients. Reduce glim for gradient coils with a low duty cycle.

Show Profile

A profile of the object at each echo time can be obtained by clicking the button **Show profile** on the Acq page. This function temporarily sets the number of phase encode steps to zero (nv=0), which signals to the sequence to acquire a single echo under the readout gradient but without any phase encoding. By default, it displays the profile for the first echo time. View the subsequent profiles by entering the command `cf=<echo number> ft`, or all of them at once by entering `flashc ft dssh`.

press

The press protocol is used to obtain a 1D NMR spectrum from a localized region, with or without water suppression. press is based on a double-spin echo.



- "Advantages of press," page 97
- "Limitations of press," page 97
- "Running the Sequence," page 97
- "Water Suppression," page 98

Advantages of press

The press experiment offers higher sensitivity advantages over the steam experiment.

Limitations of press

Outer Volume Contamination	The three slice selective pulses not only excite signals within the voxel, but also regions within the slice plane. Imperfections in the pulses result in unwanted signals in the transverse plane, which can lead to artifacts in the spectrum. Carefully placed crusher pulses can be used to destroy the undesired signals. An eight pulse phase cycling scheme is used in press to cancel out the unwanted signals and minimize artifacts in the spectrum.
J Modulation	The evolution of spins in the transverse plane causes the phase of the J-coupled spins to modulate as a function of `te` and `te2`. This may result in a spectrum that cannot be easily phase corrected.

Running the Sequence

1. Load the sequence and adjust parameters:
    a. Load the **press** protocol from the **Study Queue**.
    b. Load a **scout image** and define the **voxel ROI** using the Plan page.
    c. Set the **echo times** on the **Scan** page.
    d. Select the **Advanced** page to set additional parameters, including **spectral width** (`sw`), **acquisition time** (`at`), and **number of data points** (`np`).
2. Acquire a spectrum and reference the water peak:
    a. Click **Acquire Spectrum** on the **Advanced** page to acquire a non-suppressed test spectrum. This acquires and displays a spectrum without adding an entry to the Study Queue. Use this spectrum to reference the water to 4.7 ppm.
    b. Position the cursor exactly on the water peak.

c. Click **Set water reference**.

3. Repeat step 1 and step 2.
4. Click **Set freq at cursor** to set the transmitter frequency on the water peak.
5. Set the receiver frequency to center the spectrum on, for example, water:
   a. Click **Acquire Spectrum** on the **Advanced** page to acquire a non-suppressed test spectrum.
   b. Position the cursor exactly on the water peak.
   c. Click **Receiver ref** under the header **Offsets** on the **Advanced** page.

Clicking **Set freq at cursor** sets the global transmitter frequency, `H1offset`, at the cursor location. The offset displayed with Receiver ref is an offset relative to the transmitter offset. Start Scan automatically sets the receiver frequency (`tof`) to the correct absolute frequency.

The outer volume contamination can be reduced by applying a crusher gradient. The amplitude (`gcrush`) and duration (`tcrush`) are set under **Crushers** on the **Advanced** page; they are referred to as `te` crushers and are typically set to 1-3G/cm and 2-5ms.

The phase cycling scheme consists of 8 steps.

The press sequence is `apptype='im1D'`.

Water Suppression

Water suppression is achieved by applying a selective RF pulse at the water frequency followed by a spoiler gradient. Three water suppression methods are available:

- WET
- VAPOR
- DRY

Water suppression is activated through a check box on the **Scan** page; this sets the flag `ws='y'`. To set the water suppression frequency (`wsfrq`) on the water resonance:

1. Click **Acquire Spectrum** on the **Acq** page to acquire a non-suppressed spectrum.
2. Position the cursor exactly on the **water peak**.
3. On the **Advanced** page, click **Suppression** under the header **Offsets**.

The DRY water suppression scheme is a CHESS method (Moonen et al, *JMR* 88, 28, 1990), consisting of three consecutive rf pulses centered on the water frequency followed by spoiler gradients applied prior to the 90° excitation pulse. The amplitude (`gspoil`) and duration (`tspoil`) of the spoiler gradients are set under Crushers on the Acq page; they are referred to as CHESS crushers and are typically set as follows:.

Parameter	*Typical Value*
`gspoil`	1-3G/cm
`tspoil`	2-5ms

WET is an alternative water suppression method using four saturation pulses and is an extension of the CHESS method. The flip angles of each of the pulses is optimized and followed by gradient pulses with decreasing area. WET may be superior to CHESS in experiments with large rf inhomogeneities, uncertainty in the rf offset, or large T_1 variations across the sample.

Optimizing Water Suppression

To optimize water suppression pulses for localized spectroscopy:

- Obtain a scout image.
- Plan the voxel.
- Shim the voxel region using a localized shimming method such as GE3DSHIM.

The following parameters can be manipulated to optimize the water suppression:

- Shim — Good shimming, a linewidth of less than 10 Hz, is necessary for good water suppression.
- Flip angle
- rf pulse power
- Delay after the first rf pulse

The pulse width is inversely proportional to the bandwidth of the water suppression pulse. A pulse width of 10 ms results in a suppression of signal in a range of 100 Hz. A well shimmed system allows the use of a water suppression pulse with a narrower bandwidth, i.e., longer pulse, and reduces the effect on the rest of the spectrum.

CHESS Optimization

1. Array both the coarse and fine power levels, `satpwr` and `satpwrf`, of the CHESS pulses to optimize the water suppression.
2. Press the **Optimize** button on the Water Suppr page (Figure 31) to optimize the water suppression pulse power (or flip angle) by:
   - Setting the transmitter frequency on the water peak
   - Doing a coarse power adjustment
   - Doing a fine power adjustment

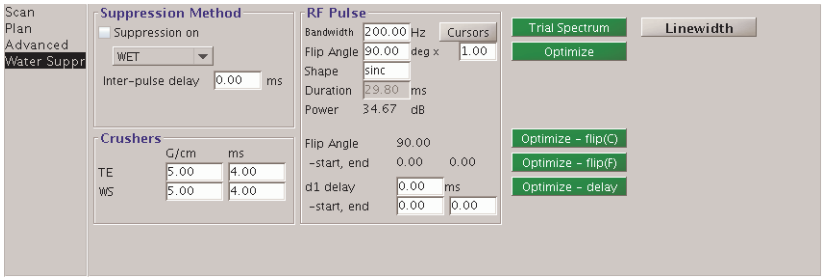


Figure 31. Water Suppr Parameter Page

WET and VAPOR Optimization

Optimize the flipangle adjustment interactively and select the proper minimum. The flipangle adjustment procedure for WET and VAPOR water suppression is as follows.

1. Set the nominal flip angle to 90 deg. and the flip angle factor to 1.0.
2. Click on **Optimize - flip(C)**.

   This measures and sets the transmitter frequency on water then arrays the flip angle factor from 0.3 to 1.7 in 0.1 unit steps.
3. Pick the optimum null.

   The optimal null (Figure 32) is the first signal going from negative to positive at spectrum #8.

a. Enter the correct flip angle factor manually if the routine does not automatically pick the correct minimum.

b. Select **Parameter arrays** in the Acquisition Menu in the tool bar.

c. Enter parameter name, `fliparray`.

View the arrayed parameter.

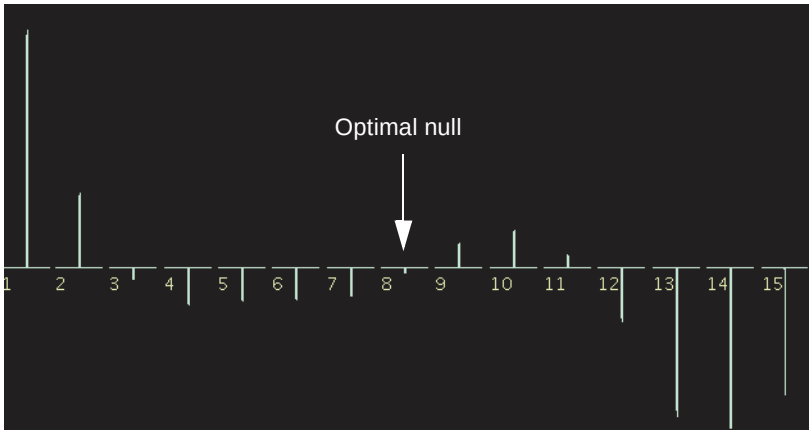


Figure 32. Optimizing the Delay

4. Optimize the power level by clicking on **Optimize - flip(F)**.

   The step size for the flip angle factor is set to 0.01 for fine adjustment. The flip angle factor is chosen as described in step 3.

Optimize the delay after the last rf pulse for WET and VAPOR water suppression schemes to further minimize the water signal as described below.

1. Optimize the power level (flip angle) calibration first.
2. Select the smallest negative signal in step 3 or step 4.
3. Set the start and end values for the delay (e.g. 0 to 4msec).
4. Click on **Optimize - delay**.

   The water signal should go from a negative signal to a positive signal. The minimum signal will be picked by the routine. The parameter, d1array, is used in the experiment and can be viewed by selecting Parameter arrays entry in the Acquisition menu.
5. Repeat if necessary.

profile1d

The profile1d protocol is used for testing and calibrating the scanner for imaging. It is based on a spinecho imaging sequence (sems) and gives a one dimensional profile along the readout axis. Slice selection is used but phase encoding is disabled. The image orientation defines the read axis as shown below.

Orientation	*Read axis*	*Slice*
Axial	y	z
Axial90	x	z
Coronal	z	y

Orientation	*Read axis*	*Slice*
Coronal90	x	y
Sagittal	z	x
Sagittal90	y	x

Advantages of profile1d

- Tests rf and gradient functionality
- Checks the position of the sample in the magnet
- Calibrates the rf pulse

Running the profile1d sequence

1. Initialize the imaging parameters in the **scan** page.
2. Set TR to 3 to 5 times T1 to allow for T1 relaxation.
3. Set TE to 20-30 ms.
4. Set the field of view and slice parameters in the **Scan** page or the **Plan** page.

   The field of view along the read dimension should cover the region of interest along that direction.
5. Set additional parameters related to the bandwidth; rf pulse, receiver gain, etc. using the **Advanced** page.
6. Click on the **Acquire Profile** button on the **Scan** page to view a profile.

Calibrating the RF pulse

1. Calibrate the power using the `spuls` protocol when setting up a new rf coil.

   This enters an approximate power calibration value is into the calibration file, `pulsecal`.
2. Initialize the imaging parameters as indicated in section, “Running the profile1d sequence,” page 101.
3. Obtain a sagittal profile and center the sample in the magnet if necessary.
4. Set the image plane to axial. This orientation selects an axial slice at the center of the rf coil and avoids the B1 field variation (fall-off) at the ends of the coil.
5. Set the power limit, in dB, for the 180^{o} pulse during power calibration. (63 dB is the maximum rf power generated by the amplifier. Reducing the power level by 3dB results in halving the rf power output.)
6. Click on the Acquire profile button and optimize the receiver gain and other parameters if necessary.
7. Click on the **Calibrate Power** button to initiate the power calibration.

   During power calibration ten profiles are collected by arraying the 90^{o} and 180^{o} pulse power levels simultaneously. The optimum power level is determined from the largest profile and printed in the message window. The profiles are also displayed on the graphic screen for verification. Reset the power limit and repeat the calibration if the profiles do not show a gradual increase to a maximum followed by a decrease.

Options

Select the appropriate amplifier if the spectrometer is equipped with both high and low power rf amplifiers by checking the entry on the **Scan** page.

quickshim

Introduction

The quickshim protocol is used to shim a sample quickly using the first order (x, y and z) shims. The procedure is similar to the FID shim method used for shimming a sample. The quickshim protocol uses a basic pulse-acquire sequence. An array of spectra are collected for a range of shim settings and the optimum shim setting is chosen based on the tallest peak. The procedure is repeated with smaller shim settings if necessary. The protocol takes advantage of the fast responding x, y and z gradients to determine the optimum shim values.

Advantages

- Fast — the x, y, and z shims optimized in about 10 seconds
- Single mouse click to start after setting the initial parameters
- Multiple iterations supported

Limitations

- Shimming — limited to x, y, and z shims
- Not a localized shimming procedure — non-selective rf pulse excites the whole sample

Running the quickshim protocol

1. Load the quickshim protocol.
2. Set up the acquisition parameters as in the case of `spuls` protocol.

   Typical parameters are:

TR	52 ms	
TE	0.5 ms	refers to the pre acquisition delay
Flip1 deg		flip angle
Width	4 µs	pulse width
Datasize	512	complex data points acquired
Averages	1	
Spectral width	10000	
Signal level	low	presig parameter

3. Acquire a spectrum and optimize the transmitter frequency and receiver gain.
4. Reduce the gain to avoid receiver overflow during the shimming process.
5. Set the shim parameters:

   Typical settings:

Load Shim	on	
Iteration	on	on
Shim step	500	50

The x shims are arrayed from -5000 to +5000 DAC units with a step size of 500 units and spectra is collected using these settings. The optimum shim setting corresponding to the maximum peak height is chosen and loaded into the hardware. Then the procedure is repeated for the y and z shims. The whole procedure is repeated using a step size of 50 units during the second iteration.

Shim Calibration (Inova Systems Only)

Calibrate the polarity of the shims prior to running the quickshim protocol. Each of the shim coils on the system must be calibrated using the procedure described below. Save the calibration file in the local (`$home/vnmrsys/qshimdir`) or system (`/vnmr/qshimdir/`) directory. Name the file `qshim.gcoil.cal` where gcoil refers to the current gradient coil name. The file contains two lines:

#XYZ_POLARITY

1 1 1

Click on the **Set Shim Polarity** button on the **Settings** page on VNMRS systems.

Shim Calibration - Alternate method

This section describes a more convenient method to determine the shim polarity. It is not necessary to position the sample inside the probe as described in the previous section.

1. Place a spherical sample in the magnet.
2. Set all the shims to zero by clicking on the **Zero all shims** button in the **Shim** page.
3. Load the `spuls` protocol.
4. Use the Manual FID Shimming panel and shim using only X, Y, and Z shims.
5. Make a note of the shim values.
6. Create a text file, `qshim.gcoil.cal`, in the `$home/vnmrsys/qshimdir` directory, where gcoil refers to the gradient coil name.

   The file should contain the following text:

   #XYZ_POLARITY

   1 1 1
7. Load the quickshim protocol.
8. Click on **Zero all shims** button.
9. Set up for shimming as described earlier.
10. Choose a single iteration and suitable shim step size.
11. Click on **Load shims** button if the option is not already selected.
12. Check the X, Y and Z shim values on the **Settings** page and compare them to the values obtained in step 5.
13. Change the sign of the polarity values in the `qshim.gcoil.cal` file if the sign of the calculated value is opposite to that obtained in the Manual FID routine.

    In the following example,

X, Y, Z shim values, using manual shimming:	1350	-517	45
X, Y, Z shim values, using quickshim method:	-1350	500	100

change the contents of the `qshim.gcoil.cal` file to:

```
#XYZ_POLARITY
-1   -1   1
```

WARNING: **If the optimum shim value is close to zero, it may not be possible to determine the shim polarity accurately because of small fluctuations in the shim value measurements. The quickshim routine with smaller step size should give a more accurate shim measurement.**

scout

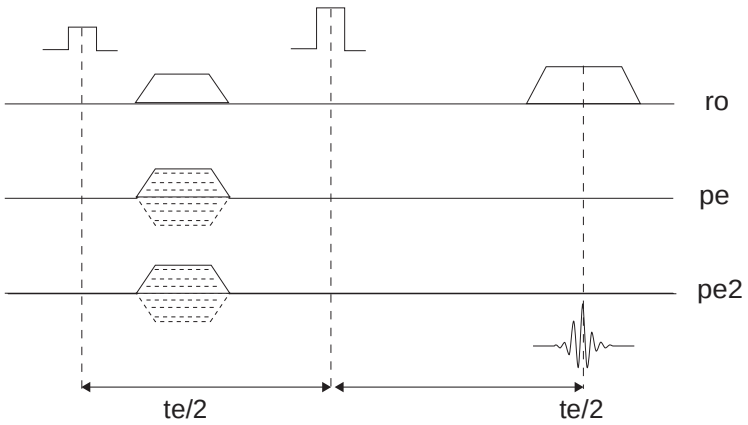
Scout is a variation of the gems protocol (see "gems," page 91) specifically designed for obtaining a quick scout image. The protocol obtains a single slice at the isocenter of the magnet in each of the cardinal planes, axial, coronal, and sagittal, in that order, using `te`/`tr` = 10/20 ms and matrix size 256x128, resulting in a total scan time of about 12 sec.

Typical FOV parameters for scout:

Human imaging	300 mm
Animal imaging	100 mm
Microimaging	30 mm

se3d

The se3d protocol is a 3D variation of the sems protocol.



Advantages of se3d

The se3d experiment gives artifact-free 3D images of high quality and signal-to-noise. The se3d experiment is well suited for:

- High-resolution T_1-weighted images (short `te`, short `tr`)
- Imaging of regions of high susceptibility
- Scans where high signal-to-noise is critical

Limitations of se3d

Long acquisition time

The primary limitation of the `se3d` sequence is the long scan time (sems has the same limitation) that effective limits the resolution in the two phase encoding directions to 32 or 64, even at a reduced repetition time. An experiment with matrix size 128x64x64 and TR=1s, the total scan time is 69 minutes.

3D limitations

The `se3d` experiment suffers from the same limited extraction capabilities as `ge3d`.

ADC overflow

Because the `se3d` sequence uses non-selective pulses with a 90° flip angle in an almost fully relaxed system, it is likely to cause ADC overflow. On animal systems, this can be avoided by setting the parameter `presig='h'`. The signal can also be reduced by adding a 10 db attenuator on the receiver port.

Running the se3d sequence

See section “ge3d,” page 65 for a description of the image orientations. Set TR to 3-5 times T1 of the sample to avoid image artifacts.

se3d is `apptype='im3D'`.

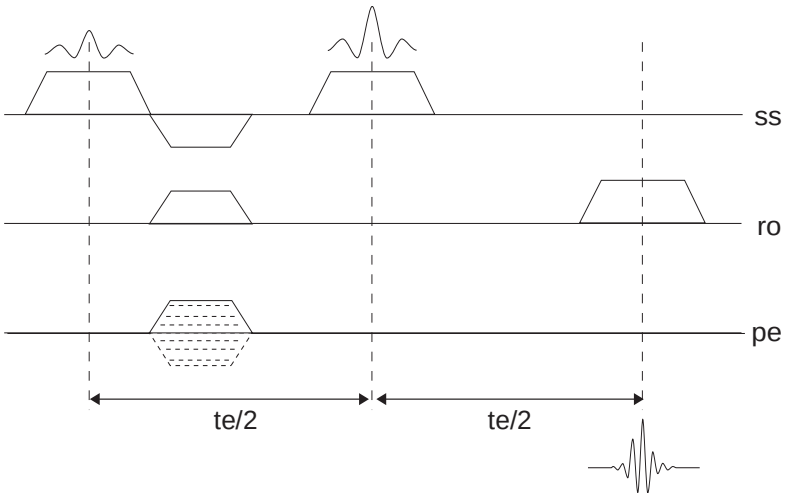
Options for se3d

- Standard sequence options — see “Standard Sequence Options,” page 114

sems

- “Advantages of sems,” page 106
- “Limitations of sems,” page 106
- “Running the sems Sequence,” page 106
- “Options for sems,” page 106

The sems protocol is a spin echo multi-slice experiment resulting in high quality images.



Advantages of sems

The spin echo experiment gives high quality, artifact-free images of high resolution and signal-to-noise ratio. The spin echo is very well suited for:

- High-resolution T_2-weighted images (long `te`, long `tr`)
- High-resolution T_1-weighted images (short `te`, short `tr`)
- Imaging of regions of high susceptibility
- Scans where high signal-to-noise is critical

Limitations of sems

- "Long Acquisition Time," page 106
- "Ghosting Artifacts," page 106

Long Acquisition Time

The primary limitation of the spin echo sequence is the long scan time. Because the spins should be allowed to return completely to equilibrium in order to maintain the T_2-weighted contrast and avoid ghosting, the `tr` is typically in the order of 3-4 seconds, resulting in a total acquisition time in the order of minutes for high resolution images.

Ghosting Artifacts

Running sems with a reduced `tr` (<2000 ms), for example to obtain T_1-weighted contrast or to reduce total scan time, often results in ghosting artifacts.

Ghosting artifacts result from residual transverse magnetization experiencing subsequent rf pulses and gradients, producing signals that are out of phase with respect to the primary spin echo signal. Running dummy scans and establishing a steady-state condition for the spins will minimized ghosting.

Running the sems Sequence

Run the sems protocols as follows:

1. Set sequence timing parameters (`te` and `tr`) and the FOV/slice parameters on the **Scan** page.

   Typical values:

   - `te` = 30 ms
   - `tr` = 3000 ms

2. Set additional acquisition parameters, such as the rf pulse definitions, bandwidth, acquisition time, and number of dummy scans on the Advanced page.

The sems sequence `apptype` is `im2D`.

Options for sems

- Standard sequence options — see "Standard Sequence Options," page 114

spuls

- "Advantages of spuls," page 107
- "Limitations of spuls," page 107
- "Running the spuls Sequence," page 107

- "Options for spuls," page 107

The spuls protocol a simple protocol consisting of an hard (non selective) rf pulse followed by acquisition.

Advantages of spuls

The spuls protocol is well-suited for the following:

- Obtaining a non-localized spectrum of the entire object for evaluation of global shim
- Global, manual shimming
- Setting the global transmitter frequency
- Calibration of a new rf coil

Limitations of spuls

Samples that are very inhomogenous may cause the local frequency and shim characteristics to vary significantly throughout the sample. Using spuls for shimming or setting the transmitter frequency may yield results that are too coarse for specific sequences.

Running the spuls Sequence

All relevant acquisition parameters (TR, number of data points, averages, etc.) are set on the **Scan** page.

The `spuls` sequence is a global acquisition and often results in a very large signal and possibly ADC overflow. On animal systems, the parameter `presig,` (see the *Command and Parameter Reference* manual) can be set to **`high`** to automatically insert a 30dB attenuator on the preamp and thus bring the signal down to a manageable level.

Using `presig` in slice- or volume-selective imaging experiments is usually not necessary where the signal is reduced due to both the limited volume and the encoding of the signal through gradients.

Use the check box **Calculate Power** in the **RF Pulse** group to select whether the RF pulse power level is calculated automatically based on the specified flip angle, or to specify the power level explicitly in dB. With the latter option, the flip angle is grayed out to signify that it is no longer applicable.

The spuls sequence is `apptype='im1Dglobal'`.

Options for spuls

- "Setting the global transmitter frequency," page 107
- "Calibration of rf Power - Coarse," page 108
- "Calibration of rf Power - New RF Coil," page 108

Setting the global transmitter frequency

Determine the global transmitter frequency automatically by clicking on the **Set frequency** button. A spectrum is acquired from which the global water frequency is determined from the largest peak; the global variable H1offset is set to this frequency. Subsequently, another acquisition is done using this frequency as the transmitter frequency.

Alternatively, position the cursor on top of the desired peak and click on **Freq at cursor**, which causes H1offset to be set to the cursor frequency.

Calibration of rf Power - Coarse

Use the **Calibrate** button under **Calibrate RF** for coarse calibration of the rf power. This function will set up an array of the rf pulse width between the two values entered above the button. Keep the command line open during this calibration. The operator is prompted via the command line whether to update the pulsecal file or not at the end of acquisition.

Calibration of rf Power - New RF Coil

1. Specify a name associated with the coil/sample to set up the power calibration on a new rf coil.

   For example, type `RFCOIL='mouse_coil'` in the command line.

2. Uncheck the Calc. Power check box on the **Scan** page.

3. Click on the **Acquire** button to initialize the parameters and acquire a spectrum.

4. Click on the **Set Frequency** button to set the transmitter on resonance or set the cursor on the resonance peak and click on the **Freq at Cursor** button.

5. Define the pulse width range start and end values for the power calibration.

   The pulse width range and power level must be chosen such that the signal goes through a minimum corresponding to a 180^{o} pulse. The calibration routine searches for the minimum signal and associates it with the 180^{o} pulse.

6. Click on the **Calibrate** button to initiate the power calibration routine.

   Ten spectra are collected and displayed in the graphics area. The smallest signal is assumed to be the 180^{o} pulse. The calibration routine prints the pulse width associated with the minimum signal. Verify that the minimum signal corresponds to the 180^{o} pulse. a message is printed if the rf coil name is already present in the pulsecal database:

   ```
   Pulsecal entry "mouse_coil" already exists
   Do you want to replace it? (y, n or q to quit now):
   Type "y" to update the pulsecal file with the new value
   and "q" (or <return>) to quit.
   ```

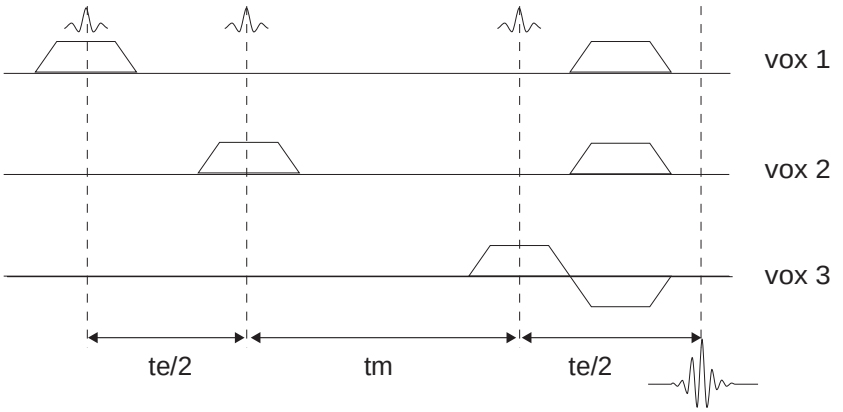
7. Repeat step 6 with new parameters.

   For example, after determining the approximate 180^{o} pulse width, set the pulse width range close to the 180^{o} pulse to obtain a more accurate pulse width.

steam

The steam protocol is used to obtain a 1D NMR spectrum from a localized region, with or without water suppression. The protocol steam is based on a stimulated echo type of experiment, and thus suffers from a lower signal-to-noise as compared to press.

This protocol is provided as part of the *Imaging _Sequences* software accessory that requires separately purchased license and password. If it doesn't appear in the Locator when sorting protocols, install the *Imaging_Sequences* from the VnmrJ CD.



Advantages of steam

The steam experiment offers some advantages over press:

- Shorter echo times because steam only has one effective echo period.
- Less sensitive to imperfections in the rf calibration and homogeneity due to typically cleaner slice profiles of 90° pulses relative to 180° refocusing pulses, and thus generally a better defined voxel.
- Optimized water suppression due to water suppression pulses during the mixing period (TM)

Limitations of steam

Reduced Signal-to-Noise

A factor of 2 loss in signal-to-noise with steam.

J Modulation

The evolution of spins in the transverse plane causes the phase of the J-coupled spins to modulate as a function of `te`. This can result in a spectrum that cannot be easily phase corrected.

Running the steam Sequence

1. On the **Scan** page:
   - Set the **echo time** (`te`) to a small value, e.g., 10-30 ms to reduce T_2 signal loss.
   - Set the **mixing time** (`tm`) to 10-40 ms.
2. Click on the **Advanced** page and adjust spectral width, acquisition time, and number of data points as necessary.
3. Click **Acquire Spectrum** to acquire a test spectrum.

This will acquire and display a spectrum without adding an entry to the Study Queue. Use this spectrum to reference the water to 4.7 ppm as follows:

1. Click **Acquire Spectrum** on the **Advanced** page to acquire a non-suppressed spectrum.
2. Position the cursor exactly on the water peak.
3. Click **Set water reference**.

4. Repeat steps 1-2 and click **Set freq at cursor** to set the transmitter frequency on the water peak.

The receiver frequency can be set manually in order to center the spectrum on, e.g., water:

1. Click **Acquire Spectrum** on the **Advanced** page to acquire a non-suppressed spectrum.
2. Position the cursor exactly on the water peak.
3. Click on the **Advanced** page and click **Receiver ref** under the header **Offsets**.

   The offset displayed with **Receiver ref** is an offset relative to the transmitter offset. Start Scan automatically sets the receiver frequency (`tof`) to the correct absolute frequency.

   Clicking **Set freq at cursor** sets the global transmitter frequency, `H1offset`, at the cursor location.

The outer volume contamination can be reduced by applying a crusher gradient. The amplitude (`gcrush`) and duration (`tcrush`) are set under **Crushers** on the **Advanced** page; they are referred to as `te` crushers and are typically set to 1-3G/cm and 2-5ms.

The phase cycling scheme consists of 8 steps.

The steam sequence is `apptype='im1D'`.

Options for steam

- Standard sequence options — “Standard Sequence Options,” page 114
- Water Suppression — Activate water suppression with the check box on the **Scan** page. Follow the water suppression setup in “Water Suppression,” page 98.

tagcine

Tagcine is a gradient echo sequence for looking at phases of the cardiac cycle and reconstruction of the images for creating CINE views of the beating heart.

Advantages

Acquisitions for one phase encode step are repeated on one slice for a number of images (controlled by the parameter `ne`). Each acquisition corresponds to different phases of the cardiac cycle. The same phase encode step is acquired for `ne` cardiac phases in the next R-R interval for next slice.

The process is repeated for the next phase encode step after a particular phase encode step is acquired for all cardiac phases and all slices. Acquisitions are triggered at the same phase in the cardiac cycle using a heart monitor. The sequence is also useful to follow the motion of something with a periodic cycle.

Provisions in the sequence for tagging provides a way to visualize the displacement of various areas of the heart. RF tagging pulses are used to place parallel stripes or orthogonal grid tags in the images. Deformations of the tags during the cardiac cycle progresses are for evaluation myocardial motion, fluid flow, or other properties of the object. Tags are sinc

modulated rf pulses preparation pulses (see *Wu et al, MRM 2002, 48(2), 389-393)* applied before each slice's cardiac phase loop. Spatial separation and width of the tags are controlled from the **Options** panel for the sequence.

Additional features of the sequence are: spatial saturation pulses and fat saturation pulse (both can be with the tagging pulses), T2 prep, and IR prep. Relaxation of the magnetization continues as the cardiac phase loop plays. Each successive cardiac phase image has a somewhat different contrast. The change in contrast is very pronounced for short T2 and the T2 preparation may be almost entirely gone by the last echo in the cardiac phase loop. Using a double inversion recovery (DIR - Black Blood contrast) suppresses the bright signal from blood and enhance visualization of the heart tissue.

Limitations

Tagcine was designed for cardiac imaging and functions similar to the normal `gems` sequence if the number of cardiac phases is set to 1 but is not as versatile as `gems`. Tagcine is sensitive to T2* and shimming. The preparation pulses are followed by the acquisition of a train of cardiac phases to provide T1- or T2- like contrast. Contrast changes in each cardiac phase limits the usefulness of the prepulses and the sequence is not suitable for quantitative measurements of T1 or T2. Do not run tagcine with both IR and T2 prep at the same time – select one not both.

Running the sequence

A series of gradient echoes acquired on a single slice each with the same phase encode step in a cardiac phase loop is the base segment of the sequence and is repeated for the next slice and cardiac phase. The phase encode step is incremented and the process is repeated after all cardiac phases for all slices are acquired for a phase encode step. The parameter for the number of acquisitions (cardiac phases) for each slice is `ne`.

The sequence is normally run with the echo time (`te`) set to its minimum value (click the **minte** check box on the **Scan** page) but not with minimum TR. A **mintr** button is provided. Set the number of cardiac phases or **Frames** on the **options** page. Three special delay parameters are provided on the **Options** page:

- R-R delay (variable name, `rrdelay`) — a user supplied parameter that inputs the nominal length of the cardiac phase cycle (from R wave to R wave). It is used in the sequence to calculate how many distinct cardiac phases can be acquired before the cardiac cycle begins again, assuming no delay between the acquisition of one phase and the next.
- Interphase delay (variable name, `idelay`) — provides additional delays between the cardiac phase acquisitions.
- Delay after the trigger (`qrsdelay`) —delays the start of the acquisition of the cardiac phase data. This delay is accessed on the options panel in the **Delay after** entry.

Additional acquisition parameters, such as bandwidth, acquisition time, and dummy scans, are accessible on the **Advanced** page.

Options

Tagging

The tagging option is accessed via the **Options** panel. Tags are applied in the readout direction, phase direction, or both to create a tag grid. Spatial separation and spatial width of the tags are set from the entries on the **Options** panel. Entry option for: **rf train width**,

rf pulse width, and **rf flip angle** are also provided (refer to *Wu et al, MRM 2002, 48(2), 389-393* for using these parameters).

IR (T1 prep)

This option uses slice selective 180^{o} pulses, crusher gradient pulses, and inversion time to produce T1-weighted contrast. The inversion pulses for each slice are sequential, followed by the inversion time for each, followed by the segments for each slice in such a way that the inversion time is the same for each slice. Typically the inversion times are long (e.g. 800 ms) to allow all the inversion pulses to be played out before the segment acquisitions start. This implementation restricts the number of slices for short (e.g. 150 ms) inversion times and is why tagcine is not recommended for short inversion time (STIR) experiments.

DIR (Black Blood)

Use the DIR (double inversion recovery) to suppress the signal from blood and make heart tissues easier to visualize. A non-selective inversion pulse and slice selective inversion pulse are applied prior to the inversion delay. The initial non-selective pulse inverts all the signals and the slice selective inversion pulse flips the spins in the imaging slice back to equilibrium state. An inversion delay, T1_null, is chosen to null the signal from blood during T1 relaxation.

T1_null = T1_blood * 0.69

Signals from blood entering the imaging slice during the subsequent gradient echo sequence are substantially suppressed.

T2prep

This option plays out a slice-selective 90-te/2-180-te/2-90 sequence before each segment acquisition. There are refocusing lobes for the 90 slice selects, and butterfly crushers around the 180º slice selective pulse. Additional crushers are played out after the second slice selective 90º pulse. These prepulses put magnetization into the xy plane, let it evolve according to T2, then store the T2-weighted magnetization along the z-axis. Since the segment acquisition follows immediately, the effects of T1 relaxation are minimal in influencing the contrast in the image.

Fat Saturation

The signal from fat is suppressed using Fat Saturation. Check the **Auto** checkbox to use the prescan fat frequency. Locate the frequency prescan at fat frequency or a user defined frequency entered. A flip angle and pulse duration for the chemically selective pulse entry is optional.

Spatial Saturation

Up to six spatial saturation bands of arbitrary orientation and thickness may be positioned from the Plan page. The **Spatial Sat** checkbox enables or disables the spatial saturation bands without affecting the positioning of the bands.

Show Profile

A profile of the object can be obtained by clicking the **Profile** button on the Advance page. The phase encoding is disabled and **etl** echoes are acquired for each slice. The last profile acquired is displayed automatically. Use the Process => Display page to view the profiles.

Imaging parameters

Crushers and spoilers are very important to the correct operation of the tagcine sequence. Listed below are the parameters for the various crushers and spoilers in the sequence.

Parameter	*Function*
`gspoil, tspoil`	Spoilers at the end of each gradient echo acquisition in the segment
`gcrush, tcrush`	Crush after each inversion pulse (T1 prep)
`gcrusht2,tcrusht2`	Crushers following the 90-180- 90 sequence (T2 prep)
`gcrush_t2180, tcrush_t2180`	Symmetric "butterfly" crushers around the 180 in T2 prep
`gcrushfs, tcrushfs`	Crushers following a fat saturation pulse
`gcrush_mtc,tcrush_mtc`	Crushers following an MTC pulse
`gcrush_sat, tcrushsat`	Crushers following spatial saturation pulses

Parameters accessed from the **Advanced** page:

Parameter	*Function*
`p1`	Segment rf pulse width
`p1flip`	Flip angle for p1 pulse- usually a relatively small tip angle (e.g. 10 °).
`p2`	`90°` rf pulse width, used for T2 prep
`p2flip`	Tip angle for p2 (usually 90°)
`p3`	Non slice selective, inversion pulse used with DIR option
`p3flip`	Tip angle for the non slice selective pulse (usually 180°)
`pi`	Inversion pulse used in T1 prep and in T2 prep
`piflip`	Tip angle for the inversion pulse (usually 180°)

Parameters accessed from the **Scan** page:

Parameter	*Function*
`tr`	Overall repetition time for the sequence
`te`	Echo time for each individual acquisition
`ne`	Number of frames, or cardiac phases, or echoes, to be acquired
`ti`	Inversion time -used in the IR option, defined as the time from the middle of the 180° pulse to the middle of the first rf pulse of the segment
`tet2`	Echo time for the T2 prep. Determines T2 contrast

4.2 Standard Sequence Options

The options that are available in most but not all sequences. Refer to the specific protocol for a listing of options available in that sequence.

Inversion Recovery

Check the **IR** check box on the **Scan** page to turn on inversion recovery. Go to the **Options** page to specify the inversion time (TI in milli-seconds) or click on Acquisition on the main menu bar, select Array, and specify a list of TI values (parameter ti, in seconds).

Magnetization Transfer

Magnetization Transfer Contrast (MTC) is obtained by applying a long RF pulse (typically 6-8ms) with a large RF power (specified as a large flip angle) at an offset of several kHz. Go to the **Options** page to specify the flip angle, rf pulse duration, and transmitter offset.

Fat Saturation

Check the **Fat Sat check box** on the **Scan** page to turn on fat suppression. Go to the **Options** page to specify the flip angle (typically 90°), rf pulse duration (usually 6-12ms, depending on the line width of the fat signal), and transmitter frequency for the fat saturation pulse. If the **Auto offset** check box is selected, the frequency found during the standard Frequency Prescan is used, otherwise any value that is entered into the Offset field is used for the transmitter offset.

Spatial Saturation

Check the **Spatial Sat** check box on the **Scan** page to turn on spatial saturation band. Go to the **Plan** page to define the saturation bands graphically.

Show Profile

Select the **Advanced** page and click on the **Acquire profile** button. The parameter `profile` is set to **'y'** (or `'yy'` for 3D experiments) and a single echo (per slice) under the readout gradient without any phase encoding is acquired. The 2D and 3D imaging sequence data is displayed in the Plan Viewport.

2D Projection

3D sequences run by clicking the 2D projection button on the Advanced page result in data acquisition with phase encoding turned off in the second or PE direction resulting in a projection image. The data is displayed in the Plan Viewport.

Trial Spectrum

Clicking on the Trial Spectrum button on the advanced page using localized spectroscopy sequences acquires a spectrum in the Plan Viewport. The data in the Plan Viewport can be evaluated for quality or optimization of the parameters without moving to the Current Viewport.

Diffusion

Check the **Diffusion** check box on the **Scan** page to turn on Diffusion Weighting. Go to the **Options** page to specify the diffusion parameters. Diffusion weighting is obtained by applying two gradients with identical duration delta (δ, parameter `tdelta`) and amplitude (`gdiff`), separated by the DELTA (Δ, parameter `tDELTA`). The gradients have the same sign in the case of a spin-echo type of sequence (sems, stems, and epi with spinecho option), or opposite sign (epi with gradient echo option).

Entry of any of gdiff, tdelta or tDELTA on the Scan page results in the calculation of the corresponding b-values according to the Stejskal-Tanner equation:

$$b = \gamma^2 \delta^2 gdiff^2 \left(\Delta - \frac{\delta}{3} \right)$$

The maximum b-value is printed in the message window and given in s/mm2. The b-values are written to the fdf header upon completion of the acquisition and can be utilized for calculation of the Apparent Diffusion Coefficient (ADC).

Diffusion weighting along different directions is obtained by selecting one of the available diffusion schemes in the Diffusion Scheme menu on the Scan page:

Parameter	*Function*
Off	diffusion gradients turned to zero
Readout	diffusion gradient applied along the readout direction
Phase	diffusion gradient applied along the readout direction
Slices	diffusion gradient applied along the readout direction
All	diffusion gradient applied along all three directions simultaneously. Notice, that this is not the same as a trace ADC map
Dual	diffusion tensor acquisition with 2 gradients on simultaneously
Dual (2)	also diffusion tensor acquisition with 2 gradients on simultaneously, but repeated twice with all gradient amplitudes reversed in sign for the second repetition

All of these options call macros for setting the diffusion gradient multiplication factors `dro`, `dpe`, `dsl` to values in the range `[-1.0; 1.0]`.

The checkbox for diffusion sets the parameter `diff` to turn diffusion weighting on (1) or off (0).

Turning diffusion **on** but selecting the **Off** scheme is not equal to turning diffusion **off**. The difference is in the sequence timing. With diffusion **on**, the time `tdelta` is inserted for the diffusion gradients, regardless of the diffusion factors. With diffusion **off**, `tdelta` is not inserted for the diffusion gradients.

The epi and stems sequences returns the entire b-matrix as well as the trace of the b-matrix. The elements of the b-matrix are given in the parameters `bvalrr`, `bvalpp`, `bvalss`, `bvalrp`, `bvalrs`, and `bvalsp`, respectively. The *b*-matrix is then given by:

$$b = \begin{bmatrix} bvalrr & bvalrp & bvalrs \\ bvalrp & bvalpp & bvalsp \\ bvalrs & bvalsp & bvalss \end{bmatrix}$$

The trace of the b-matrix is returned in the parameter `bvalue`:

```
bvalue = bvalrr + bvalpp + bvalss
```

Cross-terms between imaging gradients and diffusion gradients make a negligible contribution for the sems sequence and only the theoretical value of b is calculated.

Gradient Limitation

A gradient coil with a low duty cycle requires a reduction in the maximum allowed refocusing and spoiler gradients. Enter a smaller number for **Glim** (parameter `glim`) on the **Advanced** page, typically in the range 10-50% (of maximum gradient).

Limit the maximum gradient used for phase encoding by entering a number for **Glim PE** on the **Advanced** page (parameter `glimpe`). The parameter `glimpe` does not exist for all protocols. Create the parameter entering **`create('glimpe','real')`** on the command line.

4.3 Commands, Macros, and Parameters

Table 3 contains information about the commands, macros, and parameters that are used with imaging pulse sequences.

Table 3. Imaging Pulse Sequence Commands, Macros, and Parameters

Command	*Function*
`dconi`	Interactively adjusts 2D data displays
`dssh`	Displays an arrayed set of spectra, stacked horizontally
`flashc`	Converts compressed GEMS data set into standard VNMR file format. Needs to be executed only once on a data set
`ft`	Fourier transforms 1D data
`ft2d`	Fourier transforms 2D data
`Macro`	*Function*
`dmi`	Displays multiple images in VNMR
`decctool`	Opens tool to set eddy current, slew rate, and related parameters, using digital eddy current compensation (DECC)
`ecctool`	Opens tool to set eddy current, slew rate, and duty cycle using computer-controlled analog eddy current compensation hardware
`array`	Arrays a numeric parameter
`filter`	Sets a gaussian filter for image processing
`findpwr`	Calculates power levels using a sems profile and updates the `pulsecal` file

Table 3. Imaging Pulse Sequence Commands, Macros, and Parameters (continued)

Command	*Function*
`findpw`	Measures 180° pulse length and updates the `pulsecal` file
`ftnf`	Processes compressed data. It is equivalent to the command `ft('nf')` and can be used for processing compressed data
`ga`	Acquires and Fourier transforms data
`gems`	Loads default parameters
`go`	Submits experiment to acquisition
`imprep`	Sets up rf pulses, imaging, and voxel selection gradients
`ldrf`	Sets `resto` equal to transmitter offset frequency determined by `setof`. The value of `resto` is changed accordingly. Offset frequency is saved in the global frequency file `$HOME/vnmrsys/H1offset` by the `setof` macro.
`movetof`	Sets `tof` parameter to that specified by cursor
`offset`	Sets frequency offset corresponding to cursor location
`plan`	Defines slice parameters using a reference image
`pulsecal`	Loads rf pulse power calibration parameters
`rt`	Retrieves FIDs from a directory (e.g., `filename.fid`)
`rtp`	Retrieves parameters from a directory (e.g., `filename.par`)
`setarray`	Sets an array of values for a given parameter
`setgn`	Sets receiver gain
`setof`	Sets reference frequency for imaging (H1 offset)
`spuls`	Loads default single pulse sequence parameters relevant for imaging
`svf`	Saves current parameters and FID data in a directory (e.g., `filename.fid`)
`svp`	Saves current parameters in a directory (e.g., `filename.par`)
Parameter	*Function*
`d1`	Sets first delay length in standard two-pulse sequence and other pulse sequences
`fliplist`	Contains a list of pulse flip angles, in degrees
`fn`	Selects Fourier number in read dimension
`fn1`	Selects Fourier number in phase dimension
`gcoil`	Specifies physical gradient set currently installed, and allows updating of gradient characteristics. `gcoil` is a database file containing gradient calibration values from the `/vnmr/imaging/gradtables` directory.
`H1offset`	Global proton resonance frequency
`homo`	Enables homodecoupling control for first decoupler
`lpe`	Specifies length (field of view) in cm along phase dimension
`lro`	Specifies length (field of view) in cm along readout dimension
`np`	Sets number of points (real and imaginary) in readout dimension
`nt`	Sets number of averages
`nv`	Sets number of phase encoding steps. If `nv` is set to zero, a profile along the read dimension is obtained
`orient`	Defines orientation of imaging plane by setting the three commonly used orientations: (1) sagittal (`'sag'`), perpendicular to X axis; (2) coronal (`'cor'`), perpendicular to Y axis; and (3) transverse (`'trans'`), perpendicular to Z axis It is also possible to set the orientation to an arbitrary (oblique) plane by using the `plan` macro. For a more detailed description of `orient`, see Chapter 9, "Parameters."

Table 3. Imaging Pulse Sequence Commands, Macros, and Parameters (continued)

Command	*Function*
`p1`	Calculates length of excitation pulse, in µsec
`p1pat`	Specifies shape of excitation pulse
`pcmapapply`	Apply Phase Correction Map to Data (C); used in echo planar imaging
`pcmapclose`	Close Phase Correction Map (C); used in echo planar imaging
`pcmapgen`	Generate Phase Correction Map (C); used in echo planar imaging
`pcmapopen`	Open Phase Correction Map (C); used in echo planar imaging
`presig`	Selects preamplifier signal level (not available with human imaging systems)
`pad`	Specifies a preacquisition delay
`pss`	Specifies slice position in cm. Can be entered manually or via the `plan` macro.
`pw`	Specifies rf pulse width, in µsec.
`resto`	Specifies resonance transmitter offset frequency, in Hz. It must be set so that the transmitter is on the resonance frequency of the imaging component, usually water. `ldof` can be used to set this value from the global value in `H1offset`.
`rfcoil`	Contains rf pulse calibration entry in `pulsecal` file. The local `rfcoil` parameter is initialized from the global `RFCOIL parameter`
`tcapply`	Apply table conversion reformatting to data
`tcclose`	Close table conversion file
`tcopen`	Open table conversion file
`te`	Specifies echo time, in sec. For GEMS, it is usually set to less than 0.01 sec to minimize T_2* effects
`thk`	Specifies slice thickness, in mm
`tpwr`	Specifies pulse power output, in dB units. 63 dB is the maximum value
`tpwr1`	Specifies pulse power for the excitation pulse. The `imprep` macro sets the pulse power to the value specified by `fliplist`. For GEMS, set `tpwr1` to correspond to a 10° to 20° flip. If the `tpwr1` value is reduced by 6 dB, the flip angle is reduced by 50%. For example, reduction in the power by 12 dB corresponds to a flip angle of 22.5° (90°/4). `fliplist` provides a easy way to change the flip angle.
`tr`	Specifies recycle time, in sec. It must be set to allow for spins to return to their equilibrium state. For GEMS, it can be reduced to about 0.025 sec to 0.1 sec because of the low flip angle (5° to 30°) used for excitation.

Chapter 5. Image Viewing and Review Queue

Sections in this chapter:

5.1 Image Display and Manipulation Tools

Locations of the display and manipulation tools are shown in Figure 33. Refer to “VnmrJ Imaging Interface” on page 197, for a full description of the VnmrJ interface and icons.

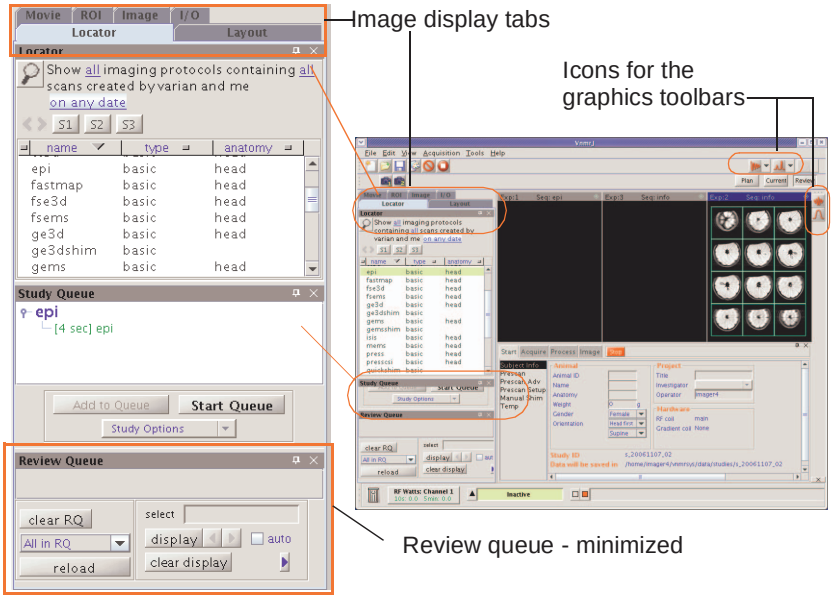


Figure 33. Image display and manipulation tools

5.2 Review Queue and Organizing Images

The review Queue (RQ) is used to organize and view images in the Review Viewport.

The Review Queue (RQ) maintains a list of scans currently loaded in the Review Viewport. Scans loaded in RQ are manipulated in the same way entries are manipulated in the Study Queue (SQ). Studies or scans are added to the RQ from the Locator (from sorting Studies or NMR data) or from the current SQ. The parent node in RQ corresponds to the study from which the data originates. Sub nodes correspond to each loaded scan and not necessarily the entire study.

Drag and drop scans to a different locations in the RQ to change their order. Nodes are updated or parent nodes are added as necessary. A parent node always corresponds to the originating study. Each scan is assigned a sequential group number as it is loaded. The group number is updated as the order of scans in RQ changes by dragging and dropping within RQ.

Loading Data into Review Queue

The choice of operation depends upon the objective.

- Add data to the RQ list — drag and drop a study or scan from the Locator or SQ into the RQ. The node is inserted where the data is dropped (if the data is not currently in the RQ).
- Add data to the RQ list and display the images in a certain frame — drag and drop a study or scan from the Locator or SQ into the frame. The node is added to the end of the list (if the data is not currently in the RQ). Images are displayed starting from the frame where the data is dropped.
- Add data to the RQ list, retrieve fid and parameter, and display the images — double click a scan in the Locator or SQ. The node is added to the end of the list (if the data is not currently in the RQ). The fid and parameters are retrieved.Images are displayed starting with the first frame.
- Reload images already in the RQ — select images using the menu on the RQ tool panel and click the reload button.

Removing Data from Review Queue

- Remove data from RQ and any related images that were displayed — drag a study, scan or image from RQ to the trash.
- Remove it from RQ and the image from the display — Select the drag tool  from the graphics bar and drag the image from the frame to the trash can.

Table Columns

A node is created in a hierarchical structure of study =>scans(s) =>image(s) when a study, scan, or image is loaded to Review Queue. The study level is attached to a scan when it is loaded. Both the scan and study levels are attached to an image when an image is loaded. The node is added to current RQ. Multiple studies can be loaded and each study may

contain multiple scans of images. A scan is treated as a group (of images). The RQ table has 12 columns.

Column	*Description and Operation*
name	Name of studies, scans and images as tree nodes in RQ. The parent node corresponds to the originating study. Double click on the node to expand the node all the way down to the individual images. Double click on the node to collapse. Rearrange nodes by dragging and dropping the names with left mouse button. Parent nodes are updated as needed. A node is copied if the control key is held while dragging and dropping the node RQ. Any parent nodes are also copied when copying a node. The number assigned to the scan (group) reflects the order of the scan in the RQ. Images in the scan have two index numbers: local index (1 to n, the total number of images in the group) and a global index that changes when the scans in the RQ are rearranged. Image indices are used for image selection. Set `aipNameFrames=2` (global) or `aipNameFrames=3` (local) and click **Display** in RQ to display the indices in the image frame.
group	This field shows group numbers and number of images in a group. A group is a scan (by default). A group contains images from the same study and same scan. When a image in group A is dropped to group B, it is added to group B only if group A and B have the same scan and study names, otherwise the image (of group A) are inserted in group B with its original scan and study names. Group B will be split in to two groups, each with their scan and study names.
display	This column contains check boxes for selecting groups for display. If a box is checked, images in that group will be displayed when clicking the display button. (see “Tools in Review Queue” on page 122 and “Image Selection” on page 123).
images	This column contains editable text fields where images in a group are selected by local image index of the group, see “Image Selection” on page 123.
frames	This column contains editable text fields where frames are selected to display a group of images. Frames are selected by frame numbers, rows, or columns, see “Image Selection” on page 123. If **auto layout** is checked, as many frames as specified will be laid out, otherwise images are displayed in the current layout. If more images are selected than current number of frames, the images are displayed in multiple batches. If a frame is selected by more than one group, and these groups are selected to display at the same time, images will be overwritten.
sort	Check the box to sort the images in the group by slices or uncheck the box to sort by echoes (or arrayed images). For example, if images are sorted by slices, and 1-2 are selected, images slice001image001echo001 and slice001image002echo001 are displayed; if images are sorted by arrayed images (or echoes) and 1-2 are selected, slice001image001echo001 and slice002image001echo001 are displayed.
slices	This column are editable text fields where slices are selected, see “Image Selection” on page 123.
echoes	This column are editable text fields where echoes are selected, see “Image Selection” on page 123.

Column	*Description and Operation*
array	This column are editable text fields where arrayed images are selected, see "Image Selection" on page 123.
ns	number of slices for a scan or slice index for an image
ne	number of echoes for a scan or echo index for an image
na	array size for a scan or array index for an image

Tools in Review Queue

RQ tool panel is located below the RQ table.

Tool	*Description*
clear RQ button	Remove all images from Review Queue and unloads all images from the browser.
select menu	Select images to reload: All in RQ – all images in the RQ Selected in RQ – reload selected images in RQ Select… – images listed in the **select** field Displayed – currently displayed images
reload button	Reloads selected images
select field	Enter images for display using "Image Selection" on page 123. The display, images, and frames field in the RQ table are automatically updated.
display button	Display selected images in RQ. If there are more images or frames than current frame layout, images are displayed as batches. This button sets aipDisplayMode = 2 (display images selected in Review Queue) and rqsort = 0 (do not globally sort images according to slices or scans, use frames selected in Review Queue).
left/right arrows	Display previous/next batch of images in selected RQ.
auto checkbox	Check to enable auto layout. The number of frames as specified in Review Queue are created automatically to display the selected images in a single batch of images. Uncheck to disable auto layout and use current frame layout .
clear display button	Clear image display and uncheck all selected groups.
expand/minimize	Toggle Review Queue table between expand and minimized.

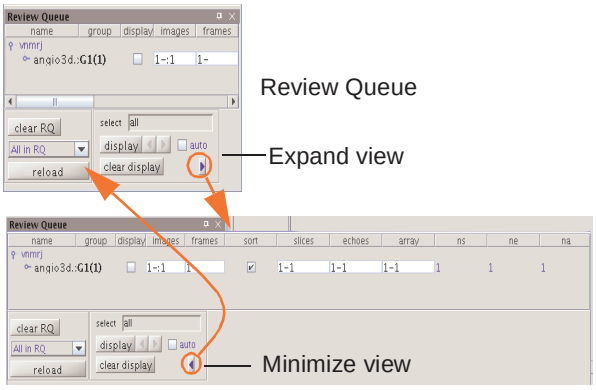


Image Display

Display images choices:

1. Double click on the image data in the Locator, SQ, or RQ.

   The images starting from the first frame are displayed.

2. Drag and drop the data to a frame.

   The images starting from that frame are displayed.

Image Selection

All viewports and images are maintained in the following tree structure:

`studies/groups/images.`

Images are selected using *selection mode* which has the following options:

Option	*result*
1	for all images
2	for images of a selected group (by click an image of that group)
3	for images selected in RQ
4	for images of selected frames
5	for images selected by a string
6	for images displayed
7	for images selected by previous command

Selection mode 5 (select images by a string) has the following syntax and arguments:

`g<number,number,...>-(image)[frame]`

`g<number,number>`	number is the group number or the number of each group who's image and frame fields are to be set the values for image and frame.
`(image)`	set the value of the image field for each group specified in group to this value. If no value is supplied, RQ table value is used.
`[frame]`	set the value of the frame field for each group specified in group to this value. If no value is supplied, RQ table value is used.

Examples:

`g1-(1-ns*ne*ma:3)`	sets the images field of all groups to 1-ns*ne*ma:3
`g1,3(1-2)`	sets the image field of groups 1 and 3 to the value 1-2
`'1-'`	select all loaded images
`'g1,3(1-)'`	select all images in groups 1 and 3
`'g1,3'`	select all images in groups 1 and 3 as selected in RQ table
`'g1[r1]g2[r2]g3[r3]'`	select selected images in group 1 in row 1, group 2 in row 2, and group 3 in row 3
`g3(1-)[9-]`	sets the image field of group 3 to 1 and the frame field to 9

If group is not specified, the ( ) for image selection can be omitted and the number will imply global indices of all loaded images.

5.3 Image Annotation Editor

The Imaging Annotation Editor, Figure 34, provides the tools designing new templates or modifying existing templates.

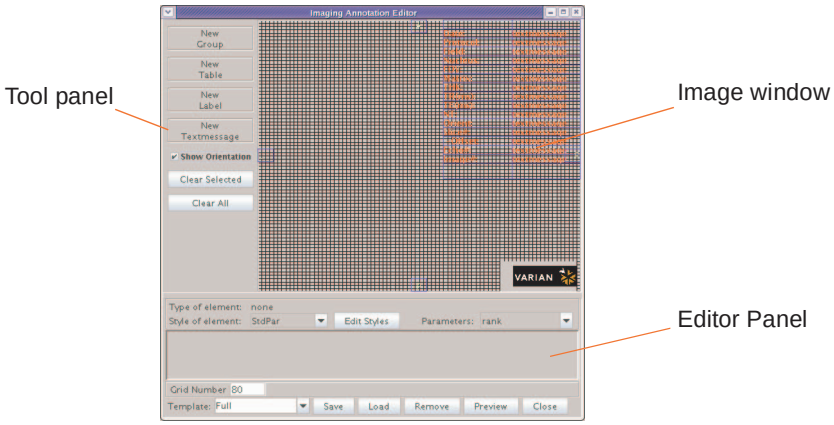


Figure 34. Image Annotation Editor

Start the image annotation editor:

1. Select **Layout tab**.
2. Click on **Edit** to start the Image Annotation Editor.

The Imaging Annotation Editor window is divided into three areas:

- Image window – the grid area that represents the image. The resolution of the grid is 30x30 by default. This is changed in the Grid Number field in the Editor panel.
- Tool panel – along the left side of the window holds tools for creating new components and buttons.
- Editor panel – along the bottom of the window allows editing of the selected component.

Annotation components are listed below:

Group	A Group is a rectangular container that holds a grouping of components. A group can be dropped at any location of the image window, where it is docked to one of eight compass rose locations: North, Northeast, East, Southeast, South, Southwest, West, Northwest.
Label	A rectangular area for either a short text string or an image icon. To display both text string and an image icon, two labels are used.
Textmessage	Text field displays the value of a parameter, or an expression. Parameters need to exist in a FDF header, or the **`procpar`** file of the scan. Select commonly used parameters from the **Parameters** menu on the upper-right corner of the editor panel. Parameters not found in the FDF header, procpar file, or not have a value, are displayed as an empty string.

The Template menu lists the templates located in:

- `$vnmruser/templates/vnmrj/annotation`
- `$vnmrsystem/templates/vnmrj/annotation`

The local template is shown if a template exists in both locations.

5.4 Regions of Interest

Regions of Interest (ROIs) are user-specified areas on the images. You can draw several general shapes of ROIs:

- Regions (polygons)  , ovals (ellipses)  , and boxes (rectangles)  define areas interior to the drawn figures.
- Points  , lines  , and curves (or polylines)  define just the area directly underneath the drawn lines.

Drawing ROIs

- Draw regions — Enter the mode for the desired shape and then drawing the figure by clicking the left mouse button and dragging the mouse to shape the figure. Release the mouse button to complete the ROI creation.
- Draw curves or regions — Drag the mouse creates a continuous trail of vertices along the path of the cursor. Releasing the mouse button and then left-clicking draws single vertices. End the creation of a curve or region by clicking the middle mouse button or double-clicking with the left button.
- Constrain lines to be horizontal, vertical, or 45° — Hold down the **Shift** key and drag one end of the line. Boxes or ovals can be forced to be square or circular by holding down the **Shift** key while dragging the mouse.
- Modify existing ROIs — press the left mouse button down on a vertex and drag the vertex to a new position. An ROI can be moved by dragging on any side of the ROI figure, far from a vertex. In the case of a very small ROI or a curve or region with continuous vertices around its perimeter, hold down the **Shift** key while moving the mouse to keep vertices from being selected.
- Modify curve and region ROIs by adding or deleting vertices — Add a vertex: Hold down both the **Control** and **Shift** keys and click on a line position on the segment to place the new vertex. Delete a vertex: drag it on top of a neighboring vertex.

Selecting ROIs

Select or deselect ROIs. When an ROI is selected, it is marked by having a small square drawn at each vertex. An ROI can be selected by going into **Select** mode  , moving the mouse near the ROI's boundary, and left-clicking. Besides selecting the ROI, this action deselects any previously selected ROIs.

- Hold down the **Shift** key and clicking the left mouse button on an ROI selects or deselects it and puts all ROIs into the same state.
- Hold down the **Control** key and click the left mouse button on an ROI selects or deselects it and puts all ROIs bound to it into the same state. ROIs that are not bound to the selected/deselected ROI are not affected.
- Click the middle mouse button to toggle between the ROI selected/deselected state without affecting other ROIs.

The **ROIs** section tab enables you to select or deselect all ROIs at once.

Deleting ROIs

Delete an individual ROI by clicking on it with the right mouse button. To delete the ROI and all ROIs that are bound to it, hold down the **Control** key and click the right mouse button. To delete all ROIs, hold down **Shift** key and click the right mouse button on any ROI. You can also delete ROIs with the **Delete Selected** button on the ROI tab.

Binding ROIs

Create identical ROIs in all of the selected frames as follows:

Choose **Bind ROI Creation** in the **Settings** panel.

When you create a group of ROIs this way they remain bound together afterwards. Modifying one ROI modifies them all, even if all frames are not selected. However, it is possible to individually select or delete ROIs.

Redraw bound ROIs dynamically as upon modification any one ROI.

1. Select the **Max Tracking ROIs** menu.
2. Select the number of ROIs that will be dynamically updated.

   Choose`0` to completely turn off dynamic updating.
3. Select **Bind ROI creation** and specify one of the following:
   - Other ROIs bound to the one being draw on are selected after being created.
   - Other ROIs bound to the one being draw on are unselected being are created.

Use the **ROI Numbering** menu to control the display of ROI numbers on the image.

1. Select **In Box**.
2. Enter number labels in a black rectangle to make it more visible.

5.5 Using and Creating Accelerator Keys

An accelerator key combines of one or more key strokes to accomplish an action associated with a mouse click over on button or as shortcuts for frequently used commands used. Access to the commands on a particular panel are not restricted by accelerator keys.

Types of Accelerator Keys

- Standard accelerator keys

  These keys work anywhere within the VnmrJ window once the VnmrJ window is selected and require one modifier key (Alt or Ctrl) or two modifier keys (Ctrl and Shift) followed by an alpha (a, b, c …) or numeric (1, 2, 3,+,- …) key.

  An example is the accelerator key combination for Zoom/Pan: `Ctrl+Shift+s`. Accelerator keys supplied with VnmrJ 2.2A are located in:

`/vnmr/templates/vnmrj/interface/KeyStrings.txt`and listed in Table 4. The Ctrl and Control keys are the same key.

Table 4. Standard Accelerator Keys

Function	*Accelerator Key*	*Command or macro executed*
Refresh	Ctrl+L	`aipDisplay('redisplay')`
Select	Ctrl+Shift+S	`aipSetState(1)`
Zoom/Pan	Ctrl+Shift+Z	`aipSetState(8)`
Vertical Scale	Ctrl+Shift+V	`aipSetState(2)`
Draw Point	Ctrl+Shift+P	`aipSetState(3)`
Draw Line	Ctrl+Shift+L	`aipSetState(4)`
Draw Box	Ctrl+Shift+B	`aipSetState(5)`
Draw Oval	Ctrl+Shift+O	`aipSetState(10)`
Draw Curve	Ctrl+Shift+C	`aipSetState(6)`
Draw Region	Ctrl+Shift+R	`aipSetState(7)`
Image Math	Ctrl+Shift+M	`aipSetState(100)`
+	Ctrl+Shift+right-click-on-image	`stepMovie('+')`
-	Ctrl+Shift+left-click-on-image	`stepMovie('-')`

- Keys that function only on a specific graphics area or widget.

  These keys are active following the selection of a specific graphics area or widget (this is referred to as focus) and can be single or multiple letter accelerator keys. Modifier keys are not required.

  Focus is gained by single clicking on the graphic area or widget to make it active. Selecting any other area graphics area or widget move the focus to the new area and makes the new area active. Only one graphics area or widget is active at any time.

  Table 5 has examples of accelerator key requiring focus on a specific area or the graphics screen or widget. The *Function*, *Key Stroke*, and *Command* as shown as they appear in fields in the Acceleratorkey Editor.

Table 5. Examples of Accelerator Keys and Commands

Function (label="string")	*Key Stroke or [KEY] (key="<key(s)")*	*Command (cmd="command<options>")*
ds	DS[N]	`ds([n])`
re-process	RP	`process`
delete rois	[DELETE]	`aipDeleteRois`
delete selected frames	[BACKSPACE]	`aipDeleteData('selected')`
display img n and amp; forward, skip n, start from clicked frame	[N]S[N]	`RQdisplay('[n]-:[n]['+aipClickedFrame+'-]')`
display img n in clicked frame	[N][ENTER]	`RQdisplay('[n]['+aipClickedFrame+']')`
display img n & forward start from clicked frame	[N]F	`RQdisplay('[n]-['+aipClickedFrame+'-]')`
display all images	A[ENTER]	`RQdisplay('1-[1-]')`
display all imgs in group n start from clicked frame	A[N]	`RQdisplay('G[n](1-)['+aipClickedFrame+'-]')`

Table 5. Examples of Accelerator Keys and Commands

Function (label="string")	*Key Stroke or [KEY] (key="<key(s)")*	*Command (cmd="command<options>")*
add a row	AR	`aipAutoLayout=0 aiplitWindow(aipWindowSplit[1]+1, aipWindowSplit[2]), RQdisplay('batch',rqnext)`
display selected imgs in group n start frame clicked frame	G[N]	`RQdisplay('G[n](1-)['+aipClickedFrame+'-]')`

Using Accelerator Keys

Accelerator keys are shortcuts for frequently used commands or actions. There are two types of accelerator keys:

- Standard accelerator keys

1. Click anywhere within the VnmrJ window and make the window the active window.
2. Press and hold the modifier key (Alt or Ctrl) or keys (Ctrl and Shift) and an alpha (a, b, c …) or numeric (1, 2, 3,+,- …) key.

- Keys requiring selection or focus.

1. Select an object (the graphics canvas, region within the graphics canvas, or widget) by moving the cursor over the object.

   The intensity of some objects will change when the cursor is over the object to indicate that focus is now on the object and other objects require clicking with the left mouse button before the focus is on the object.

   When the graphics area has the focus, the key stokes are accumulated in a buffer, key strokes are matched an accelerator key(s), the command is executed, and the buffer is emptied. Unmatched key stokes sequences are accumulated in the buffer until one of the following events has occurred: an accelerator key stokes sequence is matched to a command, time has expired, or the **`Escape`** key is pressed.
2. Type an accelerator key or keys.

Creating Accelerator Keys Requiring Focus

- "Basic Rules for Accelerator Keys" on page 128
- "Creating Accelerator Keys" on page 129

The most logical use of accelerator keys is to display images in frames selected by mouse click. Table 4 contains examples of multiple letter accelerator keys for display of selected images starts from the frame user clicked before typing the keys.

Basic Rules for Accelerator Keys

- The most useful accelerator keys have one letter key or one letter key plus numbers if desired. Using multiple letters for an accelerator is allowed.
- A letter used as a one letter accelerator key can not be used as the first key of any multiple key stroke accelerator. The buffer reads each key as it is entered, matches key to a command, and empties the buffer. Multiple key accelerators mush have unique sequences of key strokes.

- Accelerator keys patterns must be:
  letter key or letter keys – a, aa, abc …
  letter key or letter keys and number key or number keys – b1, cb1, dc23, …
  number key or number keys – 4, 56, 742, …
  number key or number keys and letter key or letters – 6a, 8cba, 321cba, …
  Letter and number keys cannot be interweaving (a3d is not an allowed key stroke).

Creating Accelerator Keys

Table 5 was derived from the file mapping key stocks to commands supplied with VnmrJ 2.2A is located in:
`/vnmr/templates/vnmrj/interface/acceleratorKeyTable.xml.`

The contents of `acceleratorKeyTable.xml` are modified or edited using the **Acceleratorkey Editor** as follows:

1. Login as either a general user (to create local user accelerator keys) or as vnmr1 (to create global accelerator keys).
2. Start VnmrJ.
3. Enter **`vnmrjcmd('edit','acceleratorKeys')`**
   The **Acceleratorkey Editor** window starts.
4. Click on the **Editor** tab.
   Editor consists a table showing existing accelerator keys that are defined by three entries: **`label`**, **`keys`**, and **`cmd`**.
   - **`label`** – a name for the keys
   - **`keys`** – combination of key stoke(s) that will be map to a command.
     Keys are not case sensitive. Strings representing a special keys are placed in square brackets so the letters are not interpreted literally as multiple single letter key strokes. The following are the special keys that can be used:

[n]	[ctrl]	[shift]	[alt]	[meta]
[space]	[enter]	[backspace]	[delete]	

   - **`cmd`** – vnmr command executed by the accelerator key(s). The command string is case sensitive.
5. Do one of the following:
   - Modify an existing acceleration key.
     a. Clicking (selecting) the row representing the accelerator keys in the table.
        The **`label`**, **`keys`**, and **`cmd`** will be shown in editable fields below the table.
     b. Make changes to any or all the fields.
   - Add a new accelerator key(s).
     a. Click on any row in the accelerator keys in the table.
        The **`label`**, **`keys`**, and **`cmd`** will be shown in editable fields below the table.
     b. Remove the existing key combination from the **`keys`** row.
     c. Define a unique key combination for the new command.
     d. Remove the existing label from the **`label`** row.
     e. Enter a table for the new command.

f. Remove the command from the **cmd** row.

g. Enter the new command (command are case sensitive and follow standard vnmr/vnmrj syntax).

6. Select the **Preference** tab.

7. Set the time out for the buffer.

   The default time out for the buffer is 2.0 seconds.

8. Set the key stroke time out.

   The key stroke time out default is 0.5 second.

   Key stoke time out applies only to numerical keys. Setting the key stroke time out to less than 0.5 seconds allows interpretation of multiple digit numbers as part of accelerator key and not interpret individual number key strokes. are, i.e., if two or more numerical keys are to be interpreted as one number, the delay between these key stokes should be less than 0.5 sec., otherwise only the first numerical key stroke will be interpreted.

5.6 Drag and Drop on Graphics Canvas

Drag and drop on graphic canvas provides a tool for direct manipulation of the images on the screen. Images can be moved to an available frame, copied to an available frame, or deleted. The display arrangement using drag and drop of images is not remembered by RQ and will be lose when the data set is reloaded and displayed.

1. Layout the images so that there are empty frames (except when deleting an image).
2. Select the  tool and move it over the desired image.
3. Choose one of the following operations on the image:
   - copy — hold the control key and left click, drag and drop into an open frame
   - delete — hold the control key and left click, drag and drop into the trash can
   - move — left click, drag and drop into an open frame

5.7 Review Queue Command (aipRQcommand) Options

The aipRQcommand is used by VnmrJ and the macros RQaction and RQ display for working with images. Functions of aipRQcommand are the following:

- "Loading and Selecting Images" on page 130
- "Displaying Images" on page 132
- "Deleting and Removing Images" on page 134
- "Manipulating Images and Other Functions" on page 135

Loading and Selecting Images

- "Loading Specified Images" on page 131
- "Selecting Specified Image or Images" on page 132

Loading Specified Images

Images are loaded and displayed only if `path` is a file, or `frameToStart` is specified. If `path` is a directory and `frameToStart` is not specified the image is loaded but not displayed.

Syntax

```
aipRQcommand('load',path, <node>, <x, y>)
aipRQcommand('load',path, <node>, <frameToStart>)
aipRQcommand('load',path, < node>)
aipRQcommand('load',path, < frameToStart>)
aipRQcommand('load', path)
```

Arguments	*Value*	*Comment*
`path`	directory of `fdf` files.	If **`path`** is a directory, image directories are loaded recursively. Each image directory is a group. If `recondisplay` in the procpar file is N and N > zero, every N images will be selected (i.e., 1-:N) for display, otherwise all images will be selected. If the number of selected images is > `rqImageNodes`, the first N image will be selected by default. If `rqImageNodes` is not defined or is zero, N is 100;
`node`	RQ node above which the new nodes will be inserted.	
	" "	*default* — an empty string and data is appended not inserted.
	<###>	id in the form of *study group image* (study number group number image number) representing the RQ node
	Examples	1 0 0 — first study 1 2 0 — second group of first study 1 2 1 — first image, second group of first study.
`frameToStart`		Frame to start the display. Frame numbers start from 1 to rows*columns.
	1	*default*
	0	Use first available frame (first empty frame or the first frame if there are no empty frame).
	<0	`abs(frameToStart)` will be used. Current display is erased.
`x,y`	Locations of the graphic area where the image(s) are dropped. Frame 1 is used if **`x,y`** is out of the range.	

Related

The following command
`aipRQcommand('load', path, <frameToStart>)`
works the same as commands:

```
aipLoadFile(path, <frameToStart>)
aipLoadDir(path, <frameToStart>))
```

Selecting Specified Image or Images

The `aipRQcommand('select')` command uses selection mode and selection string defined by parameters `aipDisplayMode` and `userselection` if `selection` is not specified.

Syntax

```
aipRQcommand('select', <selection>, <globalSort>)
```

Arguments	*Value*	*Comment*
`selection`	**First syntax**	
	`'all'`	select all images
	`'rq'`	*default* — select images selected in RQ
	`'frames'`	select images in selected frames
	`'group'`	select images in the same group of a selected frame.
`selection`	**Alternate syntax**	
	`'1-'` or `'all'`	select all images
	`'g1(1-)'`	all images in group 1
	`'g1(1-9)[3-]'`	images 1-9 in group 1 starting from frame 3
	`'g1-(1-:2)'`	every other images in all groups.
`globalSort`	`0`	sort by scans if `selection` is not `'rq'` or and alternate selection syntax
	`1`	*default* — sort by scans
	`2`	sort by slices

Displaying Images

- "Displaying Images by path" on page 132
- "Displaying Images by selection" on page 133
- "Displaying Images by key" on page 133
- "Displaying Images by batch" on page 134

These commands load and display the data and is equivalent to using the two commands; `aipRQcommand('load',...)` and `aipRQcommand('display')`.

Displaying Images by ***path***

Syntax

```
aipRQcommand('display', path, <node>, <x, y>)
aipRQcommand('display', path, <node>, <frameToStart>)
aipRQcommand('display', path, <node>)
aipRQcommand('display', path, <frameToStart>)
aipRQcommand('display', path)
```

Arguments	*Value*	*Comment*
`path`	directory of `fdf` files	If **`path`** is a directory, image directories are loaded recursively. Each image directory is a group. If `recondisplay` in the procpar file is N and N > zero, every N images will be selected (i.e., 1-:N) for display, otherwise all images will be selected. If the number of selected images is > `rqImageNodes`, the first N image will be selected by default. If `rqImageNodes` is not defined or is zero, N is 100;
`node`	RQ node above which the new nodes will be inserted	
	""	*default* — an empty string and data is appended not inserted.
	<###>	id in the form of *study group image* (study number group number image number) representing the RQ `node`
	Examples	1 0 0 — first study 1 2 0 — second group of first study 1 2 1 — first image, second group of first study.
`frameToStart`		Frame to start the display. Frame numbers start from 1 to rows*columns.
	1	*default*
	0	Use first available frame (first empty frame or the first frame if there are no empty frame).
	<0	`abs(frameToStart)` will be used. Current display is erased.
`x,y`	row #, column #	Locations of the graphic area where the image(s) are dropped. Frame 1 is used if **`x,y`** is out of the range.

Displaying Images by **selection**

Syntax

```
aipRQcommand('display', <selection>, <globalSort>, <layoutMode>)
```

This command is equivalent to:

`aipRQcommand('select',...)` plus
`aipRQcommand('display','selected',...)`

Command equivalents of `aipRQcommand('display', 'all')` are:

`aipDisplay` and `aipDisplay('all')`.

Displaying Images by **key**

Syntax

```
aipRQcommand('display', key, <globalSort, layoutMode>, <x, y>)
aipRQcommand('display', key, <globalSort, layoutMode>,
             <frameToStart>)
aipRQcommand('display', key, <globalSort, layoutMode>)
aipRQcommand('display', key, <x, y>)
aipRQcommand('display', key, <frameToStart>)
aipRQcommand('display', key)
```

Arguments	*value*	*comment*
`key`	`dir +' '+ name +'0'`	
`globalSort`	`0`	sort by scans if `selection` is not `'rq'` or and alternate selection syntax
	`1`	*default* — sort by scans
	`2`	sort by slices
`layoutMode`	`1 is default`	auto layout
`frameTo-Start`		Frame to start the display. Frame numbers start from 1 to rows*columns.
	1	*default*
	0	Use first available frame (first empty frame or the first frame if there are no empty frame).
	<0	`abs(frameToStart)` will be used. Current display is erased.

*Displaying Images by **batch***

This command display the specified batch or current batch of images. When not in auto layout mode, there may be more than one batch of images.

Syntax

```
aipRQcommand('displayBatch', <batch>)
```

Deleting and Removing Images

- "Deleting Images From the Browser" on page 134
- "Removing Images From the Browser" on page 135

Deleting Images From the Browser

This command deletes images from the Browser. Images may be selected.

Syntax

```
aipRQcommand('delete', node/path/key/'all')
```

Argument	*Value*	*Comment*
`'delete'`		Delete images
`node`	RQ node	
`path`	directory of `fdf` files	
`key`	`dir +' '+ name +' 0'`	
`'all'`		Deletes all images

Removing Images From the Browser

This command operates on single images or multiple images and both deletes images from the Browser and removes images from the RQ.

Syntax

`aipRQcommand('remove', node/path/key/'all')` — multiple images

`aipRQcommand('remove', x, y)` — single images

Argument	*Value*	*Comment*
`'remove'`		Delete images from the Browser and RQ
`node`	RQ node	
	<###>	id in the form of *study group image* (study number group number image number) representing the RQ `node`
	Examples	1 0 0 — first study 1 2 0 — second group of first study 1 2 1 — first image, second group of first study.
`path`	directory of `fdf` files	
`key`	`dir +' '+ name +' 0'`	
`'all'`		Removes all images
`x,y`	row #, column #	Remove image frame specified by location **`x,y`**.

Manipulating Images and Other Functions

Moving Nodes

Move `node1` before `node2` in the RQ.

Syntax

`aipRQcommand('move', node1/path/key, node2)`

Argument	*Value*	*Comment*
`'move'`		Move `node1` before `node2`
`node1`	source node number	Node to be moved
`path`	directory of node to be move	

Argument	*Value*	*Comment*
`key`	`dir +' '+ name +' 0'`	of node to be moved
`node2`	target node number	node above which the new nodes will be inserted.

Moving a Frame

Move image frame specified by `x1, y1` to the frame specified by `x2, y2` in the graphics window.

Syntax

```
aipRQcommand('move', x1, y1, x2, y2)
```

Argument	*Value*	*Comment*
`'move'`		Move (drag) the image to the specified location in the graphics window.
`x1, y1`	row #, column #	source frame
`x2, y2`	row #, column #	target frame

Coping a Node or a Frame

Make a copy of `node1` and insert it before `node2` (drag and drop a node while holding the cntrl key).

Syntax

`aipRQcommand('copy', node1/path/key, node2)` — node copy in RQ.

`aipRQcommand('copy', x1, y1, x2, y2)` — single frame copy in graphics window.

Copy using the mouse — **ctrl/drag** an image to a different frame

Argument	*Value*	*Comment*
`'copy'`		Move (drag) the image to the specified location
`x1, y1`	row #, column #	source frame
`path`	directory of `fdf` files	If **`path`** is a directory, image directories are loaded recursively. Each image directory is a group. If `recondisplay` in the procpar file is N and N > zero, every N images will be selected (i.e., 1-:N) for display, otherwise all images will be selected. If the number of selected images is > `rqImageNodes`, the first N image will be selected by default. If `rqImageNodes` is not defined or is zero,N is 100;
`key`	`dir +' '+ name +' 0'`	
`x2, y2`	row #, column #	target frame

Setting Node Attributes

Set the attribute values of a RQ node

Syntax

```
aipRQcommand('set', <gid/node/path/key/'all'>, attribute,
value)
```

Argument	*Value*	*Comment*
`'set'`		
`gid`		group id
`node`	<###>	id in the form of *study group image* (study number group number image number) representing the RQ node
`path`	directory of `fdf` files	
`key`	`dir +' '+ name +' 0'`	
`'all'`		all images
`attribute`	Editable column of the RQ table	examples: display, images, frame column

`value`	`yes / no`
	`1-:2`
	9 –	

Getting Node Attributes

Get the attribute value of a node (study, group, or image).

Syntax

```
aipRQcommand('get', gid/node/path/key, attribute):value
```

Argument	*Value*	*Comment*
`'get'`		Get the attribute or parameter value
`gid`		group id
`node`	<###>	id in the form of *study group image* (study number group number image number) representing the RQ node
`path`	directory of `fdf` files	
`key`	`dir +' '+ name +' 0'` of the RQ node	
`attribute`		
`value`		

Getting Other Attributes

Syntax

```
aipRQcommand('get', name):value
```

Argument	*Value*	*Comment*
`'get'`		Get the attribute

`name`	`numOfgroups`
	`numOfstudies`
	`batches`
	`batch`	

Getting Image Selection

Return current image selection in valid selection syntax.

Syntax

```
aipRQcommand('getSelection'):value
```

Reloading Selected Images

Syntax

```
aipRQcommand('reload', <mode>, <selection>)
```

Argument	*Value*	*Comment*
`'reload'`		Reload selected image
`<mode>`		default is the value of the parameter `reconMode`
	1	All images
	2	Images of selected group
	3	Images selected in RQ
	4	Images of selected frames
	5	Uses `<selection>`
	6	Images displayed
`<selection>`		default is value of parameter `rqselection`

Unselecting RQ display check boxes

Syntax

```
aipRQcommand('unselectDisplay')
```

Unselect all display check boxes in RQ.

Chapter 6. Interactive Image Planning

Sections in this chapter:

Interactive image planning enables you to plan new image scans (target scans) using previously acquired scans as the scout images. The orientation, location, and field-of-view (FOV) of scans are determined by graphically manipulating overlays of target scans on one or more scout images (see Chapter 7, “Image Processing in VnmrJ ” on page 149 for more information on displaying images).

6.1 Scan Types

Four types of scans, see Table 6, can be planned using Image Planning: slices, radial, volume, voxel, and 2D CSI.

Table 6. Scan Types

Scan Type	*Description*
Slices	Slices have the same orientation and FOV. The location of slices varies only by slice position (`pss`), i.e., the location is shifted along the axis that is perpendicular to the plane (the *z* axis). By default, the slices are equally spaced, but the space can be adjusted by sliding the slices along the *z*-axis or by deleting selected slices.
Volume	A 3D volume is a stack of equally spaced scans with the gap implicitly set by the size of the second phase-encoded dimension. Since individual scans cannot be adjusted independently, a 3D volume is represented as a box without showing individual slices.
Voxel	Voxels are represented the same as volume but with smaller FOV.
2D CSI	2D CSI scans are slices with two phase-encoding axes; i.e., the axes are `lpe` and `lpe2` instead of `lpe` and `lro` as they are for slices.

6.2 General Features

The interactive image planning interface, shown in Figure 35, consists of the following features:

- Overlays on the scout images that graphically represent target image scans and which can be interactively manipulated.
- A plan control panel for menus, action buttons, display options and parameter entries.

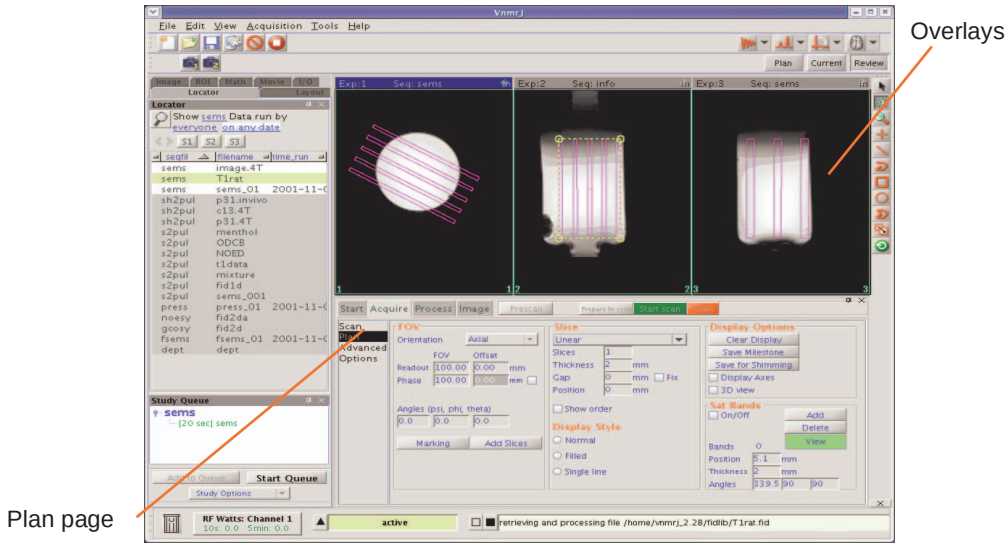


Figure 35. Interactive Image Planning Interface

Scout Images

Any previously acquired images can be used as scout images and multiple images can be displayed for planning. Double-clicking a completed scan in the Study Queue (while in the Plan viewport) will clear the display and load those images. Dragging from the Study Queue onto the graphics area adds images from the scan to the display without clearing already displayed images.

Overlays

The intersection of the planned target image orientation and position with the displayed scout images is shown as a color overlay (stripes or center lines) on the images. When you manipulate an overlay on one scout image, the intersections with other images are updated in real time. The scout images for planning can have arbitrary orientation. The appearance of overlays depends on the orientation of the scout images, i.e., the same target scans might look different on different scout images. The 3D representation of the target scans can also be shown to get a better perspective of the orientation. Other display options are described on page 144. The prescription (planning) can be saved as a milestone and be called back any time for the same protocol or for different protocols in the same study. Planning can also be directly copied to a different protocol.

6.3 Starting Image Planning

To start interactive image planning:

1. Select the **Plan viewport**.
2. Load and display **scout images** if no scout images are displayed.
3. Load the next scan if it is not already loaded.
4. Click on the **Acquire tab** and select the **Plan** page.
5. Select a localization type from the **Localization** menu.

   The Localization menu contains a list of default localizations (or scan type, see section 6.1 “Scan Types,” on page 139):
6. Select an image orientation from the **Prescription** menu, Table 7.

   The Prescription menu contains a list of default prescriptions, plus prescriptions automatically saved for each node of the study. The following default prescriptions are available:

Table 7. Image Planning Prescription Menu Options

Prescription	*Description*
Current	Current prescription parameters are used to determine the overlays of the target image scans.
Axial	Orientation of the target scans is transverse (`theta=0`, `psi=0`, `phi=0`).
Coronal	Orientation of the target scans is coronal (`theta=90`, `psi=0`, `phi=0`).
Sagittal	Orientation of the target scans is sagittal (`theta=90`, `psi=90`, `phi=0`).
3 Planes	Acquire the 3 cardinal orientations: axial, coronal, sagittal, in that order (`theta=0,90,90`, `psi=0,0,90`, `phi=0,0,0`).
Milestone	If a milestone prescription is ever saved in the current workspace, it is read and shown; otherwise nothing is shown. If a new milestone is saved during planning, when you click Milestone again, planning is restarted with the latest milestone.
Shim Voxel	For fastmap shimming, a voxel needs to be selected as the shim region. This selection retrieves the last saved voxel for fastmap shimming.

Use the **add slices** button to start planning. After selecting a different localization, the add slices button changes to add voxel, add 2D CSI, etc. accordingly. This button creates an overlay that is perpendicular to the selected scout image. The added slices are oriented and placed so the marks are maintained by one of the slices.

6.4 Using Marks in Image Planning

The position and orientation of a slice may alternately be specified by marking up to three points at arbitrary locations on one or more images. Marked points may be placed on images having different slice pointer or orientation. Use the following procedure to mark image features with up to three marks:

1. Click on **marking** in the **Plan** page.

   The cursor changes into a pencil.
2. Click the left mouse button on the image to mark the image.

   To remove the mark, click the right mouse button.

- No marks are used — Click the **add slices** button to add the target scans at the center of the selected scout image. The scans are oriented the same way as when one mark is used.
- One mark is used — The orientation of the plane is not defined and is chosen arbitrarily chosen as perpendicular to the image plane with the first phase encoding axis of the target and scout image planes parallel.
- Two marks are used — The target plane has one degree of freedom, i.e., the rotation about the axis defined by the two marks. The orientation is chosen so the plane is perpendicular to the image or one of the images if the marks are on two different images.
- Three marks are used — The slice plane is uniquely defined. Orientation of the target scan is the same as the image if all three marks are on the same image.
- All cases — The target scans are centered at the center of the marks (average position of the marks). The position is constrained to `ppe=0` if **ppe** is not checked
- Mark is placed on the overlay of target scans — That mark is considered used. Clicking the **add slices** button adds an overlay without using the mark to determine the orientation of the target scans. Placing one mark and click **add slices** to add a stack add the mark to the stack and is now used.
- Clicking **add slices** again, places a stack in the center of the scout image. Marks can be used for voxel saturation bands and other localizations.

Positioning and Orienting Scans

Marks determine only the initial position and orientation of the scans. Fix the scans at he current position by double clicking on the mark and turing the mark into a pin. A stack anchored by one pin cannot be moved but can be rotated about the pin. Use two pins to fix the position and orientation of a stack.

Double-clicking the mark toggles it between pin and mark.

Removing Marks

Click the mark with right mouse button to remove a mark.

6.5 Overlays

Click on the Select tool  to select and move an overlay; resize, rotate, and remove a scan; select and move a slice in a stack; or change the slice order in a stack.

- “Selecting an Overlay” on page 143
- “Resizing an Overlay” on page 143
- “Rotating an Overlay” on page 143
- “Moving an Overlay” on page 143
- “Selecting and Moving a Slice” on page 143
- “Changing Slice Order” on page 144
- “Removing Overlays” on page 144

Selecting an Overlay

Click the overlay to select (or activate) an overlay. The outline of the selected stack is highlighted.

Resizing an Overlay

Resize a scan by dragging a corner or edge of the overlay.

Resizing in Two Dimensions

Resize the target scans as follows:

1. Place the cursor over a corner.

   A red box appears and the corner is highlighted.

2. Hold down the left mouse button to grab the corner.
3. Drag the corner to resize the overlay.

Resizing in One Dimension

The following procedure is another way to resize a scan.

1. Place the cursor on one of the edges of the outline polygon. The edge is highlighted.
2. Click and drag the highlighted edge to resize the overlay with the rest of the edges fixed. Use the right mouse button to symmetrically resize the overlay.

Fix the gap between slices when resizing a stack by checking the button **fix gap** or **fix angle**. Slices are added or removed to keep the gap constant. The gap is changed to keep the number of slices constant if **fix gap** is not checked.

Rotating an Overlay

Rotate an overlay as follows:

1. Place the cursor over a corner.

   A red box appears and the corner is highlighted.

2. Press the right moue button.

   The red box will become a red circle.

3. Drag the circular handle to rotate the overlay about its center.

   Rotate an overlay about an arbitrary point by marking and double clicking the point. The point becomes a pin that anchors the rotation axis.

Moving an Overlay

Move an overlay (and a mark) as follows:

- Drag it with the left or right mouse button.
- Hold down the shift key and drag the object with the left mouse button.

Selecting and Moving a Slice

Select a slice of a stack by double-click on the slice.

A selected slice can be moved along the *z* axis of the stack (or rotated about the axle of the radial scans). Remove the selected slice by clicking on the **Delete** button. Restore a stack can to the original spacing and number of slices with the **Restore stack** button.

Changing Slice Order

Slices of a stack (including radial) are sequentially ordered by default. Click on the **Show order** button to show the slice order,. Alternate the order of the slices using the menu on the lower-right corner of the Plan panel.

Removing Overlays

Use the **Delete** button to remove a selected overlay or a slice of the overlay or remove all overlays at once using the **Clear** button.

6.6 Display Options

The display options are listed in Table 8 and are applied to the selected stack (i.e., overlays of the stack on all images). Display options are applied to the first stack (most likely the only stack) if no stack is selected. Any combination of display options is allowed. For example, **intersection**, **3D view**, **3D axes**, **show order**, and **fill stripes** can be all applied at the same time.

Table 8. Display Options

Display Option Check Box	*Description*
intersection	By default, this box is checked. It turns on/off the display of the intersection overlay.
3D view	Check this box to show the 3D view of the scans. The *z* axis is differentiated by the intensities of the color. Closer (away from the screen) is brighter, farther (into the screen) is darker. The highlight and handles of an overlay are not affected by 3D display because the manipulation of the scans is based on the 2D intersection overlay.
3D axes	Check this box to show the 3D axes of the outline of the scans. The axes are labeled as `lro` and `lpe`.
show order	Check this box to show the slice order without going into the “change order” mode.
stripes/center lines	Check this box to toggle between slice omitted and center line displays. When the intersections of the target scans appear as overlays on the scout images, they are represented by one or more 2D polygons by default. If the target planes are perpendicular to the scout images, the intersections are stripes or rectangles. In other cases, the shape of the intersection is less predictable. The slices can be represented by planes without thickness, i.e., the overlay is the center lines of the slice.
fill stripes	Check this box to show stripes as empty or filled (solid). By default, stacks, volumes, voxels appear as empty stripes or boxes. Saturation bands appear as filled stripes.

6.7 Copying Current Planning to a New Protocol

The current planning is automatically copied to the new protocol when a new protocol is retrieved from the Study Queue. Current planning is not automatically copied when data or parameter sets are retrieved. Click the **refresh** button in the **Plan** panel to copy planning to the current parameter setting.

6.8 Saving and Retrieving Prescriptions

Save current planning with the **save milestone** button. Planning can be called back any time in the current workspace. Planning is saved to a file in the directory of the current workspace. To save planning to a user-specified file or retrieve planning from a user-specified file, use the command:

```
gplan('savePrescription',path)
```

or

```
gplan('LoadPrescription',path)
```

6.9 Commands

The Plan page associates a menu, button, entry, etc. with commands that facilitate interactive image planning. All image planning commands take the following form:

```
gplan (function_name, arg1, arg2,...)
```

The command `gplan` is used instead of the macro `iplan` to avoid conflict with `iplan`.

`function_name` is the name of an image planning function surrounded by single quotation marks.

`arg1, arg2,...` are arguments for the function, if relevant.

Functions

Many function names contain the word stack, because internally all types of planning are represented by stacks. Radial scans are a stack with the slices varied by fan angle instead of by the shift along *z*-axis as a regular stack. A volume is a stack with a single thick slice. A voxel is a single thick slice stack ten times smaller than volume. A saturation band is a single slice stack without FOV.

The codes for different types of planning status are listed in the following Table 9.

Table 9. Planning Status Codes

Code	*Type*
0	Regular stack
1	Radial scans
2	Volume
3	Voxel
4	Saturation band
5	2D CSI

Image planning functions listed in Table 10 can be executed by the `gplan` command. If the type is not specified, the parameter `iplanDefaultType` is used.

Table 10. Image Planning Functions

Function	*Action*
`addAstack(int type)`	Adds a stack of the given type. `type=0`, type is not given, `type` =–1, the default type will be used.
`alternateSlices(int mode)`	If `mode=0`, restores the order. `mode=1` alternates slices. `mode=-1`, toggles between the two modes.
`clearStacks()`	Deletes all stacks.
`deleteSelected()`	Deletes selected stack or slice (only one is selected at a time).
`deleteSlice()`	Deletes selected slice.
`disCenterLines()`	Shows intersection overlay of stack as center lines or stripes.
`disStripes()`	Shows intersection overlay of stack as stripes.
`endIplan()`	Ends image planning.
`getActiveStacks()`	Starts planning with overlays calculated from current parameters.
`getCoronal()`	Starts planning with overlays determined with default parameters and coronal orientation.
`getDefaultSize()`	Gets default FOV.
`getDefaultSlices()`	Gets default number of slices. Used to update an entry. Because default parameters are not variable, they can be accessed only through functions.
`getDefaultStacks()`	Starts planning with overlays determined from default parameters and orientation of scout image.
`getDefaultThk()`	Gets default thickness of slices.
`getGapMode()`	Returns gap mode.
`getMilestoneStacks()`	Starts planning with overlays determined from saved milestone parameters.
`getPrevStacks()`	Starts planning with previous parameter set.
`getSagittal()`	Starts planning with overlays determined with default parameters and sagittal orientation.
`getTransverse()`	Starts planning with overlays determined with default parameters and transverse orientation.
`loadPrescription(char* path)`	Loads prescription from a given file.
`refresh`	Redraws/refreshes overlays.
`removeAstack(int index)`	Removes the stack with the given index. Stack indices begin with zero. If `index` is not given or `index=-1`, the selected (active) stack is deleted.
`restoreStack()`	Restores stack to its original spacing and number of slices.
`saveMilestoneStacks()`	Saves current planning as a milestone prescription. `Milestone` is saved in both memory and to a file.
`savePrescription(char* path)`	Saves current planning to a given file.
`setDefaultSize(float size)`	Sets default size (FOV) to `size`. All dimensions are set with the same size.

Table 10. Image Planning Functions

Function	*Action*
`setDefaultSlices(int ns)`	Set default number of slices to `ns`.
`setDefaultThk(float thk)`	Set default thickness of slices to `thk`.
`setDefaultType(int type)`	Set the default type to `type`
`setDisplayStyle(int mode)`	Show stripes or lines `mode=0`, shows stripes `mode>0`, shows lines `mode=-1`, toggles between the two style.
`setDraw3D(int mode)`	Show/hide 3D view of scans. `mode=0`, does not show 3D `mode>0`, shows 3D `mode=-1`, toggles between the two modes
`setDrawAxes(int mode)`	Show/hide 3D axes of scan outline. `mode=0`, does not show `mode>0`, shows `mode=-1`, toggles
`setDrawInterSection(int mode)`	Turn on/off intersection overlay. `mode=0`, does not show intersection `mode>0`, shows intersection `mode=-1`, toggles
`setDrawOrders(int mode)`	Show/hide slice order. `mode=0`, does not show `mode>0`, shows `mode=-1`, toggles
`setFillPolygon(int mode)`	Show empty/filled stripes. `mode=0`, shows empty `mode>0`, shows filled (solid) `mode=-1`, toggles
`setGapMode(int mode)`	Fix/unfix gap mode. `mode=0`, gap is not fixed `mode>0`, gap is fixed
`setMarkMode(int mode)`	Remove/activate one mark each time it is executed. `mode=0`, remove mark `mode>0`, activate mark If all marks (maximum number is 3) are removed or activated, it does nothing. When a mark is activated (`mode>0`), cursor changes into a pencil. Clicking a graphic area places a mark on the area and the cursor turns back into an arrow.
`setValue(char* paramName, float value, int index)`	Sets parameter values.
`startIplan(int type)`	Start/restart image planning with the **Active** prescription, and sets the default type as `type`. `type=0`, `type` not given `type =-1`, type determined by current parameters.

The parameters listed in Table 11 are used in image planning. The current value of these parameters is updated when an action is complete (e.g., planning is initialized or restarted, a stack is added, the display is refreshed, or the mouse is released after manipulating the overlay).

Table 11. Image Planning Parameters

Parameter	*Description*
gap	Gap between slices.
lpe	FOV of first phase encoding dimension, used for lope, vox1.
lpe2	FOV of second phase encoding dimension, used for lpe2, vox3.
lro	FOV of read out dimension, used for lro and vox2.
ns	Number of slices.
phi	Euler angle, used for phi, sphi, vphi.
psi	Euler angle, used for psi, spsi, vpsi.
ppe	Shift of stack center along first phase encoding dimension. Used for ppe, pos1.
pro	Shift of stack center along readout dimension. Used for pro, pos2.
pss	Shifts of slices along *z* axis.
pss0	Shift of stack center along *z*, the axis perpendicular to the plane. Used for pss0 and pos3.
radialAngles	Fan angle of radial slices.
theta	Euler angle, used for theta, stheta, vtheta.
thk	Thickness of slices or saturation bands (satthk).

Chapter 7. Image Processing in VnmrJ

Sections in this chapter:

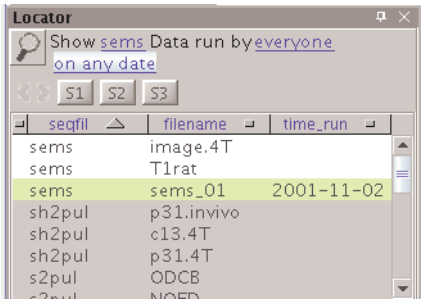
Data in a **Study** panel data is automatically processed into images and the images are displayed at the end of the scan. This chapter explains how to modify the display of the images.

7.1 Image Processing Controls

The image processing panels provide tools for manipulating image display, analysis, and printing.

Locator

The locator panel holds the study queue and, if the review port is active, the review queue.

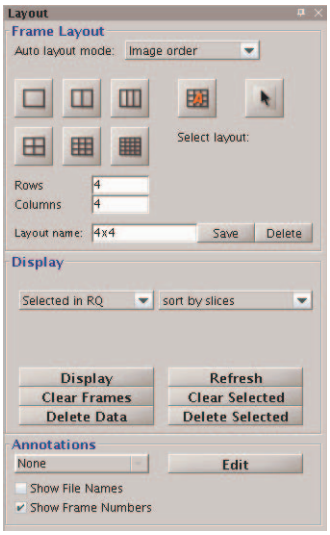


Layout

The Layout tab is used for selecting which images are displayed in which layout.

Frame Layout

The Frame Layout area provides buttons to quickly select one of the commonly used layouts: 1, 2, 3, 2x2, 3x3, 4x4.



	Auto button. Automatically layout enough frames to display the images.
Select layout	Menu selection of user saved layouts
Rows	Enter the number of rows in a layout
Columns	Enter the number of columns in a layout
Layout	Shows name of the current layout
Save	Save a frame layout with the default row x column name or enter a name in the Layout field and click the **Save** button.
Delete	Delete a saved layout by selecting the selected frame layout
	Select tool allows the user to select frames.
Slider bar	 .If there are more images than frames in the current layout, a slider bar appears. Images are displayed in batches corresponding to the frame layout. Click the slider and display the next batch of images

Display

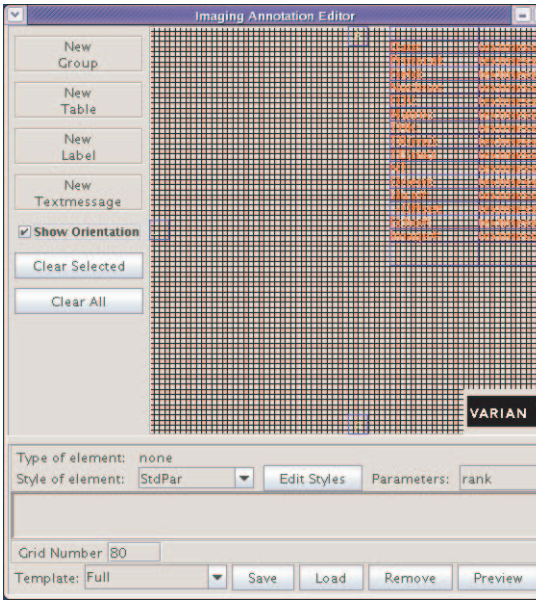
You can choose which images to display.

Menus	*Item*	*Description*
Display	All	Display all images in the review queue.
	Selected Frames	Displays images in selected frames.
	Selected in Review Queue	Display the images selected
	Select…	Opens the text entry field **Specific**. Enter image selections for display in the field next to **Specific**.
sort (global)		Drop down menu to select multiple scans
	no sort	Display images in frames specified in the review queue.
	sort by scans	Display images by scans.
	sort by slices	Display images by slice – use if multiple scans are selected.

Buttons	*Description*
Display	Display the images selected from the menu.
Clear Frames	Clear the selected frames.
Delete Data	Delete (unload) the data from review queue.
Refresh button	Refresh the display.
Clear Selected	Clear the image from selected frame without unloading the data.
Delete Selected	Delete (unload) the data associated with selected frame.

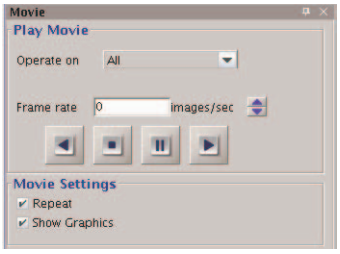
Annotations

Select an annotations options.

Menu selections	Full	A listing of most imaging parameters.
	Medium	Short + TE/TR/FOV
	None	No annotations at all.
	Short	L/R,A/P,I/S + image number
	Subject info	Name, ID, age.
Editor button	Opens **Imaging Annotation Editor**, refer to "Image Annotation Editor" on page 124.	

Movie

Use the Movie tab to setup images for a movie display. The movie appears in the frame selected when starting the movie. The **Operate on** menu selection determines the frames or images used in the movie.

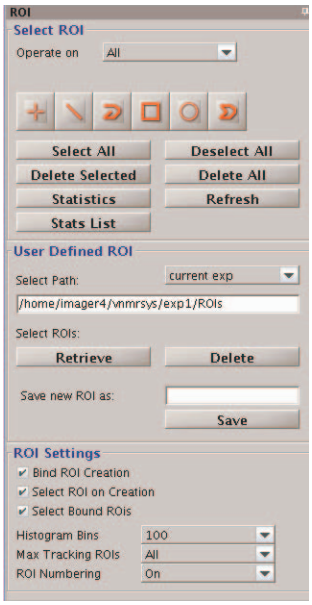


Operate on	All — use all images. Selected Frames — use the images selected frames.
Frame rate	Enter a value or use the up/down arrows. Enter the new frame rate and click the play button to enter a new frame rate while the movie is playing. The and buttons step the images one at a time either backward or forward if the frame rate is set to 0.
Repeat	Checked — the movie runs until you click the stop or pause button. Unchecked — the movie stops at the last frame.
Movie buttons	Play movie in reverse. Stop play. Pause play. Play movie forward.
Show Graphics	Checked — displays image ROIs and annotations associated with that image. Unchecked — displays only the images.

Region of Interest – ROI

ROI Panel

The ROI tools are described in 5.4 “Regions of Interest,” on page 125. The ROI is scaled in size with the image as the operator zooms in/out or pans. Changing the image intensity scaling does not affect the ROI (s). Changing the frame layout (e.g., from a single frame to 3x3) moves and scales the ROI appropriately. The operate on menu button determines which images are affected when creating new ROIs or when an ROI is retrieved from a file.



Menu or Button	*Description*
Operate on menu	All Selected Frames Selected in RQ Select… Group… Displayed
Select All	Select all ROIs
Deselect All	Deselect all ROIs
Delete Selected	Delete selected ROIs
Delete All	Delete all ROIs
Statistics	Opens a window displaying: • ROI statistics • Single point information • Histogram for a single square, circle, or polygon • Profile for a straight or curved line • Plot for multiple selected ROI's Use this window to do the following: • Segment an ROI to clear either the ROI or the background. • Associate the statistics with a specific file.
Stats List	Display the contents of the file with the ROI statistics.
Refresh	Redraw images and ROIs. ROI segmentation cannot be undone. Reloaded images into the review view port and apply a new segmentation.
Select Path: menu Select Path: field	Select a path — **current exp** or **current study** from the drop down menu. The selected path is displayed in the **Select Path** field below the menu. A path must be selected or a full path from root entered in the **Select Path** field before a user defined ROI can be saved, retrieved or deleted.
Retrieve	Retrieve user defined ROI to images specified using the operate on menu.
Delete	Delete user defined ROIs that are currently selected. The Delete and Backspace keys on the keyboard also delete currently selected ROIs
Save	Save selected ROIs to a file in the path specified in the **Select Path** field. Select the ROI by clicking on it with the select tool .

ROI Settings

Setting	*Function when Setting is Selected or Value Specified*
Bind ROI Creation	Bind all ROI's. All ROI's move and change in unison.

Select ROI on Creation	ROI is selected as it is drawn
Select Bound ROI's	All ROI's created on multiple images are selected when they are created. Un-check the box to select only the current active ROI.
Histogram Bins	Specify the number bins in histogram statistics
Max tracking ROI's	Specify the maximum number of ROI's that can be bound together.
ROI numbering	Turn on ROI numbering. Un-check to turn off numbering.

Image

The Image tab contains controls for modifying the image intensity, zoom, and rotations.

VS Mode Selected from Operate On Menu

- "Individual" on page 154
- "All" on page 154
- "Displayed" on page 155
- "From Header" on page 155
- "Group" on page 155
- "Selected in RQ" on page 155

Individual

Applies to individual images or frames.

Selection	*Operation*
Rescale	Auto scale is applied to each loaded image.
Load	Auto scale is applied to each image as it is loaded.
Mouse action	Scaling is applied only to selected image.
VS Page	Changes are applied to all images in selected frames or all images if no frames are selected.

All

Default values are shown on the VS Page and determined by one of the following:
—from the first selected frame with an image
—from the first frame with an image defines the default if no frames are select
—not changed if there are no images are displayed

Selection	*Operation*
Rescale	Sets the scaling of all loaded image to the current defaults or applies a default of 0.1 if no scaling is defined.
Load	Scale new images using current default. If no default is defined, auto scaling is applied to the first image and scale values applied to succeeding images
Mouse action	Applies scaling to all images
VS Page	Applies to all loaded images

Displayed

Applies to images currently displayed.

Selection	*Operation*
Rescale	Apply common auto scaling values to currently displayed images.
Load	Apply auto scaling to loaded images.
Mouse action	Apply to displayed image

From Header

Applies the VS for images saved in the auxiliary FDF header file. These files have the same name as the data file and add extension.aux to the file name, e.g. `image001.fdf.aux`.

Users with write permission can save auxiliary head files and any user can read the files.

Selection	*Operation*
Rescale	Apply VS setting saved with each image to all loaded images. Images that do not have a VS setting file are not affected.
Load	Use the saved VS file to scale the images, if the file does auto scale the first image and apply the values to the remaining images.
Mouse action	Apply to selected image.
VS Page	Apply to all images in selected frames or all images if no frames are selected.

Group

All images in a common directory.

Selection	*Operation*
Rescale	Auto scale each loaded group and apply the scaling to each image in the group.
Load	Auto scale is applied to the group containing a new image. This is not recommended for large groups of images.
Mouse action	Applies to all images in the group.
VS Page	Apply to all images in selected frames or all images if no frames are selected.

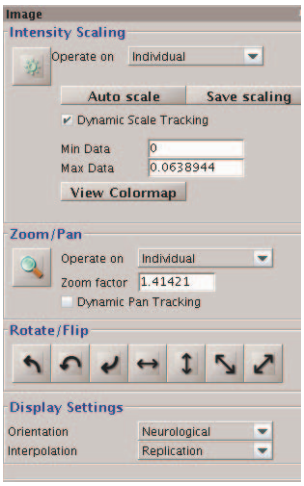
Selected in RQ

Applies to images defined in the RQ

Selection	*Operation*
Rescale	Apply common auto scaling values to all images in the (OG).
Load	All images are rescaled to a common value when a new image is added. This is not a recommended practice. Load the new images in a new OG and rescale them. Images not in the OG are auto scaled individually. Removing image from the OG does not affect the scaling of the remaining images.

Mouse action	Applies scaling to all images in the OG.
VS Page	Applies to all images in selected frames. Any image included in the OG are also scaled. If no frames are selected, changes are applied to all loaded images.

Intensity, Zoom/Pan, and Rotate/Flip



Button or Field	*Selection and Description*
	Select frames tool
	Switch to image intensity scaling mode. Mouse up/down – image intensity Mouse left/right –contrast
Auto scale	Adjusts the window and level so that the middle 98% of the histogram spans from black to white. If the bottom part of the window is less than 5% of the window width, the bottom of the window is set to 0 intensity (black). Selecting a group of images adds the pixels from all the images to the histogram and then auto scales.
Save scaling	Saves the current scaling to the auxiliary FDF header files and is retrieved when **From** **Header** is selected from operate drop down menu.
Dynamic Scale Tracking	Check to scale images during mouse movement or un-check to scale after mouse button is released.
Min Data	Image data corresponding to black
Max Data	Image data corresponding to white
View Colormap	Open Image Colormap window, see "VScale–Adjusting Contrast and Intensity," on page 162
	Switch to zoom mode.
Zoom factor	Enter a value to change the zoom factor. Click the left/right mouse buttons to zoom in/out. Drag holding the middle mouse to pan
Dynamic Pan Tracking	Check to zoom images during mouse movement or un-check to zoom after mouse button is released.
Rotate/Flip	The allow you to rotate, flip, or mirror the image.
Extract group	Active only if 3D imaging data is loaded. Refer to "Extract–Loading 3D Image Data" on page 162.

Display Settings

Option	*Selection*	*Description*
Orientation	Neurological	Display the left side of the patient is on the left side of the screen in the supine, head first position.

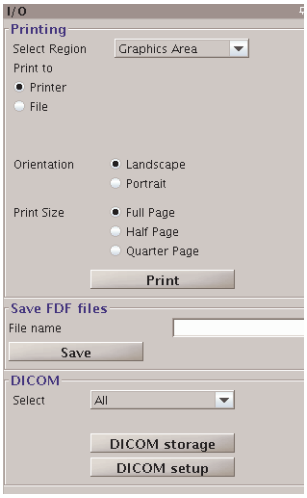
	Radiological	Display the right side of the patient is on the left side of the screen.
	Pixel order	Display is determined by the acquisition order of the data set.
Interpolation		Typical screen resolution is higher than the image resolution. Use one of the following options to determine how the acquired image is displayed.
	Replication	Default mode. The intensity of the image pixel is replicated in all the appropriate screen pixels.
	Linear	Linear interpolation between neighboring screen pixels producing a smooth transition between image pixels.
	Quadratic	Quadratic interpolation between neighboring screen pixels a smooth transition between image pixels.

I/O

Set up printing options for printing to a file or printer for hardcopy output.

- "Printing" on page 157
- "DICOM" on page 158
- "Math" on page 158

Printing



Button or field	*Selection and Description*
Selected Region	Graphics Area – print graphics area Selected Frames – print selected frames VnmrJ Screen – print entire VnmrJ screen
	Select **File** to send output to file. Enter a path or click **Browse…** and select a path. Select output format: JPEG, GIF, TIFF, or BITMAP
	Select **Printer** for hardcopy output Select **Orientation** – Landscape or Portrait Select **Print Size** – Full , Half , or Quarter Page
Print	Send output to either the printer or to file as selected in **Print to**.
Save FDF files	Save selected images and new FDF files with the user supplied filename. The filename and directory are shared between Save FDF files and Printing to a file.

DICOM

Save image data in DICOM storage format.

Menu	*Selection*	*Description*
Select	All in RQ	Stores all images in the review queue.
	Selected Frames	Stores images in selected frames.
	Selected in Review Queue	Stores the images selected through the entry fields in Review Queue.
	Select…	Open text entry field **Select images**. Enter image selections in the field.
	Group	Stores all images in the group
	Displayed	Stores all images currently displayed
DICOM storage	Sends DICOM files in the DICOM image archive server for storage	
DICOM setup	Opens the setup popup – refer to the *VnmrJ Installation and Administration* manual for more information.	

Math

The Math panel provides tool to perform image arithmetic by entering simple math expressions or functions. See Chapter 8, “Math Processing,” page 169 for information about Image Math.

Acquisition Parameter POPUP

Display acquisition parameters for selected image.

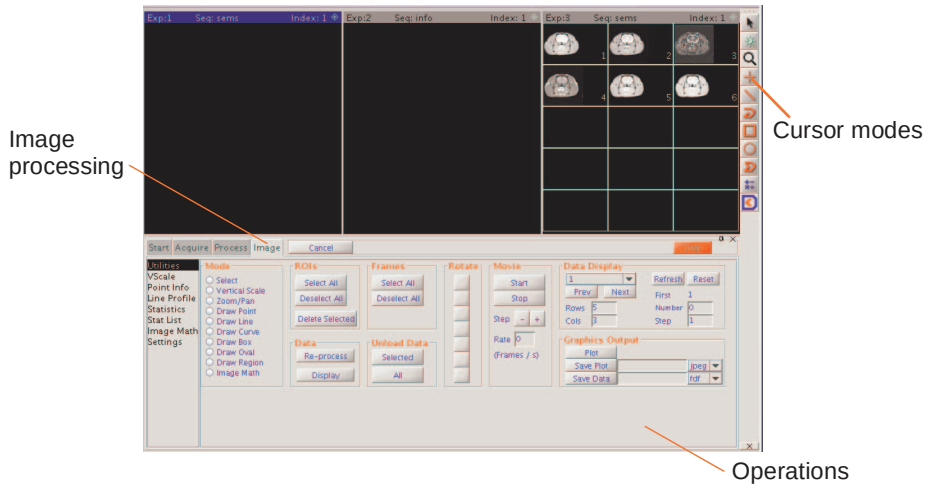
1. Click and hold the right mouse button while the pointer is over the image of interest.

   A popup window containing the acquisition parameter for the image will appear after approximately three seconds.

2. Click anywhere on the VnmrJ screen (not on the popup) to dismiss the popup.

7.2 Image Processing

Access most of the image processing tools from the **Image** panel.



Use the panel to perform the following image processing operations. For descriptions of these operations, see section 7.3 “Processing Images,” on page 161.

- **Utilities** panel has the controls for image and movie display. Use it to select and delete ROIs and images.
- **Vscale** enables you to control the “vertical scale” (intensity and contrast) of images.
- **Point info** shows information about “Point” ROIs.
- **Line profile** shows information about “Line: and “Polyline” ROIs, including a plot of image intensity as a function of distance along the line.
- **Statistics** shows information about all ROIs, including histogram plots. Use it to segment images or ROIs and save statistics summary to a file.
- **Stat List** shows file of summary statistics.
- **Image Math** performs image arithmetic, either with simple expressions or externally defined processing functions.
- **Settings** adjusts properties of the image processing interface.

Most routine actions are accessed from the **Utilities** panel and various defaults set with **Settings** panel. The remaining operations are for more specialized actions.

Using Cursor Modes

Image Processing has different “cursor modes” to perform different operations. Change modes by selecting one of the buttons along the left-hand side of the VnmrJ canvas or use an accelerator key combination to enter each mode; the accelerators are printed in the tool tips for the buttons. For example, **control+shift+V** enables the Vertical Scale mode  . Table 12 shows the key combinations for all modes.

Table 12. Key Combinations

Button	*Mode*	*Key Combination*	*Function*
	Select	control+shift+S	Selects a ROI.
	Vscale	control+shift+V	Adjusts vertical scale of images.
	Zoom	control+shift+Z	Magnifies and “pans” images.
	Point	control+shift+P	Draws a point or cursor.
	Line	control+shift+L	Draws a straight line.
	Curve	control+shift+C	Draws a polyline.
	Box	control+shift+B	Draws a rectangular box.
	Oval	control+shift+O	Draws an oval.
	Polygon	control+shift+R	Draws a polygon.
	Drag mode		Enter drag mode in review queue.
	Return		Go to image display menu.

Selecting Frames

The appropriate mode for most operations is **Select**, which is the only mode that shows the normal arrow cursor. Select a frame by going into **Select** mode and moving the mouse inside the frame of the image to change, but near the edge of the frame. The frame changes color when the mouse is correctly positioned.

- Select a frame — Click the left mouse button near the edge of the frame. Any other frames that might have selected will be deselected. Small corner tabs appear on the frame to show that it is selected.
- Toggle between a frame's selected or deselected state without affecting the selection of other frames — Click the middle mouse button on a frame.
- Toggle between the selection or deselection state of all frames — Hold down the **Shift** key and click the left mouse button on a frame. This action makes all other frames match the state of the frame that you clicked on.

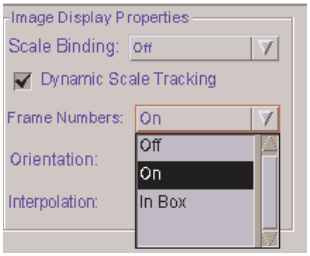


Figure 36. Showing Frames

- Show the frame number of each frame in its lower-right corner — Click on the **Settings** selection, shown in Figure 36. In the **Image Display Properties** section, click on **Frame Numbers** and select **On**.
- Select or deselect all frames at once — Use the buttons on the **Utilities** panel.

7.3 Processing Images

Use the following controls in the **Image** panel to process images:

Utilities–Controlling Image and Movie Display

Use the controls in the **Utilities** section, Figure 37, of the **Image** panel to display images.

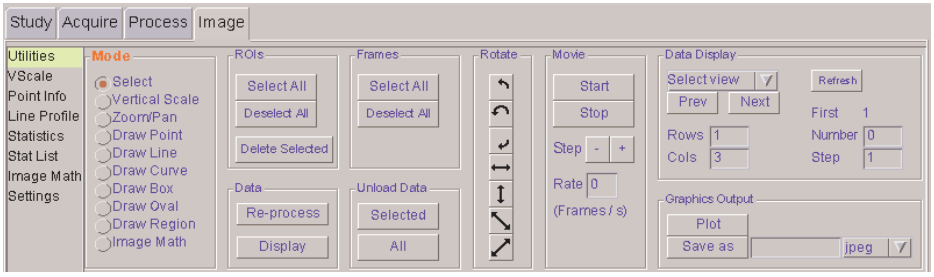


Figure 37. Utilities Panel

The **Data Display** section contains the primary viewing controls. Click on **Select view** to see a menu of choices for specifying the number of image frames into which you want the canvas divided. If none of the choices is what you want, use the **Rows** and **Cols** fields to specify an arbitrary matrix of frames. By default, the number of frames determines the number of images that will be displayed. Click on the **Next** button to see the next group of images.

Set **Number** to a positive value to limit the number of images shown. Zero is ignored and all the images the frames allow are displayed. Set **Step** to a value (2, 3, etc.) to show only every second, third, etc. image. Press the **Return** key or click on **Refresh** to see the result.

Seeing Specific Images (Movie-Step)

Use the **Movie-Step** buttons control which image are seen in each frame.

1. Select the frame to change in the **Movie** section of the panel and in the **Step** line.
2. Click the – or + button to cycle through the available images or move the mouse to the desired image while holding down both the **Control** and **Shift** buttons and left-clicking or right-clicking the mouse to select the frame and changes the image in one operation.

Removing Data (Unload Data)

Unload data that is not wanted it so that it will not show when cycling through the images. Click on **Unload Data-Selected** to remove the data shown in the selected frames, or **Unload Data-All** to remove all data.

Rotating Images

Change the displayed orientation of images in the **Rotate** section of the **Utilities** panel. The buttons rotate (positive angle is counter clock wise rotation) or flip the image in various ways suggested by the button labels. These actions always apply to all the selected images (also see the **Orientation** selection in the **Settings** panel, shown in Figure 41).

Cycling through Images

The **Movie** section in the **Utilities** panel controls viewing of the loaded images in a cinematic loop. This function cycles through all the loaded images in the selected frame at a specified rate. Any previous vertical scale and zoom adjustments are not preserved in the movie.

Extract–Loading 3D Image Data

Loading a 3D data set enables the **Extract** group of the **layout** folder. Use this page to extract 2D slices from the 3D data set. To extract images, do the following steps:

1. Choose an orientation.
2. Enter the range of slice numbers and the slice increment.
3. Click on **Extract Slices** or **Extract MIP**.

The MIP (Maximum Intensity Projection) is an image that is synthesized from all the specified slices by setting each pixel to the maximum value of that pixel over all the slices. Slice numbers run from 1 to the number of slices. A suggestion for the maximum slice number is printed to the right of the **Last Slice** entry box. It is based on the number of slices in that orientation in the current experiment which will commonly be the same size as the loaded data set.

VScale–Adjusting Contrast and Intensity

Adjust the contrast and intensity (window and level) of images with the middle mouse button. Clicking the middle mouse button on an image sets the image contrast to make the point under the cursor white. Hold down and drag the middle button to adjust both the contrast and intensity. Dragging the mouse back and forth changes the contrast; dragging it up and down changes the intensity. To automatically scale an image, hold down the **Control** key and click anywhere on the image with the middle mouse button.

An additional feature is available by going into the **Vertical Scale** mode  . The cursor becomes a sun. In this mode, the left mouse button duplicates the actions of the middle mouse button. Furthermore, clicking the right mouse button makes the selected point appear as black.

Vertical scaling might affect only the image that you click on or it might affect multiple images. Control how many images are vertically scaled with **Scale Binding** in the **Image Display Properties** section of the **Settings** panel. Choose **All Frames** to make scale changes apply to all the displayed images. Choosing **Selected Frames** changes all selected

images when clicking on any selected image. Selecting **Off** limits rescaling to the image that are clicked on.

Detailed control of vertical scaling is available in the **VScale** panel, shown in Figure 38. To open the panel, click on **VScale**.

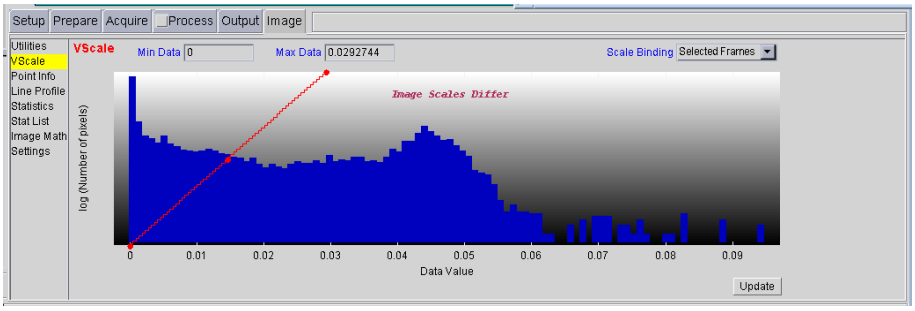


Figure 38. Image Colormap Window

Use the controls in the **VScale** panel to:

- Manually set the data values that correspond to the black and white levels (respectively, **Min Data** and **Max Data**).
- Modify the shape of the data-value-to-intensity-transfer-function to enhance the contrast at the low or high end of the intensity scale.

The **VScale** page has a graph that shows, as a red line, the data value (on the *x*-axis) versus screen intensity (on the *y*-axis). In the background, the graph has a histogram showing the (logarithm of the) number of image pixels in each interval of data values. All the selected images are included in the histogram. If no images were selected, all the displayed images are included in the histogram. Use the mouse to drag the control points on the graph. Changes that you make in this panel apply to all the selected images or, if you do not select any images, to all displayed images. The **Scale Binding** menu in the **VScale** page is duplicated in the similarly named portion of the **Image Display Properties** section on the **Settings** page.

Magnifying the View

Click on  to enter the zoom mode (the cursor becomes a magnifying glass) and magnify the view of a specific region of an image by zooming in on it.

Zooming In

Click the left mouse button on a point in an image to zoom in on that point. Each click of the mouse button increases the zoom scale by a factor selected in the **Settings** panel. Use the **Zoom Factor** menu in the **Zoom and Pan** section to select the magnification factor.

Zooming Out

Click the right mouse to zoom out by the same factor.

Centering a Zoomed Image

Recenter the image in the frame (pan) by holding down the **Shift** key, clicking the left mouse button, and dragging the image or by dragging the image with the middle mouse button.

Zooming and Panning Multiple Images

Bind panned and zoomed images so that when one image manipulated the changes are made to all other images or selected images.

1. Select the **Settings** panel.
2. Select the **Binding** menu in the **Zoom and Pan** section.
3. Select **Off**, **Selected Frames**, or **All Frames**.
4. Select whether “bound” images track the image being panning in real time or are only updated when the mouse button is released.

Point Info–Getting Information on Point ROIs

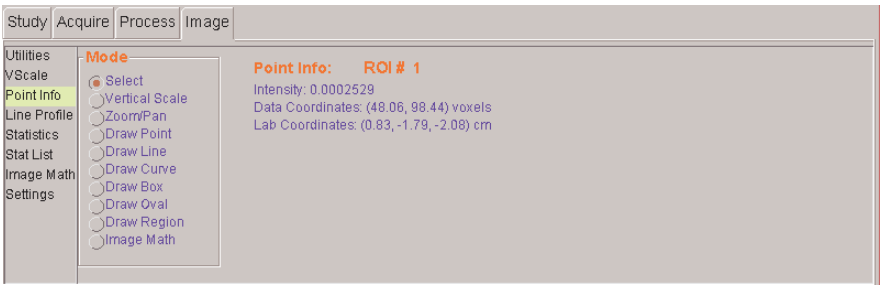


Figure 39. Point Info Panel

This section of the **Image** panel, shown in Figure 39, shows additional information about point ROIs. The information is about the point that was most recently created, modified, or selected with a left mouse click. The Intensity (data value), Data Coordinates (*x*, *y* position in the data matrix), and Lab Coordinates (position with respect to the magnet isocenter) are displayed for that point. If you draw a second point, the panel also shows the distance between the current point and the previous point that had data displayed. Both the actual distance in 3D space is shown and the distance from the projection of the previous point onto the current image plane.

Line Profile–Getting Information on Line and Curve ROIs

This section of the **Image** panel, shown in Figure 40, shows information that is specific to line and curve ROIs. The information is about the line or curve that was most recently created, modified, or selected with a left mouse click. The primary display is a plot of data values along the line. For lines, selecting the **Show MIP** toggle button switches the profile

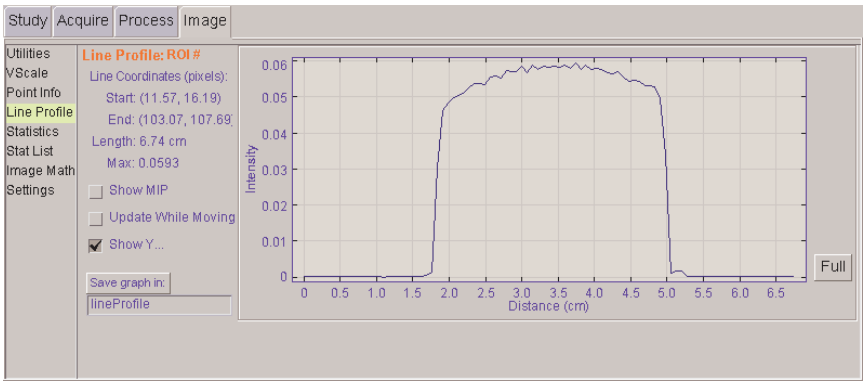


Figure 40. Line Profile Panel

display to a maximum intensity projection of image intensities onto the line. Clicking the **Save graph in** button saves the plot data in a file with a specified name. If you are in a study, the file is put the current study directory; otherwise, the data goes into the current experiment directory.

Statistics–Getting Information About ROIs

This panel shows information about selected ROIs. If you select only one ROI, it displays a histogram of the intensities (or data values) within that ROI (see "Scatterplots" on page 165 if you select more than one ROI). In addition, **Statistics** lists various summary statistics about the ROI such as mean voxel data value, area, and volume of the ROI. The statistics and the graph are updated when the ROI is modified. If you select **Dynamic Update**, the statistics and graph are updated in real time as you drag around the ROI.

Histograms

Select the resolution of the histogram (the number of intensity bins that it is divided into) from the **Settings** panel. The range of intensities covered can be selected in the **Statistics-Histogram limits** section of the **Statistics** panel. This setting specifies the range of values plotted on the *x*-axis of the histogram plot. It also limits which voxels are considered in the printed ROI Statistics values. Voxels with data values outside of the limits are not included in the averages or in the area or volume calculations.

Segmenting Images

Set cursors on the histogram to indicate a range of intensities to keep while voxels with data values outside this range are reset to zero. Set the left and right cursor positions by left-clicking or right-clicking the mouse on the histogram plot. Then click on one of the **Do segmentation of:** buttons at the bottom of the panel.

- **Images** operates on all selected images and zeros all voxels in the image with values outside the range.
- The **ROIs** buttons zero all the voxels outside the specified range and operate on all images with a selected ROI. **ROIs (Clear Bkg)** also zeros everything outside of the selected ROIs, while the **ROIs (Keep Bkg)** button preserves all voxels that are outside the selected ROIs.

Scatterplots

Select more than one ROI and the **Statistics** panel displays a scatterplot showing some summary statistics as a function of ROI. Use the **Scatterplot Axis Values** menus to select what to plot. Save the graph data (for either histograms or scatterplots) in a text file by clicking the **Save graph in** button.

Stat List–Seeing Statistics

Save the summary statistics in a text file by first filling in a file name and then clicking the **Save stat** in button. View the contents of this file by clicking on the **Stat List** button.

Image Math–Entering Math Expressions or Functions

The Math panel provides tool to perform image arithmetic by entering simple math expressions or functions. See Chapter 8, "Math Processing," page 169 for information about Image Math.

Settings–Adjusting Image Processing Properties

Use the **Settings** panel, shown in Figure 41, to adjust properties of the image processing interface.

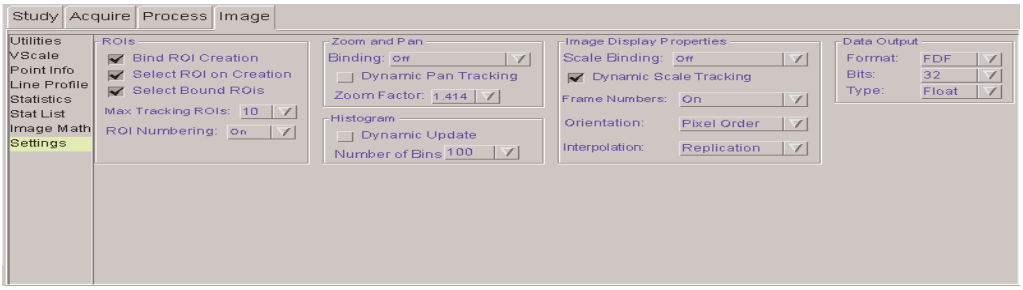


Figure 41. Settings Panel

The **Orientation** button enables you to select the orientation of displayed images.

- Selecting **Pixel Order** shows the fast data direction from left to right and the slow data direction from top to bottom.
- **Neurological** puts the subject's right to the right of the screen.
- **Radiological** puts the subject's right to the left of the screen.

The **Interpolation** button in the **Image Display Properties** section of the panel enables selection of how displayed screen pixel intensities are interpolated when the data voxels cover more than one screen pixel. Click the arrow to see more interpolation choices. The selection **Replication** shows each data voxel in a solid color. **Linear** or **Quadratic** interpolate pixel values between nearby data points.

Zoom and Pan Settings

Adjust the behavior of the Zoom/Pan mode  with the controls in the **Zoom and Pan** section of the **Settings** page. Use the **Binding** menu to choose whether changes made to one image affect only that image, apply to all images, or apply to all selected images. Only the selected image with the cursor on moves in real time while dragging the mouse and panning an image to move many images at once; the other images are updated after the mouse button is released. Select **Dynamic Pan Tracking** to make all images update in real time. Use the **Zoom Factor** menu to choose how much to zoom in or zoom out when you click the left or right button.

7.4 Advanced Image Processing Commands

Table 13 lists advanced image processing commands.

Table 13. Image Processing Commands

Command	*Function*
`aipDeleteData` or **`aipDeleteData('sel')`**	**`aipDeleteData`** unloads all image data from memory and clears the screen. **`aipDeleteData('sel')`** deletes data that is displayed in the selected frames and clears the selected frames. If the same data is deleted in two frames (only one of which is selected), the data is still available as long as it remains displayed in that frame. But, it will be unloaded from memory as soon as that frame is cleared or another image is displayed.

Table 13. Image Processing Commands (continued)

Command	*Function*
aipDeleteFrames	Clears the screen.
aipDeleteRois	Deletes all selected ROIs.
aipDisplay	Displays as many of the loaded images as will fit in the existing frames. If there are no existing frames, it splits up the screen into at least **aipFrameDefaultMax** frames with a split that is appropriate for the aspect ratio of the first image.
aipDisplay('all')	Clears the currently displayed data, resplits the screen into enough frames to show all the loaded images, and displays all the images. Makes a screen split that is appropriate for the aspect ratio of the first image.
aipDisplay('redisplay')	Redraws everything exactly as it was last drawn.
aipDisplay('batch' [,'first] [,'last] [,'next'] [,'previous] [,'show'])	Displays a "batch" of images in the existing frames according to the values in the parameter **aipDisplay[1:3]**. **'show'** must be present for anything to actually be displayed. **'first'** initializes the display to the first batch of images. **'last'** initializes the display to the last batch of images. **'next'** updates **aipDisplay[1]** (the number of the first image to show) to show the next batch before the images are displayed. Updating is done after any **first** or **last** operation. **'previous'** updates **aipDisplay[1]** to show the previous batch before the images are displayed. Updating is done after any **first** or **last** operation. The order of the arguments is unimportant. Normally, use **'show'** alone to do a redisplay function, or one of the **first**/**last**/**next**/**previous** options plus **'show'**.
aipExtract(['xy'|'yz'|'xz'], first_slice [, last_slice [, incr]])	Extracts 2D slices from a 3D data set.
aipExtractMip(['xy'|'yz'|'xz'], first_slice [, last_slice [, incr]])	Extracts a Maximum Intensity Projection from a 3D data set.
aipFlip(0 | 45 | 90 | 135)	Reflects the image display about an axis with the specified orientation.
aipLoadDir(dirpath)	Loads all images in the specified directory. It does not delete already loaded data. Image files must be in FDF format.
aipLoadFile(filepath)	Loads an image in the specified file. It does not delete already loaded data. Image files must be in FDF format.
aipMathExecute or **aipMathExecute(parname)**	Executes an Image Math expression. Without an argument, it executes the current expression. With a string argument, it interprets the string as the name of a GLOBAL string parameter and uses the string stored in that parameter as the math expression.
aipPrintImage	Sends the images in all selected frames to a DICOM printer. The displayed area of the data is scaled according to the value of the **aipPrintScale** parameter, which is in percent. That is, if the display part of the image measures 120 by 150 voxels on the original data, and **aipPrintScale=200**, and an image of 240 by 300 pixels is sent to the printer. The current vertical scaling is also applied to the printer image.
aipRotate(90 | 180 | 270 | -90)	Rotates the image counter-clockwise by the indicated number of degrees. (The arguments **270** and **-90** are equivalent.)

Table 13. Image Processing Commands (continued)

Command	*Function*
aipSegment('r[oi]') or **aipSegment('i[mage]')**	Performs image or ROI segmentation on selected ROIs or images.
aipSelectFrames('all' | 'none')	Selects or deselects all frames, depending on whether the argument is **all** (the default) or **none**.
aipSelectRois('all' | 'none')	Selects or deselects all ROIs, depending on whether the argument is **all** (the default) or **none**.
aipSetDebug	Not for general use.
aipSetExpression	Not for general use.
aipSetState(mode_number)	Sets the mouse mode to the given integer value.
aipSetVsFunction	Not for general use.
aipSomeInfoUpdate	Updates the line profile and point information.
aipSplitWindow	Clears the screen and splits it into some number of windows. With no arguments, it splits the screen into enough frames to display all the currently loaded data, up to the limit specified by the user **("aipFrameDefaultMax")**. You might get a few more frames if that is the efficient way to split up the screen.
aipSplitWindow(n)	Splits the window into at least **n** frames.
aipSplitWindow(r,c)	Splits the window into **r** rows by **c** columns.
aipSplitWindow(n,w,h)	Makes at least **n** frames, splitting the screen optimally for images with an aspect ratio of **w**/**h** (width and height).
aipSplitWindow('all' [,w,h])	Makes at least enough frames to display all the loaded images. Specify **w** (width) and **h** (height) to specify an aspect ratio of **w**/**h**. The default aspect ratio is **1**.
aipStatUpdate	Recalculates the data for the ROI Statistics page.
aipTestListener	Not for general use.
aipTestMouseListener	Not for general use.
aipWriteData	Writes out selected images in various formats. The format is controlled by the parameter **aipWriteFmtConvert**. The output file is named according to the parameter **aipWritePath**, which is appended with a serial number indicating the selected frames that it came from. The string parameter **aipWriteFmtConvert** contains a format ID, followed by a space, followed by a shell script to convert FITS output data into the desired format. The script uses **"$1"** to signify the input file and **"$2"** to indicate the base path of the output file. The script should append an appropriate suffix to the output file, such as **.gif**.
continueMovie(speed)	Continues movie from frame where `stopmovie` command was issued.
resetMovie(speed)	Stop movie and end movie mode, reset conditions to state prior to the start of the movie.
startMovie(speed)	Shows a movie of selected images in the first selected frame. The frame rate is **speed** frames per second.
stepMovie('+' | '-')	Goes to the next (**+**) or previous (**-**) frame in a movie.
stopMovie	Stops a currently running movie.

Chapter 8. Math Processing

Sections in this chapter:

Operations in image math are defined as either expressions or functions:

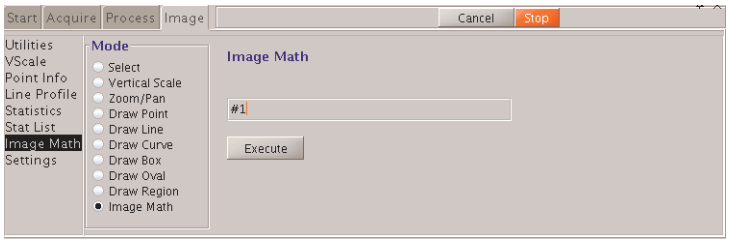
- *Expressions* are specified by typing any legal C expression into the **Image Math** page, using symbols such as `#5` to specify images. The expression is applied to each data pixel, and each output data pixel value is a function of the values of the corresponding data pixels in the input images. Operations can involve an arbitrary number of input images, as well as the X and Y coordinates of the data pixel within the image.
- *Functions* are used for operations that cannot be specified in a single expression and are written in the form of a C subroutine.

Image math works on either 2D or 3D data sets. The image operands must all be the same size for operations with expressions.

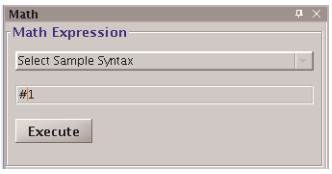
8.1 Opening Image Math

To run Image Math, do the following:

1. Click on **Image Math** to open the Image Math page.



2. Do either of the following:
   - Type an expression or function in the field.
   - Select Math from the vertical panel, click on **Select Sample Syntax** menu, and retrieve a predefined function and use it as an example.



3. Specify which images are to be operated on by the expressions or functions.

Images are specified by their graphic frame (Gframe) numbers using symbols (such as `#n`) in which `n` is the number of a Gframe containing an image. The graphical frame number and image numbers may not be the same.

4. Use the following procedure to automatically enter Gframe numbers:

   a. Open the **Image Math** page.

   b. Click the mouse cursor inside a Gframe.

   The number of that frame is entered in the Image Math equation area at the current cursor location. If the cursor is positioned just after a #, only the Gframe number is entered, and any preexisting number is deleted; otherwise, a # and the Gframe number are inserted.

8.2 Image Math Expressions

Legal expressions are in the form of standard C expressions, with the image specifiers, `#n`, treated like "float" type C variables in evaluating the expression. For example, the following expression calculates the average of the images in Gframes 1, 2, and 3 and puts the result in Gframe number 4:

```
#4=(#1+#2+#3)/3
```

Click on the **Execute** button to carry out the operation after typing the expression. The expression is evaluated for each data pixel to calculate the output image.

The first time an expression is entered and executed, it is edited and inserted into a C program, which is then compiled and stored in the directory `$INITDIR/math/expressions/bin` as a dynamically loadable library. This library is then linked to the running VnmrJ program, and the input images are passed to the routine containing the user's new expression. This routine calculates the output image and then returns to VnmrJ, which loads it into the appropriate Gframe. Finally, the library is unloaded. If the same expression is used a second time, possibly with different image numbers, the compilation step is skipped in the above sequence, because the precompiled program can be used.

Variables Used in Image Math Expressions

Certain variables can be used in an expression. Variables `i`, `j`, and `k` respectively contain the column, row, and plane of the current data pixel, as shown in this example:

```
#3 = abs(i-j)<30? #1 : #2
```

This expression copies a 60 pixel wide diagonal band of image #1 into Gframe #3 and sets the rest to image #2. An expression should not modify `i`, `j`, or `k`.

The C construct "*expression0? expression1:expression2*" is a compound expression that returns the value of *expression1* if *expression0* is true (or nonzero) and the value of *expression2* otherwise. The variables width, height, and depth contain the number of columns and rows in the image. For example, the following expression copies image #1 to Gframe #2, leaving a 6-pixel-wide border of zeros around the edge:

```
#2=i>5&&i<width-6&&j>5&&j<height-6?#1:0
```

An expression should not modify width, height, or depth.

These `i`, `j`, `k`–width, height, and depth–variables appear to make it possible to construct a synthetic image without any input image. However, some input image is required in order to establish image parameters such as width and height, as well as everything else that is in the file header, for example:

```
#2=(#1,exp(-((width/2-i)*(width/2-i)+(height/2-j)*
   (height/2-j))/2500.0))
```

This expression creates a Gaussian spot in the middle of the image that is 100 data pixels wide. The output image has the same shape and size as image #1. Note that the denominator 2500 is written in floating point (2500.0) so that the division does not give truncation errors and that the `exp()` function gets a float type argument, as it expects.

The C construct "*var=(expression1,expression2)*" is used in the previous example. Expressions in parentheses are evaluated left to right and only the value of the last expression is kept. So, in this case, *var* is set equal to the value of *expression2*. In this example, the value *expression1* is only a dummy to give the program information about the image format, but it could affect the final value; for example, `var=(x=2,x+3)` sets `var` equal to `5` and `x` equal to `2`.

Finally, there are variables available for temporary storage that are not preassigned any values. The variables `x`, `y`, `z`, and `r[0]` through `r[99]` are available for you to store floating point values. The variables `ii`, `jj`, `kk`, and `n[0]` through `n[99]` are integer variables. These variables can be used for efficiency, to avoid recalculating complicated expressions, as in the following example:

```
#2=(#1, x=width/2-i, y=height/2-j, exp(-(x*x+y*y)/2500))
```

In this example, unlike the previous example, 2500 is written as an integer, because temporary variables `x` and `y` are floats that force the division to be done in floating point. Using temporary variables like this often makes expressions more readable.

8.3 Image Math Functions

Sometimes you might need to perform an operation that cannot be put into a single C expression; such cases require user functions. An Image Math function is distinguished from an expression simply by whether the first field to the right of the equals sign is the name of an existing function. The following example shows how user function `foo` is activated:

```
#11 = foo ##1-8 "bar" 7
```

The expression calls `foo`; passes it images 1 through 8, the string `bar`, and the number `7` as input; and puts the output of `foo` in frame 11.

Image Math function specifications are not parsed as C expressions, so the syntax format is not strictly defined. Use the style in the last example to assure compatibility with future versions of image math. Double quotation marks are required around every string argument to be passed.

Specifying Images in Functions

Image Math functions allow lists, or "vectors," of images to be specified. The following form is the most general form for specifying an image vector:

```
#(image_list)
```

`image_list` is a list of frame numbers separated by commas, and optionally including ranges of frame numbers denoted by hyphens.

The statement:

```
#11 = maxof #(1,3,8-10,6)
returns the maximum of images 1, 3, 8, 9, 10, and 6.
```

The simple `#3` notation, as used in Image Math expressions, specifies a vector with one element, and is equivalent to `#(3)`. If the vector only contains one range of consecutive frame numbers, it can be abbreviated as `##1-10`.

A construction like `#1 #3 #8 #9 #10 #6` does *not* specify a vector of images but rather six vectors, each containing one image. Programs, such as `maxof`, treat the two cases identically, but others, such as `fit` discussed on page 179, do not.

Image Math functions can also produce more than one output image. Specify the output images as an image vector:

```
##11-12 = maxof ##1-10
```

In this example, `maxof` writes the maximum intensity image to frame 11 and writes a map of which image had the maximum intensity for each pixel in frame 12. The following construction produces only one output image; the `#12` frame is ignored:

```
#11 #12 = maxof ##1-10
```

A vector of images is specified any of three ways:

- `#1` specifies a vector with one element.
- `##1-10` specifies a vector with a single range of image numbers.
- `#(1-10,21,31)` specifies a vector with an arbitrary list of images.

Creating a New Image Math Function

Defining the `maxof` function involves defining a function called `mathfunc` in a file named `maxof.c`. (The process is similar to defining a user pulse sequence by defining the `pulsesequence` function in a file named after the sequence.) Function files are kept in the directory `$INITDIR/math/functions/src`. The following procedure is an example of how you would define the file `maxof.c`, shown in Figure 42, in that directory.

Entering a File Header

First, enter the following line at the beginning of the file:

```
#include "imagemath.h"
```

`imagemath.h` declares the global variables and functions needed to access the input and output images (`imagemath.h` also includes the most commonly needed standard UNIX headers, including `math.h`).

Defining the mathfunc Function

Next, define the `mathfunc` function. `mathfunc` first checks to see if the input being passed is valid. If the input is not valid, `mathfunc` returns a FALSE value to the caller (if the function encounters no errors, `mathfunc` should return TRUE). Be aware that `nbr_infiles` and `input_sizes_differ` are global variables declared in `imagemath.h` and get set before the `mathfunc()` subroutine is called.

The `maxof` math function also calls the `want_output()` routine to ensure that there is someplace to put the first output image; `want_output(n)` returns TRUE if you have asked for the `n`th output image. The first image number is `"0"`.

Setting Image Dimensions

Input images are all the same size (`input_sizes_differ` is FALSE) store their common dimensions are in the global variables `img_width`, `img_height`, and `img_depth`. The product of these three variables is in `img_size`. Functions that handle input images of different sizes require the arrays `in_width[]`, `in_height[]`, `in_depth[]`, and `in_size[]`. These arrays determine the width, height, depth, and

```
/*@(#)maxof.c 1.3 06/27/97 (c)1997 Varian Associates*/
#include "imagemath.h"

int
mathfunc()
{
    int i;
    int j;
    int imgnbr;
    float ymax;

    if (nbr_infiles<1 || input_sizes_differ ||!want_output(0)){
        return FALSE;
}
    create_output_files(2, in_object[0]);

    for (i=0; i<img_size; i++){
        imgnbr = 0;
        ymax = in_data[0][i];
        for (j=1; j<nbr_infiles; j++){
            if (ymax < in_data[j][i]){
                ymax = in_data[j][i];
                imgnbr = j;
           }
        }
        out_data[0][i] = ymax;
        if (want_output(1)){
            out_data[1][i] = imgnbr + 1;
        }
}
    return TRUE;
}
```

Figure 42. `maxof.c` File

size for each individual image (unless otherwise mentioned, all arrays start indexing from 0, in typical C fashion).

Allocating Memory

The `create_output_files()` function allocates memory for all the requested outputs, making them all the same size as the input images. `maxof` limits the number of output images to two, and gives images header characteristics like those of the first input image.

Pixel Looping

The `maxof` function then loops over all the pixels in the input images:

- `img_size` has the number of pixels per input image.
- `nbr_infiles` has the number of images.
  The `nbr_infiles` variable has the total number of images in all input image vectors. To access individual image vectors, use the variable `nbr_image_vecs`, which provides the number of image vectors, and the array `in_vec_len[]`, which provides the number of images in each vector.
- `in_data[j][i]` has the `i`th pixel in the `j`th input image.

The maximum value in the ith pixel is written to the first output image, addressed as `out_data[0][i]`. Check the desired output number 0 at the beginning of the routine when defining `mathfunc`. Determine if output number 1 is required and, if it is required, write the index of the image with the maximum value in output image number one.

- `IN_DATA(i,j,k)` references the kth pixel of the jth image in the ith vector.

Compiling a New Function

Creating and compiling a new Image Math function is done manually. Familiarity with the basics of the `make` utility is a prerequisite for users who write their own math functions. Back up the `$INITDIR/math/functions/src` directory before preceding. All of the original files are available in: `/vnmr`.

Create a function using the following procedure:

1. Create a file that defines the function `mathfunc` (e.g., `myfunc.c`). This file must reside in the `$INITDIR/math/functions/src` directory.
2. Edit the make file to add `myfunc.c` to the list of source files.

   The `make` files for various operating systems are:

   - Solaris — `makemathfunc`
   - Linux — `makemathfunc.lnx`.

   The `make` macro variable `USRSRC` is a list of the source files for simple user programs, those that only involve one source file.
3. Use a text editor to modify the definition of `USRSRC` in the file `makemathfunc` to include the new function, for example: `USRSRC = maxof.c myfunc.c`

   Put a backslash (\) as the last character on the line to continue on the next line if the list exceeds a single line.
4. Add a target section in the make file that performs the same task as the other simple file targets; copy one of the existing targets and replace the file name as appropriate: Example, the target section for `snr` is:

   ```
   snr: ufuncs.o snr.o
      $(CC) -o snr -m32 -fPIC ufuncs.o snr.o $(LIBFLAG)
      rm -f $(BINDIR)/snr
      ln -s $(SRCDIR)/snr $(BINDIR)/snr
   ```

   For a function called `myfunc`, the target section becomes;

   ```
   myfunc: ufuncs.o myfunc.o
      $(CC) -o myfunc -m32 -fPIC ufuncs.o myfunc.o
      $(LIBFLAG)
      rm -f $(BINDIR)/myfunc
      ln -s $(SRCDIR)/myfunc $(BINDIR)/myfunc
   ```

   Note how all instances of the string `snr` are changed to `myfunc` (7 times). Note also that per the rules for make files, a tab character – not spaces – must precede the commands in the target sections.
5. Make sure that the file Makefile is a symbolic link to `makemathfunc` for Solaris, or `makemathfunc.lnx` for Linux
6. Edit the file.
7. Enter the following command: **`make depend`**

This command updates the list of files that the program depends on and changes the makemathfunc file (a warning `fit.c` includes `userfit.c` more than once! appears, which is normal.). Enter `make depend` only after you change `#include` directives in a file or change the makefile itself.

8. Enter `make myfunc` to compile the `myfunc` routine.

Variables, Macros, and Functions Available to User Functions

This section lists global variables, macros, and functions for use in `mathfunc` routines.

Global Variables

Except where noted, global variables are initialized before `mathfunc` is called.

`int nbr_image_vecs`	Number of image vectors passed to the user's program.
`int in_vec_len[]`	Array of length `nbr_image_vecs` giving the number of images in each input image vector.
`int vecindx[]`	Array of length `nbr_image_vecs` giving the index in the `in_object[]` and `in_data[]` arrays of the first member of each image vector. The rest of the members of a given vector sequentially follow in those arrays.
`int nbr_infiles`	Number of input images in all the image vectors put together.
`int input_sizes_differ`	Set to TRUE if the input images are not all identical in size. If the images are all the same size, it is set to FALSE.
`int img_width, img_height, img_depth,img_size`	If all input images are identical in size, these arrays have their dimensions. The `img_size` is the total number of data pixels.
`int in_width[], in_height[], in_depth[],in_size[]`	If input images vary in size, use these arrays to get the sizes of the individual images. The dimension of these arrays is `nbr_infiles`.
`FDFptr in_object[]`	Array of dimension `nbr_infiles` containing pointers to all the input image structures, and which can be treated either as a single array, containing every input image in every image vector, or as several arrays placed "end-to-end," one for each image vector. The starting index of each vector in the whole array is given in `vecindx[]`.
`float *in_data[]`	Array of dimension `nbr_infiles` containing pointers to all the input data arrays, and which can be treated either as a single array, containing every input image in every image vector, or as several arrays placed "end-to-end," one for each image vector. The starting index of each vector in the whole array is given in `vecindx[]`.
`int pixel_indx`	Used in the `fit` program to indicate which pixel is currently being `fit`. It can be referenced by the user's FUNCTION, JACOBIAN, or GUESS routines.
`int nbr_strings`	Number of strings passed to the user's function.
`char *in_strings[]`	Array of dimension `nbr_strings` containing pointers to all the strings passed to the user's function.
`int nbr_params`	Number of numerical constants passed to the user's function. In the `fit` program, this is modified in `fit.c` so that it does not reflect any threshold value that might have been passed.

`float in_params[]`	Array of dimension `nbr_strings` containing all the numerical values passed to the user's function. In the `fit` program, this variable is modified in `fit.c` so that it does not reflect any threshold value that might have been passed.
`int nbr_outfiles`	Number of output files that caller has requested from user function. In the `fit` program, this variable can be adjusted downward if more output files are requested than `fit` knows how to supply.
`int out_width[], out_height[], out_depth[], out_size[]`	Arrays of dimension `nbr_outfiles` that have the size of each output image. These arrays are initialized to match the size of the last input image, but you can adjust them before calling `create_output_files()`.
`FDFptr out_object[]`	Array of dimension `nbr_outfiles` containing pointers to all of the output image structures. It is initialized by `create_output_files()`.
`float *out_data[]`	Array of dimension `nbr_outfiles` containing pointers to all of the output image data arrays. It is initialized by `create_output_files()`.

Macros

`IN_DATA(vec,img,pixel)`	References pixel number `pixel` in image number `img` in input image vector number `vec`.
`TRI_ELEM(matrix,row,col)`	(In `fit` routines only). If `matrix` stores the lower triangle of a symmetric matrix, references the matrix element in row `row` and column `col`. Requires `row >= col`.

Functions

`FDFptr clone_ddl`	Makes an identical copy of the image structure `old_ddl`. If `dataflag` is FALSE, only the header values are copied, otherwise the data are also copied. Function Prototype: `FDFptr clone_ddl (FDFptr old_ddl, int dataflag)`

`FDFptr create_ddl`	Creates an image data structure of the given width, height, and depth, and returns a pointer to the structure. Function Prototype:
	`FDFptr create_ddl(int width, \`
	`int height,int depth)`

`int create_output_files`	Creates up to `n` output `files` (actually, just data structures in memory). File sizes are given by `out_width[]`, `out_height[]`, `out_depth[]` arrays. This function loads `out_object[]` and `out_data[]` with pointers to the data structures and data arrays, respectively. Function Prototype: `int create_output_files (int n, FDFptr cloner)`

`void *getmem`	Equivalent to system `malloc()` function, except that any memory allocated this way is freed when the user function is done. `size` is the number of bytes of memory to allocate. Function Prototype: `void *getmem (size_t size)` ***CAUTION:* Do not use `free()` to release memory allocated by `getmem()`.**
`int want_output`	Returns TRUE if output image number `n` is requested. If three images are specified for output in the Image Math command line, `want_output(n)` returns TRUE if `0<=n<=2`; otherwise, this function returns FALSE. Function Prototype: `int want_output(int n)`

`get_header_int`	Gets the value of an integer-type header variable. The variable `name` is read from the image referred to by `handle`. The value of the variable is put into the integer pointed to by `pvalue`. Returns a logically true (nonzero) value on success, and a logically false (zero) value on failure. Function Prototype:
	`int get_header_int(handle, \`
	`  name,pvalue)`
	`FDFptr *handle;`
	`char *name;`
	`int *pvalue;`

`get_header_double`	Gets the value of an double-type header variable. The variable `name` is read from the image referred to by `handle`. The value of the variable is put into the location pointed to by `pvalue`. Returns a logically true (nonzero) value on success, and a logically false (zero) value on failure. Function Prototype:
	`int get_header_double(handle, \`
	`  name,pvalue)`
	`FDFptr *handle;`
	`char *name;`
	`double *pvalue;`

`get_header_string`	Gets the value of an character-array-type header variable. The variable `name` is read from the image referred to by `handle`. A pointer to the character string is put into the location pointed to by `pstring`. Returns a logically true (nonzero) value on success, and a logically false (zero) value on failure. Function Prototype:
	`int get_header_string(handle, \`
	`  name,pstring)`
	`FDFptr *handle;`
	`char *name;`
	`char **pstring;`

`get_header_array_int`

Gets the value of one element of an integer-array type header variable. The `index` member of the variable `name` is read from the image referred to by `handle`. The value of the element is put into the location pointed to by `pvalue`. Returns a logically true (nonzero) value on success, and a logically false (zero) value on failure. Example:

```
int get_header_array_int  \
(handle,name,index,pvalue)
FDFptr *handle;
char *name;
int index;
int *pvalue;
```

`get_header_array_double`

Gets the value of one element of a header variable that is an array of doubles. The `index` member of the variable `name` is read from the image referred to by `handle`. The value of the element is put into the location pointed to by `pvalue`. Returns a logically true (nonzero) value on success, and a logically false (zero) value on failure. Example:

```
int get_header_array_double  \
   (handle,name,index,pvalue)
FDFptr *handle;
char *name;
int index;
double *pvalue;
```

`get_header_array_string`

Gets the value of one string from a header variable that is an array of strings. The `index` string from the variable `name` is read from the image referred to by `handle`. A pointer to the character string is put into the location pointed to by `pstring`. Returns a logically true (nonzero) value on success, and a logically false (zero) value on failure. Example:

```
int get_header_array_string  \
   (handle,name,index,pvalue)
FDFptr *handle;
char *name;
int index;
char **pstring;
```

`get_image_width`

Returns the number of pixels in the *fast* image dimension. Function Prototype:

```
int get_image_width(handle)
FDFptr *handle;
```

`get_image_height`

Returns the number of pixels in the *medium* image dimension. Function Prototype:

```
int get_image_height(handle)
FDFptr *handle;
```

`get_image_depth`

Returns the number of pixels in the *slow* image dimension. Function Prototype:

```
int get_image_depth(handle)
FDFptr *handle;
```

`get_object_width`

Returns the width of the region imaged, in centimeters. Function Prototype:

```
double get_object_width(handle)
FDFptr *handle;
```

`get_object_height`	Returns the height, in cm, of the region imaged. Function Prototype:
	`double get_object_height(handle)`
	`FDFptr *handle;`

`get_object_depth`	Returns the depth of the region imaged, in centimeters. Function Prototype:
	`double get_object_depth(handle)`
	`FDFptr *handle;`

`get_dll_data`	Returns a pointer to the array of floats that represent the image. Function Prototype:
	`float *get_ddl_data(handle)`
	`FDFptr *handle;`

8.4 The fit Program

The `fit` program is provided as a general-purpose routine to fit a function to a series of images. Output is one or more images that give the parameter value as a function of pixel location. Add new functional forms to be fit, as described in "Adding New Functional Forms" on page 181.

For example, to run the `fit` program on T_1 data, type the following statement in the Image Math window:

```
##11-17 = fit ##1-8 "t1" "ti" .01
```

Look at the first two fields:

- `##11-17` specifies the *number of output images*, in this case, seven. These images contain, respectively, the three parameters of the fits, the RMS residuals, and the formal sigmas of the parameters. Reduce calculation time by asking for fewer output images. In this example, images that not asked for are not calculated. In practice, residuals take negligible time to calculate, and parameter sigmas increase the calculation time by less than a factor of two.
- The first field to the right of the equal sign (=), in this case, `fit`, is the *name of the program to run*. Since `fit` exists in $INITDIR`/math/functions/bin`, Image Math does not try to parse the name as an Image Math expression.

The remaining fields are passed to the `fit` program:

- `##1-8` is the *list of input images*.
- `t1` is the *type of fit* required. (`t1` does *not* need to be the first string parameter. Rather, the first string that names a known fit type is taken as the fit type specification.)
- `ti` is the *independent variable of the fit*, whose value is found in the header of the input images. Often, the desired independent variable values are put in the header when the image files are created (with `svib`), because any arrayed parameters will have their values put in. If the header parameter name happens to be the same as the fit type, enter the same string twice.
- Parameter `.01` is the *threshold value*. Pixels that have values in all the images with absolute value less than the threshold return zeroes in the output images. The default is 0.

Other string arguments can be entered on the command line:

- The string `quick` can be used to force nonlinear fits to bypass the iterative fitting procedure and use the initial guess for the parameter values as the final result. Depending on the accuracy of the initial guess function, this result might be useless, or

nearly as good as the results of the nonlinear fitting procedure. `quick` is also useful for checking the accuracy of a guessing function.

- The string `noderiv` directs the nonlinear fitting routine not to use derivatives of the fitting function with respect to the parameters that might be provided. In this case, the fitting routines will estimate derivatives numerically from finite differences. This option is mainly useful for testing.
- The strings `prev` or `noprev` are used to force the `USE_PREVIOUS_PARAMETERS` flag on or off. Be aware that `prev` breaks the `abst1` and `absqt1` routines, because their guess routines modify the data.

Types of Fits

Shown in the Table 14 are the types of fits available: `t1`, `qt1`, `abst1`, `absqt1`, `t2`, `adc`, and `shames2`:

Table 14. Fit Types

Name	*Functional Form*	*Fit Parameters* *P0*	*P1*	*P2*
`t1`	$y=(M(0)-M_o)*\exp(-t/T1)+M_o$	T1	M(0)	M_o
`qt1`	$y=A*(1-2*Q*\exp(-t/T1))$	T1	A	Q
`abst1`	$y=\lvert(M(0)-M_o)*\exp(-t/T1)+M_o\rvert$	T1	M(0)	M_o
`absqt1`	$y=\lvert A*(1-2*Q*\exp(-t/T1))\rvert$	T1	A	Q
`t2`	$y=M(0)*\exp(-t/T2)$	T2	M(0)	
`adc`	$y=M_o*\exp(-b*ADC)$	ADC	M_o	
`shames2`	$y=BV*SBV_o*\exp(-t*alpha)+PS*SBV_o*(1-\exp(-t*alpha))/(alpha*(1-hct))$	BV	PS	

- `t1` and `qt1` are alternative formulations for three parameter fits to T_1 data.
- `abst1` and `absqt1` are alternative formulations for three parameter fits to absolute value T_1 data.
- `t2` is a standard two-parameter fit to T_2 data.
- `adc` is a two-parameter fit to diffusion weighted images. The fitted parameters are the Apparent Diffusion Coefficient and the reference level.
- `shames2` is a two-parameter fit for image enhancement by a contrast agent as a function of time. The fitted parameters are for blood volume and permeability. There are three fixed parameters that can be set from the command line: `alpha`, `SBV0`, and `hct`. The following command is an example:

  ```
  #11=fit ##1-8 "shames2" "x" 0.01 0.136 0.13 0.37
  ```

  In this command line, the first constant (`0.01`) is interpreted as the *threshold level*; any pixels with an absolute intensity less than this value are not fit, but given zero values in the output images. This first constant is read by the basic fitting routine; any further constants can be read by the user function.

  The next example sets the following parameter values:

  ```
  alpha=0.136
  SBV0=0.13
  hct=0.37
  ```

  These parameters are also the default values.

Pass additional images on the command line. The first extra image is used as a baseline reference; its pixel value is subtracted from all the normal input images. The following command is an example.

```
#11=fit ##1-8 #9 "shames2" "x"
```

The `fit` routine uses `#9` as the *reference image*. Up to three more additional images can be specified to set pixel dependent values of `alpha`, `SBV0`, and `hct`; these values override any "constant" values specified on the command line, such as:

```
#11=fit ##1-8 #9 #10 "shames2" "x"
```

Now, the `fit` routine sets `alpha` differently for each pixel, according to the value in image `#10`. The `fit` routine also uses `#9` for a baseline.

User variables are defined in the second section of a fitting file as static (local to the current file). However, on compilation, all your `xfit.c` files are combined with `fit.c` into one file, so names should be unique among all fitting functions.

Adding New Functional Forms

Additional functional forms can be handled by supplying a C language file that defines the function and how to fit it. Take the following steps to add new fitting functions:

1. Create a file of C source code containing your fitting function. The format of this file is described in detail in "Function Definition Files" on page 181.
2. Edit the file `userfit.c` to include your new file.
3. Make sure that the file `Makefile` is a symbolic link to `makemathfunc`.
4. Enter **`make depend`** to update `makefile` to recognize your new file.

   The command `make depend` changes the `makemathfunc` file (a warning `fit.c includes userfit.c more than once!` appears, which is normal). Enter **`make depend`** whenever you change `#include` directives in a file or change the `makefile` itself.
5. Enter **`make fit`** to create the new version of the `fit` program.

Whenever you click on the **Execute** button in the **Image Math** panel, the current version of `fit` is loaded and executed.

Function Definition Files

By convention, your fitting files should be named `xxxfit.c`, where `xxx` is the type of `fit`. For example, the file `t1fit.c` is divided into two sections with preprocessor directives:

```
#ifdef FUNCSELECTION
first section
#else
second section
#endif
```

The first section contains a fragment of C code that selects the type of fit; several macros are defined to make the job easier (macros are indicated by ALL CAPITAL letters.) The following example is taken from `t1fit.c`:

```
IF_FITCODE("t1"){
   N_PARAMETERS = 3;
   FIT_TYPE = NONLINEAR;
   FUNCTION = exp_function;
```

```
   JACOBIAN = exp_jacobian;
   GUESS = exp_guess;
   PARFIX = t1_parfix;
   return TRUE;
}
```

These macros are defined in the following table:

IF_FITCODE	Compares your fit type string to a given string, and executes the following lines, enclosed by braces, { }, if the strings match. (Case differences are ignored in the comparison.) The bracketed lines show what needs to be done in case of a match.
N_PARAMETERS	Set to the number of parameters in the fit. In this case, the number of parameters is fixed, but it could depend on arguments on the Image Math line.
FIT_TYPE	Set to one of the following values: LINEAR is a function in the following form: `y = C(x) + P0*f0(x) + P1*f1(x) + ...` where P0 and P1 are the parameters to be estimated, and the constant C, (which might depend on x) and the functions f0 and f1 of the independent variable x are the same for every pixel. LINEAR problems are solved by calculating your "design matrix" (containing the fn(x) at each x) and inverting it to get a matrix that transforms a vector of observed (y-C) values into a vector of parameter values. Thus, matrix inversion needs to be done only once, and the calculation for each pixel simply involves subtracting the constant C from the observed y values and doing a matrix multiply. LINEAR_RECALC_OFFSET is the same as LINEAR, except that C can be a function of pixel number. In `y = C(x) + P0*f0(x) + P1*f1(x) + ...` your FUNCTION is called with a zero parameter vector for each pixel in order to reevaluate C(x). LINEAR_RECALC is also the same as LINEAR, but now both C and the fn functions can be a function of pixel number. This means that you must construct a new design matrix and invert it for each pixel. NONLINEAR (the default) is used for functions that do not have any of the previous forms. The most desirable functions might be in this category.
FUNCTION	Set to the name of the subroutine that calculates the function values. The specifications for this function are on page 183.
JACOBIAN	Always optional and is useful only for NONLINEAR functions. It is set to the name of the subroutine (supplied by you) that calculates derivatives of the function with respect to each parameter. If a you do not provide a routine, derivatives are estimated by the nonlinear fit routines. Providing derivatives normally only slightly speeds up fit routines.

GUESS	Used only for NONLINEAR functions. It is set to the name of a routine (supplied by you) that calculates an initial guess for the parameter values. Sometimes, fixed initial guesses might work for all sets of data. In such cases, you can omit setting GUESS and instead specify default values with the following command
	`set_default_parameters(3, 0.0, 1.0, 0.0);`
	where the first argument, 3, is the number of following arguments; the remaining arguments are the default values. You must provide at least as many values as there are parameters in the fit. If completely fixed guesses do not work, but the same guess can be used for every pixel in the image, you can specify the command
	`GUESS = fixed_guess;`
	which allows the initial guesses to be passed on the command line. These guesses would be `n_parameters` constants after the constant for the threshold value.

USE_PREVIOUS _PARAMETERS	Used only for NONLINEAR functions. Setting to TRUE should speed up the fit if the routine uses a fixed guess or if the GUESS function is likely to be very far off; for example: `USE_PREVIOUS_PARAMETERS = TRUE;` This command means that the first pixel is fit with the values from the GUESS function or fixed guess values, but that subsequent pixels use the parameters from the last successful fit for the guess. If the fitting routine fails with these previous parameters, the GUESS function or fixed guess values are used to try the fitting routine again. This option can speed up the overall fit time by an order of magnitude if the initial guess is not very accurate. For most data, if it is possible to find an initial guess that will make the fit converge (even if it takes many iterations), an initial guess is almost as good as using an accurate guessing function.
PARFIX	Set only if the parameters in the functional form specified in the FUNCTION are different from what you want to be reported. This method is used in `t1fit.c`, where the functional form of the fit is `y = P0 + P1 * exp(x * P2)` but the parameters reported are for the fit of `y = P2' + (P1' - P2') * exp(-x/P0')`. Therefore, `t1_parfix` calculates the estimated `Pn'` from the estimated `Pn`, and also calculates new covariances. Writing a `parfix` routine involves extra work, but the routine might be an advantage over having to specify different functions for fits that are equivalent but use different parameters.
`return TRUE;`	Must be entered before the closing brace, *}*.

Additional information can be included before the `return TRUE;` statement, as shown in a fragment of the `shamesfit.c` file in Figure 43. In this fragment, `FIT_TYPE` is made to depend on the number of image vectors passed, and additional numerical parameters on the command line (after the threshold value) are used to set values of variables used in calculating the function. Note that the `nbr_params` variable is set to the number of numerical values on the command line after the threshold value. User variables are defined in the second section as “static” (local to the current file). However, on compilation, all your `xfit.c` files are combined with `fit.c` into one file, so names should be unique among all fitting functions.

The second section in an `xxxfit.c` file contains the user-supplied functions that are mentioned in the first section. First, there is `FUNCTION`, which calculates the values of your fitting function. `FUNCTION` is the only routine needed for any of the varieties of linear fits. It calculates a vector of *y* values given a vector of *x* values and a vector of parameter values. Figure 44 is an example. Note that the `nparams` variable is not used in this routine because `exp_function` is only used for three-parameter fits. Fitting an nth order

```
#ifdef FUNCSELECTION
  IF_FITCODE("shames2"){
    N_PARAMETERS = 2;
    FUNCTION = shames_function;
    switch (nbr_image_vecs){
      case 1:
        FIT_TYPE = LINEAR_FIXED;
        break;
      case 2:
        FIT_TYPE = LINEAR_RECALC_OFFSET;
        break;
      default:
        FIT_TYPE = LINEAR_RECALC;
        break;
  }
  if (nbr_params > 0) alpha = in_params[0];
  if (nbr_params > 1) sbv0 = in_params[1];
  if (nbr_params > 2) hct = in_params[2];
  return TRUE;
}
#else   /* not FUNCSELECTION */

/* Constants for Shames model */
static float alpha=0.136; /* Time Const for [CA-plasma] signal decay */
static float sbv0=0.13;   /* Initial value of [CA-plasma] signal */
static float hct=0.37;    /* Hematocrit */
...
```

Figure 43. Fragment of `shamesfit.c` File

```
static void
exp_function(int npoints,   /* Nbr of data points */
             int nparams,   /* Nbr of parameters-NOT USED */
             float *params, /* nparams parameter values */
             int nvars,     /* Number of indep variables-NOT USED */
             float *x,      /* npoints*nvars values of indep vars */
             float *y)      /* Function values OUT */
{
  int i;
  for (i=0; i<npoints; i++){
      y[i] = params[0] + params[1] * exp(x[i] * params[2]);
  }
}
```

Figure 44. FUNCTION Specifications

polynomial, for example, `nparams`, specify the order. Similarly, `nvars` is not used because `exp_function` only deals with one independent variable.

`JACOBIAN` is the second routine. Given vectors of parameter values and *x* values, `JACOBIAN` calculates the partial derivative `dy/dp` at each *x* value for each parameter. Note that it returns what looks like the transpose of the Jacobian as it is usually defined. This transposition is the result of the underlying fitting routines, which are derived from Fortran routines. Compared to `C`, Fortran stores arrays in transposed order. The definition of a JACOBIAN routine is shown below.

```
static void
exp_jacobian(int npoints,   /* Nbr of data points */
             int nparams,   /* Nbr of parameters */
             float *params, /* nparams parameter values */
             int nvars,     /* Number of indep variables */
             float *x,      /* npoints*nvars values of indep vars */
             float **dydp)  /* Derivative values OUT*/
{
  int i;
  for (i=0; i<npoints; i++){
    dydp[0][i] = 1;
    dydp[1][i] = exp(x[i] * params[2]);
    dydp[2][i] = dydp[1][i] * x[i] * params[1];
  }
}
```

The third routine is the `GUESS` function, which is required for nonlinear fits and is usually the most difficult routine to define. Accurate first guesses will usually speed up the fit considerably, as well as ensure that it does not converge to a spurious local minimum. Since the guess algorithm is idiosyncratic for each function, you determine how the function is defined. The signature of the function is shown below.

```
static int
exp_guess(int npoints,   /* Nbr of data points */
          int nparams,   /* Nbr of parameters-NOT USED */
          float *params, /* Parameter values OUT */
          int nvars,     /* Number of independent vars-NOT USED */
          float *x,      /* npoints*nvars values of indep var */
          float *y,      /* npoints values of dependent variable */
          float *resid,  /* Quality of fit OUT--OPTIONAL */
          float *covar)    /* Covariance matrix OUT--OPTIONAL */
```

For an example of a trivial guess function, see `fixed_guess` in the file `fit.c`. Note that the returned values `resid` and `covar` are optional, which means that you must test these pointers to verify that they are nonzero before trying to store values.

TRI_ELEM Macro

The covariance matrix contains only `(nparams * (nparams+1))/2` values, rather than `nparams*nparams`. Only the lower triangle of this symmetric matrix is stored. The storage order is:

`C(0,0), C(1,0), C(1,1), C(2,0), C(2,1), C(2,2), C(3,0), ...`

The TRI_ELEM macro is provided to easily reference any element of a matrix stored in this format. The syntax `TRI_ELEM(mat,row,col)` references the element of the matrix at the row and column. This macro requires that `row` be greater than or equal to `col`.

PARFIX Routine

With PARFIX, estimated parameters can be combined to form estimates for other parameters that were not explicitly fit. There are some potential pitfalls involving the covariances between parameters. For example, the estimate of the sum of two parameters is

`E[p0 + p1] = E[p0] + E[p1]`

but, the estimated value of their product is

```
E[p0 * p1] = E[p0] * E[p1] + Covar[p0, p1]
```

This value is the direct result of the covariance definition. Because calculating the variance of the newly synthesized parameters can be fairly complex, avoid using PARFIX routines. Instead, directly write functions in terms of the parameters you actually want to know.

8.5 Signal-to-Noise Ratio, Ghosting, and Related Functions

Signal-to-Noise Ratio (snr)

The `snr` function measures the signal, noise, and ghosting level, Signal-to-Noise Ratio (SNR), and Percentage Image Uniformity (PIU).

Usage

```
#output_frame = snr #input_frame N R "comment"
```

The `snr` function takes as input two optional numbers:

- `N` — the size of a mean filtering kernel applied to the input image(s) prior to analysis; it defaults to 11 for 128x128 (or larger) images and to 5 for smaller images.
- R — the percent of the diameter of the object that is used to measure the PIU; it defaults to 80%.
- `"comment"` A string input reflected in the output text to distinguish results from different analyses.

Example:

`#2 = snr #1 "axial"` (a single image)

`#2 = snr #1 3 "ax5"` (a single image with a 3x3 filter kernel)

`#2 = snr #1 5 100 "axial"` (a single image with 5x5 filter, using 100% of object)

`##4-6 = snr ##1-3 "cor"` (3 images)

The `snr` function assumes a reasonable amount of signal in all images but does not assume the images are of the same object or orientation, see Figure 45 for an example.

Use the function `snrme` to analyze a series of multi-echo images of the same object but with varying intensity (see below).

Output

A filtered image with radius as used for PIU analysis is output for each input image. The number of output and input frames must be equal. All pixels outside of the object are zeros, except for a single pixel in the center of the maximum ghost which is maintained in order to facilitate manual inspection of the ghost location.

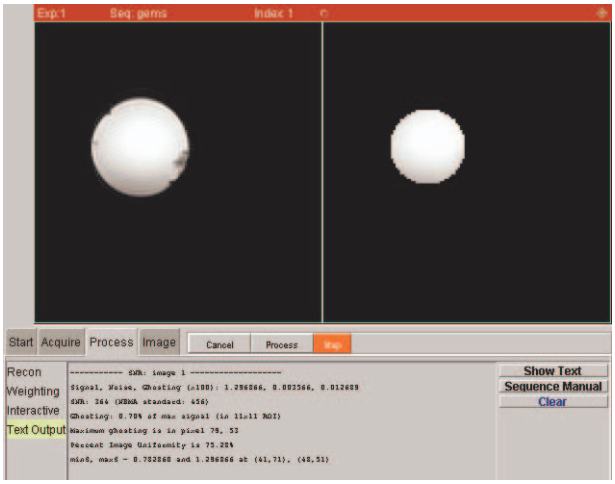


Figure 45. SNR Input and Output images

The following numbers are reported:

- Intensity Levels for signal, noise, and ghost (multiplied by 100)
- SNR (and SNR according to the NEMA standard)
- Ghosting as percent of signal
- The pixel location of the maximum ghost
- Percent Image Uniformity
- Minimum and Maximum signal (multiplied by 100), and the pixel location of these signals.

All calculated values are printed in the Text Output window of the Process folder and appended to the file "`SNR_measurements.txt`" in the current directory.

Algorithm

1. The object is identified through a simple histogram analysis algorithm, which separates signal from noise, assuming two primary peaks.
2. The noise level (meanN) is calculated as the average intensity in 4 regions outside the boundaries of the object: top left corner (outside the object), top-right, bottom-left, and bottom-right. We could use all "non-image" pixels, but this includes ghosting.
3. The input image is filtered with a mean-function using an NxN filter kernel. The default is 11 (5 for smaller images) for a 10x10 or 5x5 ROI.
4. The signal level is determined as the maximum signal (maxS) found in the object in the filtered image.
5. The ghosting level is determined as the maximum signal (meanG) found outside of the object but in the same band in the phase encoding direction in the filtered image.

The SNR is calculated as the maximum signal divided by the noise `(maxS/meanN)`.

NEMA standard SNR divides the `maxS` by the true standard deviation of the noise, `s0`. Assuming a gaussian distributed noise with mean 0 (zero) and standard deviation s0, the magnitude noise will follow a Rayleigh distribution with mean 1.253s0 and standard deviation 0.665s0. The NEMA SNR is calculated as: `maxS/(meanN/1.253)`.

The ghosting is reported as the maximum intensity (meanG) in the region that falls outside the boundaries of the object in the phase encoding direction in the filtered image (minus the noise level) divided by the average signal level `((meanG-meanN)/(maxS)`.

The Percentage Image Uniformity is calculated as `(1 - (maxS-minS)/(maxS+minS))*100`, where `maxS` and `minS` are the largest and smallest values within the object in the filtered image.

Stability (stats)

The stats function measures the standard deviation and peak-to-peak variation as a function of the mean signal intensity within a series of images.

Usage

```
#output_frame = stats ##input_frames N R "comment"
```

The stats function takes as input two optional numbers:

- N — the size of a mean filtering kernel applied to the input image(s) prior to analysis; it defaults to 11 for 128x128 (or larger) images and to 5 for smaller images. Entering 0 (zero) bypasses the filtering.
- R — the percent of the diameter of the object that is used to measure the average standard deviation within the object. The default is 80%.
- `"comment"` A string input reflected in the output text to distinguish results from different analyses.

The number of output frames must be at least 1 and no more than 4, see Figure 46 for an example of the output.

Example:

`#101 = stats ##1-60` (statistics on images 1-60, one output image)

`#101 = stats ##5-60` (skip the first 4 images)

`##101-102 = stats ##5-60` (two output images)

`##101-104 = stats ##5-60` (four output images)

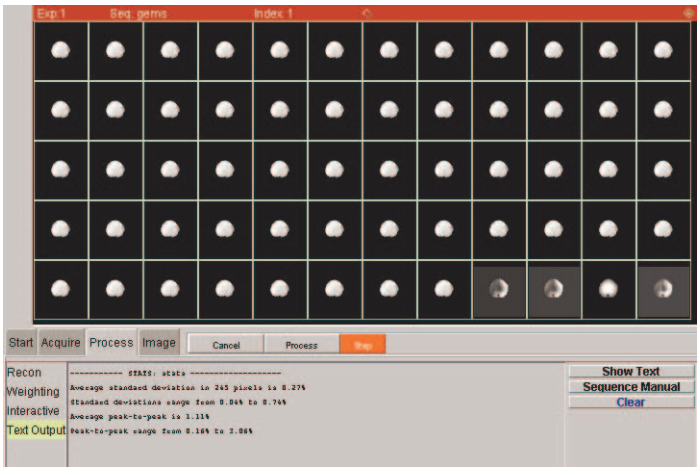


Figure 46. Stats: Input and Output Images

Output

The stats function can output up to four images:

1. Standard deviation as percentage of mean
2. Peak-to-peak as percentage of mean
3. Mean
4. Standard deviation (absolute value)

The following numbers are reported in the Text Output window of the Process folder:

- Standard deviation as percentage of mean averaged over the object
- Average peak-to-peak as percentage of mean (if peak-to-peak output image is selected)
- Appends calculated values to the file STAB_measurements.txt in the current directory.

Algorithm

The object is identified through an analysis similar as for the `snr` function. The mean, standard deviation, standard deviation as a percentage of mean, and peak-to-peak as a percentage of mean are calculated on a pixel-by-pixel basis within the object.

The center 4 pixels are ignored (values set to zero), by default, to avoid affects of DC artifacts on the result. The optional argument, `nodc`, forces inclusion of the center pixels.

Limitations of the Image Analysis Functions

- Reported numbers may not reflect the values over the entire object if the object is not circular (e.g., a sagittal view of a bottle).
- Consequently, the calculations may report erroneous numbers for any of the following:

  Pronounced dielectric effect leading to large signal inhomogeneities

  Histogram analysis from a signal/noise yields a threshold that is too large resulting underestimating the size of the object.
- The part of the object that falls outside of the circular region may be interpreted as ghosting, leading to a very large ghosting level.
- Reduced SNR and ghosting level and potentially negative ghosting reported if there are artifacts in the corner regions of the image and the estimated noise level is too large.

snrme

Similar to `snr`, except that the object is identified on the first image alone and the object limits applied to all subsequent images.

Usage

```
#output_frame = snrme #input_frame N R "comment"
```

object

The object is identified through a simple histogram analysis algorithm, and the object boundaries (top- and bottom-most row, left- and right-most columns) are determined. Output is an image with the background set to zero.

Usage

```
#2 = object #1
```

circ

The object is identified as with the object function, but the output is the approximated circular object. Optional input is the percentage of the radius to use as the object.

Usage

```
#2 = object #1 R
```

R is the percentage, default 100%.

filter

The input image is filtered with a mean-function using an NxN filter kernel.

Usage

```
#2 = filter #1 N
```

N defaults to 11.

8.6 Problems with Image Math

Run-time Errors

Image Math has no automatic run-time validation of math operations. Check data values, as shown in these examples:

```
#1=(#2==0)?0:#1/#2
#2=sqrt(fabs(#1))
#5=(#1<=1.0e-6)?log(1.0e-6):log(#1)
#5=log(#1<1.0e-6?1.0e-6:#1)
```

If a user function has bugs (such as using uninitialized pointers) that result in memory violations, the entire VnmrJ program is core dumped. Core dump files result because, while your function is running, it is actually part of VnmrJ.

CAUTION: **Before performing possibly illegal operations, check data values.**

Image Math expressions can be written that will kill VnmrJ, e.g. `#2 = #1 + *(float *)0`

CAUTION: **Be careful when programming and testing new user functions.**

Run-time error messages might be found in the console window and a core dump file can be in the current VnmrJ directory.

Compilation Errors

Image Math does not generate a legal C program if an illegal expression is entered and the message line shows: `Math: Program did not compile`

Compiler errors are also written into the console window.

Chapter 9. Digital Eddy Current Compensation

Sections in this chapter:

This chapter describes the digital eddy current compensation (DECC) module and decctool, the associated software interface. DECC is used in microimaging, horizontal imaging, and whole-body imaging.

9.1 The DECC Module

The DECC module consists of the DECC board, the Smart DAC (SDAC) board, and associated cables (a power supply is sometimes also supplied with the module in certain standalone situations.) A functional block diagram is shown in Figure 47.

DECC relies on digital signal processing technology to create appropriate compensating signals, the calculation being based on parameterized compensation requirements applied to the digital signal from the gradient waveform generator boards (WFGs). The parameters are sent to the board over the APbus. The compensating signal is scaled as appropriate and added into the main gradient signal on the SDAC, and sent out to the gradient power supplies.

The SDAC board is an improvement over previous versions of gradient DAC boards; the following signal strength and/or conditioning controls can now be set via the APbus:

- Shim input scaling
- DECC input scaling
- Rise time (slew rate)
- Output gain
- Output polarity

The SDAC board is a low-power current driver that is used for compensating B0 shifts. When B0 shifts are too large for this on-board current driver, a jumper setting turns the signal into voltage mode so that an appropriate external current amplifier can be used.

9.2 Theory of Preemphasis

This section is a brief theoretical description of preemphasis (also known as eddy current compensation), the module, the software, and a few key terms. Referred to other NMR and MRI literature for more background. This chapter does not provide any descriptions of methods for measuring eddy current effects.

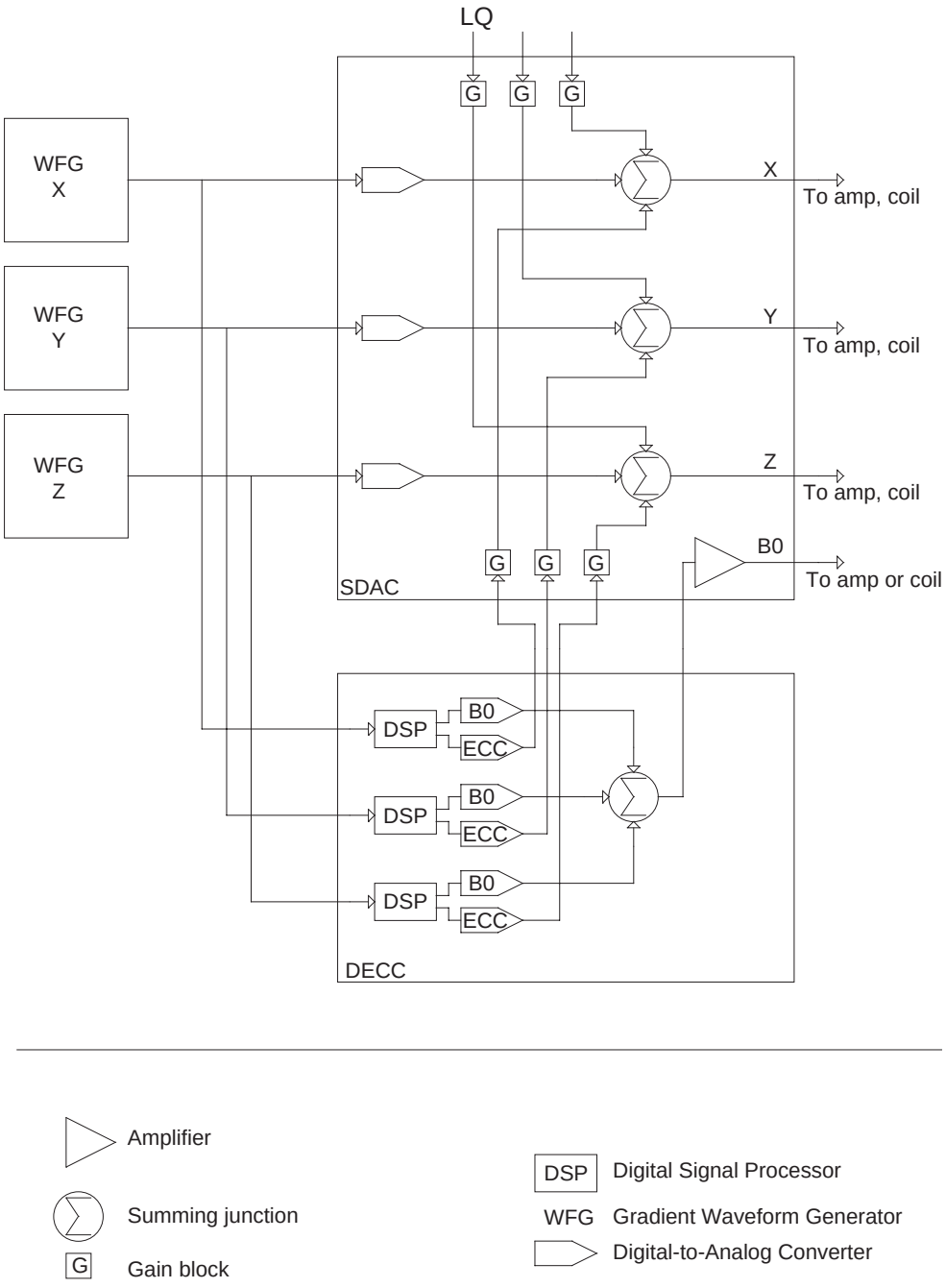


Figure 47. DECC Module Block Diagram

Measuring Two Samples

Sample I is located at the center of the gradients (center of X, Y, and Z) and sample II centered in X and Y but offset from the Z center. The assumptions used in this example are: the samples are point-like, have very narrow linewidths. and the NMR frequency for each sample can be measured at any time and independently of each other.

Apply a simple pulse-acquire (to either sample) at a time T following a B0 field gradient pulse, as shown in Figure 48. Applying a rf pulse-acquire sequence that is short compared to the gradient and eddy current times and vary the time T between the gradient and the rf pulse results in a series of spectra with the spectral lines offset from the zero-gradient spectrum that converge to the zero-gradient frequency at long T times.

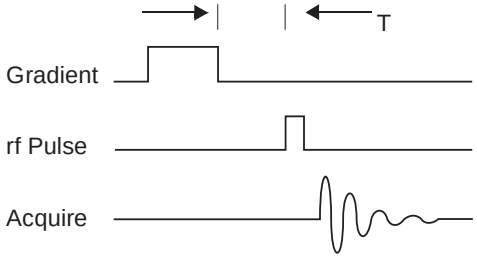


Figure 48. RF Pulse-Acquire Sequence

The empirical relation ship between the line frequency of time T is as follows:

$$f(T) = f_0\left[1 - \sum_{k=1}^{N} A_k e^{-T/\tau_k}\right] \qquad \text{[Eq. 5]}$$

A_k and τ_k are characteristic of conducting structures of the magnet within which the eddy currents reside. A_k can be negative for shielded gradients. Eddy currents act to oppose the field (Lenz's law) that caused them. Each of the magnet's conducting structures give rise to a term in the summation in Equation 5.

Eddy current fields contain two major components; a B0 component and a gradient component (first order or linear term). Each component consists of a set of terms which decay according to Equation 5. B0 terms are independent of spatial position and influence the NMR signal at sample I and II equally. Linear or gradient terms influence the NMR signal differently depending on the magnitude of the gradient field at I and II. The samples in this example are along the *z* axis and the Z gradient is pulsed and yields terms known as Z–>Z main terms. Terms resulting in the B0 shift are known as the Z–>B0 terms.

Gradients arise in the *z* axis (or cross terms) from gradients applied along one of the other axes instead of along the *z* axis. X–>Z cross terms arise from a pulse applied along the *x* axis. Y–>Z cross terms arise from a pulse along the *y* axis.

Eddy current effects result from variety of main terms, cross terms, and B0 terms, all of which can be corrected with DECC.

9.3 Using the Decctool Interface

This section describes how to use the decctool interface.

Modifications using DeccTool can only be make by the system hardware administrator, typically this is vnmr1. Any investigator can used the tool to view a gradient coil calibration. The systems reads the information imbedded in the gradient coil ID, loads the correct gradient calibration file when the gradient coil is changed, and makes the necessary configuration changes to VnmrJ.

Opening decctool

1. Click on **Tools** on the main menu.
2. Select **System Settings…**
3. Click on **Gradients and ECC** to open DeccTool, see Figure 49.

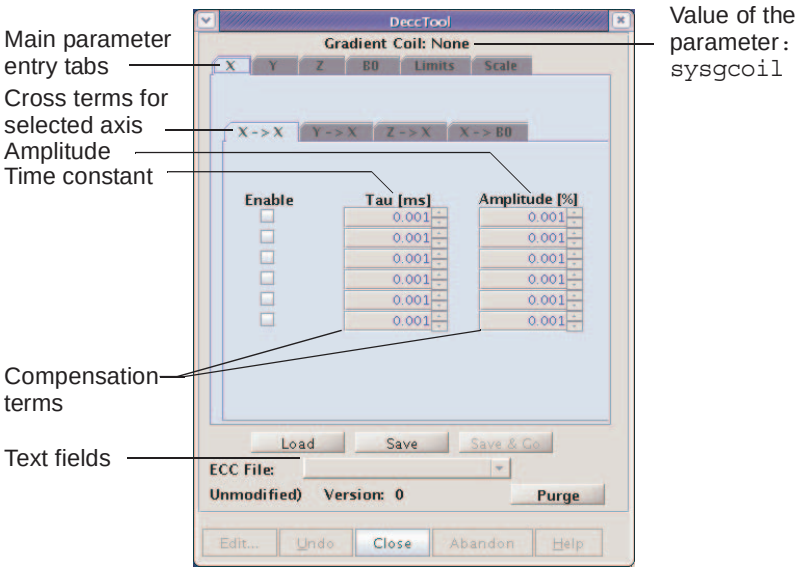


Figure 49. decctool Window

4. Click in the **ECC File** field to activate it. Type a name of your choice, then click on the **Save** button. **Do this step now before proceeding**.

Loading and Saving Files

The name of the magnet gradient coil, which is the value of the `sysgcoil` parameter (`None` in Figure 49), is shown at the top of the decctool window. The master file name used internally to hold the ECC values is named after the coil used. Compensation parameters are associated with the coil-magnet combination in use.

The values for the parameters in the master file are displayed when the decctool window opens. No name in the **ECC File** field. Create a scratchpad file for the parameter settings operations by entering a filename in the **ECC File** field.

The **Load** and **Save** buttons are enabled. **Load** and **Save** buttons operate on the scratchpad file and simultaneously overwrite the master file. **Do not click** on the **Load** and **Save** buttons before reading the following sections and learning how to uses the interface.

Loading a File

1. Enter a name in the **ECC File** field or click the pulldown menu arrow to select a file.

   Select a specific version of a file by including a version number extension in the file name (e.g., `test.7`). The latest version is loaded if no version number is provided.

2. Click on **Load**.

   The parameters in the parameter-entry panels are simultaneously loaded from the file named in the **ECC File** field and also saved to the master file.

Saving a File

1. Enter a name in the **ECC File** field or click the pulldown menu arrow  to select a previously named file.
2. Click on **Save**.

   The parameters in the parameter-entry panels are simultaneously saved in the file named in the **ECC File** field and in the master file.

   Previous copies are kept and named with an extension incremented by one from the previous version. The number of the current version is listed below the **ECC File** pulldown menu.

   Delete old copies of files by clicking on **Purge**.

   Version number in the **ECC File** field is ignored and the file is saved with a version number one higher than the highest existing version.

Starting Experiments

The **Save & Go** button performs the same operation as the **Save** button and starts the current experiment. Become familiar with the operation of `decctool` before using the **Save & Go** button.

The **Save & Go** button runs the macro `deccgo` that performs a `go` command by default. Change the operation of `deccgo` by either writing a new `deccgo` macro or by defining a `deccgo` parameter executed by the default `deccgo` macro.

Example: Make **Save & Go** execute the `au` command. Enter the following in the input window:

```
string('deccgo')
deccgo='au'
```

Modifying X,Y, and Z Compensation Parameters

Tabs indicating provide access to each of the five main parameter entry panels:

- **X** — x-channel parameter entry (with four subpanels)
- **Y** — y-channel parameter entry (with four subpanels)
- **Z** — z-channel parameter entry (with four subpanels)
- **Limits** — set duty-cycle and rise time
- **Scale** — set various gains

Changing Time-Constants and Amplitude Values

The **X**, **Y**, and **Z** parameter entry panels are select using the tabs to and open a subpanel. Each subpanel has four tabs for the cross terms effecting the gradient.Change the time-constant and amplitude values as follows:

1. Click on **X**, **Y**, and **Z** parameter tab to select a subpanel of cross terms.
2. Click on a the tab representing the cross term of interest.
3. Place a **check** in the box under the **Enable** column to select time-constant and amplitude pair.

   The message at the bottom of the decctool window has changes from **(Unmodified)** to **(Modified)** after check box to change a time constant and amplitude is changed.

4. Set a time constant by entering a number in the field under **Tau (ms)** or click on the up or down arrows to the right of the entry field.

   The message at the bottom of the decctool window has changes from **(Unmodified)** to **(Modified)** after a time constant and amplitude is changed.

5. Hit **Return** after typing a value.
6. Set an amplitude by entering a number in the field under **Amplitude(%)** or click on the up or down arrows to the right of the entry field.
7. Hit **Return** after typing a value.
8. Repeat step 3 through step 6 for each time-constant and amplitude pair that will be used to define the cross term up to the maximum pairs allowed in each panel.
9. Repeat step 2 through step 6 for each cross term of interest.
10. Repeat step 1 through step 9 for each parameter panel as required.
11. Press **Load**.

Values displayed in the various text fields that are the same as the master file are unmodified. Values that have changed from the master file are modified.

Selecting or Deselecting Values

Place a check in the box under the **Enable** column to make a the time-constant amplitude pair active. Removing the check from the box makes the pair inactive. Disabling (unchecking) the time-constant amplitude pair sends values of zero for that particular ECC term to the system.

Setting Rise Time and Duty Cycle

Use the **Limits** panel to set Rise time (slew rate) and Duty cycle. These settings occur on the SDAC board. Duty cycle sets a limit for the gradient pulses—if the duration exceeds this value, an error signal is generated.

Setting Gains

The **Scale** panel is used to set various gains on the SDAC board.

The ECC gain setting affects the ECC signal coming into the summing junction on the SDAC board where the ECC is combined with the main gradient signal. The value in the X, Y, and Z parameter entry values fixes the amplitude correction that is applied to the gradient and is generally not affected by the ECC scale factor in the Scale window. If the ECC scale does need to be changed, the values of the ECC parameters do not need to change. The purpose of having this scale factor available is related to resolution of the DAC creating the compensation waveform, and only in rare circumstances is the scale factor of concern.

The Shims scale factor controls the gain of the incoming shims. The x1, y1, and z1 shims are summed into the gradient signal on imaging systems.

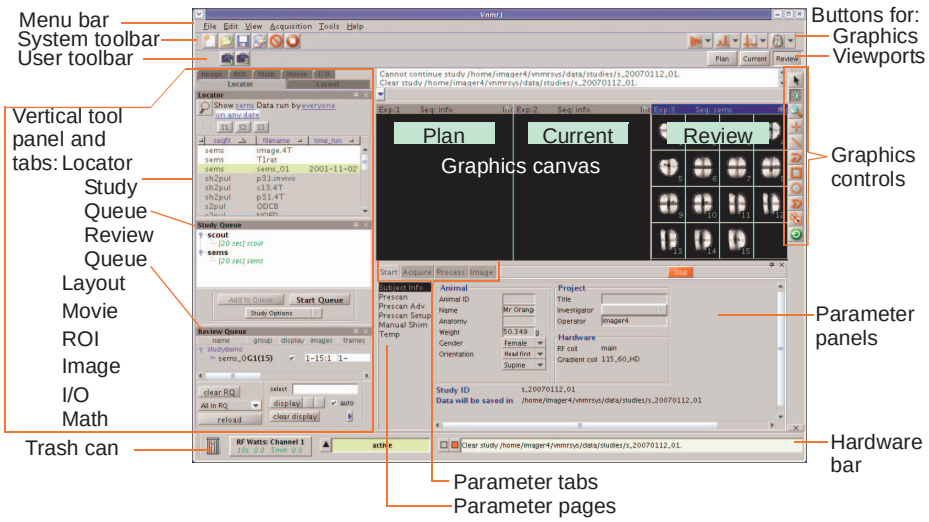
Overall scale sets the gain on the entire set of signals—gradients, compensation, and shims. This is used mostly to correctly set the size of the image for the applied demand gradient. It accepts negative values, so it can also be used to reverse the polarity of the gradient signal.

Closing decctool

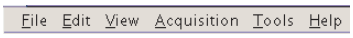
Click on the **Close** button at the bottom of the decctool window to close decctool.

Appendix A. VnmrJ Imaging Interface

The VnmrJ interface is shown below. This chapter describes major areas of the interface. Details about the procedures, operations, etc. controlled through the interface are documented in this and other manual.



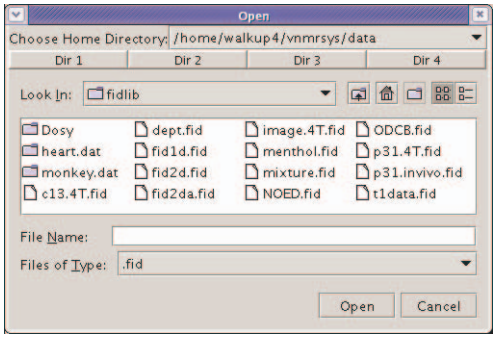
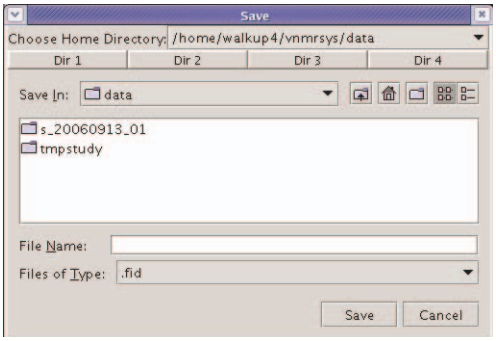
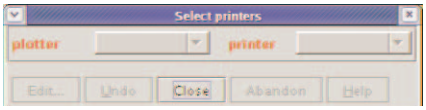
A.1 Main Menu Bar



The main menu bar for the account administrator provides the following items:

File Menu Selections

The menu selections are for the File menu are: .

Menu Items	*Descriptions*
New Workspace	Make a new workspace of the next available workspace number.
Open	Opens up the file navigation window to the locate the required file. Click the **file** and click on the **Open** button to open or **drag and drop** the file on to the graphics screen. 
Save as …	Opens the file navigation window to the locate the required directory. Enter a **file name** in the Save as field and click **OK** to save. 
Auto Save	Saves data using directories specified in Save data setup…
Save data setup …	Opens the Save Data Setup window — customize where data is saved and customize the file naming, see "Setting Up Study Data Directories and Templates," in the *VnmrJ Installation and Administration* manual.
Printers...	Opens a window for selecting printers and plotters.  Only printers and plotters defined through VnmrJ Admin are displayed, see the manual *Host Computer Setup for VnmrJ* for information about connecting printers and plotter
Exit VnmrJ	exits VnmrJ.

Edit

The Edit menu selections are:.

Edit Menu Items	*Descriptions*
Create protocols	See "Making a New Protocol," page 30 and "Making a Composite Protocol," page 30.
Tool Bar	Opens the tool bar editing tool. Refer to the *VnmrJ System Administration* manual for more details.
Display options...	Opens a window for setting symbolic colors and fonts in the interface.
Parameter Pages…	Opens the parameter panel editing tool.
Viewports	Opens the Viewport Settings panel to set the number of viewports. Select a radio button from 1 to 9 to set the number of viewports, see "Viewports," page 210 for more details.
Annotation…	See "Annotations," page 151.
Edit config profile…	Opens the Edit User Config Profile window.

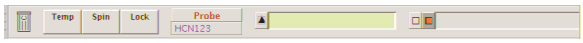
View

The View menu selections are:

View Menu Items	*Descriptions*
Command Line	Displays the command line if it is hidden — account owner only.
Experimental Panel	Adds the experiment panel to the vertical panel protocol tab.
Parameter Panel	Opens the horizontal parameter panels if they are hidden.
Study Queue	Adds the study queue panel to the vertical panel protocol tab.
Layout	Layout tab is used for selecting which images are displayed in which layout, see "Layout," page 150.
Movie	Movie tab to setup images for a movie display, see "Movie," page 152.
ROI	ROI tools see 5.4 "Regions of Interest," page 125 and "Region of Interest – ROI," page 152.
Image	Image tab contains controls for modifying the image, see "Image," page 154.
I/O	Printing and DICOM options, see "I/O," page 157.
Toolbars	Opens a pop-out menu. Place check next to a tool bar to show the tool or remove the check to hide the tool bar.
System Toolbar	 Refer to "System Tool Bar," page 202 for a description of system tool bar functions.
User Tool bar	 Refer to"User Toolbar," page 203 for a description of system tool bar functions.

View Menu Items	*Descriptions*
Graphics Toolbars	See "Graphics Toolbars," page 205.

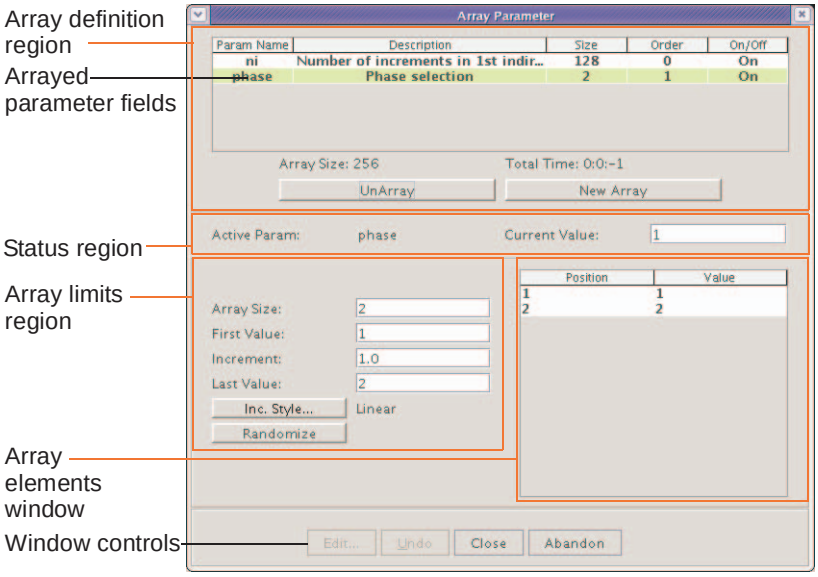
Hardware Toolbar



Acquisition

The Acquisition menu selections are:.

Menu Items	*Descriptions*
Parameter arrays…	Open Array Parameter window



Window Region

Array definition

Arrayed parameter field columns:

Parm Name – enter name of arrayed parameter.

Description – displays text description of array.

Size – displays number of steps or increments in the array.

Order – displays precedence for running the array – double click in the field and enter the array order. Arrays with sequential numbers create a full matrix (array A x Array B) and each array can be a different size. Arrays with the same order number (and the same size) creates a diagonal array.

On/Off – Array is used / array not used

Fields and buttons

Menu Items	*Descriptions*
	Array Size field – shows size of selected array.
	Total Time field – shows estimated time to compleat the array.
	UnArray button – remove selected parameter from the list of arrayed parameters.
	UnArray button – add new row to list of arrayed parameters.
	Status – show active parameter during acquisition and parameter's current value.
	Array limits
	Array Size field – enter the size of the array and press return.
	First Value – enter the starting value of the array and press return.
	Increment – enter the array increment and press return.
	Last Value – enter the ending value of the array and press return.
	Inc. Style … button – click and select linear or exponential.
	Randomize button – click to toggle between a random and ordered array.
	Array elements
	Change the value of the array element by double clicking on the value of the array element associated with the array position, entering a new value, and pressing **Enter**.
	Window buttons
	Edit—Not active.
	Undo—Click to undo click again to restore the change.
	Close—Closes the window.
	Abandon—Closes the window and removes all entries
Use Study Queue	Check this box to enable the study queue and to facilitate building a protocol.
Abort Acquisition	Data acquisition is stopped.

Tools

The tools menu selections available are:

Menu Items	*Descriptions*
Update locator	Opens a submenu that provides choices for updating the different parts of the Locator.
Import files to locator	Opens a window for importing files to the locator.
System Settings...	Opens the System Settings window, which enables you to set system parameters.
System Settings Window tabs and Buttons	
System config	**button —** inactive if user is not the system administrator, typically vnmr1.
Gradients and ECC…	**button** — Starts Decctool, see "Digital Eddy Current Compensation," page 191.

Menu Items	*Descriptions*
Gradient Tables …	**button**— opens Gradient Tables window with a drop down menu listing of available systems coils. Click on the desired coil and click on close to select the coil.
System tab	**Application mode** – Walkup, Standard, or imaging. **Receiver gain used by qtune (0-60)** – enter a value in the field. **Autosave data after acquisition** Check box: enabled if checked **Trash study node preferences** – set options from drop down menu: • Customized study nodes: deleted, skipped, or not allowed. • Completed study nodes: not allowed, skip, delete
Display/Plot tab	**Process data on drag-and drop —** Check box: enabled if checked. **Set display from plotter aspect ratio (wysiwyg) —** Check box: enabled if checked. **Spectrum updating during phasing (0-100)** — set the percentage of the display that is updated during interactive phasing. 100 is recommended **Max # of pens** — number of plotter pens to use **Show Tooltips —** Opens a window for saving the current locator view **—** check box: enabled if checked. **Max # of items to show in locator**– enter a value in the field.Values larger than 2000 slow the locator response. Refer to appendix on locator administration in the *VnmrJ Installation and Administration* manual for more information on working with the database. **Display only matching items in locator —** check box: enabled if checked. **Day Limit of files in Locator (neg = forever)** — Enter a value. **Turn off locator—** check box to turn the locator off.
Browser…	Opens a VJ Browser window to navigate and search directories for files.
Locator…	See “Locator,” page 213.

Help

Starts VnmrJ online help. The help files must be loaded from the VnmrJ Manuals CD. Or, the CD must be left in the CD-ROM drive.

A.2 System Tool Bar 

The tool bar is directly below the menu bar. These buttons provide quick access to common functions. The tool bar and buttons can be edited. Click on **Edit** and **Select Tool** to start the

editor, refer to *VnmrJ Installation and System Administration* manual for more information. The following tools are the default available in this tool bar:

Button	*Function*
	Create a new work space.
	Open the file browser to locate a directory, select a file, and load the file. Click on the file to load and click on the **Open** button to load the file into the current workspace (experiment).
	Save As… Opens a file browser to locate a directory, name a file, and save a data set. Enter a file name in the **File Name:** field, select the **file type** from the drop down menu, and click on the **Save** button.
	Open the display options Styles and Themes window.
	Cancel command.
	Stop acquisition.
	Show the fid display toolbar.
	Show the spectrum display toolbar.
	Show the 2D data toolbar (grayed out if the data set is 1D).
	Show image display toolbar

A.3 User Toolbar

Button	*Function*
	Save the current screen layout (graphics, a parameter panel, locator sizes). Click on one of the buttons and press the mouse button for five seconds to save the layout. Click on the button again to return to the saved layout.
	Plan, Current, and Review viewports.

A.4 Hiding and Showing the Toolbars

1. Click on **View** from the main menu.
2. Select **Toolbars**.
3. Check on a **toolbar name** to toggle the tool bar on (place a check mark to the left of the toolbar name) or off (remove the check mark to the left of the toolbar name).

A tool bar with an **X** at the bottom can be hidden or closed by clicking on the **X**.

A.5 Locator

The locator provides access to data sets, experiments, shim sets, and commands, see Appendix B, “Locator” for more information about the locator.

A.6 Study Queue

The Study Queue is used to set up and view studies. The Study Queue holds a list of scans or protocols that have been previously acquired or are set up for future acquisition. Scans can be acquired in any order, independent of their position in the Study Queue. Study data is saved automatically as it is acquired. As scans are run, they are shuffled up in the Study Queue so that scans that have been run are listed in the order they were run at the top of the Study Queue. However, if you skip any scans within a composite protocol, those skipped scans remain in place.

A new study is initiated by selecting Clear Study from the Study Options menu at the bottom of the Study Queue. Clear Study closes the previous study and clears the Study Queue, which becomes available for a new study. A study identification tag is automatically generated and assigned to the study.

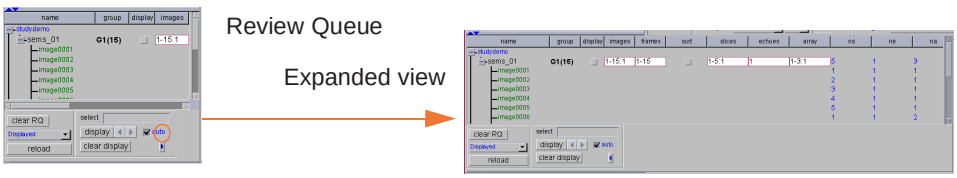
Each scan in the Study Queue can be in one of seven states:

- Ready – the protocol has just been loaded from the Locator, but not yet viewed by the operator.
- Customized – the operator has at some point loaded this protocol into the Plan viewport to view or modify parameters, but has not submitted the protocol for acquisition.
- Active – currently loaded into the Plan viewport.
- Queued — protocol is queued for acquisition when the Start Queue button is pressed
- Executing – actively acquiring data.
- Completed – acquisition completed successfully and data is available.
- Error – the protocol was submitted for acquisition but an error occurred and the acquisition did not complete.
- Skipped – the protocol was dragged to the trash.

As soon as a protocol is submitted for acquisition, it is marked with a lock icon to indicate that the parameters can no longer be modified. If the scan completes successfully, it is marked with a spin-echo icon to indicate that it contains actual data.

A.7 Review Queue

The Review Queue is a tool for organizing and viewing images. Refer to 5.2 “Review Queue and Organizing Images,” page 120, for more details.



A.8 Graphics Toolbars

The graphics control bar for the active viewport is to the right of the graphics canvas. Use the buttons in the bar to control the interactive display in the graphics canvas.The graphics control bar is to the right of the graphics canvas. Toolbar actions include integral displays, phasing, threshold adjustments, and other actions.

Common Graphics Display Toolbar Controls

The following tools are common to 1D, nD, and fid display toolbars.

Icon	*Description*
	Zoom in
	Zoom out
	Select zoom region
	Redraw display
	Return to previous tool menu

1D Display Spectrum Toolbar Controls

Icon	*Description*
	Two cursors in use, click to toggle to single cursor
	One cursor in use, click to toggle to two cursors
	Click to expand to full spectral display
	Pan or move spectral region
	Integral display
	Display scale
	Toggle threshold on or off
	Phase spectrum

Display FID Toolbar Controls

Icon	Description
	Two cursors in use, click to toggle to single cursor
	One cursor in use, click to toggle to two cursors
	Click to expand to full fid display
	Pan and stretch
	Showing real and imaginary - click to zero imaginary
	Showing real and zero imaginary - to show only real
	Showing real only — click to show real and imaginary.
	Toggle scale on and off.
	Phase fid

Imaging and nD Display Tools

- "Imaging Tool Bar," page 206
- "Imaging Tools Menu Selections," page 207
- "nD Graphic Tools," page 208

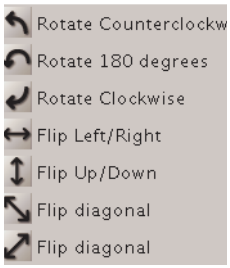
Imaging Tool Bar

Icon	Description
	Imaging tools, click to start imaging tool bar.
	Tool bar handle - grab and drag tool bar to any location within the VnmrJ screen.
	Select
	Image scaling.
	Select zoom region.
	Draw a point.
	Draw a line.
	Draw a curve

Icon	Description
	Draw a box.
	Draw an oval
	Draw a region.
	Drag an object.
	Return to previous menu.
	Close tool bar. Click to close the tool bar.

Imaging Tools Menu Selections

Icon	Description
	Imaging tools menu select.
	Image scaling.
	Manual image scaling Automatic image scaling
	Zoom in
	Open frame layout sub-menu
	1 Frame 2 Frames 3 Frames 2x2 Frames 3x3 Frames Automatic
	Open region of interest tools sub-menu.
	Draw a point.
	Draw a line.
	Draw a curve
	Draw a box.
	Draw an oval

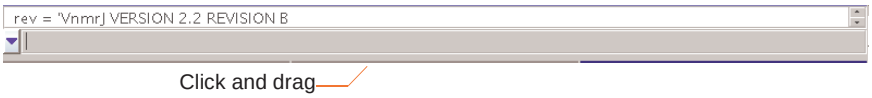
Icon	*Description*
	 Draw a region.
	Show Statistics
	Select All
	Delete All
	Open rotation tools sub-menu.
	
	Open movie tools sub-menu.
	 Start movie.
	 Stop movie
	Open annotation sub-menu.
	None Short Medium Full Subject-Info

nD Graphic Tools

Icon	*Description*
	Box cursors in use, click to toggle to dual cursor
	Dual cursor in use, click to toggle to box cursors
	Click to expand to full fid display
	Pan and stretch
	Show trace
	Show projections
	Click on  to horizontal maximum projection across the top of the 2D display.

Icon	*Description*
	Click on  to horizontal sum projection across the top of the 2D display.
	Click on  to vertical maximum projection down the left side of the 2D display.
	Click on  to vertical sum projection down the left side of the 2D display.
	Rotate
	Increase vertical scale 20%.
	Decrease vertical scale 20%.
	Phase spectrum.
	Click on  to select the first spectrum.
	Click on  to select the second spectrum.
	Peak pick.

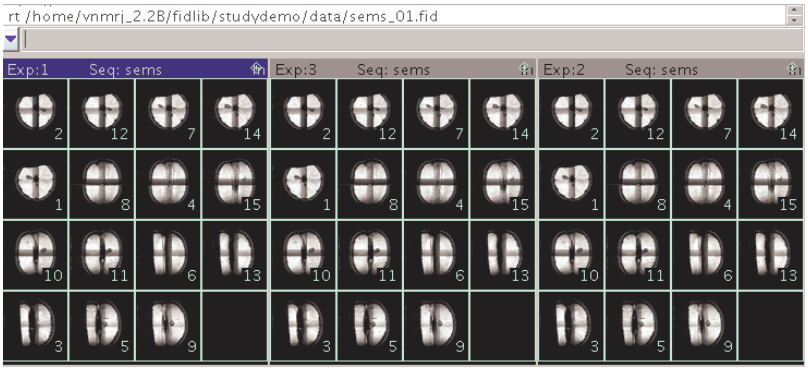
A.9 Advanced Function Bar



Move cursor over the top of the graphics screen until it turns into a double arrow. Left mouse click, hold, and drag down to open command entry field and a text output field. Close the field by moving cursor over the top of the graphics screen until it turns into a double arrow. Left mouse click, hold, and drag up to close command entry field and a text output field clicking once on the button. Any command or macro can be entered into this command window. Error and information messages are displayed in the scrolling text window above the command line in addition to the hardware bar. Command history can be shown if you click on the arrow with the left mouse button. Select a command from the command history by highlighting it and pressing **Return** to execute it.

A.10 Graphics Canvas

This portion of the interface, shown in below with three images, is used to display and interact with graphic and text information.



- Resize the graphics canvas by clicking on the canvas boundary line with the left mouse (the cursor changes form) and dragging the line (e.g., between graphics and parameter templates or between graphics and locator).
- Expand the graphics canvas and hide the parameter templates area by clicking the **x** on the upper right hand corner of the parameter template. Show the parameter panels by clicking on **View** on main menu and selecting **Parameter Panel**.
- Flip the parameter templates behind the graphics canvas, create a Parameter Panel tab on the left side of the graphics window, and expand the graphics canvas by clicking the push pin on the upper right hand corner of the parameter template. Place the cursor on the tab to display the parameter panel.
- Resize the graphics display and display the parameter panel by placing the cursor on the tab to display the parameter panel and clicking on the push pin on the upper right hand corner of the parameter template.
- Reduce any vertical panel to a horizontal tab to the left side of the VnmrJ screen by clicking on the push pin. When all the vertical panel tabs are reduced to horizontal tabs the graphic canvas expands to the full width of the VnmrJ screen. Display any tab by placing the cursor on the tab. Fix the tab in place by clicking on the push pin.

A.11 Viewports

A study is run using the three viewports: Plan, Current, and Review. Move between the viewports by clicking on the buttons on the upper right corner of the VnmrJ window, above the graphics canvas.

The Plan viewport is used for setting up acquisition and processing parameters for the next scan. Typically, the scout image is displayed for graphical planning. A scan is submitted to acquisition by clicking the Start scan button, at which point the parameters are transferred to the Current viewport where acquisition is initiated. After the acquisition is started, you can go back to the Plan viewport and set up the next scan and perform the graphical planning. Images are selected as scout images for planning by double-clicking any completed scan in the Study Queue while in the Plan viewport.

Completed scans and error scans can be loaded from the Study Queue into the Review viewport for analysis. Double-clicking a completed scan clears the graphics area before

loading the images. Drag a completed scan onto the graphics area to avoid clearing the graphics before displaying.

Images appear in the Current viewport as they are acquired.

A.12 Folders

Select parameter panels by clicking on the tabs across the top of the panels.

Use the **Start** panel to control the start and end of a study.

Use the **Acquire** panel to set acquisition parameters.

Use the **Process** panel to adjust processing parameters and process data.

Use the **Image** to perform image processing. See Chapter 7, “Image Processing in VnmrJ,” for more information on interactive image processing.

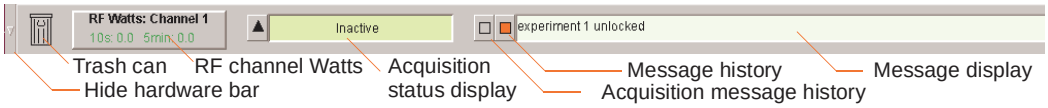
Within each panel, there is a vertical list of pages to help navigate among the parameters.

To edit a page, select the **Edit** menu, then select **Parameter Pages**. This template editor is also useful for viewing commands and parameters that are used in the panels.

A.13 Action Controls

To the right of the parameter panel selection tabs are a series of buttons that change, depending on the currently displayed panel. The buttons appear when a tab is selected (buttons not active on a data station are shown in gray).

A.14 Hardware Bar



The hardware bar contains the following:

- “Trash Can,” page 212
- “RF Watts,” page 212
- “Acquisition Status Details,” page 212
- “History of Acquisition Messages,” page 212
- “History of All Messages,” page 212
- “Message Display,” page 212

The right portion displays the current state of the acquisition system and system messages.

Hiding and Showing the Hardware Bar

Click on the arrow icon to the left of the trash can to hide or show the hardware bar.

Trash Can

Dragging an item to the trash can from the Locator or other area generally removes the item and adds it to the trash can.

Double-clicking on the trash can enables you to view items in the trash can area. In this mode objects can be restored from the trash can by selecting them and then clicking the **Restore items** button. To exit this mode, double-click on the trash can.

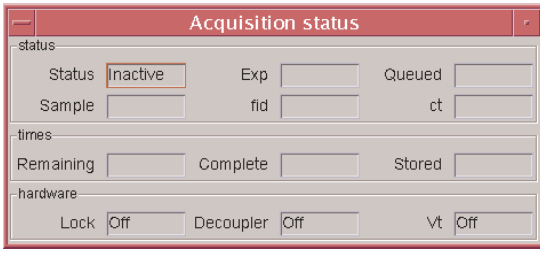
CAUTION: **Emptying the trash can deletes data from the disk.**

RF Watts

Click on this icon to open a window showing a history of rf power appears. To close the window, click on the icon again. Click the right mouse button on this icon to open a window enabling channel selection.

On human imaging systems, this button opens a window that displays the rf power as a function of time.

Acquisition Status Details



Click on the  icon. To close the window, click on the icon again to open a window showing acquisition status details.

History of Acquisition Messages

Click on the  icon To see a history of all acquisition messages. Click on the icon again to close the window. Click the right mouse button within the scrolling message window to change the text view options.

History of All Messages

To see a history of all spectrometer messages, click on the  icon. To close the window, click on the icon again. Click the right mouse button within the scrolling message window to change the text view options.

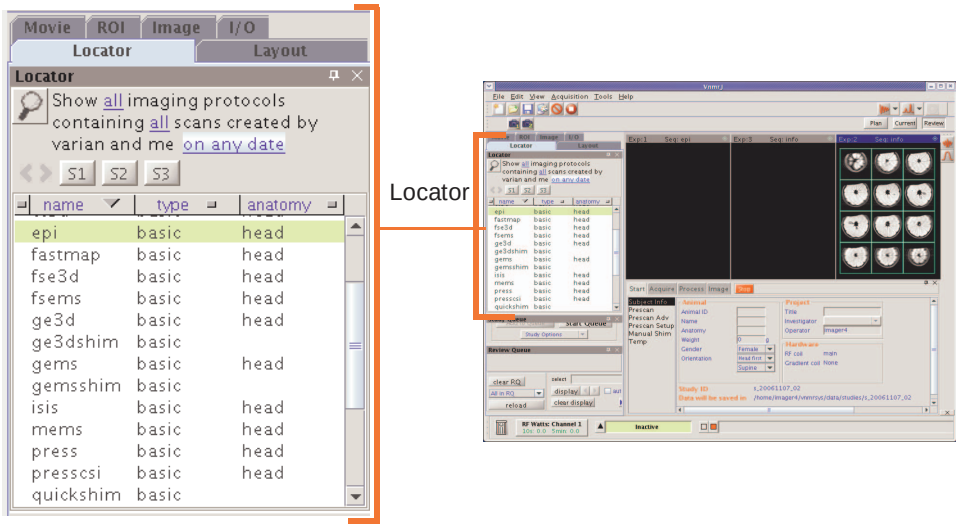
Message Display

The message display shows the last message that occurred. Messages can be informational, a warning, or an error message.

Appendix B. Locator

Sections in this chapter:

The locator, shown below, is a database browser that provides access to data sets, experiments, shim sets, commands, and other things. Additional information on setting up the locator data base are found in the *VnmrJ Installation and Administration* manual



The Locator enables access to information on all or part of the disk environment. The scope of the Locator’s actions is determined by the administrator who sets the global and local the scope of the Locator.

The Locator works similar to a directory or file manager and uses minimal filtering of the information. Rather than only showing the files that satisfy the requirements, it shows two or three lists of information. With two lists, one list shows the items (or objects) that satisfy all terms of the search while the other list shows the objects that do not. Where some terms have a boolean relationship, the Locator shows three lists:

- Objects that meet all criteria
- Some of the boolean terms met
- Remaining objects

The determination of which of these lists it are shown is determined by the construction of the underlying Locator statement.

The Locator displays three attributes for each object within each list. Object attributes are not limited to those in the Locator statement. Any one of the attributes can be designated as the sort attribute, in which case the objects in each list are sorted by the value each has for this attribute.

B.1 Locator Settings and Interface Elements

The Locator interface elements are described in the following sections:

Locator Settings

Set the locator settings as follows:

1. Click on **Tools** on the main menu.
2. Click on **Systems Setting** tool.
3. Select the **Display/Plot** tab.

Max # of items to show in locator– enter a value in the field.Values larger than 2000 slow the locator response. Refer to appendix on locator administration in the *VnmrJ Installation and Administration* manual for more information on working with the database.

Display only matching items in locator — check box: enabled if checked.

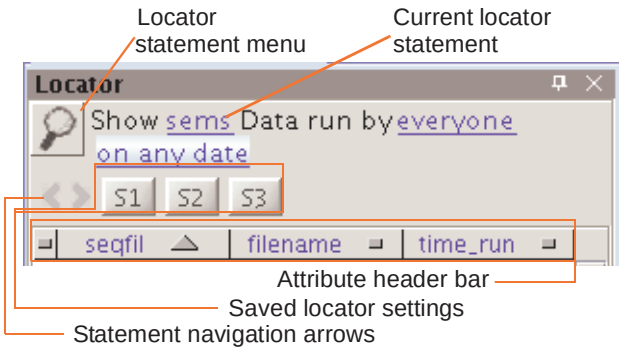
Day Limit of files in Locator (neg = forever) — Enter a value.

Turn off locator— check box to turn the locator off.

Locator Statements and Menu

A magnifying glass and the current locator statement are at the top of the Locator.

The magnifying glass is the menu of currently available locator statements. This menu includes both statements provided by Varian, Inc. and those customized and saved by the user.



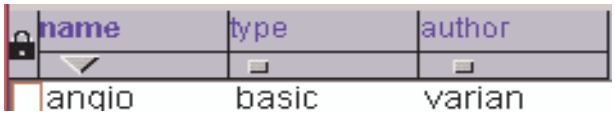
Locator statements are statements in which a word or phrases are colored and underlined in a manner similar to links in a web page. Each link hides a menu of choices, of which the currently displayed phrase is an example. The choices available vary with the types of data currently known to the locator.

Navigation in the Locator

Below the locator statement is a pair of arrows (statement navigation arrows), which enable you to move forward and back through past locator operations, applying each to the current locator environment. Thus a set of locator statements can be rapidly applied in a changing environment.

Attributes

Below the icons is the **attribute header bar**. This bar enables you to select the attributes displayed and to arrange the objects in each list in a number of ways.



The **padlock** enables locking an object against archival. This feature is not yet implemented.

The next three fields are the currently displayed attributes. Change any column by clicking on the attribute label and selecting a different attribute from the drop-down list. Below each label is its hot zone. The hot zone can be either a **block** or a **triangle**. Only one attribute at a time has a triangle and it is this attribute that serves as the sort term for each list.

- Click on a **block** to sort by this attribute.
- Click on the **triangle** to reverse the sort order.

The boundaries between the attribute labels are adjustable. Simply place the mouse cursor on the boundary you wish to adjust. Wait for the adjust cursor. Click and drag the boundary to its new position and release.

Objects in the locator are available for a number of actions. A single click selects an object. The selected object can then be dragged to another part of VnmrJ in which case the action taken will depend on the type of object and where the object is dropped. Alternatively a double click on an object will cause the most likely action to occur. These actions will be discussed shortly.

The value of an attribute might be longer than the width of the column in the locator. A tool tip appears for a period of time when the mouse cursor rests on an attribute value. The tool tip contains the full value of the attribute.

Attribute Lists

The list of attributes in the drop-down lists are controlled by configuration files. There are three file names, for three different types of items in the locator. These are:

- shuffler_param_list for 'vnmr data' and 'vnmr parameter' files
- study_param_list for 'study' items
- data protocol_param_list for 'protocol' items

Each of these can exist for each of the appmode types and for individual users. That is, appmode types of imaging, standard (experimental liquids & solids), and walkup. The attributes visible in the drop down menu for each appmode type, will be controlled by files in the appropriate directories. If a user does not have an individual file, the file in the appropriate appmode directories will be used. If there is no file in the imaging or walkup

directories listed above, then the file in `/vnmr/shuffler` will be used. If users have their own individual files, the attributes listed in it must also be in the appmode directory file. That is, a user's files can limit attributes shown, but cannot add to the list of attributes shown beyond the attributes in the system files.

Wildcards

Wildcards can be used in attribute values, but not for the attribute name itself. For example, `'file*'` to specify the attribute `'filename'` is not allowed. Selecting an attribute of `'filename'` and editing the selection value to be `'p31*'` to show all files whose names start with `'p31'`. `'?31*'` is allowed and shows all file starting with any single character followed by `'31'`, followed by `0` or more characters. The leading `'?'` allows upper or lower case `'P'` and any other character. This does not apply to dates.

The following wildcards can be used:

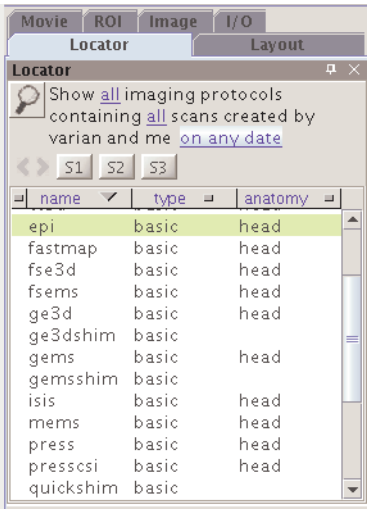
- `'*'` or `'%'` can be used to match any number of characters
- `'?'` or `'_'` can be used to match any single character

B.2 Using the Locator

Use the mouse to select or drag-and-drop items in the locator interface.

- "Searches," page 216
- "Dragging and Dropping from the Locator," page 216
- "Editing File Names from the Locator," page 217
- "Configuration Files," page 217

Searches



Clicking the magnifying glass with the left mouse button brings up a menu of searches. Selecting one changes the *search sentence* displayed at the top of the locator. The result of the search is displayed in the list. Those items in the white part of the list satisfy the search sentence. Those in the gray part do not. Three attributes are displayed for each item found. These correspond to the three columns in the list. Clicking on the attribute name at the top of the list with the left mouse button brings up a menu of attribute choices.

Dragging and Dropping from the Locator

Clicking on an item in the locator list selects that item and drag it to the graphic area or the parameter panel area to cause the appropriate action. For example, dragging a data set to the graphic area retrieves that data set into the current workspace (experiment) and displays the spectrum. Dragging a workspace to the graphic area joins that workspace (experiment) with the graphic area. Double-clicking on an item performs the same action as dragging the item to the graphics canvas.

Dragging-and-dropping an object will have an action appropriate to the context. In many cases the same effect will be obtained by double-clicking on an object. Some examples are:

- Dragging a protocol into the experiment queue adds the protocol into the queue.
- Dragging a study into the experiment queue loads the study into the queue.
- FIDs are retrieved into the current workspace. If Autoprocess on drag-and-drop is enabled is System Settings, process macro is invoked so that the FID is transformed.
- Double-clicking a workspace joins that workspace. Drag-and-drop does the same.
- Double-clicking a parameter set loads that set in the current workspace, as will a drag-and-drop.
- Double-clicking a shim set loads the shims. Drag-and-drop to the current shim buttons also loads the shims into acquisition.
- Dragging either data or shims and dropping them in the trash (lower left in the hardware bar) deletes the object (removes the file from the disk).

  Retrieve an objects from the trash can by double-clicking on the trash can, selecting an object, and clicking the **Restore items** button.

Editing File Names from the Locator

When a new file is added to the locator from within VnmrJ, the new item appears in its appropriate spot in the Locator, and it appears in green at the top of the locator window. If one of the columns in the Locator is *filename*, click on the green editing filename and change it.

Press **Return** or click on another line after changing the file name. The old filename is to removed and the new one added. The Locator redisplays to show the new name.

Configuration Files

Configuration files for the locator are contained in the following directories for the different appmode types:

Interface	*Directory*
Standard (experimental)	`/vnmr/shuffler`
Imaging	`/vnmr/imaging/shuffler`
Walkup	`/vnmr/walkup/shuffler`
Individual users	`$vnmruser/shuffler`

B.3 Locator Statements

Sorting Locator Statements

- “Sort Protocols,” page 218
- “Sort Studies,” page 218
- “Sort Workspaces,” page 218
- “Sort NMR Data,” page 218
- “Sort Records,” page 219
- “Sort Parameter Files,” page 219
- “Sort Shimsets,” page 219

Sort Protocols

The statements in this category show the list of NMR imaging protocols. The two sort options provided are

- by scan and type
- by anatomy and coil.

Sort Studies

The statements in this category allow you to sort by study parameters:

- by project
- by gender and age
- by scan and coil

Sort Workspaces

The statements in this category allow you to sort by workspaces parameters:

- All
- by group

Sort NMR Data

Entries show the known NMR data sets, but differ in the actual format of the statement as well as the initial set of attributes shown. The most comprehensive statement is the last one, **by user defined attributes and date** (this is also the one that is least likely to be used, but it is discussed here to explore the scope of the data statements).

The generic statement is shown in Figure 50.

There are seven separate underlined choices in this statement: `seqfil, sems, anatomy, all, everyone, time_run, and on any date.`

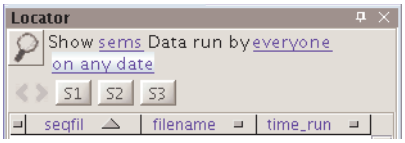


Figure 50. Generic Locator Statement

Clicking on any of the underlined phrases produces a drop-down menu of the choices in this position. The menus are environment sensitive so they will not display choices that do not exist. For example, if the first phrase is **`seqfil`**, then the second phrase will have only those pulse sequence choices that the locator has found in the data. Thus, **`sems`** will not appear in the drop-down menu unless there is some data that has been run with **`seqfil='sems'`**.

The logic of this statement is of the form:

Show attributes A and B of type C with additional limitations.

First, the additional limitations phrases enable you to select the owner of the data. This selection is determined by the administrator at the time a directory is made available to the Locator.

Second, the additional limitations enable reordering by date. There are various dates associated with data, for example, the time started or the time saved. Specify these date fields several ways or alter the date two ways:

- Using the left or right arrows to decrease or increase the date by one day each click.

All other statements supplied by us are simpler than the generic one. If there are certain statements that you use frequently, these can be promoted to the top of the menu simply by saving them again as your local variants.

Sort Records

The statements in this category show the list of record files that can be sorted as follows:

- by seqfil
- by study

Sort Parameter Files

The statements in this category show the list of NMR parameter files. Two major categories of parameter files are **System Param Files** and **My Param Files**. You can also select the statements **Test Files** and **by user defined attributes** to do other selective searches. After you select a category, the locator statement changes, e.g., **Show Test Files**.

Sort Shimsets

The statements in this category enable you to access the shim sets that you have saved. Note that the shim sets are saved with an automatically generated file name and with a descriptive shim name provided by you. This is one instance where the UNIX file name is less appropriate to sort on as an attribute than is the descriptive name.

Sort Command Macros

The generic statement in this category enables you to find a VnmrJ command or macro based on its attributes. The locator enables you to reorder commands and macros by a number of attributes. Once you find the command that you wish to use, a double click will execute it.

Sort Pulse Sequence Macros

The generic statement in this category enables you to reorder the set of macros used to setup different experiments, based on attributes that categorize the type of experiment, for example, 1D, 2D, or 3D. Double-clicking on a macro executes it, setting up the current workspace to run this experiment.

Appendix C. DICOM® Conformance Statements

Sections in this chapter:

C.1 DICOM Conformance Statements for Storage on VnmrJ

DICOM conformance statement for MIR CTN Applications are found at:

http://wuerlim.wustl.edu/DICOM/ctn-docs/conformance.pdf

- or -

http://www.erl.wustl.edu/DICOM/ctn-docs/conformance.pdf

Additional information can be found at:

http://www.erl.wustl.edu/DICOM/ctn-docs/doc_index.html

C.2 DICOM Conformance Statements for Print-SCU on VnmrJ

This appendix describes the DICOM conformance statement for VnmrJ that serves as DICOM Print Service Class User (SCU). In order to comply with the DICOM V3.0 specification, only standard Service Object Pair Classes (SOP) is used.

The following summarizes the sequence of real-world activities.

1. Establish Association

   VnmrJ will initiate associations by using TCP/IP protocol.

   The attributes of both Application Entities are defined in the file `/vnmr/dicom.cfg`.

Attribute	*Description*
AeTitle	Title of Application Entity of Printer Service Provider.
Hostname	hostname of Printer Service Provider.
Port	port number which Printer Service Provider will accept associations.
ScuTitle	Title of Application Entity of Printer Service User.

In this step, the following SOP Class is used:

SOP Class Name	*SOP Class UID*
Printer	1.2.840.10008.5.1.1.17

2. Create Presentation Look Up Table

   If Printer support Presentation LUT then it will request the PresentationLUT UID from Printer Service Provider.

   In this step, the following SOP Class is used:

SOP Class Name	*SOP Class UID*
Presentation LUT	1.2.840.10008.5.1.1.23

   The following attributes are set:

Attribute Name	*Tag*	*Default Value*
Presentation LUT Shape	(2050,0020)	IDENTITY

3. Create Basic Film Session

   VNMR will ask SCP to create Basic Film Session. In this step, the following SOP Class is used:.

SOP Class Name	*SOP Class UID*
Basic Film Session	1.2.840.10008.5.1.1.1

   Some attributes defined in the file `dicom.cfg` are sent to SCP.

Attribute Name	*Tag*	*Default Value*
Number of Copies	(2000,0010)	1
Print Priority	(2000,0020)	LOW
Medium Type	(2000,0030)	CURRENT
Film Destination	(2000,0040)	CURRENT
Illumination	(2010,015e)	1000
Reflected AmbientLight	(2010,0160)	10
Referenced Presentation LUT Sequence	(2050,0500)	None
Referenced SOP Class UID	(0008,1150)	PresentationLUTSOPClass
Referenced SOP Instance UID	(0008,1155)	Unique Identifier

4. Create Basic Film Box

   In this step, the following SOP Class are used:

SOP Class Name	*SOP Class UID*
Basic Film Box	1.2.840.10008.5.1.1.2

Some attributes defined in the file `dicom.cfg` are sent to SCP:

Attribute Name	*Tag*	*Default Value*
Image Display Format	(2010,0010)	STANDARD\1,1
Annotation Display Format ID	(2010,0030)	None
Film Orientation	(2010,0040)	PORTRAIT
Film Size ID	(2010,0050)	None (Printer Default)
Magnification Type	(2010,0060)	None (Printer Default)
Smoothing Type	(2010,0080)	None (Printer Default)
Border Density	(2010,0100)	None (Printer Default)
Empty Image Density	(2010,0110)	None (Printer Default)
Min Density	(2010,0120)	None (Printer Default)
Max Density	(2010,0130)	None (Printer Default)
Trim	(2010,0140)	No
Configuration Information	(2010,0150)	None
Requested Resolution ID	(2020,0050)	None

5. Set Basic Grayscale Image Box

   In this step, the following SOP Class is used:

SOP Class Name	*SOP Class UID*
Basic Grayscale Image Box	1.2.840.10008.5.1.1.4

Some attributes defined in the file `dicom.cfg` are sent to SCP:.

Attribute Name	*Tag*	*Default Value*
ImagePosition	(2020,0010)	1
Polarity	(2020,0020)	NORMAL
Requested Image Size	(2020,0030)	None (Printer Default)
Requested Decimate Crop Behavior	(2020,0040)	None
Grayscale Image Sequence	(2020,0110)	None
Samples Per Pixel	(0028,0002)	1
Photometric Interpretation	(0028,0004)	MONOCHROME2
Rows	(0028,0010)	rows of image data
Columns	(0028,0011)	columns of image data
Photometric Interpretation	(0028,0004)	MONOCHROME2
Pixel Aspect Ratio	(0028,0034)	1\1
Bits Allocated	(0028,0100)	8
Bits Stored	(0028,0101)	8
High Bit	(0028,0102)	7
Pixel Representation	(0028,0103)	0

6. Send Image Pixel Data

   The Raw Image data will be send to printer.

7. Delete Basic Film Box

   Send Delete Basic Film Box Request to printer.

8. Delete Basic Film Session

   Send Delete Basic Film Session Request to printer.

9. Delete Presentation LUT

   Send Delete Presentation LUT Request to printer.

10. Release Association

C.3 Dicom File Generation

Introduction

DICOM file format is a standard file format used in the Medical imaging field.

This file format is recognized by most image analysis, display and printing software. DICOM files contain a header with various experimental and image related parameters followed by image data. The data is commonly 8- or 16-bit integer type. For example, a multi-image

dataset is arranged in the following order:

```
Header - Image#1 - Image#2 - etc.
```

The VNMR software generates images with an ascii (text) header and binary data (FDF format). In the case of 2D images, each image is stored as a separate file labelled slicexxximagexxxechoxxx.fdf, where, xxx refers to a number, such as slice number or echo number. The extension fdf refers to the FDF file format, used in Varian spectrometers and the parameters associated with the image are stored in a separate parameter (text) file, procpar. A limited set of the imaging parameters are contained in the FDF file header whereas all acquisition and processing parameters are contained in the procpar file. The images after a scan are stored in a directory, for example, gems_01.img.

```
gems_01.img/
slice001image001echo001.fdf
slice002image001echo001.fdf
slice003image001echo001.fdf
procpar
```

The DICOM file generation routine converts the images into DICOM files. The user may specify a single (default) or multiple image output. In the former case all slices are saved as a single, pseudo-3D image and in the latter case individual slices are generated.

A single image output is represented by:

```
DICOM_Header - Slice#1 - Slice#2 - Slice#3
```

In the case of multiple image output:

```
DICOM_Header - Slice#1
DICOM_Header - Slice#2
DICOM_Header - Slice#3
```

The resulting files are stored in the users local directory, as:

`$home/vnmrsys/dicom/image.dcm` -single image output

In the case of multiple image output the images are named,

`slicexxximagexxxechoxxx.dcm`.

Similarly, 3D images can also be generated by the dicom conversion routines.

Using the Review Q and Locator

1. Select the Review VP.
2. Clear all previously loaded files in the Review Queue - click on Clear RQ.
3. Load the fid file. Using the locator, double click on a previously acquired dataset.

   This action will load the raw data (.fid) and image file into the Review viewport. You may also use the file browser to select the fid file and load it into the Review VP. The Process routine is called to process and display the images. (It is necessary to load the fid file because the DICOM header is initialized using the parameters saved with the fid file.)
4. Enter a filename or the full path and filename.
5. Select the I/O Tab in the vertical panel area and click on the DICOM storage button. The DICOM file, image.dcm, will be saved in the $home/vnmrsys/exp# directory (default).

Interactive Mode

1. Clear all the images displayed in either the Plan or Review viewport.
   a. In the review VP click on Clear RQ
   b. In the plan VP, Image => Unload Data, All
2. Load the raw data (.fid) file. Using the file browser, double click or drag and drop the .fid file into display window.
3. Initialize the processing parameters if necessary. Using the Process panel, you may change the zerofilling (fn, fn1) or apodization (gf, gfs) parameters.
4. Click on the Process button to process and display the images.
5. Select the I/O Tab in the Image display area and click on DICOM storage button to generate the DICOM file.
6. A single output file will be saved in the specified file.

Other options:

- `dicomstore` — generates a single image output (default), same as dicomstore('single')
- `dicomstore('single')` — generates a single image output
- `dicomstore('multi')` — generates a dicom image for each slice, or array element. The images will carry the same base name as the fdf file but with a .dcm extension.

Generating DICOM Files Automatically During a Study

1. Add the dicomstore macro to the execprocess parameter:
   a. Click on **Edit**.
   b. Select **Create Protocol.**
   c. Select **Configure EXEC parameters.**
2. Add `dicomstore` to the Processing commands

   e.g. `im2D('proc') dicomstore`

   or

   `execprocess = 'im2D(`proc`) dicomstore'`
3. Save the protocol
4. The dicom files (.dcm) will be created after image processing and then saved in the study data directory along with the (.fdf) images.
5. Enable or disable the DICOM file generation by creating the parameter, `dicomflag`.

   `create('dicomflag','flag')`

   The default condition is equivalent to `dicomflag='y'`, which generates the DICOM files. Set `dicomflag='n' to` disable.

Customizing the DICOM Header

The DICOM header is created using a parameter template, `/vnmr/user_templates/plot/dicom.default`. The macro, `dicomhdr`, initializes the DICOM header by reading the template and the parameter information loaded into the present workspace. The user may specify the parameter information to be stored in the DICOM header by creating a customized template file. The `dicomhdr` macro selects the template in the following order:

- `$home/vnmrsys/templates/dicom/seqfil`
  `-seqfil` refers to the pulse sequence name
- `dicompath/seqfil`
  `-dicompath` parameter contains a directory name:
  `/vnmr/user_templates/dicom/seqfil`
  `$home/vnmrsys/templates/dicom/default`
- `/vnmr/user_templates/plot/dicom.default`
  — default, system file

Additional Notes

- A template (text file) of the DICOM file header is generated in `$home/vnmrsys/dicom/tmp/ctn.input` file.
- All intermediate files are put in a temporary directory, `$home/vnmrsys/dicom/tmp`.
- In the case of 2D images,
  Rows = Read dimension size
  Columns = PE dimension size
  Frames = no of images or slices
- In the case of 3D images,

Rows = PE#1 dimension size

Columns = read dimension size

Frames = PE#2 dimension size

Limitations

1. Some parameters in the DICOM header may not be initialized.
2. Image orientation parameters are not set correctly.
3. It is assumed that the parameters in the present viewport correspond to the displayed image.
4. When arrayed, multi-slice images are selected a single DICOM image file will contain all the images. The DICOM file generation programs do not distinguish between the slices and arrayed images.

Appendix D. NMR Imaging Concepts

Sections in this chapter:

This chapter introduces the basic concepts necessary to understand MRI experiments and become familiar with the terminology and principles in simple experiments in conventional NMR because this chapter focuses on MRI-related topics. NMR concepts can be easily understood when the process of a simple imaging experiment is analyzed. The 2D spin-warp imaging sequence that is commonly performed in MRI is used in this chapter as an example to illustrate principles and experimental aspects related to NMR.

The spin-warp imaging sequence is based on the 2D Fourier transform principle for converting the time domain NMR signals into image data. Most of the other imaging techniques are also based on the Fourier transform idea and can be regarded as variations of the spin-warp method.

D.1 Basic Imaging Principles

This section contains a brief introduction to nuclear magnetic resonance (NMR) imaging, magnetic resonance spectroscopy, chemical shift imaging, the 2D spin-warp imaging sequence, and lists several additional references for more information about NMR imaging.

NMR Imaging

NMR imaging, or MRI, is used to obtain a map of the distribution of spins in a sample (for example, protons in water). The inherent properties of the spins—such as spin density (T_1, T_2, T_2*), diffusion coefficient, etc.—affect the signal intensity in imaging experiments, which makes the contrast in the resulting images easy to distinguish. This feature of distinguishing different sample regions based on NMR-related properties makes imaging an important tool in clinical, biological, and material sciences.

For example, clinical MRI scanning techniques are the preferred method for distinguishing various soft tissues in the body. The spin density (T_1 and T_2) of water in different tissue regions makes the contrast between tissues easy to distinguish. Experimental techniques can be designed to further enhance the contrast between tissues. Special imaging techniques can also be used to study flow, perfusion, diffusion, and susceptibility effects.

Methods for Obtaining Spectral and Spatial Information

Magnetic resonance spectroscopy (MRS) is the study of spectroscopic information in different spatial regions in a sample. Volume-localized spectroscopic methods are used to obtain spectral information from specific locations in a sample. Chemical shift imaging (CSI) methods are another related class of experiments that are designed to provide both spectral and spatial information from a single experiment.

2D Spin-Warp Imaging Sequence

2D spin-warp imaging is one of the simplest imaging sequences commonly used in NMR imaging. Most of the other imaging sequences are variations of this fundamental sequence.

In "Basic Imaging Principles," page 229, the basic principles of imaging are discussed based on the spin-warp sequence. The information in that section is primarily meant to help a novice grasp the basic principles and terminology of NMR imaging. The chapter contains a description of the experimental aspects of NMR imaging so that you can understand the correlation between the parameters and the resulting image. For a more theoretical understanding of the imaging experiments, refer to any basic text or reviews on MRI.

References

The manual *Getting Started* contains more general information about the software interface. Consult the online help or the PDF files on the manuals CD for additional information on commands, macros, and parameters.

D.2 Time Domain to Spatial Domain Conversion

As an example of Time domain to spatial domain conversion, consider a tube of water inserted within an NMR probe and placed in the center of the magnet. The magnet produces a homogeneous field in the region surrounding the water sample. A single pulse experiment yields an NMR signal that, on Fourier transformation (FT), produces the frequency spectrum of the sample, as shown in Figure 51.

A single line at the resonance frequency, f_0, is obtained. The frequency is defined by the following Larmor equations:

$$f_0 = \gamma' \cdot B_0 \qquad \text{[Eq. 6]}$$

$$\gamma = 2\pi \cdot \gamma' \qquad \text{[Eq. 7]}$$

In Equation 6 and Equation 7, γ is the gyromagnetic ratio (rad.gauss^{-1}sec^{-1}) and B_0 is the magnetic field strength (gauss).

For protons, γ is 2.6752×10^4 rad.gauss^{-1} sec^{-1} and γ' is 4257 Hz.gauss^{-1}. In MRI, the magnet strength, B_0, is usually expressed in tesla (1 T = 10,000 gauss), whereas in conventional NMR, magnet strength is commonly referred to in terms of the proton resonance frequency in MHz.

The frequency spectrum that is displayed in NMR is referenced with respect to the rf transmitter frequency. The center of the spectrum refers to the carrier frequency. Therefore, spectral components that are above (positive) and below (negative) can be measured by NMR. In MRI, the spatial-frequency components are measured with respect to the resonance frequency of the major component in the sample, usually water. Therefore, the carrier is placed on the water resonance frequency, f_0, as part of the initial setup procedure. Now, the center frequency in the spatial-frequency domain refers to the origin, or the center, of the gradient frame of reference.

In addition to the standard equipment in NMR spectrometers, imaging systems are equipped with *X*, *Y*, and *Z* field gradient coils that are designed to produce linear field gradients along the *x*, *y* and *z* directions, respectively. In MRI, these field gradients are used to get the spatial information from the sample. The *x*, *y*, and *z* gradient fields are orthogonal to each other and their origins lie at the center of the gradient system. The field produced in each direction is linear and ranges from a negative value to a positive value; the field at the origin is zero.

Consider the water sample shown in Figure 51 and apply a linear field gradient along the *y* direction, ranging from a negative value to a positive, as shown in Figure 52.

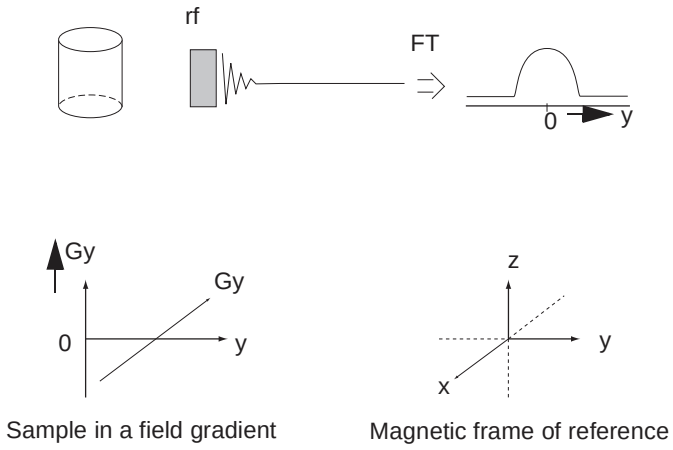


Figure 52. Effect of a Field Gradient Along Direction *y*

In Figure 52, the field along the *y* direction is no longer constant but varies linearly, depending on the position *y*. The field at a particular location, *y*, is defined by *y*.*Gy*, in which

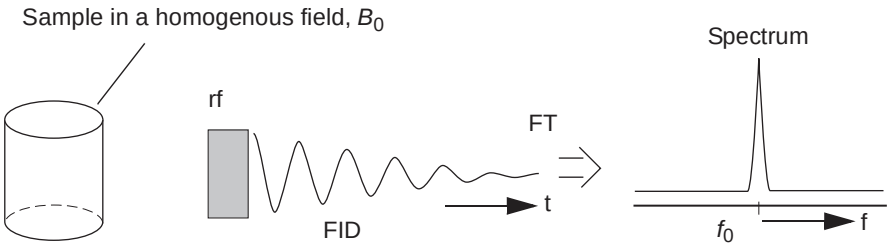


Figure 51. Frequency Spectrum Produced by an NMR Signal

Gy (in gauss/cm) refers to the field gradient along *y* direction. Therefore, the spins along the *y* direction experience a unique field depending on the location of the *y* direction.

The frequency, *fy*, of the spins at various *y* locations is defined by the following equation:

$$fy = \gamma' \cdot (B_0 + y \cdot G_y) \qquad \text{[Eq. 8]}$$

In this equation, *y* refers to the *y* location (in cm) and *Gy* refers to the applied field gradient (in gauss/cm).

Equation 8 is the most important equation in MRI because it correlates the spatial position of the spins, *y*, to the measured parameter, *fy*. That is, the frequency spectrum measured is a direct reflection of spatial information (along *y*) because, as shown in Equation 9,

$$fy \propto \gamma \qquad \text{[Eq. 9]}$$

when *y*=0, Equation 9 is the same as Equation 6 and Equation 7, so the frequency at the origin of our frame of reference is equal to the resonance frequency of water, f_0. It is necessary to place the rf transmitter frequency at f_0 so that images can be spatially referenced with respect to the origin of our reference frame or the center of the magnet.

Under the previously described conditions, a single-pulse sequence yields a spectrum that contains a continuous range of frequencies, as shown in Figure 53.

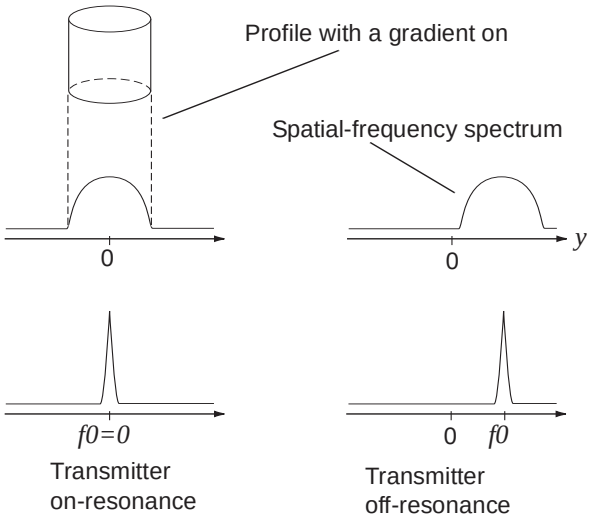


Figure 53. Frequency Ranges

The frequency spread is a direct reflection of the spatial position of the spins along the *y* direction. Signal intensity is directly related to the amount of water at various positions along *y*. The tube of water appears as a semicircle in the center of the spectrum. The *spatial-frequency* spectrum, shown in Figure 53, is also referred to as a *profile* or *projection* of the sample along the *y* direction.

The projection resolves the spatial-frequency components along a single direction. But an imaging sample is three-dimensional, so more imaging must be done to visualize our sample in 3D space. Many experiments have been designed in the past to uniquely identify and map the spin distribution in the sample. Each experiment has its own advantages and limitations. Experiments based on the spin-warp techniques are the most commonly used in MRI. Therefore, it is useful to understand how these experiments resolve the spatial-frequency components of a 3D sample.

The 2D spin-warp experiment contains the following three parts, which correspond to the *preparation*, *evolution*, and *detection* steps in a conventional 2D NMR experiment:

- Slice selection
- Phase encoding
- Readout

D.3 Logical to Laboratory Axes Transformation

Imaging experiments require a coordinate transformation from logical axes (slice select, phase encode, and readout) to laboratory axes (X, Y, and Z) for the applied gradients. Table 15 lists the standard orientations.

Table 15. Standard Orientations

orient	*psi*	*phi*	*theta*	*slice select*	*phase encode*	*readout*
trans	0	0	0	Z	X	Y
cor	0	0	90	Y	X	Z
sag	90	0	90	X	Y	Z

Oblique angles would involve a *mixing* of the laboratory axes. This coordinate transformation occurs in software or in hardware using the Coordinate Rotator board (if installed):

- **Software** – when the `Gradients` entry is set to `WFG+GCU` in the Config window (or the global parameter `gradtype='www'`).
- **Hardware** – if a Gradient Coordinate Rotator board (01-905404-01) is installed and when the `Gradients` entry is set to `Gradient Coordinate Rotator` in the Config window (or the global parameter `gradtype='rrr'`).

With the Coordinate Rotator board installed, it is necessary to download to the board the coefficients required for the transformation. This download is accomplished with the pulse sequence element `rotate();`.

This element is actually a macro for the fully expanded pulse sequence element, `rotate_angle`:

```
rotate_angle(psi,phi,theta,offsetx,offsety,offsetz,delayx,delayy,delayz)
```

`psi`, `phi`, and `theta` arguments are the traditional angles of rotation.
`offsetx`, `offsety`, and `offsetz` arguments are static shim offset values that can be added to the laboratory axis gradients.
`delayx`, `delayy`, and `delayz` arguments are gradient amplifier delay values.

The pulse sequence element `rotate()` uses the values of `psi`, `phi`, and `theta` in the parameter set and sets the shim offsets and the amplifier delays to zero.

`rotate()` downloads the necessary numbers to the Coordinate Rotator board in order to accomplish the matrix multiplication and add calculation for the coordinate rotation. The time of the download is included in `apdelay.h` as `INOVA_CRB_ROTATE` and is equal to 60.0 microseconds.

The calculation of the rotated gradient output requires 3.1 microseconds and is accomplished at each waveform generator strobe. Therefore, waveform generator dwell times should not be less than 4 microseconds. This is in good agreement with the DAC update rate of 4 microseconds.

Another pulse sequence element, `init_crb()`, can be used explicitly in a pulse sequence to set the rotation matrix to `unity` and the shim offsets and gradient amplifier delays to `zero`. This element would be used to apply a gradient on a specified laboratory axis without any coordinate transformation.

It is also possible to have more than 1 `rotate()` pulse sequence element in a pulse sequence. For example, a gradient at the standard orientation of `psi`, `phi`, `theta` and

then an additional gradient for saturation bands would be accomplished with the following code:

```
status(A);
xgate(ticks);

rotate();     /* default angles psi, phi, theta */
```

(other events or options in the pulse sequence go here)

```
/* spatial sat pulses.  */
if (sat[0] == 'y') {
   for (j=0; j<nsat; j++) {
      obspower(satpwr);
      obspwrf(satpwrf);
      poffset(satpos[j],gsat[j]);
      rotate_angle(spsi[j],sphi[j],stheta[j],0,0,0,0,0,0);
      oblique_gradient(0.0,0.0,gsat[j],spsi[j],sphi[j],stheta[j]);
      delay(trise);
      shapedpulse(satpat,psat,zero,rof1,rof2);
      zero_all_gradients();
      delay(trise);
   }
rotate();     /* set back to default = psi, phi, theta */
   obl_gradient(gcr,gcr,gcr);
   delay(tcrush);
   zero_all_gradients();
   delay(trise);
}
/*End of spatial sat pulse*/
```

The `rotate()` pulse sequence element is ignored in a pulse sequence if `gradtype` is NOT set to `'rrr'`, so it is harmless to have it there. The element has been added to Varian's standard imaging pulse sequences.

The Coordinate Rotator board works with the following imaging pulse sequence elements:

```
obl_gradient(LEVEL1,LEVEL2,LEVEL3)
oblique_gradient(LEVEL1,LEVEL2,LEVEL3,psi,phi,theta)

obl_imaging_shapedgradient(PAT,WIDTH,LVL1,LVL2,LVL3,LOOPS,WAIT)
oblique_imaging_shapedgradient(PAT,WIDTH,LVL1,LVL2,LVL3,psi,phi,theta, LOOPS,WAIT)

obl_shapedgradient(PAT1,PAT2,PAT3,WIDTH,LVL1,LVL2,LVL3,LOOPS,WAIT)
oblique_shapedgradient(PAT1,PAT2,PAT3,WIDTH,LVL1,LVL2,LVL3,psi,phi,theta, LOOPS,WAIT)

pe_gradient(STAT1,STAT2,STAT3,STEP2,VMULT2)
phase_encode_gradient(STAT1,STAT2,STAT3,STEP2,VMULT2,nv/2,psi,phi,theta)

pe2_gradient(STAT1,STAT2,STAT3,STEP2,STEP3,VMULT2,VMULT3)
phase_encode3_gradient(STAT1, STAT2, STAT3, 0.0, STEP2, STEP3, zero, VMULT2, VMULT3, 0.0, nv/2, nv2/2, psi,
     phi,theta)

pe3_gradient(STAT1,STAT2,STAT3,STEP1,STEP2,STEP3,VMULT1,VMULT2,VMULT3)
phase_encode3_gradient(STAT1, STAT2, STAT3, STEP1, STEP2, STEP3, VMULT1, VMULT2, VMULT3, nv/2, nv2/2,
     nv3/2, psi, phi, theta)

pe_shapedgradient(PAT,WIDTH,STAT1,STAT2,STAT3,STEP2,VMULT2,WAIT,TAG)
phase_encode_shapedgradient(PAT,WIDTH,STAT1,STAT2,STAT3,STEP2,VMULT2, nv/2,psi,phi,theta,one,WAIT,TAG)

pe2_shapedgradient(PAT,WIDTH,STAT1,STAT2,STAT3,STEP2,STEP3,VMULT2,VMULT3)
phase_encode3_shapedgradient(PAT, WIDTH, STAT1, STAT2, STAT3, 0.0, STEP2, STEP3, zero, VMULT2, VMULT3,
      0.0, nv/2, nv2/2, psi, phi, theta, 1.0, WAIT)

pe3_shapedgradient(PAT,WIDTH,STAT1,STAT2,STAT3,STEP1,STEP2,STEP3,VMULT1,VMULT2,VMULT3)
phase_encode3_shapedgradient(PAT, WIDTH, STAT1, STAT2, STAT3, STEP1, STEP2, STEP3, VMULT1, VMULT2, VMULT3,
     nv/2, nv2/2, nv3/2, psi, phi, theta, 1.0, WAIT)

pe_oblshapedgradient(PAT1,PAT2,PAT3,WIDTH,LVL1,LVL2,LVL3,STEP2,VMULT2,WAIT,TAG)
pe_oblique_shaped3gradient(PAT1,PAT2,PAT3,WIDTH,LVL1,LVL2,LVL3,STEP2, VMULT2,nv/2,psi,phi,theta,WAIT,TAG)

pe2_oblshapedgradient(PAT1,PAT2,PAT3,WIDTH,STAT1,STAT2,STAT3,STEP2,STEP3,VMULT2,VMULT3)
pe3_oblique_shaped3gradient(PAT1,PAT2,PAT3, WIDTH, STAT1, STAT2, STAT3, 0.0, STEP2, STEP3, zero, VMULT2,
     VMULT3,0.0,nv/2,nv2/2, psi, phi, theta, 1.0, WAIT)

pe3_oblshapedgradient(PAT1,PAT2,PAT3,WIDTH,STAT1,STAT2,STAT3,STEP1,STEP2,STEP3,VMULT1,VMULT2,VMULT3)
pe3_oblique_shaped3gradient(PAT1,PAT2,PAT3, WIDTH, STAT1, STAT2, STAT3, STEP1, STEP2, STEP3, VMULT1, VMULT2
     VMULT3,nv/2, nv2/2, nv3/2, psi, phi, theta, 1.0, WAIT)
```

D.4 Slice Selection

Magnetic resonance images are displayed as 2D pictures in either grayscale or color scale for further analysis. The 2D images represent the NMR signals taken from a *slice* in the sample, as shown in Figure 54. It is possible to selectively obtain signals from a slice by using a slice-selection process. During the preparation phase of the experiment, only the signals from a predetermined slice are pulsed so that only those excited spins contribute to the resulting image. Slice selection involves using a selective rf pulse in combination with a slice-selection gradient.

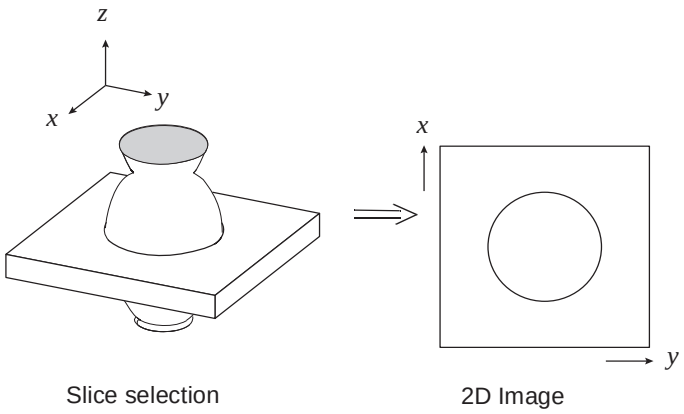


Figure 54. 2D Image Resulting from a Slice Selection

The section "Time Domain to Spatial Domain Conversion," page 230, described how the presence of a field gradient causes a spatial frequency spread (profile) along the gradient direction, shown in Figure 53. In the example shown in Figure 55, the profile along the z direction is rectangular because the signal intensities from the sample at various points along z are equal.

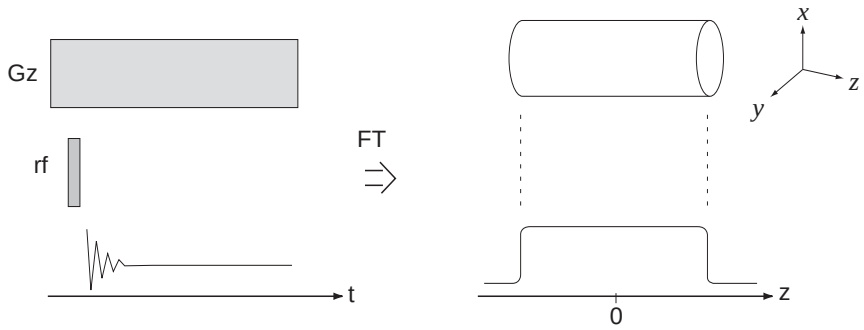


Figure 55. Rectangular Profile

The use of the hard pulse excites all of the spins in the sample because the excitation bandwidth is wider than the frequency spread of the profile. However, if a soft, selective pulse is used, a narrow bandwidth of the profile at the carrier frequency is excited. In other words, spins corresponding to a narrow slice at $z = 0$ are selectively excited. The resulting profile, referred to as the *slice profile*, is shown in Figure 56.

Ideally, a rectangular slice profile is preferred. A rectangular profile can be achieved by using a shaped pulse with its amplitude modulated in the form of a sinc function, as shown in Equation 10:

$$sin(\theta)/\theta \qquad \text{[Eq. 10]}$$

The phase θ is given in Equation 11:

$$\theta = 2\pi\nu t \qquad \text{[Eq. 11]}$$

In Equation 11, ν is the modulation frequency of the sinc function and t is the time axis.

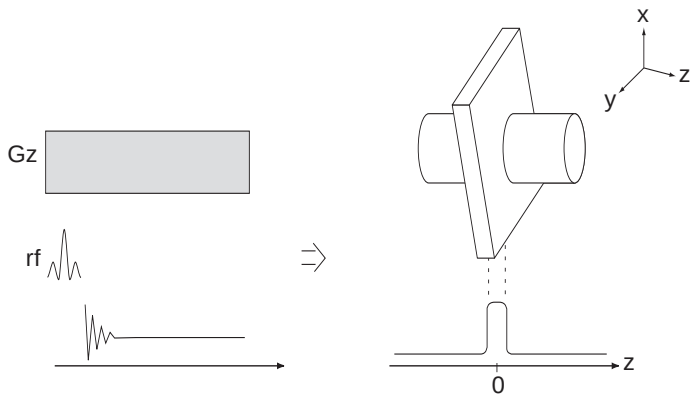


Figure 56. Slice Profile

Theoretically, the resulting excitation profile can be predicted by taking the Fourier transform of the sinc function, which in Equation 10 is rectangular in the frequency domain, as shown in Figure 57.

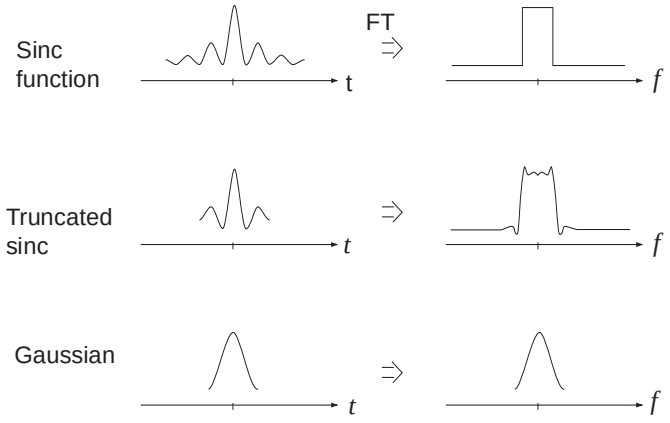


Figure 57. Sinc Function, Truncated Sinc Pulse, and Gaussian-Shaped Slice Profiles

However, in practice, because of experimental limitations such as T_2*, the pulses are limited to about 4 ms or less. The resulting truncated sinc function has an excitation profile, as shown in Figure 57.

Gaussian-shaped pulses are also used for slice-selection purposes. The Gaussian pulse produces a profile that is also a Gaussian, as shown in Figure 57. In general, this simplified approach is only true for short (about 30^o or less) flip angles. At larger flip angles, pulses show large behavior that is not ideal because of the nonlinear response of the NMR spins. The pulse shapes can be optimized to produce more ideal pulse characteristic for specific applications. For example, the rf pulses can be optimized by computer-iterative procedures to give slice profiles that are closer to rectangular shape. Such pulses minimize contamination of the image from regions outside the slice region of interest. The optimization procedures can also produce pulses that are closer to ideal in terms of flip angle and phase response across the slice profile.

So far, we have assumed the transmitter frequency is on-resonance, which corresponds to a slice plane at z = 0. It is also possible to excite a slice at any location along the slice direction by changing the rf transmitter frequency during the excitation phase of the experiment, as shown in Figure 58.

For offset slice selection, the transmitter offset frequency depends on the amplitude of the slice gradient that is applied and is defined by the following equation:

$$(fs - f_0) = \gamma' d \cdot gss \qquad \text{[Eq. 12]}$$

In this equation, *fs* is the transmitter frequency (in Hz) that is needed to excite a slice at distance *d* (in cm) from the origin, f_0 is the resonance frequency (in Hz) of water, and *Gss* is the slice-select gradient (in gauss/cm).

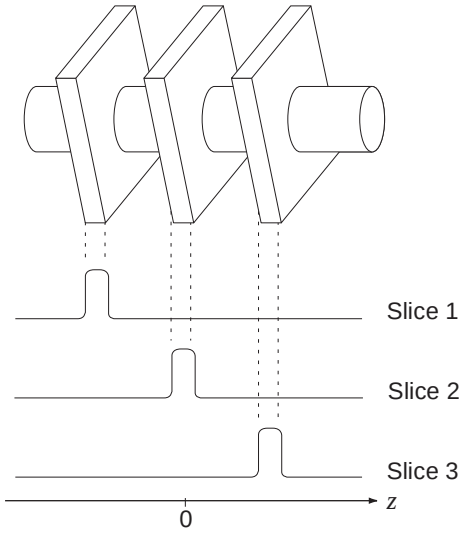


Figure 58. Multislice Excitation

Note: You must return the transmitter reference frequency to the original position during the detection stage of the experiment for proper referencing of the resulting profile.

Slice thickness is directly related to the bandwidth of the excitation pulse. For a sinc pulse, the excitation bandwidth *w* (in Hz) is defined by the following equation:

$$w = 2/\lambda \qquad \text{[Eq. 13]}$$

In Equation 13, λ refers to the wavelength (in sec) of the sinc pulse.

The slice thickness parameter is dependent on the slice gradient because the slice gradient affects the frequency spread or the profile along the slice direction. Equation 14 represents the relationship between the band width of the rf pulse *w* (in Hz), slice gradient *Gss* (in gauss/cm), and slice thickness *st* (in cm).

$$w = \gamma' \cdot Gss \cdot st \qquad \text{[Eq. 14]}$$

The presence of a slice gradient during the slice-selection pulse has an undesirable effect on the signal. The signals lose phase coherence, which results in a rapid signal loss. This signal loss can be restored by applying a gradient of opposite sign, as shown in Figure 59.

The amplitude of the slice rephasing gradient, *Gsd*, can be obtained by the following equation:

$$k \int_{t_7}^{t_4} gss \cdot dt = \int_{t_4}^{t_7} gss \cdot dt \qquad \text{[Eq. 15]}$$

In Equation 15, the factor *k* is approximately equal to 1. Equation 15 simply means that the shaded areas in Figure 59 must be approximately equal for maximum refocusing of the spins after the slice-selection pulse.

Some experimental macros and parameters related to slice selection are listed in Table 16. For more information on macros, parameters, and commands, refer to the online help *Command and Parameter Reference*.

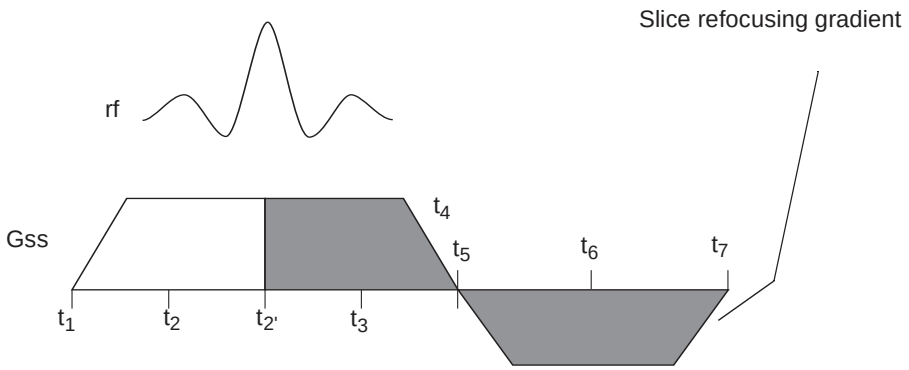


Figure 59. Signal Loss Restoration

Table 16. Experimental Macros and Parameters

Macro	*Function*
`plan`	Displays a menu that provides access to the target scan plan utilities. `plan` allows users to define slice positions, offsets `gap`, and the number of slices by using a graphical tool. The parameters can then be transferred to a target experiment using the `transfer` macro.
Parameter	*Function*
`ns`	Sets the number of slices to be acquired for multislice sequences.
`pss`	The position of slice offset, in cm. `pss` is an arrayed parameter; therefore, an arbitrary number of slices can be directly entered. A more convenient way to enter slice offset parameters is to use the `plan` macro.
`resto`	NMR resonance offset frequency, in Hz.
`thk`	The slice thickness, in mm.

D.5 Frequency Encoding

In the presence of a readout gradient, the spatial-frequency components can be directly visualized by observing the profiles along that direction. Even though the presence of a readout gradient during the FID signal gives the necessary information, in practice it is desirable to collect an echo signal. The echo signal, when Fourier transformed, generates only absorption components in the resulting spatial-frequency spectrum or profile. The broad dispersive components are cancelled because of the symmetry of the echo signal.

The cancellation of dispersive components is a big advantage when dealing with imaging data because the image or profile can be generated by simply calculating the absolute value without the need for any phase correction. An echo signal can be generated by first dephasing the excited spins by using a readout gradient pulse and then rephasing the spins by reversing the sign of the gradient. When the area of the rephasing gradient equals the area of the dephasing gradient, a “gradient echo” is formed, as shown in Figure 60.

The readout gradient is applied during the acquisition time, `at`, so that the echo appears at the center of the acquisition window, a condition that is assured if the shaded areas in Figure 60 are equal, as shown in the following equation:

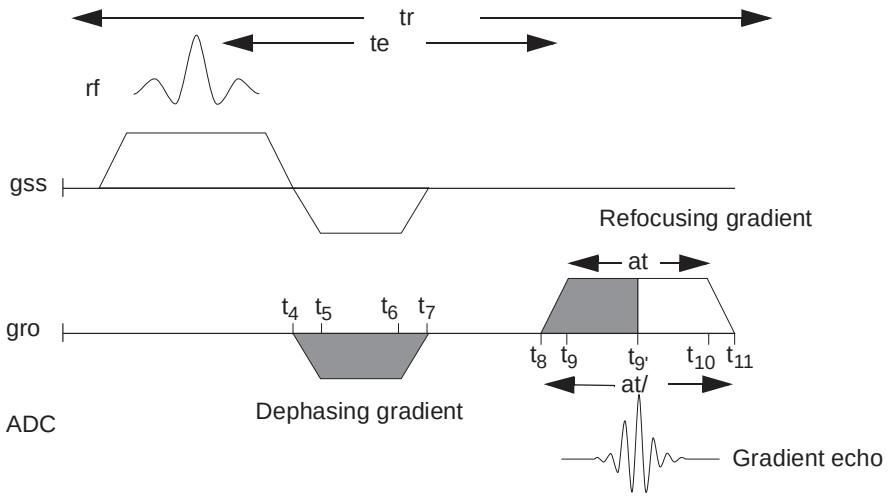


Figure 60. Readout Gradient and Gradient Echo

$$\int_{t_3}^{t_4} gro\,dt = \int_{t_5}^{t_6} gro\,dt \qquad \text{[Eq. 16]}$$

The Fourier transform of the echo signal gives the profile along the readout direction; only the signal from the selected slice contributes to the profile. The sequence shown in Figure 60 is commonly used to observe the profile during the initial setup of imaging experiments. The profile can be very useful in doing the following procedures:

- Positioning the sample along the readout direction.
- Checking or calibrating the rf pulse power.
- Setting the receiver gain.
- Checking the signal-to-noise ratio.
- Optimizing the pulse sequence parameters such as `te` and `tr`.

Readout gradient strength determines the frequency spread of image components in a profile. Therefore, the spectral width must be sufficiently wide to resolve all the spatial-frequency components along the readout direction. Otherwise, frequency components outside the spectral window cause “fold-over” artifacts.

The readout gradient and spectral width determine the *field of view* along the readout dimension, defined by the following equation:

$$sw = \gamma' \cdot gro \cdot lro \qquad \text{[Eq. 17]}$$

In Equation 17, `gro` (in gauss/cm) is the readout gradient, `lro` is the field of view along the readout dimension (in cm), and `sw` is the spectral width or bandwidth (in Hz). The spectral width is related to the acquisition parameters, defined by the following equation:

$$sw = (np/2)/at \qquad \text{[Eq. 18]}$$

In Equation 18, `np` is the total number of (real plus imaginary) points digitized, and `at` is the acquisition time (in sec). The maximum bandwidth, `sw`, is determined by the digitizer used on the system. A typical 16-bit digitizer, used on most imaging systems allows a

spectral bandwidth limit of 500 KHz, whereas some 12-bit digitizers, used in solids NMR systems, allow a maximum bandwidth of 5 MHz. The parameter `np` is usually set to approximately 128 or 256.

D.6 Phase Encoding

During slice selection (the preparation phase of an experiment), it was possible to restrict the signals to a plane. Spatial-frequency distribution in a plane is achieved by using the evolution (phase encoding) and detection (readout) phases of a 2D NMR experiment. In a spin-warp imaging experiment, a 2D dataset is collected and each orthogonal dimension contains information about the phase encode and readout dimensions, respectively.

Slice selection and frequency encoding (detection phase) are easily visualized by viewing the slice profiles and readout profiles, shown in Figure 55 and Figure 61. The concept of phase encoding is less obvious because information is preserved in the second dimension as a phase modulation. Fourier transformation along the second dimension provides spatial-frequency information. Spatial information corresponding to the phase dimension is encoded by the use of a gradient pulse during phase encoding, as shown in Figure 61.

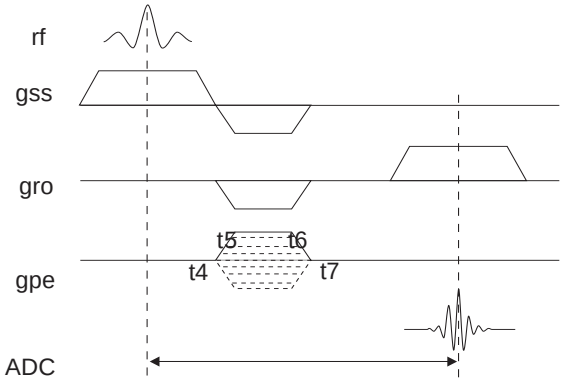


Figure 61. Gradient Echo Imaging Sequence

For example, consider a spin at a specific location, *y* (in cm), along the phase encode dimension. The phase of the spin, ϕ, is affected by the phase encoding gradient amplitude, `gpe`, and its duration, `tpe`. For an arbitrary pulse, the phase is proportional to the integral area of the gradient pulse, defined by the following equation:

$$\phi = \int_{t4}^{t7} \gamma \cdot y \cdot gpe \cdot dt \qquad \text{[Eq. 19]}$$

In this equation, ϕ is the phase in radians. For a square pulse, Figure 19 reduces to the following expression:

$$\phi = \gamma \cdot y \cdot gpe \cdot tpe \qquad \text{[Eq. 20]}$$

In Equation 20, `tpe` is the phase encode time (in sec).

From Equation 20, it is clear that either `tpe` or `gpe` can influence the phase of the resulting NMR signal. In the spin-warp experiment, the phase encode gradient is varied (rather than the phase encode time) from scan to scan in a stepwise manner. Therefore, the phase of the spins at location *y* are phase-modulated in a predictable linear fashion. The modulation frequency is directly proportional to the spatial location *y*. Fourier transformation along the phase encoding direction converts the time domain and phase modulation into spatial-frequency domain.

The field of view along the phase encode dimension is related to the gradient step size. Therefore, it is convenient to define the parameter `pestep`, which is equal to the incremental area of the phase encode gradient pulse, defined by the following equation:

$$\texttt{pestep} = \int_{t4}^{t7} gpe \cdot dt \qquad \text{[Eq. 21]}$$

The number of 2D phase encode steps to be acquired is determined by the parameter `nv`. `nv` experiments are run when the phase encode gradients are set to the values, defined by the following equation:

$$\texttt{pestep} \cdot (n - (nv + 1)/2) \qquad \text{[Eq. 22]}$$

In Equation 22, n = 1, 2, 3,... `nv`. Equation 22 ensures an equal number of positive and negative phase encode gradients are applied during the phase encode time `tpe`. For example, if `nv = 4`, the gradient amplitudes are stepped in half-integral units of

−1.5, −0.5, +0.5, +1.5

The phase-modulated nature of the imaging experiment would normally produce unwanted dispersion components in the final image. This problem is avoided by phase encoding with both positive and negative values of the gradient to create a pseudo-echo signal along the phase encode dimension that is transformed with pure absorption components. Therefore, as in the case of the gradient echo signal, an absolute value calculation yields an image without the need for any phase correction.

The field of view along the phase dimension is related to the step size of the phase encode gradient and is defined by the following equation:

$$lpe = 1/(\gamma' \cdot \texttt{pestep}) \qquad \text{[Eq. 23]}$$

In Equation 23, `lpe` is the field of view along the phase encode dimension, in cm.

It is important to choose the parameters so that the field of view, `lpe`, is greater than the spatial frequency spread along the phase encode dimension, or else the spatial components that lie outside the field of view will cause fold-over artifacts.

D.7 Image Resolution

Image resolution defines the ability to separate the signal arising from adjacent regions in the object being imaged. Decreasing the resolution improves the appearance of the actual shapes of the separate parts of an object. An image is displayed as a 2D digitized picture and each digital element is referred to as a *pixel* (or picture element). In the case of a 3D image, each digital element is referred to as a *voxel* (or volume element).

Resolution of an image depends on two factors:

- Frequency spread over the field of view, which is determined by gradient strengths `gpe` and `gro`.
- Pixel size, which is determined by the number of complex data points in the readout dimension, `np`/2, and the number of phase encode steps, `nv`.

Minimum resolution is determined by linewidth, which determines whether the signal from one region can be confined to a single pixel. Linewidth is mainly determined by spin-spin relaxation time and also susceptibility and inhomogeneity at a specific location in the sample.

Resolution along the phase encode dimension is defined in the following equation:

$$Rpe = lpe/nv \qquad \text{[Eq. 24]}$$

Similarly, resolution along the readout dimension is defined by the following equation:

$$Rro = lro/(np/2) \qquad \text{[Eq. 25]}$$

To illustrate image resolution, assume the image is from a sample consisting of three spheres filled with water, as shown in Figure 62.

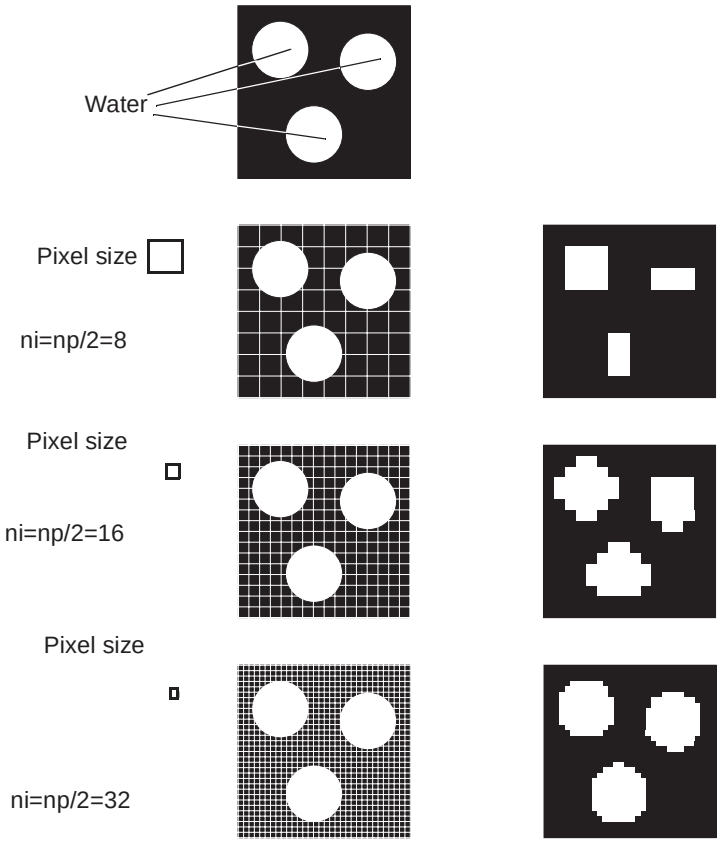


Figure 62. Image Resolution of Three Water-Filled Spheres

When the number of data points is small, one pixel can contain both a large region that does give an NMR signal and a large region that does not give an NMR signal. The lack of NMR signal causes the edges of the object to be poorly defined and can cause overlap between adjacent structures so that the separate objects cannot be distinguished from one another. As the number of data points (and/or gradient frequency spread) is increased, the signal from any given point is better able to be confined to a single pixel, so the amount of overlap between adjacent structures diminishes and the image is better defined.

The usual number of chosen data points is 128 or 256. A smaller number results in insufficient resolution and can also cause artifacts created by truncation of the time domain signal. A larger number of points along the phase encode dimension (`ni` or `nv`) significantly increases the data acquisition times. More points along the readout dimension increase the acquisition; therefore, the echo times are increased, which leads to loss of signal caused by the T_2* effect. The number of data points is usually set to a power of 2, as required by the Fourier transform. Sometimes image presentation can be improved by *zero-filling*, that is, by increasing the number of image points along the phase and readout dimensions. However, this method does not improve the inherent resolution of the image.

D.8 Spatial Frame of Reference

The section “Image Resolution,” page 242, described the NMR method for resolving the spatial dimension along a particular direction. In reality, a sample is a three-dimensional (3D) object. Therefore, it is necessary to be able to resolve the spatial information in 3D space. It is convenient to define a frame of reference for dealing with a 3D sample. The orientation of the magnetic fields produced by the gradient coils inside the magnet defines a coordinate system for imaging experiments. An understanding of the workings of this coordinate system will help you to operate the imaging instrument.

The origin of the whole system lies at the center of the magnet, which is also the center of the gradient coil system. Gradients produce a zero field in the center of the magnet. Therefore, the frequency associated with the origin or magnet center is the resonance frequency for the particular nuclear substance intended for imaging. For example, water is the chemical substance most often imaged for the proton, and the frequency at the origin of the gradient reference frame puts the NMR signal from water “on-resonance.”

There are two types of imaging magnets:

- Narrow bore, vertical magnets, which are used for MRI microscopy (MRM)
- Wide-bore, horizontal, magnets, which are used for larger samples

In the case of horizontal magnets, shown in Figure 63, the *z* axis is defined as being in the direction along the bore of the magnet, going from the cable end (back) of the magnet to the sample end (front) of the magnet. The *x* and *y* directions in the horizontal magnets and refer to the left-right and top-bottom orientations respectively, as shown in Figure 63.

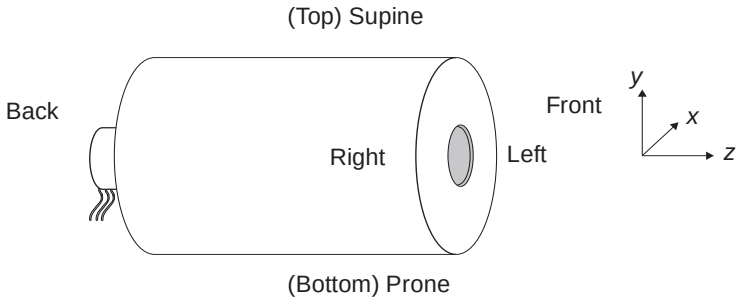


Figure 63. Horizontal Magnet

However the *x* and *y* directions in vertical bore magnets are less obvious because of the cylindrical symmetry of those magnets, shown in Figure 64.

During installation, the gradient coils and shim coils are aligned and fixed so that they are symmetrical with respect to the center of the magnet. For imaging, you must place the rf coil in the magnet center and position the sample within the rf coil.

The image planes are referenced with respect to the gradient frame of reference. The three commonly referenced planes are *sagittal*, *coronal*, and *transverse* and they respectively refer to the planes that are perpendicular to the *x*, *y*, and *z* axes, as shown in Figure 64. Images can also be obtained from arbitrary, or *oblique*, planes. The `plan` macro in VNMR allows you to define oblique planes by using a graphical tool and a reference image. For some applications, you might want to collect a 3D volume image instead of a 2D slice image. For a 3D volume image, it is possible to analyze or view the data by using 3D image analysis routines.

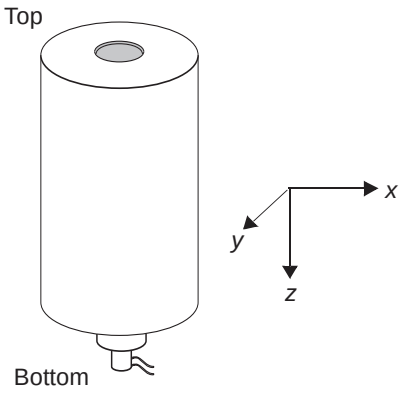


Figure 64. Vertical Magnet

D.9 Image Reconstruction

The imaging data is collected as a 2D arrayed time domain signal, *S(t1, t2)*, in which `t1` and `t2` respectively refer to the phase encoding and readout dimensions. (For historic reasons, in conventional 2D NMR, the subscript numerals 1 and 2 respectively refer to the phase encoding and detection dimensions.)

When the signals are viewed along either the phase encode or readout dimension, the time domain signals take the form of an echo signal. Fourier transformation (with respect to `t1` and `t2` using the `ft2d` routine) yields the spatial-frequency data, *S(F1, F2)*. The symmetry properties of the echo signal yields only absorption-mode components in the dataset, *S(F1, F2)*, without any undesirable dispersion mode components. The yield of only absorption-mode components is a significant advantage in imaging because the final image can be obtained by simply taking the absolute value spectrum, $|S(F1, F2)|$, without the need for any phase correction.

The appearance of the image can be improved or modified by *digital filtering*. Filter functions can either be applied in the time domain or the spatial domain. In the case of time domain data, t=0, point is in the center of the time axis. Therefore, an apodization function symmetrical to t=0 should be applied. For example, a gaussian (“shifted”) function has the effect of improving the signal-to-noise of the resulting image at the expense of loss of resolution (“blurring”) of the image. Another common way to improve the image appearance is to *interpolate* the image during the display process. Interpolation is also equivalent to *zero-filling* the data in the time domain.

D.10 Important Imaging Parameters

This section describes three important timing parameters—`tr`, `te`, and `ti`—that are used during the performance of imaging experiments.

tr – Recycle Time

The `tr` parameter defines the time between the beginning of one scan and the next.

It is important to allow sufficient recycling time so that the excited spins have sufficient time to return to equilibrium. In the case of a 90° excitation pulse, a recycle time of >4.T_1 must be allowed. If the recycle time is too short, the signal gets saturated, which results in a gradual loss of signal intensity, eventually reaching an equilibrium or steady-state condition. However, this T_1-dependent signal variation can be exploited to enhance T_1 contrast in the images.

In experiments involving quantitative work such as relaxation studies and pulse power and receiver gain calibration, `tr` must be set to greater than 4.T_1 to avoid erroneous results. In experiments such as FLASH, the flip angle is set to approximately 5° to 30° and `tr` is set to small values (about 10 µsec to 50 µsec) so that the images can be acquired very rapidly. Table 17 lists the approximate relaxation times, at 4.7 T, of some commonly used liquids.

Table 17. Relaxation Times

Liquid	*Time*
Doped water (1 g CuS04/liter)	0.6 s
Vegetable oil	0.3 s
Tap water	3 s
Degassed distilled water	26 s

te – Echo Time

Unlike in conventional NMR spectroscopy, imaging experiments usually generate either gradient- or spin-echo signals. The resulting signal intensity therefore depends on the echo time, `te`. Echo time is the time between the center of the rf excitation pulse and the position of the echo maximum, as shown in Figure 65.

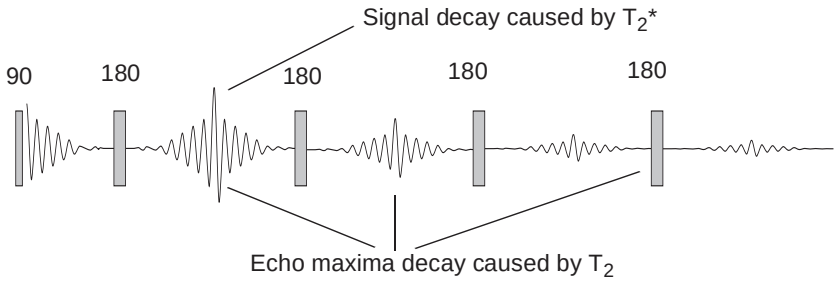


Figure 65. Signal Intensity

Echo time delay results in some loss in signal because of spin dephasing, which is caused by T_2* effects. T_2* is defined as a combination of spin-spin relaxation (T_2), magnetic field inhomogeneity, and susceptibility effects. Susceptibility effects are caused by interactions of the magnetic field with the heterogeneous sample, which produces localized field gradients within the sample. T_2* effects tend to get worse at higher fields. Signal loss caused by T_2* effects is exponential. Therefore, at long `te` values, a dramatic loss of signal intensity can result, leading to degradation of image quality.

It is therefore advantageous and sometimes even necessary to shorten the `te` value to improve image quality. However, there is a limit to the minimum `te` because echo time depends on the acquisition time and the rf and gradient pulse delays in the sequence. The shortest, achievable echo time depends mainly on maximum gradient performances such as maximum gradient strengths, rise times and residual eddy currents. However, `te` delay can also be used to enhance the T_2 or T_2* contrast in images. For example, in functional MRI, brain activity causes localized susceptibility in the brain, which is enhanced by using the

gradient echo imaging techniques. The T_2* effects of solid materials are very short (<100 µs), so special experimental techniques need to be used to obtain images from such samples.

ti – Inversion Time

`ti` is an important contrast parameter in imaging. The inversion time contrast between different components in the sample can be enhanced by performing a `ti` inversion recovery sequence (`ti ir`).

The `ti ir` imaging sequence involves applying a 180° inversion pulse and a delay, `ti`, at the beginning of a conventional imaging sequence. The inversion pulse flips the magnetization to the *z* direction. The spins return to equilibrium, exponentially, with a time constant inversion time, as illustrated in Figure 66.

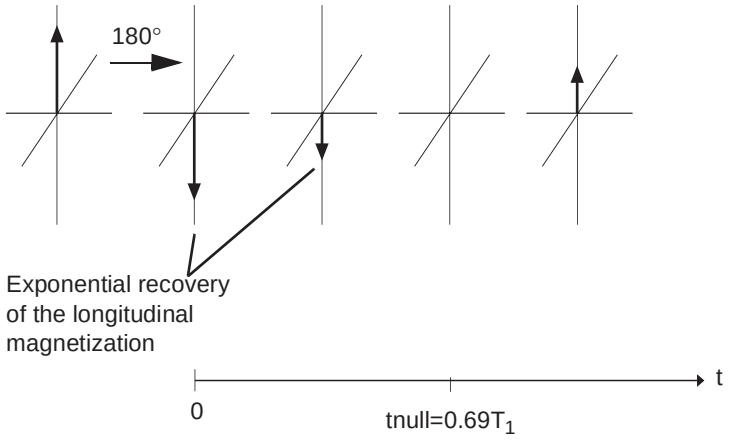


Figure 66. Equilibrium Magnetization

Sampling the magnetization after the inversion time delay results in varying signal intensities, depending on the `ti` of the spins. Notice that the signal is negative at short inversion times and gradually becomes positive at longer inversion times. When `ti=(0.69.T1)`, the signal is zero, as shown in Figure 66. If the sign of the intensities is to be retained in the images, it is necessary to phase correct the images instead of taking the absolute value mode. `ti ir` imaging experiments can be inefficient because of the long recycle time required to allow the spins to return to equilibrium.

Symbols

Numerics

A

B

C

D

E

F

G

M

N

O

P

Q

R

S

T

U

V

W

Z