LX ASP 2
New Features Manual

2286472-100 Rev. 0 (12/00)

Medical Device Directive

These products conform with the requirements of council directive 93/42/EEC concerning medical devices, when they bear the following CE Mark of Conformity:

CE 0459

This equipment generates, uses, and can radiate radio frequency energy. The equipment may cause radio frequency interference with other medical and non-medical devices and radio communications. To provide reasonable protection against such interference, the:

GE Signa LX Systems

comply with emissions limits for (Group 2, Class A) Medical Devices as stated in EN 60601-1-2. However, there is no guarantee that interference will not occur in a particular installation.

If this equipment is found to cause interference (which may be determined by turning the equipment on and off), the user (or qualified service personnel) should attempt to correct the problem by one or more of the following measure(s):

- reorient or relocate the affected device(s);
- increase the separation between the equipment and the affected device;
- power the equipment from a source different from that of the affected device; and/or
- consult the point of purchase or service representative for further suggestions.

The manufacturer is not responsible for any interference caused by using interconnect cables that are not recommended or by unauthorized changes or modifications to this equipment. Unauthorized changes or modifications could void the user's authority to operate the equipment.

Do not use devices that transmit RF Signals (**cellular phones**, transceivers, or radio controlled products) in the vicinity of this equipment as they may cause performance outside the published specifications. Keep the power to these types of devices turned off when near this equipment.

The medical staff in charge of this equipment is required to instruct technicians, patients, and other people who may be around this equipment to fully comply with the above requirement.

Immunity/Emissions Exceptions: Note the exceptions from the EMC test results. Check with the business EMC engineer for this information.

In accordance with the international safety standard IEC 601-1, this system is a Class I device, acceptable for Continous Operation, having ordignary protection against ingress of water with type B applied parts and is not for use in the presence of flammable anesthetics.

CAUTION: User to call or contact the local authorities for disposal of the MR System at the end of its useful life.

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Contra-indications for Use

The use of the MR system is contraindicated for:

⇨ Patients with electrically, magnetically or mechanically activated implants (e.g., cardiac pacemakers and ferrous/electrically activated cardiac catheters) because the magnetic and electromagnetic fields produced by the MR system may interfere with the operation of these devices.

⇨ Patients with intracranial aneurysm clips.

Implant and Prosthesis Hazards

WARNING: The magnetic field of the MR system can cause a ferrous implant (e.g., aneurysm clip, surgical clip, cochlear implant, etc.) or prosthesis to move or be displaced, possibly resulting in serious injury. Patients should be screened for implants, and those patients with implants should not be scanned. Prostheses should be removed before scanning to help prevent injury

WARNING: Induced electrical currents and heating can occur in the region of metallic implants. Patients with implants should not be scanned.

WARNING: Electrical discharges between conductive devices with points or sharp edges and the MR coils can panic a patient, causing him or her to injure him/herself. To help avoid such reactions, avoid placing any metal objects (e.g., limb braces, traction mechanisms, stereotactic devices, etc.) into the MR magnet. For further safety cautions and information, please refer to Volume 1, Chapter 1 and other MR operating documentation.

FRFSE (Breath-Hold T2-Weighted Exam)

Description

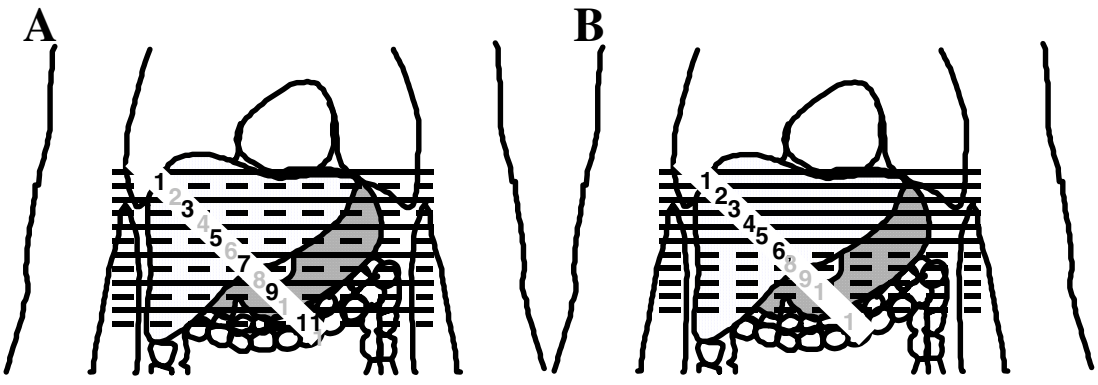
This pulse sequence includes the following modifications for breath-hold T2-weighted abdominal imaging:

- ⇨ Optimized Slice-Ordering Scheme
- ⇨ Blurring Cancellation
- ⇨ Fast Recovery T2 Enhancement

Optimized Slice-Ordering Scheme

When multiple acquisitions are required to collect the number of slices specified, the conventional *FSE* and *FSE-XL* implementations will acquire slices by default in an interleaved fashion as shown in Figure 1(A), i.e. if two acquisitions are required for twenty slices, slices 1, 3, 5…19 will be acquired in the first acquisition and slices 2, 4, 6…20 will be acquired in the second acquisition. Normally, two acquisitions will be required to collect axial slices of the liver with appropriate slice thicknesses. If the patient holds his/her breath so that one acquisition is completed per breath-hold, the default slice acquisition scheme will acquire axial slices covering the entire liver in each breath-hold, interleaving the slices from subsequent breath-holds. Because it is impossible for the patient to hold his/her breath at exactly the same location on each breath-hold, the liver will be at different actual locations in the scanner during each breath-hold. This means that axial slices from subsequent breath-holds are not correctly interleaved relative to the slices acquired in the first breath-hold. In this scheme, it is even possible to miss portions of the liver entirely.

Figure 1



The improved acquisition scheme for liver imaging is detailed in Figure 1(B). In this method, axial slices are acquired in groups of contiguous slices, starting with the first group located at the top of the liver, with each subsequent group located progressively more inferiorly until the entire liver is covered. (The groups can also be acquired starting from the bottom of the liver and progressing to the top over subsequent breath-holds if preferred). One group of slices is acquired per breath-hold, interleaving slices within each group during the breath-hold to reduce cross-talk effects. The ability to overlap groups of slices prevents the possibility of missing tissue between groups of slices if the patient does not hold their breath at the same location over subsequent breath-holds.

Blurring Cancellation

Blurring Cancellation has been implemented as a User CV for *FRFSE-XL*. This feature acquires k-space twice, in reverse order. Turning this User CV to ON decreases ghosting on *FSE* images, but can add to acquisition time in some cases. If shorter breath-holds are desired (especially 1 NEX), this User CV can be turned OFF, but ghosting will be increased.

Note: There are now two versions of FSE. When FSE-XL is selected from the PSD menu screen, this uses a shorted ESP(Echo Spacing) and may give more slices per TR due to

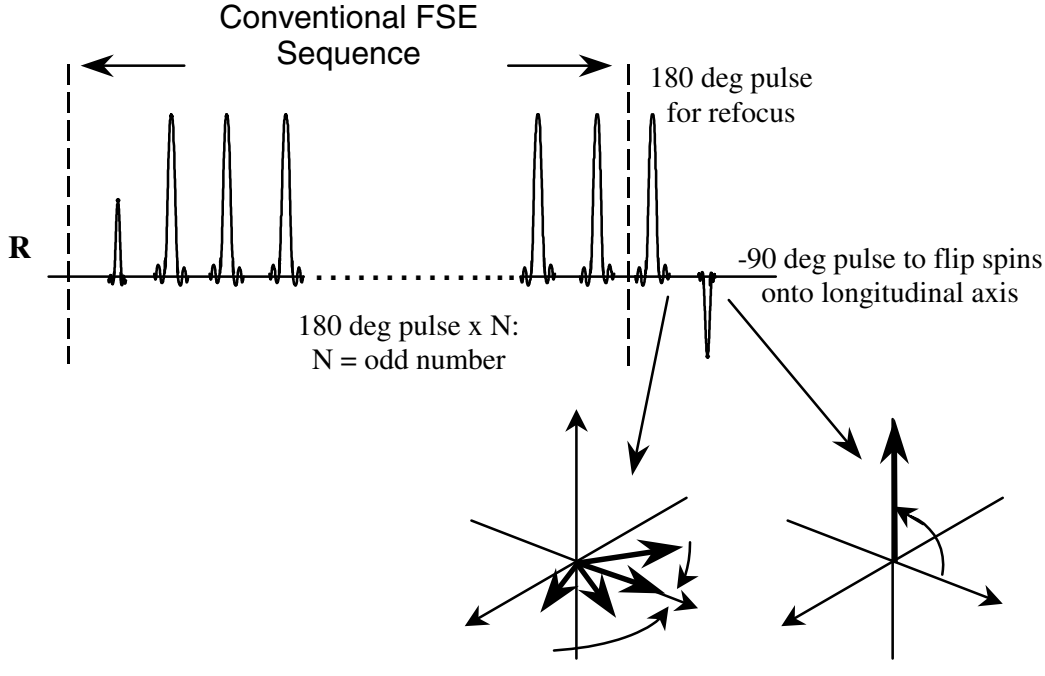
the shorter ESP and may vary depending on the other parameters.

The other version of FSE-XL is activated by selecting FSE-XL from the PSD menu screen and typing “fseopt” in the PSD field. This version gives you blurring cancellation and the new slice ordering.

Fast Recovery T2 Enhancement

The Fast Recovery T2 enhancement has also been added to this sequence to increase the signal from long T2 components in the liver. *FRFSE-XL* uses additional RF pulses after the last acquisition window to drive the recovery of longitudinal magnetization (see Figure 2). An additional 180 degree refocusing pulse is played out after the last echo in the *FSE* echo train is acquired. A -90 deg pulse is then used to drive the refocused magnetization back up onto the longitudinal axis, instead of allowing it to recover via T1 processes. After several TR intervals, a steady state longitudinal magnetization is established with a net enhancement of the long T2 components. For long echo trains, signal from fluid can be dramatically enhanced in these images.

Figure 2



Pulse Sequence Set-Up

- ⇨ Pulse Sequence Selection: You select *FRFSE-XL*.
- ⇨ Acqs Before Pause must be set to 1 to enable breath-hold slice ordering. This will allow a pause between groups of slices for free breathing.
- ⇨ Blurring Cancellation: On the User CV page, Blurring Cancellation can be selected by setting this CV equal to 1 (default = 1, off = 0). This feature decreases ghosting especially on 1 NEX scans, but increases the breath-hold duration.
- ⇨ Slice Definition: Overlap groups of slices as shown in Figure 1(B) in the Graphics Prescription window:
  - (a) Define the first group of slices with the maximum number of slices per acquisition.
  - (b) Place the cursor over the last slice, hold down the **SHIFT** key, left click, and define a second group of slices. Again, prescribe the maximum number of slices per acquisition.
  - (c) Move the second group to overlap with the first group of slices.
- ⇨ SAT Bands: Select both the S and I SAT pulse and “concatenated” to place a group of SAT bands at the limits of each group of slices.
- ⇨ Always use 0.75 phase FOV to maximize efficiency.

Note: FRFSE can be used with multiple NEX, respiratory triggering and for other body parts.

Recommended Protocols

Timing Parameters	*1 Breath-Hold Low-Res*	*2 Breath-Hold Hi-Res*	*2 Breath-Hold (for more slices)*
Pulse Sequence	FSE	FRFSE-XL	FRFSE-XL
Type-in PSD	FSEOPT	-----	----
Imaging Options	TRF, FCf	TRF, FCf	TRF, FCf
User CV Blurring Cancellation	On (1)	On (1)	On (1)
TR/TE	4900/90	2000/90	2500/90
Echo Train Length	31	21	20
Bandwidth	41	32	41
FOV	32 or greater	32 or greater	32 or greater
Matrix	256 x 128	256 x 192	256 x 160
Phase FOV	0.75	0.75	0.75
Slice Thickness	7 – 8/mm	7 – 8/mm	7 – 8/mm
Spacing	1 – 2/mm	1 – 2/mm	1 – 2/mm
NEX	1	1	1
Acquisition Time	24/s	20/s	25/s
Fat Sat	optional	optional	optional
Number of Slices	18 (Fat Sat on) 19 (Fat Sat off)	20 (Fat Sat on or off)	13 (Fat Sat on) 14 (Fat Sat off)
SAT bands	S/I concat	S/I concat	S/I concat
Freq	R/L	R/L	R/L
Acquisitions B/4 Pause	1	1	1

Dual-Echo SPGR

Description

This pulse sequence acquires both out-of-phase and in-phase images in the same breath-hold using a dual-echo GRE technique. Total acquisition time for the images is reduced by half compared to acquiring the echo separately, and discrepancies in slice locations between breathholds are removed.

Pulse Sequence Set-Up

- ⇨ PSD Selection: Select Fast SPGR or Fast GRE, then select 2 echoes. The system automatically sets the lowest possible in and out of phase TE, based on the other parameters selected. TR can be increased to increase slice coverage, however, the flip angle must also be increased to maintain T1 contrast.
- ⇨ Multiple Breath-hold Slice Definition: If more than one acquisition is required to cover the liver, # of Acqs Before Pause must be set to 1.To overlap groups of slices as shown in Figure 1(B) in the Graphics Prescription window by:
  - (a) Define the first group of slices with the maximum number of slices per acquisition.
  - (b) Place the cursor over the last slice, hold down the **SHIFT** key, left click and define a second group of slices. Again, with the maximum number of slices per acquisition.
  - (c) Move the second group to overlap with the first group of slices.
- ⇨ SAT Bands: Select both the S and I SAT pulses to reduce flow artifacts from the aorta and IVC. If more than 1 acquisition is required, select “concatenated” to place a group of SAT bands at the limits of each group of slices.
- ⇨ Always use 0.75 phase FOV to maximize efficiency.

Timing Parameters	*Hi-Res*	*Med-Res More Slices*	*Med-Res Shorter BH Time*
Pulse Sequence	Fast SPGR or Fast GRE	Fast SPGR or Fast GRE	Fast SPGR or Fast GRE
Imaging Options	ZIP512 (optional)	ZIP512 (optional)	ZIP512 (optional)
TR	150	180	150
Flip Angle	75	85	75
FOV	32 or greater	32 or greater	32 or greater
Matrix	256 x 192	256 x 160	256 x 160
Phase FOV	0.75	0.75	0.75
Slice Thickness	7 – 8/mm	7 – 8/mm	7 – 8/mm
Spacing	1 – 2/mm	1 – 2/mm	1 – 2/mm
NEX	1	1	1
Acquisition Time	23/s	23/s	19/s
Fat Sat	optional	optional	optional
Number of Slices	15*	18	15
SAT bands	S/I	S/I	S/I
Freq	R/L	R/L	R/L

* 15 slices will be obtained with TE = out-of-phase AND TE = in-phase for a total of 30 images in this series.

SSFSE Improvements

Description

The SSFSE feature extends the maximum ETL in *SSFSE* to give higher spatial resolution in the phase direction. The new pulse sequence allows high resolution matrices of 512 x 352 to be obtained, but you must choose the maximum TE. You can control the actual TE using a combination of RBW and phase resolution.

The new features associated with the Extended ETL SSFSE are:

- ⇨ Extended ETL's when utilizing maximum TE.
- ⇨ Intermediate TE's can be chosen based on RBW and ETL selections.
- ⇨ RBW selections from 7.84kHz to 62kHz can be chosen.

A second modification to the pulse sequence has been made to allow multiple slices (angles) to be obtained in the same series. This means you only have to define the multiple slices once in Graphics Prescription page utilizing radial or partial radial.

- ⇨ There is a new entry called Radial Direction under the Graphic Rx screen that controls the angle between the slices of a radial prescription. (For example if you select 5 slices in a radial and do not type anything in the partial radial field, your graphic Rx will look like a wagon wheel with a 20 degree angle between each slice. If you select 5 slices and then type 5 degrees in partial radial field your graphic Rx will look more like cat whiskers and there will be 5 degrees between each slice.)

Each acquisition is triggered by pressing the SCAN button, and all slices are stored in the same series. This modification enables multi-angle MRCP (magnetic resonance cholangiopancreatography) with one prescription for all LX platforms.

Pulse Sequence Set-Up

⇨ PSD Selection: Select *SSFSE* on PSD screen.

⇨ Select maximum TE, the system will use the maximum TE possible for the RBW and frequency resolution chosen. This will enable higher phase resolution.

- Increasing RBW, decreasing frequency and phase resolution, or using a fractional phase-FOV will decrease the maximum TE.

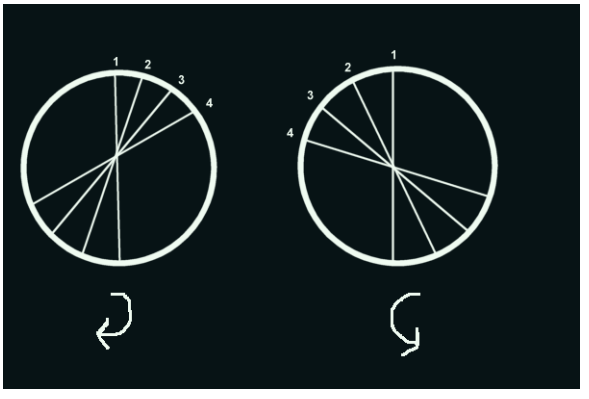
⇨ Graphic Prescription: Prescribe slices using the radial parameters.

Scan Parameters	***Low-Res***	***Hi-Res***
Pulse Sequence	SSFSE	SSFSE
TE	max	max
RBW	31kHz	62kHz
Matrix	256 x 256	320 x 320
FOV	36	32
Phase FOV	1	1
Slice Thickness	40 – 60/mm	20 – 40/mm
Fat Sat	yes	yes
Freq	S/I	S/I
Scan Plane	Oblique	Oblique

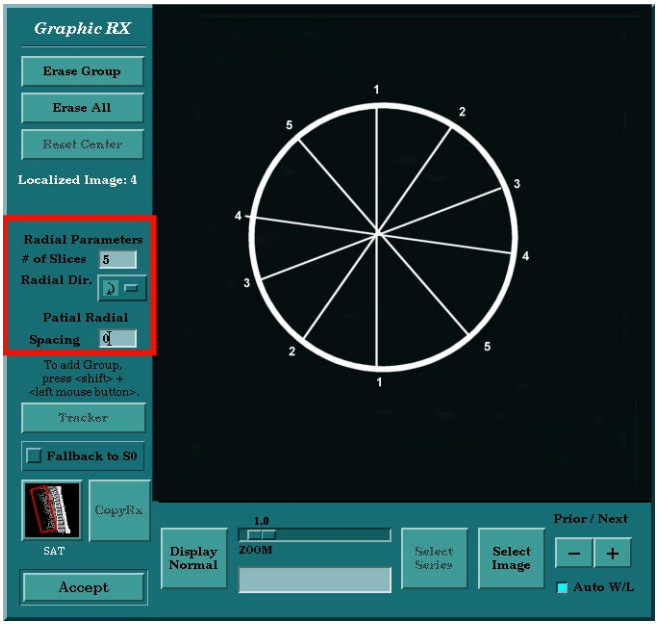
Radial Set-up

The Radial Direction button 

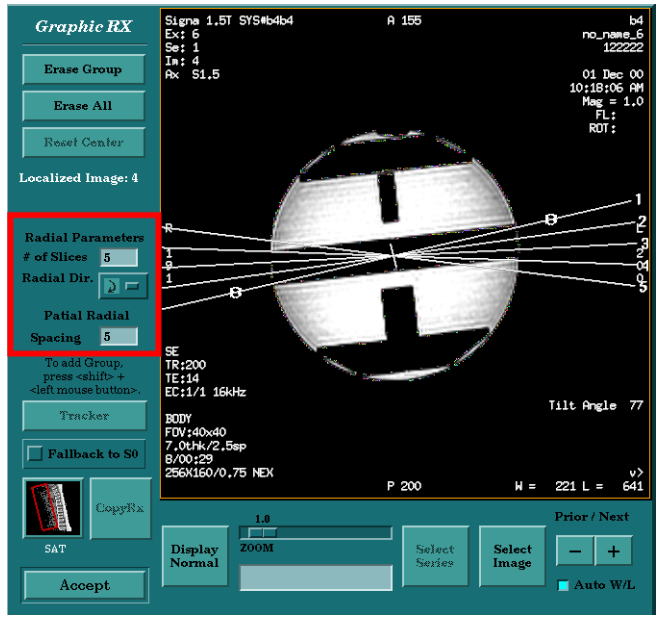
is a pulldown menu that sets the image #'s direction to clockwise or counterclockwise.



To prescribe the scan, enter a value in the # of slices field and click on the image in the Graphic Rx screen. (If you "draw" the slices using the cursor, you won't be able to get the angles.) If you prescribe 5 slices and keep a partial radial spacing of 0, your slices Rx will look like this:



If you prescribe 5 slices and select a partial radial spacing of 5 for example, your Rx will look like this: (cat whiskers)



To prescribe another group, again enter the # of slices in partial radial spacing, hold down the **SHIFT** key and place the cursor on the image where you want the slices. Repeat as necessary.

You must first enter the # of slices and the radial spacing before placing the cursor on the image and clicking. Once the Rx is drawn on the image, you can't change it. Instead you must select **[Erase Group]** or **[Erase All]**, enter in new values and then click on the image to see the new Rx.

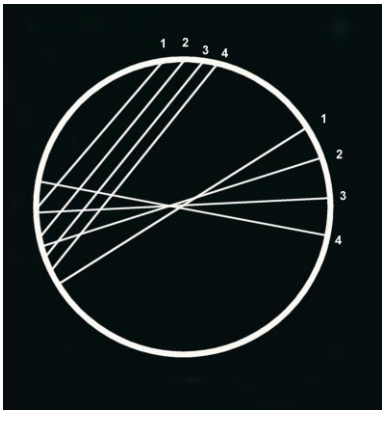
⇨ Set the # of Locs before Pause to:

- 0 if all slices are at the same angle. That will allow you to scan all the slices in 1 breath-hold, or type in any number to break up the group for multiple shorter breath holds.
- 0 or 1 when prescribing a radial. If you choose 1, the system will pause after each slice and you need to press **[Scan]** to scan each slice. Although 0 is also compatible, it will cause cross talk where the slices intersect.

⇨ The maximum number of slices in the largest group when utilizing MSMA (multi-slice, multi angle). That will enable you to scan one group (angle) at a time.

Note: After entering your graphic Rx, enter the number of Locations before Pause. The # of Locs before Pause can be of a confusing nature. If you select 0, you don't have to push the scan button for every slice (angle), but you will probably have cross talk problems. If you select 1, you control the scan, so you could let the tissue relax by waiting a few seconds before pressing the scan button.

Since each slice is an angle and each angle is a group, the maximum # of Locs before Pause is always 1 unless you prescribe an oblique group on the same series. For example, if you prescribe a radial scan with 4 slices and an oblique group with 8 slices, you could enter 8 in the # of Locs before pause. You would start the scan, the system would acquire those 8 slices, then you would hit scan four more times (one for each slice) to acquire the radial. The oblique slices in the group (single angle) would let you select 4 (or whatever number of locations before pause). See example below:



Ultra-Short TR for 3D Fast GRE

Requirements

- ⇨ Octane Computer
- ⇨ SGD-(gradient) based EchoSpeed, EchoSpeed Plus, HighSpeed or HighSpeed Plus MR System

Description

This feature is an enhancement to the current product 3D Fast Gradient Echo, 3D Fast GRE/SPGR, 3D Fast TOF GRE/SPGR, PSD that makes shorter minimum TRs available.

Shorter TR's in 3D Contrast Enhanced Magnetic Resonance Angiography (MRA) are translated to reduced scan time. This allows you shorter overall scan time, more coverage, and higher spatial resolution. Shortened TRs, when combined with elliptical centric view ordering, allow a larger fraction of k space to be acquired during the arterial phase of the bolus, resulting in better contrast between arteries and background, and greater suppression of venous signal.

In a multiphase exam, shorter TRs are translated to a higher temporal resolution. Multiphase 3D CEMRA (contrast enhanced magnetic resonance angiography) with sufficient temporal resolution allows the arteries of interest to be imaged without the enhancement of parenchyma, improving the conspicuity of the arteries.

Turbo Mode

Turbo Mode is only available on SGD-(gradient) based EchoSpeed, EchoSpeed Plus, HighSpeed or HighSpeed Plus MR Systems. It reduces the width of the RF pulse and allows shorter TR periods. The Turbo Mode option is located under User CVs.

Systems available with the option of turbo mode will be given the options of 0=off, 1=faster and 2=fastest.

Set-up

Scan Timing

Coil	Body
Mode	3D
Pulse Sequence	Fast TOF SPGR
Imaging Option	Fast
TE	Minimum
TR	System Default
Flip	less than 30°
Bandwidth	62 kHz
Frequency Matrix	256
Phase Matrix	192
FOV	36cm or greater
Nex	.5
Phase FOV	0.8
Slice Thickness	3
User CV	Turbo Mode 2
Locs Per Slab	42
Plane	Coronal
Options	zip x 2

The new 3DFGRE will provide default choices for Frequency and Phase resolution, and round user input to the nearest allowable value.

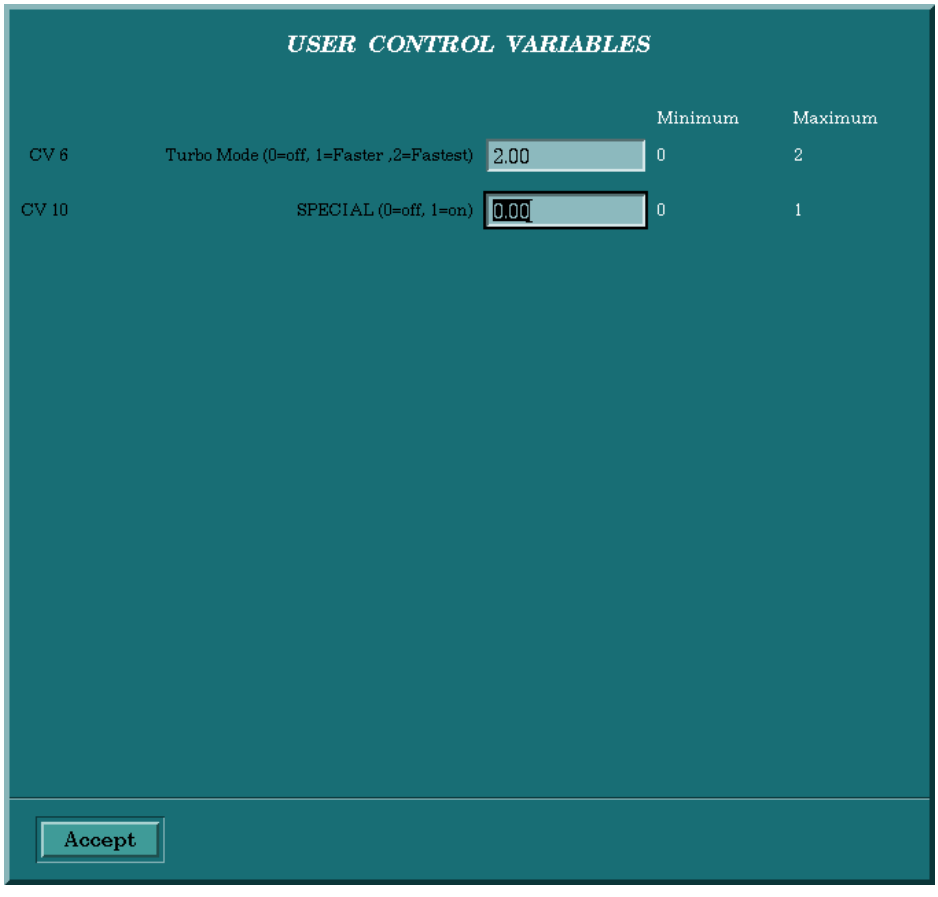
It will also provide default selections for FOV, slice thickness, and the locations per slab. You can change these defaults within the limits determined by the PSD.

Note:

You must select Turbo mode before selecting the matrix.

The minimum TR increases as slice thickness decreases, and flip angle, bandwidth, and matrix increases.

User CV Screen



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High B-Value DW-EPI

Requirements

⇨ Signa MR/i and LX SmartSpeed, HiSpeedPlus and EchoSpeedPlus systems.

⇨ Diffusion-Weighted EchoPlanar Imaging (DW-EPI) purchase option.

Description

High B-Value DW-EPI provides the following improvements to Diffusion-Weighted EchoPlanar Imaging (DW-EPI):

⇨ The ability to obtain B-Values up to 2,500s/mm^2 on MR/i or LX SmartSpeed systems; up to 4,000s/mm^2 on MR/i or LX HiSpeedPlus systems; 7,000s/mm^2 on MR/i or LX EchospeedPlus systems.

⇨ The minimum allowable echo time (TE), based on the defined B-Value.

⇨ Multiple NEX image averaging for DW-EPI sequences.

In a DW-EPI sequence, the prescribed B-Value can be achieved with different combinations of gradient amplitude and duration. The gradient duration directly affects the minimum TE for a DW-EPI sequence. As gradient amplitude increases, the duration needed to obtain the prescribed B-Value can be decreased.

Before ASP software, the diffusion gradients were applied at a fixed duration while the amplitude was varied to obtain the selected B-Value. A fixed gradient duration results in a fixed TE value. The TE value in this case is approximately 100ms. Two potential problems exist with the method:

(1) The TE is approximately the same value regardless of the B-Value. At high B-Values, SNR is reduced. The SNR reduction, coupled with the lower SNR associated with long TEs (approximately 100ms), decreases total SNR in the images.

(2) The maximum B-Value that can be achieved is 1000s/mm^2 on MR/i and LX systems. Higher B-Values may help eliminate T2 shine-through, improve visualization of white matter tracks, and may be useful in differentiation of sub acute versus chronic infarcts.

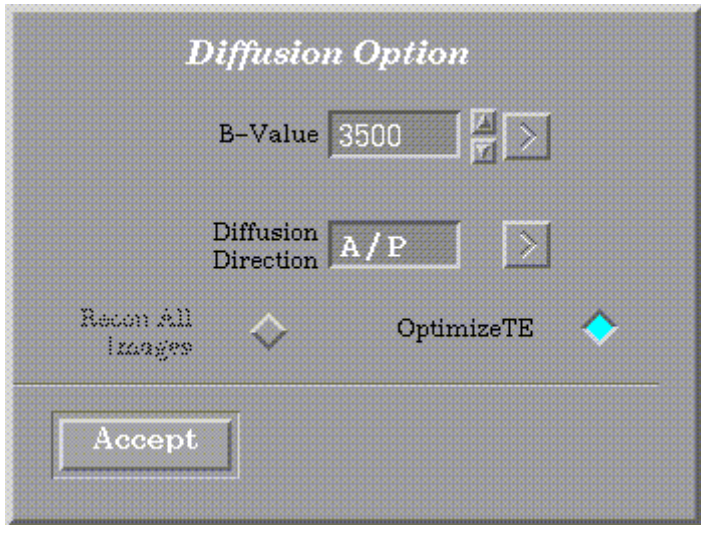
To overcome these potential problems and offer more options in B-Value selections, High B-Value DW-EPI has been developed. High B-Value DW-EPI calculates the minimum gradient duration needed to achieve the prescribed B-Value. DW-EPI calculates the minimum gradient duration needed to achieve the prescribed B-Value while utilizing the maximum gradient amplitude allowed for a system's gradient configuration. The benefits of this method are:

(1) Decreasing gradient duration will decrease the TE for B-Values of 1000 or less on MR/i and LX systems.

(2) B-Values greater than 1000 can be defined on MR /i and LX systems.

In the additional parameters area, select the DWI screen.

Both methods of applying the diffusion gradients are available for use. Selections made at the Diffusion screen define which method is implemented. Optimize TE needs to be selected to get the higher B-Values. If you want the same images as before ASP, you would want Optimize TE off.



B-Value	The menu offers only a few selections. The desired B-Value can be entered manually. The maximum depends on the state of Optimize TE. When enabled, Optimize TE permits higher values, when off, B-value options are restricted to lower values.
Diffusion Direction	The direction of the diffusion gradients is defined here: All, L/R, A/P, or S/I for orthogonal planes; All or Slice for oblique planes. The diffusion images reflect the motion of water molecules in the selected diffusion direction.
Recon All Images	Systems with a research agreement are able to reconstruct the directional diffusion images, (L/R, A/P, or S/I) when All is the diffusion direction.
Optimize TE	ON is the default. When Optimize TE is on, maximum gradient amplitudes are employed while the minimum possible TE, based on the B-Value, will be used. Higher B-values are also available. When turned off, B-Values are limited and gradient duration is fixed, resulting in a TE of approximately 100ms.

The gradient configuration of the system determines the maximum B-Value. The following chart can be used to determine the maximum for a system with or without Optimize TE enabled.

System	*TE*	*Maximum B-Value*
MR/i and LX Smart-Speed systems		
Optimize TE OFF	Approximately 100ms	1,000s/mm^2
Optimize TE ON	Minimum TE is used and is based on the prescribed B-Value.	2,500s/mm^2
MR/i and LX HiSpeed-Plus systems		
Optimize TE OFF	Approximately 100ms	2,200s/mm^2
Optimize TE ON	Minimum TE is used and is based on the prescribed B-Value.	4,000s/mm^2
MR/i and LX EchoSpeedPlus systems		
Optimize TE OFF	Approximately 100ms	2,200s/mm^2
Optimize TE ON	Minimum TE is used and is based on the prescribed B-Value.	7,000s/mm^2

Multiple NEX Image Averaging

Another benefit to High B-Value DW-EPI is Multiple NEX Image Averaging. One to sixteen NEX can be prescribed for a DW-EPI sequence. High B-Value imaging can lead to a significant suppression of water signal and loss of SNR. Multiple NEX can be used to improve SNR in diffusion-weighted images. Of course, as the number of NEX increases, scan time increases accordingly. This increase in scan time may be offset by the benefit of improving SNR.

Applications

⇨ The high B-Values available with Optimize TE enabled may help to differentiate between sub-acute infarcts and chronic infarcts.

⇨ At low B-Values (<1000 for LX and MR/i) with Optimize TE enabled, lower TEs are achieved. This provides increased SNR as compared to images obtained at longer TE values, provided the B-Values remain the same.

⇨ Multiple NEX image averaging can be used to improve SNR, especially when using high B-Value.

Considerations

⇨ The peak gradient amplitude is limited by the constraints of the gradient subsystem; therefore, there is a limit to the minimum TE and the maximum B-Values that can be achieved for a given MRI system.

⇨ Using multiple NEX imaging increases the need for bulk acquisition memory (BAM). If the system cannot allocate enough BAM for the series, a message will be posted. The following parameters can be decreased to decrease the amount of BAM needed: frequency matrix, phase matrix, number of slices, or number of NEX.

⇨ If the selected B-Value cannot be achieved, an error message will be posted.

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3D Focal CSI

Description

Magnetic Resonance Spectroscopy (MRS) is a device that provides, in a non-invasive manner, the signal intensities of molecules containing hydrogen present in a specified region of interest in the body. Chemical Shift Imaging (CSI) is an effective and efficient method of simultaneously characterizing the spatial distribution and spectral frequency content of signal producing species in a magnetic resonance (MR) examination. Voxel localization is used to limit data acquisition to a particular volume of interest (VOI) and to exclude unwanted signals. In voxel localized CSI, spatial distribution is encoded using magnetic field gradients incremented on successive acquisitions to produce spatially dependent phase changes. Such phase encoding can be applied on three orthogonal axes to dimensionally characterize the excited volume in three dimensional (3D) space. The field of view (FOV) over which the signal is encoded may be independent of the bounds of the excited volume.

The frequency content of each spatial location is evaluated by detecting the time dependence of the signal, the Free Induction Decay (FID), in the absence of magnetic field gradients. Fourier transformation along the phase encoded axes separates the data into spatially separated FIDs. Fourier transformation of the FIDs yields the spatially localized frequency plots, or spectra.

Compared to 2D chemical shift imaging, automated voxel localized three-dimensional (3D) chemical shift imaging provides more efficient coverage of the brain tissue. The feature is optimized for use in the brain where lipid signals are restricted to the edges of the skull and can be avoided by volume positioning and outer volume suppression (OVS) rather than in-volume signal suppression. This feature builds upon the current technology for acquiring single voxel and two-dimensional (slice oriented) CSI data by enabling

encoding of the third dimension in a user-friendly manner.

3D Focal CSI

Probe-P Single Voxel (Probe/SV), probeSI, and 3D Focal CSI can all be accessed from the PROBE-P pulse sequence. For example, when you choose PROBE-P from the PSD menu, the mode of operation will be based on the selections of frequency and phase matrices, and the locations per slab.

If the phase matrix, frequency matrix, and Locs per Slab are all set to 1, you will acquire single voxel data. If the phase and frequency matrices are greater than 1 (the options are there to select the same resolutions that exist for the current 2D product) and Locs per Slab is set to 1, you will acquire single slice, multi-voxel data (same as the probeSI product). When all three (frequency matrix, phase matrix, and Locs per Slab) are greater than 1, you will get the 3D behavior which will return data in the appearance of a multi-slice version of probeSI. The data will be analyzable in a very similar (but multi-slice) fashion as probeSI.

Mode of Operation	*Parameter*	*Selection*
PROBE/SV	Locs per Slab	1
	Phase Matrix	1
	Frequency Matrix	1
probeSI	Locs per Slab	1
	Phase Matrix	>1
	Frequency Matrix	>1
3D Focal CSI	Locs per Slab	≥8 *
	Phase Matrix	≥8 *
	Frequency Matrix	≥8 *

* Only even numbers from eight to 16 are valid.

The distance between the slices is controlled by the Spacing field. Select the parameters for the Field of View (FOV), Voxel Thickness, Phase matrix, Frequency matrix and the Locs per Slab before

selecting the Spacing. The Phase FOV is not a selectable option, the system will choose this for you.

Matrix	*Phase FOV*
8 x 8, 16 x 16	1
8 x 10, 8 x 12, 8 x 14, 8 x 16	.5
10 x 8, 12 x 8, 14 x 8, 16 x 8	.5
All other matrices	1

The matrix sizes in the above table correspond to Frequency x Phase.

The following are approximate scan times using the given parameters.

TR	*Locs per slab*	*Frequency*	*Phase*	*Nex*	*Approximate Scan Time*
1000	8	8	8	1	8:32 min
1000	8	10	10	1	13:20 min
1000	8	16	16	1	34:08 min
1000	16	8	8	1	17:08 min

3D Focal CSI Options

Very Selective Spatial Saturation

As spectroscopy imaging becomes more prevalent and targeted at challenging areas of the anatomy, effective spatial saturation of unwanted signals becomes more critical. Very Selective Spatial Saturation (VSS) provides an effective means to saturate signals within a chosen plane. The saturated plane is characterized by flat transmission and stop bands, and very narrow transition bands. This allows you to apply saturation bands very close to the VOI without affecting signals within the VOI because of unwanted overlap with the saturation transition band. VSS pulses also have a very high effective bandwidth, and are therefore very appropriate for use in regions of

high inhomogeneity, or in cases where chemical shift is important. Sharply defined bandwidths are necessary to cut out unwanted signals near or within volumes of interest without unduly impacting the signals of interest. Slice selective Very Selective Saturation RF pulses are designed to provide improved spatial saturation performance with no increase in the time required for the pulse sequence. VSS pulses can be used with Probe-P single voxel, probeSI, and 3D Focal CSI.

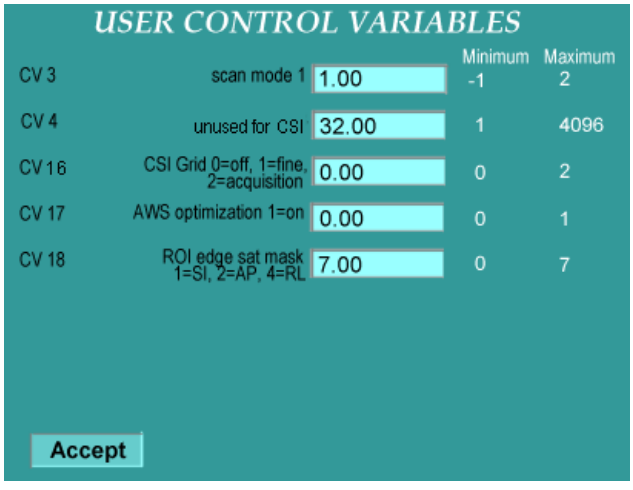
In the default mode, VSS provides the use of six fixed-position saturation bands bordering and surrounding the MRS-mode prescribed Volume of Interest (VOI).

The default VOI edge sat bands can be turned on and off by a user control variable (UserCV) which appears on the UserCV screen when default sat bands are available. The UserCV allows independent on-off control of the sat bands placed at Right/Left (R/L), Anterior/Posterior (A/P), and Superior/Inferior (S/I) edges of the VOI.

Additionally, up to four explicitly prescribed SAT bands can be placed on the same localizer image used to prescribe the PROBE-P voxel. The four explicit sat bands can be graphically prescribed using the Saturation Prescription screen on a localizer image. Choose the same axis plane that was used to place your VOI scan prescription. The saturation bands may be changed in thickness and angle and may be placed anywhere on the image by dragging or by explicitly entering the coordinate. The prescription process gives you visible feedback of the sat band positioning and thickness. The true thickness is displayed numerically in millimeters. These bands help refine the VOI. FOV edge sat bands can also be chosen on the Saturation Prescription screen, but no explicit position is given. The thickness can be changed by typing it in the thickness field.

UserCVs

There are five UserCVs entries; only 4 are relevant when prescribing a CSI acquisition, CV4,"total number of scans is not used." The default display is:



⇨ **Scan Modes** allows for four choices, two imaging modes (-1 and 0) and two spectroscopy modes (1 and 2):

Scan Mode = -1 scans and displays an image of the slice centered within the voxel with narrow Sat bands placed at the edges of the prescribed voxel. This image clearly shows the location of the voxel in reference to the entire slice and can be used to confirm the location of the voxel. Reduce the TR and TE to reduce the scan time.

Scan Mode = 0 scans and displays an image of the voxel. This displays only the signal from the prescribed volume. Reduce the TR and TE to reduce the scan time.

- Scan Mode = 1 reconstructs the chemical shift images centered on the localizer images within the 3D volume. The spectra will be at the exact locations as the localizer images. When using the CSI display tool, the overlay localizer

images are the **exact** matches to the metabolic images. This is the default mode.

- Scan Mode = 2 acquires chemical shift images with the prescribed number of phase encoding steps, center spacing, and locs per slab. When displayed, the overlay localizer image is the **closest** match to the metabolic image.

NOTE

A message appears in the FuncTool command window stating “Not a perfect match.”

NOTE

If UserCV 15 steady state appears on the User CVs window, select one and continue to scan. Notify the service engineer the system needs calibration.

⇨ **Grid**

- 0 = No Grid.
- 1 = Fine Grid (reconstructed matrix 32 x32 represents the zero-fill).
- 2 = Acquisition Matrix (the grid cell size is determined by the FOV/phase matrix value).

⇨ **AWS (Automatic Water Suppression) Optimization**

- 0 = Off. This is the default and the recommended value. The prescan time is decreased with AWS off.
- 1 = On. Only use 1 (on) if you know from past experience that the default water suppression will not be acceptable or if you wish to use the optimization portion of the Auto Prescan process.

⇨ **ROI edge sat mask**

- Enables the placement of Very Selective SAT bands around the VOI. Select one of the following:

Selection	*Sat Band Placement*
0	Off (no SAT bands)
1	Superior (S) and Inferior (I)
2	Anterior (A) and Posterior (P)
3	S/I and A/P
4	Right (R) and Left (L)
5	R/L and S/I
6	R/L and A/P
7	R/L and A/P and S/I

Reset Center Option on Graphic Rx

Reset Center allows you to change the center of the voxel prescription to the desired image location. A message appears on the left side of the Graphic Rx window displaying the image number of the localized image, as well as, stating if the prescribed voxel is within the scanning limits.

Setup

This procedure is only for prescribing a spectroscopy scan from a localizer and not for displaying the spectra. For some spectroscopy exams more than one localizer scan plane may be needed in order to preview the anatomy that will be in the probe volume.

Note

Minimize the time between the localizer scan and the spectroscopy acquisition to decrease chances of patient movement and to ensure accurate position.

Note

The selected values in the center column of the following table are only an example of what could be used and are NOT to be considered recommendations by GE Medical Systems.

Note

Because of sequence dependencies, it is best to prescribe a 3D CSI examination by selecting (in this order) **Locs per slab**, **frequency matrix**, and **phase matrix** before selecting any other values on the scan desktop. Similarly, you should choose the voxel thickness value before entering the Graphic Rx window.

RX Manager Screen		
RX Manager	New Series	Select New Series from RX Manager, Click on Patient Position if the Patient Protocol screen appears.
Patient Position Area		
Patient Position	Supine	3D Focal CSI is most frequently used in neuro scanning so the patient position and entry selections reflect that.
Patient Entry	Head First	
Coil	Head	
Series Description		Enter a suitable series description. If a description is not entered, the system will enter one. The series description default is the selected scan mode, PSD, and imaging options.
Imaging Parameters Area		
Plane	Axial	3D Focal CSI is compatible with any scan plane including oblique and 3-Plane localizers; select the same plane as the localizer scan plane. This is different from the normal prescription process. Typically, an axial is prescribed from a sagittal or coronal. With probe, an axial must be prescribed from an axial localizer.
Mode	MRS	Select MRS
Pulse Sequence	PROBE-P	Select PROBE-P
Imaging Options	EDR	Use Extended Dynamic Range on all PROBE-P scans. Click **[Accept]** to register the selections.

UserCVs Screen		
Scan Mode	1	Select a scan mode of -1 to acquire an image of the slice centered within the voxel with sat bands at edges, 0 for the voxel imaging mode, 1 to reconstruct the CSI images on the exact centers of the localizer images (this is the default mode), or 2 to acquire and reconstruct the CSI images as prescribed.
Total number of scans	Default	Unused for CSI.
Steady state	1	Continue to scan, contact service engineer to calibrate system.
Grid	0	0 = No Grid. 1 = Fine Grid (reconstructed matrix 32 x32 represents the zero-fill). 2 = Acquisition Matrix (the grid cell size is determined by the FOV/phase matrix value).
AWS Optimization	0	0 = Off. Uses predefined water suppression parameters during the scan. This eliminates the water suppression process in prescan and thus reduces prescan time. 1 = On. Use if experience indicates the water is better suppressed in comparison with AWS=Off (0).
ROI edge sat mask	7	Allows placement of additional sat bands. Refer to ROI edge sat mask table previously listed in this chapter.
Scan Timing Area		
# of echoes	1	3D Focal CSI is only compatible with 1 echo.
TE	144msec	In the spectroscopy acquisition modes (1 or 2), select a recommended TE of 144, or 288. As in all other MR scans, the longer the TE, the less the SNR. With a TE 144ms the lactate peak is exactly inverted; at TE 288ms the lactate peak is not inverted.
TE2	N/A	
TR	1000 ms	If the scan mode = 1, select a typical TR of 1000ms. A longer TR results in increased SNR at the expense of increased scan time. If the scan mode = 0 or -1, (voxel image) select the shortest allowed values for TR.
TI (Inv. Time)	N/A	
Flip Angle	N/A	
Echo Train Length	N/A	
Bandwidth	N/A	The Receiver Bandwidth is automatically selected for probe scans and cannot be selected.
Bandwidth 2	N/A	

Scanning Range Screen		
FOV	24	Choose the same FOV as the localizer image.
Voxel Thickness	50	Choose a voxel thickness large enough to cover the anatomy or pathology. The lower limit is 3mm and the upper limit is 100mm.
Locs per Slab	8-16	Choose the number of locations per slab. For 3D Focal CSI, acceptable values are even numbers from 8 to 16.
Spacing	Desired choice	Selecting the Locs per slab before Spacing allows for more Spacing choices.
Graphic RX Screen		
Image	Left mouse button	Click on the image to display the voxel for Graphic Rx. Select the adjustment handle to re-size. Drag the voxel ROI to deposit at desired location. Position the voxel for the anatomy and pathology. Select **[Accept]**.
[+] Next and **[-]** Prior	Click **[+]** and **[-]**.	To page through the localizer images to check the position of the voxel. The center of the voxel will be the center image of the localizer series, which is the first image that appears when you enter Graphic Rx.
Reset Center	Click **[Reset Center]**. (If Necessary.)	To change the center of the voxel prescription to the desired image location. If you Reset Center a message will appear on the left side of the Graphic Rx window.
Erase	Click **[Erase].** (If Necessary.)	To eliminate the voxel volume from the screen and start over.
Accept	Click **[Accept]**.	To confirm the cursor position and exit Graphic Rx.
Acquisition Timing Screen		
Frequency Matrix	8-16	Choose the frequency matrix. Acceptable values are even numbers 8-16. As the frequency value increases, the spatial resolution increases and the scan time increases. The FOV divided by the frequency value determines the CSI grid cell size in the frequency dimension.
Phase Matrix	8-16	Choose the phase matrix. Acceptable values are even numbers 8-16. As the phase value increases, the spatial resolution increases and the scan time increases. The FOV divided by the phase value determines the CSI grid cell size in the phase dimension.

NEX	1	As the NEX value increases, the SNR increases and the scan time increases.
Phase FOV	N/A	Not a selectable option, the system will choose one for you according to the rules listed earlier in this chapter.
Frequency DIR	A/P	Select the default value.
Auto Center Freq.	Water	Always select water.
Flow Comp DIR	N/A	
Autoshim	On	Always turn on Autoshim.
Phase Correct	N/A	
Scan Operations Screen		
Save Series	Click **[Save Series]**.	This closes the scan prescription screen and accepts the prescription.
Prepare to Scan	Click **[Prepare to Scan]**.	This will download the series.
Auto Prescan	Click **[Auto Prescan]**.	Auto Prescan completes the following: Sets the CF, TG, and RG. Determines the gradient field current offsets for increased homogeneity. Determines the flip angle of third water suppression pulse when AWS = 1.
Scan	Click **[Scan]**.	Initiates the acquisition.

Considerations

- Up to four saturation bands can be selected for a scan prescription when the default saturation bands are in use. When more than four are selected, there is not enough time available for all the requested saturation bands. When this condition is detected by the system, the default saturation bands are deleted in deference to the explicitly prescribed sat bands. The S/I bands will be deleted first, followed by the A/P bands, and then the R/L default saturation bands.
- If you copy and paste a PROBE/SV sequence and adapt to scan a 3D Focal CSI sequence, note when selecting the Locs per slab an advisory window appears with the frequency matrix selection. Selecting [Accept] places this value into the frequency matrix field. Remember to change the Locs per slab to the desired value.

- Homogeneity is more critical than water suppression to obtain a successful CSI acquisition. The linewidth should not be greater than 15. If the linewidth is greater that 15 try one or more of the following:

(a) Make the voxel smaller.

(b) Move the voxel to avoid regions of large susceptibility change.

(c) Move the voxel to avoid anatomy known to cause linewidth problems.

(d) Move the voxel to avoid disease regions (hemorrhage) that are known to cause linewidth problems.

- The suppression level (Supp Lvl) percentage, shown on the Advisory Panel, should be between 95-99%. If the value is less than 95% run prescan again, if the value is still low you may need to reposition your voxel over more homogeneous anatomy.
- Upon scan completion, a number Chemical Shift storage images appear in the AutoView window. Each one of these CSI storage slices contains a collection of frequency specific data centered at the stated slice location.

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3D Focal CSI Display

Description

Chemical Shift Images acquired with the Probe-P pulse sequence are displayed by selecting a display tool such as **[MIROI]** or **[Functool CSI]** from the browser. Select the 3D CSI series from the browser, a message window appears asking you to select a localizer. Select the localizer series that you used to prescribe the 3D CSI scan.

The initial display consists of five areas: the command window, and four display viewports. The chemical shift viewport appears in the upper left (UL), the spectral grid viewport in the upper right (UR), the metabolite image viewport in the lower left (LL), and the reference viewport in the lower right (LR). The chemical shift viewport defaults to No Smoothing.

Whenever a protocol is selected from the **[Get Protocol]** menu, a Function parameters window is displayed over the bottom viewports.

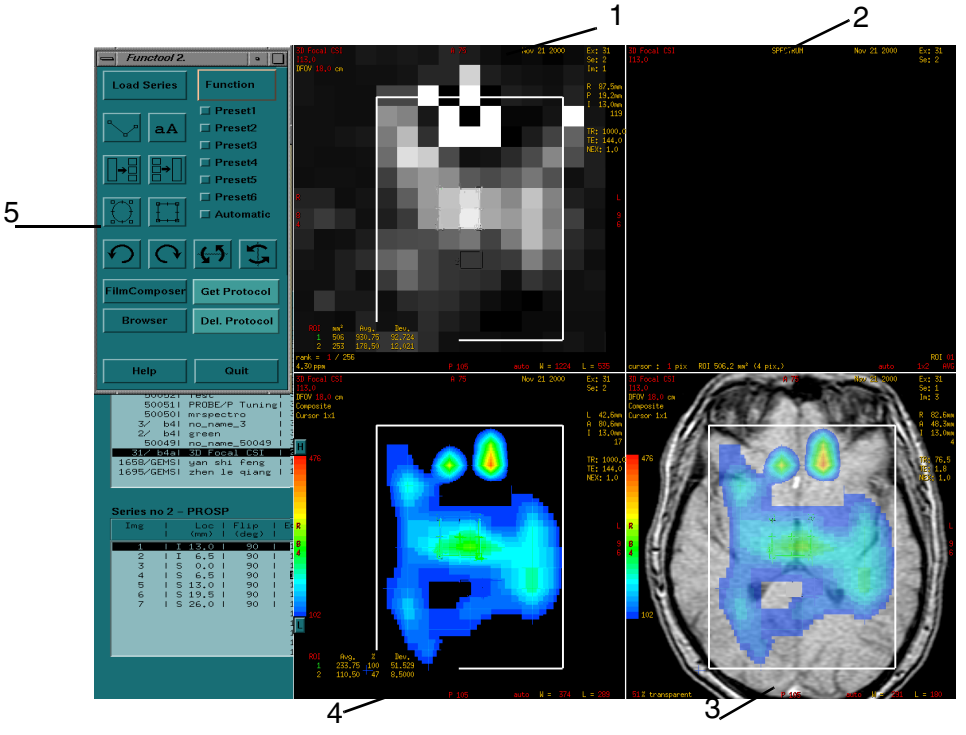


Figure 1: Example of the first screens displayed by the post-processing tool using a 3D CSI series.

1 - Chemical shift viewport (Upper Left-UL),

2- Spectral grid viewport (Upper Right-UR),

3 - Reference viewport (Lower Right-LR),

4 - Metabolite image viewport (Lower Left-LL),

5 - Display command window.

Section 1- Concepts, Applications, and Terminology

General features of the probe-P CSI display tool are described in this section. Features specific to each viewport are discussed later in this chapter.

Region-of-Interest (ROI) and Spectrum Colors: ROIs are outlined by a purple or a green line (Figure 2). A green ROI is the active ROI and usually has resizing and movement handles as part of the green outline. A purple ROI is inactive or deselected, and cannot be moved, resized, deleted, or copied. An

active ROI is deselected if you select another ROI from the command window. The active ROI is also deselected if you click anywhere on a viewport except on the cursor area, outline, on another ROI (in the UL, LL, and LR viewports), or spectrum (in the UR viewport). The same color code is used in the spectral grid (UR) viewport; purple corresponds to the spectra or information lists from inactive ROIs, and green to the spectrum or list from the active ROI. A third color – white – is used on the spectral grid (UR) viewport to distinguish the spectrum or list that corresponds to the current cursor location on any of the other viewports.

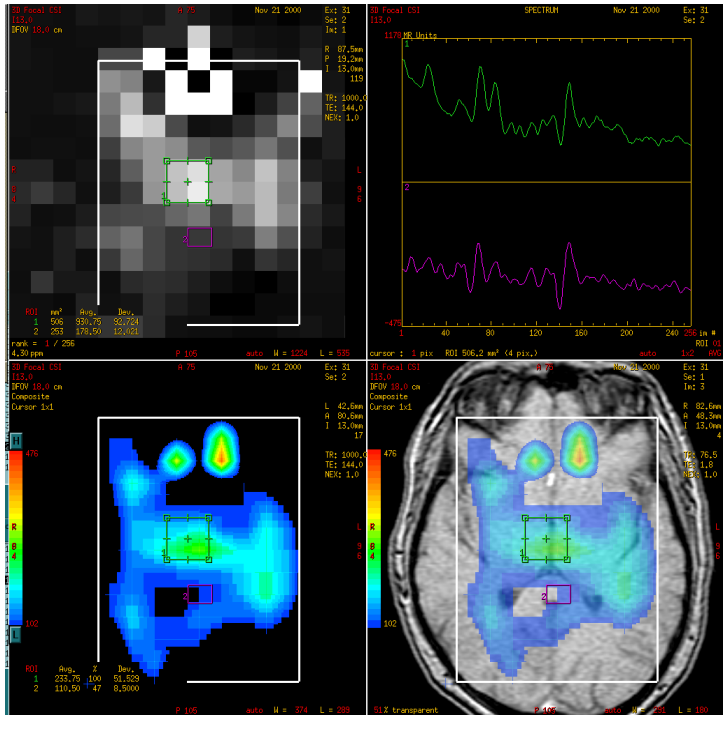


Figure 2: Typical Probe-P display with two ROIs, a reference image, and spectra.

Mouse use: The mouse buttons behave in a different manner when used in different areas of the viewports.

When clicked, or clicked and dragged over an active annotation (the red or bright white, alphanumeric characters in a viewport) the mouse buttons behave in a manner defined by, or consistent with the active

annotation. Active annotations for each viewport are described in Sections 3 – 6.

When clicked in other areas of a viewport, the three mouse buttons behave in a fairly standard manner.

The left mouse button is used in combination with the cursor to select objects (e.g., a spectrum in the UR viewport or an ROI in any of the other three viewports), to drag or resize selected objects, to draw ROIs (when used with the **Shift** key), or to communicate a location to the display tool programs.

The middle mouse controls the viewport window width and level of the chemical shift (UL), of the metabolite image (LL), and the reference image (LR) viewports.

The right-click brings up viewport specific menus.

Keyboard use: The **arrow** keys can be used to increase or decrease items selected with the cursor – the behavior is identical to using the left and right mouse clicks, respectively.

You can use the **Ctrl-X**, **Ctrl-C**, and **Ctrl-V** key combinations to delete, copy, or paste an active (green) ROI. The **Shift** key is used with the left mouse button to draw an ROI.

You can use **Alt-F3** to raise and lower overlapping window on the desktop. For example, if you select **[Browser]** on the command window, the browser screen covers the display viewports and command window. To uncover the display viewports and command window, place the cursor anywhere on the Probe-P display tool and select **Alt-F3**. This key sequence can be used to raise and lower windows on any of the LX desktops.

Active annotations: Active annotations are the **red**, or **bright white** (on a black/white monitor), numbers, words, or acronyms displayed on the viewports (Figure 2). The active annotations respond or perform an action when the cursor is placed on the item and a mouse button is clicked, or clicked and dragged. You can increase or decrease active numbers by placing the cursor over the number, and clicking the left or right, respectively. Similarly, you can scroll the active numbers by clicking and dragging the middle button.

You can also use the **left** and **right** cursor keys on the keyboard to increase or decrease a numeric value. Clicking on a red or bright white word allows you to change the display, or the location of a display. For example, to move the numeric lists that are displayed on the chemical shift, metabolite image, and reference viewports, click on the **ROI** active annotation and then drag and drop the list on another area of the viewport.

The **auto** active annotation automatically scales the display in a viewport. For the three viewports that display images or maps (UL, LL, and LR), clicking on **auto** automatically adjusts the window width and level of the displayed image/map. On the spectral grid (UR) viewport, selecting **auto** (or pressing the **Spacebar** on the keyboard) scales all spectra in that viewport to the active (green) spectrum. In this case, the maximum and minimum points in the active spectrum define the maximum and minimum spectrum display limits. A common scale allows you to compare and contrast signal intensities from several ROIs.

The **patient name**, displayed in red, or bright white, in the top left corner of each viewport, is an active annotation. Clicking the **patient name** displays a menu with the selection **[Hide patient name**]. The patient name region changes to ******** on all the viewports. You can redisplay the patient name by clicking the ******** and selecting **[Show patient name]**.

The **slice location**, displayed below the patient name, is an active annotation. You can page through the slice locations by clicking or clicking and dragging on this annotation. Multiple ROIs can be drawn on a slice or the slices of a 3D Focal CSI series. The ROIs are numbered sequentially in the order in which they are drawn on the slices.

Active annotations specific to each viewport are discussed in Sections 3 – 6.

Data smoothing conventions – The pixel smoothing feature that is a standard part of the MIROI or Functool software, should **not** be used with Probe-P maps. Keep the **"cursor : # pix" at 1.** Normally, the chemical shift images and metabolite maps in the three image views are displayed using simple pixel replication or smoothed using a bi-cubic smoothing algorithm. In addition, depending on the size of the cursor, a "regional" filter is applied to the images or maps. The size of the filtered region corresponds to the number of pixels used to define the cursor size. This means the information from 4, 9, 16, 25, 36, 49, 64, 81, or 100 neighboring pixels is smoothed. The number of pixels is given by the "cursor : **#** pix …" active annotation on the spectral grid viewport, or by the "cursor 1x1 …" display on the image viewports as shown in Figure 2. To avoid this "regional" data filter, set the cursor size active annotation to read "cursor : **1** pix …" on the spectral grid viewport. If you use any other cursor size, the numeric values corresponding to an ROI or pixel will vary depending on the size of the cursor.

Image Pan/Zoom: Images or maps are displayed in three of the 4 viewports (Figure 2). Standard image annotations such as – DFOV, and A/P, R/L, and S/I that contain **red** or **bright white** numbers indicate that these are active annotations:

"DFOV **24.0** cm", "A **120**", "R **120**", "L **120**", and "P **120**".

You can zoom by clicking on the DFOV **24.0** entry. You can pan the image by clicking and grabbing the **120**s. Zoomed, pixel replicated images with a split ROI are

shown in (Figure 3). Select **[Display normal]** on the shortcut menus to undo the pan or zoom.

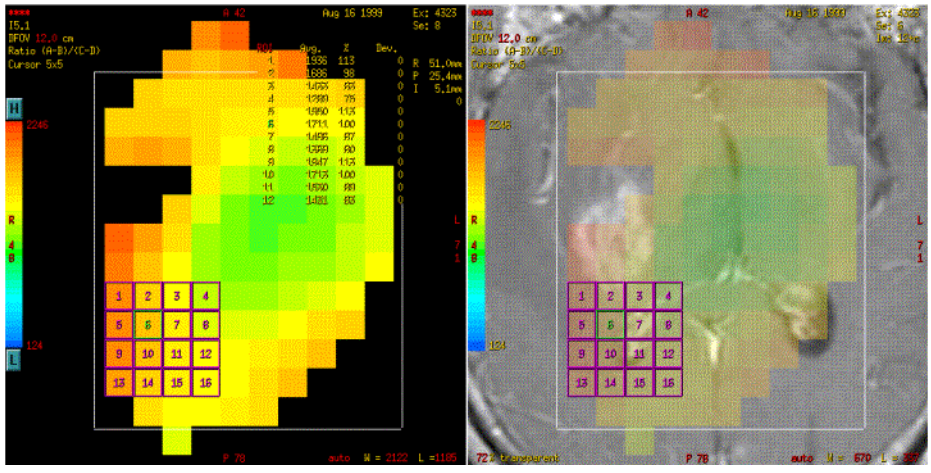


Figure 3: A zoomed display of a pixel replicated metabolite map and a split ROI.

Shortcut Menus: There are shortcut menus for each of the viewports with selections that allow you to modify the current and subsequent displays. Shortcut menus are accessed with a right-click anywhere on a viewport, except on an active (red or bright white) annotation, and drag and release on the desired option. The specific menus for each viewport are described in Sections 3 – 6.

Viewport Shortcut Menu Items

The following items may appear on the viewport shortcut menus.

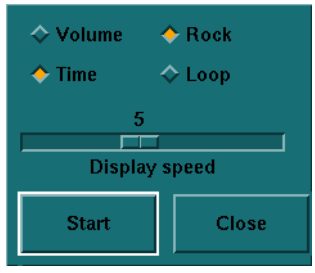
You can toggle between **No smooth/Smooth**, **Hide/Show grid**, **Hide/Show Press ROI,** and **Show/Hide SAT bands** to show or hide these functions.

Feature	*Description*
Create Annotate	Allows you to create annotation in the UL, LL, and LR viewports. Cursor must be in one of the 3 viewports.
Color Ramps	Allows you to change the color of the display. There are six choices: Rainbow (the default), Hot iron, Puh thallium, 3 colors, Gray levels, Inv. Rainbow (Inverted Rainbow).

Display Normal	Restores to the default image display if you have panned and/or zoomed the image. Window/level are not restored.
Hide/Show graphics	Must have cursor in viewport, selecting hides or shows graphics in that viewport only.
Hide/Show grid	Places the CSI acquisition grid over the image.
Hide/Show PRESS ROI	Hides or shows the voxel placement.
Hide/Show SAT bands	The graphically prescribed SAT bands are drawn on the reference image.
Movie	Allows you to view the chemical shift images, in the upper left viewport, in a movie mode, and allows you view the slices of the metabolite map in the lower left viewport, in a movie mode. Can use to check for patient motion.
Save all	Saves all the images of the series to the Browser as reformatted images.
Save view	Saves the current view to the patient data base as a screen save image in a separate series.
Smooth/No Smooth	Invokes a bi-cubic interpolation of the pixel data in the image, or a simple pixel replication, respectively.

The **Movie** option is available only in the upper left and lower left viewports. When selected a window opens allowing selection of movie display modes. Selecting Volume pages through the CSI slices or the metabolite slices, depending on the viewport. Selecting Time highlights different signal intensities on the CSI image, and is only available on the chemical shift viewport. Rock and Loop are options for the sequence in which images are displayed. Rock alternates forward and reverse mode when the last image of the series is reached, for example: a series with four images displays 1, 2, 3, 4, 3, 2, 1. Loop is for continous

forward display of images, for example: a series with four slices displays 1, 2, 3, 4, 1, 2, 3, 4.



Section 2 - The Command Window

The command window allows you to select CSI display tool functions. Placing the cursor over the buttons allows you see the tool tips describing the button's function.

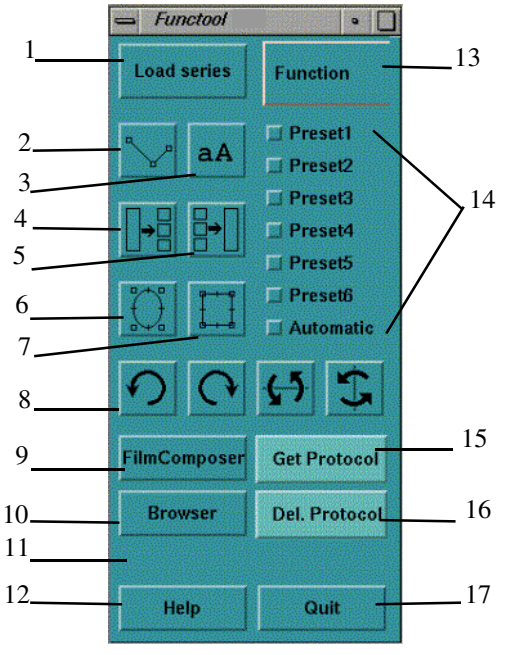


Figure 4: Display Tool Command Window.

No:	*Description*	*Function*
1	**[Load Series]**	Loads the selected exam, series and images from the Browser into the display tool.
2	**[Polygon] or [Spline]**	Used to create a polygon or spline region of interest. Click while pressing **Shift** and drag to draw. Selecting the icon again will toggle between polygon (straight lines) and spline (curved lines). You can edit by dragging on the drawn figure.
3	**[aA]**	Used to type annotation on an viewport.
4	**[Split ROI]**	Used to split an ROI into multiple single–pixel ROIs.

5	**[Merge ROI]**	Used to return a split ROI to the original ROI.
6	**[Ellipse]**	Used to create an elliptical ROI.
7	**[Square]**	Used to create a square ROI.
8	**Rotate Buttons**	Used to rotate or flip the displayed image.
9	**[Film Composer]**	Opens the Film Composer in the lower right hand corner of the monitor.
10	**[Browser]**	Opens the Browser for series or image selection.
11	**Message Line**	Area reserved for posting messages concerning display operation.
12	**[Help]**	Provides a quick reference of commonly used commands.
13	**[Function]**	The menu of statistical algorithms. You can choose from the General, Research, or Spectroscopy categories. Each of these categories has a sub-menu of metabolites or ratio of metabolites to select.
14	**Preset 1-6, Automatic**	Preset and automatic window level options.
15	**[Get Protocol]**	A pull down menu of pre–defined and previously saved protocols.
16	**[Del. Protocol]**	A pull down menu of protocols available to delete.
17	**[Quit]**	Closes or quits the display tool, returning to the browser.

Region of Interest

To place an ROI on the chemical shift, metabolite image, and reference viewports select either **[square ROI]** or **[ellipse ROI]**. A green (active) ROI is drawn at the center of the three image viewports. The ROI can be moved or resized by clicking on the resizing and movement handles on the ROI – the handles are only present on an active ROI. Alternatively, you can select **Shift**, left-click and drag to draw an ROI.

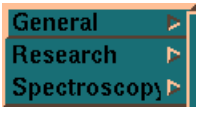
Once an ROI has been placed on the viewports, it can be split or divided to display the reconstructed CSI pixels contained within the ROI as shown in Figure 3. To split the ROI, select **[split ROI]**. To return to the merged or single ROI, select **[merge ROI]**. Note that an ROI of any shape – rectangle, ellipse, or freely drawn – is composed of the square, reconstructed CSI pixels. By selecting **[split ROI]** you can always see which CSI pixels contribute to the ROI, and to the numeric information displayed or listed for the ROI. Once the ROI has been split it is possible to move and delete the individual CSI pixels.

Rotate Buttons

Use the Rotate buttons to change the orientation of the images. To return to the original display right-click on the image and select **[Display Normal]** from the shortcut menu. You cannot flip or rotate the graphs.

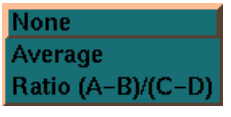
Function Menu

The Function menu allows a number of choices to display the CSI data. These choices differ from the selections on the **[Get Protocol]** menu, in that the Function menu selections cannot be modified and include no information concerning the definition of the protocols.

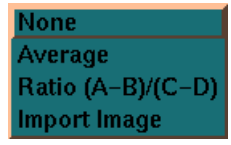


The Function menu selections opens to a set of metabolite selections.

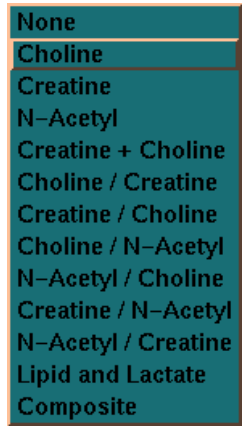
The General menu displays the following choices:



The Research menu displays the following choices:



The Spectroscopy menu displays the following choices:



The map of the metabolite or ratio of metabolites is displayed.

If you select a metabolite or ratio, such as Creatine/ Choline a dialog box appears with the options for **[Compute]**, **[Save Protocol]**, **[Close]**, and **[Help]**.

⇨ **Compute** - Clicking allows the changes that you make to the parameters on the panel are invoked by clicking **[Compute]**. Whenever you click **[Compute]** the protocol title on the Function parameters panel, the function view, and the composite view is changed to the generic “Average” or “Ratio (A-B)/(C-D)”.

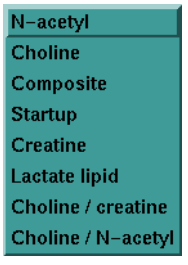
⇨ **Save Protocol** - Clicking allows you to save the metabolite or ratio as a protocol that can be stored and recalled for future use. Enter the name of the new protocol on the entry field on this panel. To accept, and create the new protocol, click **[OK]**. Click **[Cancel]** to leave the “Save protocol” panel without creating the new protocol. User created protocols can be deleted at any time by clicking **[Del. Protocol]** on the Main Control Panel.

⇨ **Close** - Allows you to exit from the Function parameters dialog box. Generally you will only use **[Close]**.

⇨ **Help** - Clicking **[Help]** enlarges the Function parameters panel to include an explanation of the protocol, simple algorithmic information, and definitions of the parameters. **Help** allows viewing of the absolute value for the selected metabolite or ratio. This value cannot be changed, it is for viewing only.

Get Protocol

Selecting **[Get Protocol]** displays the metabolite map or metabolite ratio map using the pre-defined spectral regions to calculate the metabolite or ratio maps.



- **N-acetyl** – displays the averaged, absolute pixel values from CSI image 143 through image 154 as a metabolite map,
- **Choline** – displays the averaged, absolute pixel values from CSI image 64 through image 74 as a metabolite map,
- **Composite** – displays the averaged, absolute pixel values from CSI image 64 through image 222 as a metabolite map,
- **Startup** – displays the averaged, absolute pixel values over the region 50-200. This is a good picture of the excited ROI.
- **Creatine** – displays the averaged, absolute pixel values from CSI image 78 through image 88 as a metabolite map,

- **Lactate lipid** – displays the averaged, absolute pixel values from CSI image 183 through image 222 as a metabolite map,
- **Choline/creatine** – displays a map of the ratio of the choline, 64 -74 region, to the creatine, 78 – 88 region,
- **Choline/N-acetyl** – displays a map of the ratio of the N-acetyl, 143 – 154 region, to the choline, 64 – 74 region.

Section 3 - The Chemical Shift or Upper Left (UL) Viewport

Individual chemical shift images, are displayed as non-zipped images, and are displayed in gray scale in this viewport. No smoothing is the default mode for displaying images in this viewport. The individual rank images can be used to characterize the homogeneity through the prescribed PRESS voxel, and the spatial variation of the water suppression. The rank is the number assigned to the image when the images are sorted by increasing time. Large variations in both will appear as dark and light regions as in (Figure 5). Each rank image corresponds to the spatial distribution of one of 256 equally spaced frequencies between 4.3 and 0.49 PPM.

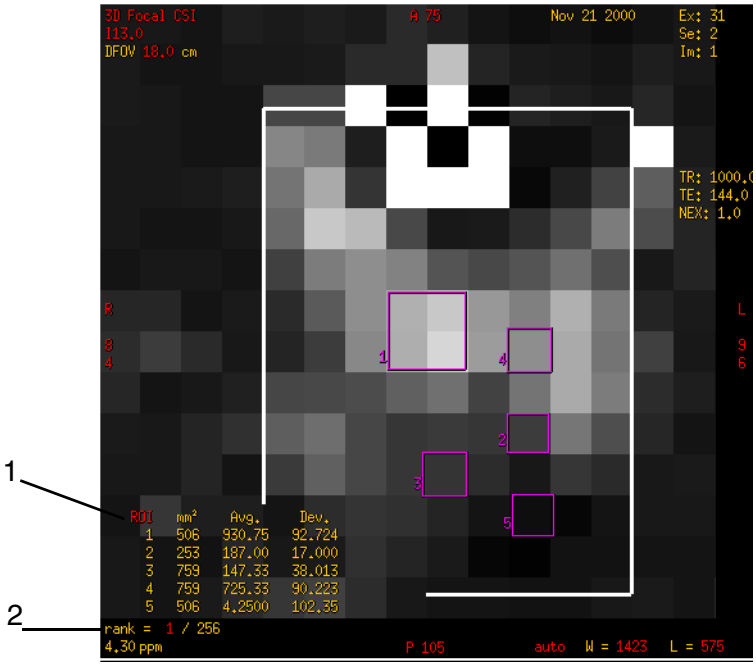


Figure 5: The chemical shift viewport, rank=1 display with five ROIs.

Initially, the first of the 256 chemical shift images is displayed, as indicated by the rank = **1** / 256 (2) entry displayed at the bottom left of the viewport. The rank number of the displayed chemical shift image is an active annotation and can be changed with the mouse buttons or the **arrow** keys. A right mouse click decreases the rank number and a left mouse click increases the number.

General information for each ROI is printed in this window. In the example (Figure 5), a column of ROI numbers (1) labeled "**ROI**", a column labeled "mm^2" which lists the area in millimeters for each ROI, and a column labeled "Avg." are displayed in the bottom left corner of the viewport. The average of the signals from the pixels in each ROI is listed in the "Avg." column. Depending on the selected metabolite a "Dev." column may appear showing the standard deviation. The ROI

list can be moved to another part of the viewport by clicking and dragging the ROI label with the middle mouse.

The Chemical Shift Viewport Menu: The default shortcut menu contains eight selections. Right-click in the upper left (UL) viewport to access this menu. Once an ROI, other graphic object, or annotation has been placed on the viewport, other toggle items are added to the menu such as Hide/Show graphics and Hide/Show annotation.

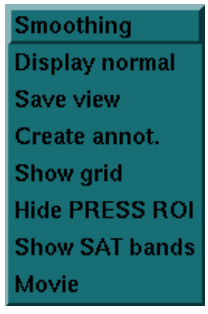


Figure 6: Chemical shift viewport menus.

Section 4 - The Spectral Grid or Upper Right (UR) Viewport

One to at least 250 spectra can be displayed in this viewport; the initial display is blank. Three display colors are used for the spectra; green for the spectrum from the “active” ROI, purple for spectra from any other ROIs, and white for the spectrum corresponding to the cursor location when the cursor is used to select a spatial region on one of the image display viewports. The signal intensity for each of the 256 points in a spectrum can be listed for the spectra from 1- 8 ROIs (Figure 7). This list is accessed with a right-click in the spectral grid viewport and drag to select **List values**. You can click on the image number located at the top of the list (indicated by the red or bright white text) to scroll through the list. Left-click to increase and right-click to decrease the image number. (For example, the “Rank im #,” number 65 in Figure 7.)

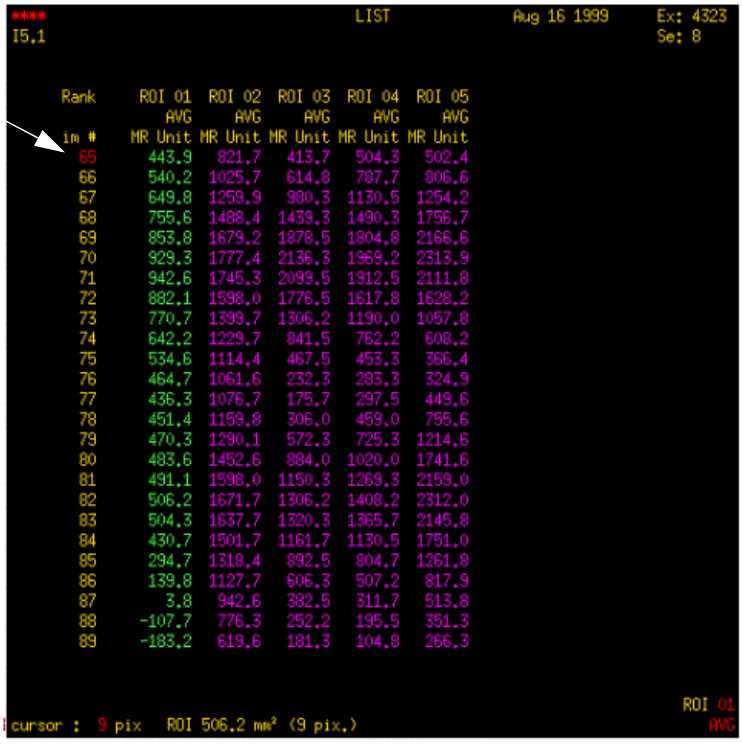


Figure 7: Spectral grid viewport with a list of signal intensities from five ROIs.

When you move the cursor on the spectrum or spectra displayed in the spectral grid viewport, two white lines intersect on the display and two numbers are displayed in white along the x- and y-axes (Figure 8). The x-axis number corresponds to the image rank number or to the PPM value of the chemical shift image (the 4.30 to 0.49 PPM region of the spectra is displayed). The y-axis number corresponds to the signal intensity at the cursor location on the spectrum.

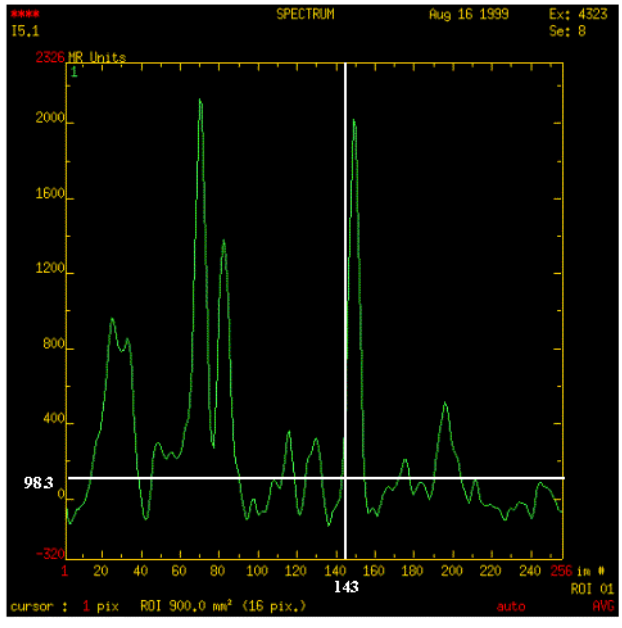


Figure 8: Using the cursor to display the signal intensity at a point in the spectrum.

You can also display the rank or complete chemical shift image in the chemical shift viewport (UL) for a given point in a spectrum by double clicking on a spectrum. For example, if you double click on the spectrum at point 143, the display in the chemical shift viewport will change to the 143rd rank or chemical shift image, and the UL display will be “rank = 143 / 256”. The image number (im #) is the default for the x axis, to change, right-click in the spectral grid viewport, drag to **Set x units** and select **ppm**.

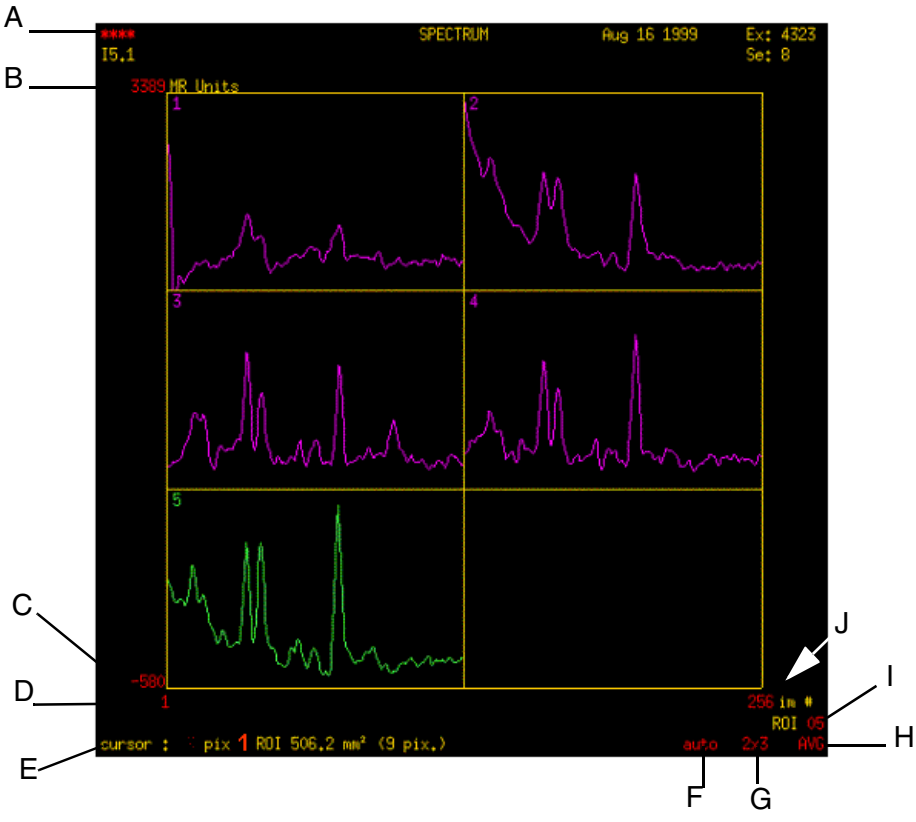


Figure 9: Spectra displayed in the spectral gird viewport.

Active annotations: There are ten active annotations in this viewport. In Figure 9, the active annotations, starting at the top left and moving down, are:

- (A) ******** – the patient name, which has been hidden in Figure 9.
- (B) **3389** – the current y-axis maximum value, used to scale the spectra.
- (C) **-580** – the current y-axis minimum value, used to scale the spectra.
- (D) **1** – the current x-axis starting image, used to zoom the spectra – units are points or rank image as shown in Figure 9, or PPM.

- (E) **cursor: 1 pix** – i.e., the number of pixels averaged to produce the cursor spectrum, and used to determine the extent of the cursor size smoothing region. **Set the value to one to avoid cursor size smoothing.**
- (F) **auto** – click to automatically scale the vertical spectra to the active spectrum (ROI) – pressing the **space bar** has the same effect. Select either an ROI or a specific spectrum in the UR viewport and click **auto**. The other spectra are vertically scaled to the selected ROI or spectrum.
- (G) **2x3** – click to toggle between the display of separate spectra, as shown in Figure 9, or to display the spectra superimposed on one frame, i.e., **1x1** (Figure 10).
- (H) **AVG** – click to toggle between the four spectrum display selections, AVG, MAX, MIN, and DEV (standard deviation) – these selections are explained later in the chapter.
- (I) **ROI 05** – indicates the active spectrum (ROI), click to change the active spectrum, clicking on the word “ROI” deselects the active spectrum (ROI).
- (J) **256 im #** – the current x-axis ending image, used to zoom the spectra – units are points or rank image as shown in Figure 9. If you set x units to PPM (using the shortcut menu, accessed with a right-click), the x (horizontal) scale changes to 4.30 - 0.49 ppm. With the cursor over the active annotation of 0.49, a right click will increase this value and a left click will decrease this value, the range is 0.49 - 4.29 ppm.

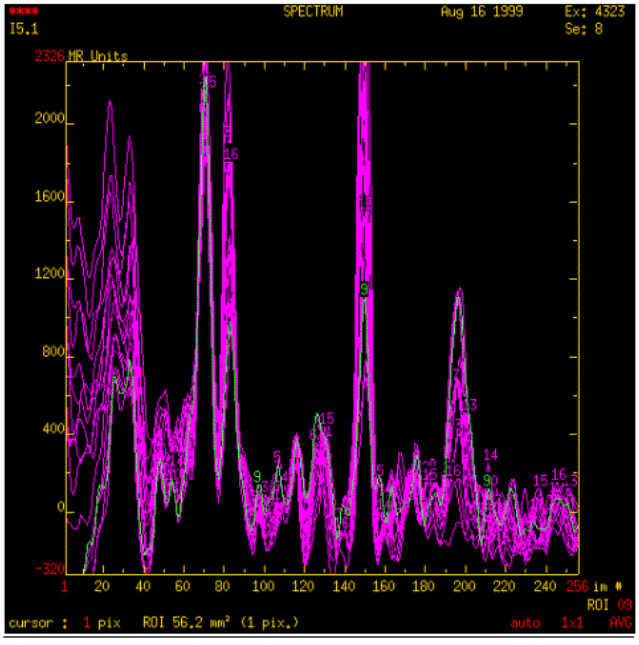


Figure 10: Superposition of 16 spectra in the spectral grid viewport.

Active Spectrum (ROI): In the spectral grid viewport, to change the active spectrum (ROI) click on the spectrum, or click on the ROI active annotation. The active spectrum is always drawn in green.

Y-axis and Spectrum Scaling: Spectra can be scaled to fit the display window by clicking, or clicking and dragging the y-axis maximum and minimum active annotations. It is also possible to automatically scale the active spectrum to fit the display window or a frame by pressing the **Spacebar** on the keyboard, or clicking on the **auto** active annotation. If more than one spectrum is displayed, all spectra are scaled to the active spectrum (ROI) with these selections. Unless explicitly changed, the scale stays the same.

X-axis, Image Rank and the PPM Scale, and Spectrum Zooming: You can zoom the spectrum by clicking on the x-axis limits to select the region of the spectrum that you wish to display. Each spectrum

consists of 256 points, one for each of the 256 Chemical Shift or rank images stored in a CSI data set. The spectra cover a frequency range from 4.30 to 0.49 PPM.

The PPM (parts-per-million) scale relates all resonant frequencies (peaks) to a standard frequency (i.e., on a Signa system to *in vivo* water at 4.7 PPM), and is independent of the field strength. At 1.5T, a change of 1.0 PPM corresponds to a change of approximately 64Hz. The N-acetyl groups resonate at 2.0 PPM, a frequency that is 2.7 PPM or 173Hz lower than the resonant frequency of the hydrogen atoms in the water molecule.

Unfortunately the resonant frequency of the hydrogen atoms in the water molecule is temperature dependent, while the resonant frequencies of the metabolites are relatively constant between 10-50°C. A water temperature change of one degree Celsius (1°C) corresponds to a frequency change of 0.6Hz (approximately 0.01 PPM). For example, the resonant frequency of water at 21°C is about 10Hz lower than the frequency of water at 37°C (body temperature). The PROBE/SVQ, probeSI, and 3D Focal CSI spectra are processed assuming tissue water resonates at 4.7 PPM, i.e., the tissues are at or near 37°C. When acquiring data from a phantom at a temperature other than 37°C, the quantitative analysis program will often fail, and/or the reconstructed spectrum may be shifted by the temperature dependent shift of the water resonance from 4.7 PPM.

Cursor Location Spectrum: The spectrum associated with the cursor location is the spectrum from one pixel, or an averaged value of the spectra from 4, 9, 16, 25, 36 ,49, 64, 81, or 100 pixels. The number of pixels is selected by clicking on the cursor : # pix active annotation at the lower left of the viewport. The cursor spectrum is always displayed in white, and is always the last spectrum in a multi-spectrum display.

Note:

Before displaying any metabolite or ratio maps, set the cursor value to one to avoid additional smoothing (based on the size of the cursor) of the maps.

Superimposed Spectra or Individual Spectra: In the initial or default display of multiple spectra – the 1x1 active annotation, (Figure 10) the spectra are superimposed on the display. The spectra are scaled to the maximum and the minimum values found in the set of selected spectra or to the last scale selected. Separate spectra, one for each ROI, are displayed in smaller individual frames for an NxN active annotation. In Figure 9, the five spectra are displayed as a 2x3 array, and the active annotation is 2x3.

Spectrum Average or Compression Techniques: The spectra or signal intensity lists can be displayed using one of 4 different methods to combine the data from more than one pixel. The four methods are:

AVG - displays the average of the pixel values,

MAX - displays the maximum pixel value for each point,

MIN - displays the minimum pixel value for each point,

DEV - displays the standard deviation for each point.

For spectra corresponding to a single pixel the AVG, MAX, and MIN methods produce identical spectra and intensity lists, and the DEV selection produces straight lines. Typically the default AVG selection should be used to display the spectra.

The Spectral Grid Viewport Menu: This shortcut menu has several options and toggle options, that can be accessed with a right-click in this viewport. If an option is selected, the menu contents change. The

default shortcut menu and the sub-menu selections are:

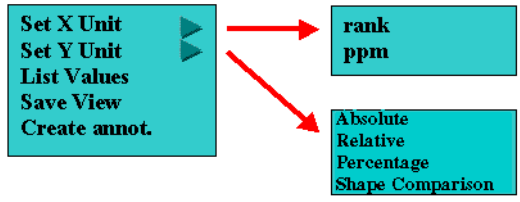


Figure 11: Spectral grid viewport menus.

If you place an ROI on one of the image viewports or you use **Create annot.**, additional items are added to the shortcut menu as shown in Figure 12:

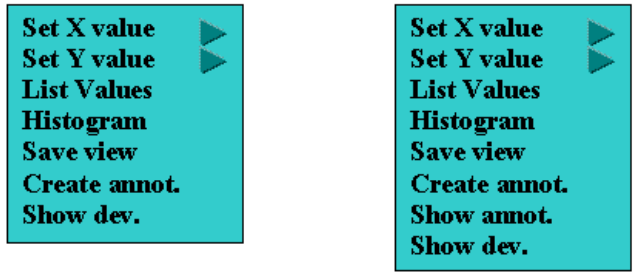


Figure 12: Expanded spectral grid viewport menus.

The toggle selections in the menu are: **List Values** and **Spectrum**, and **Show/Hide dev.** The **Show/Hide annot.** toggle selection only appears if you select **Create annot.**

⇨ Under **Set X Unit** you have the option of choosing **rank** or **ppm**: Sets the x-axis unit label. The choices are points (image rank) or PPM (parts per million). Each spectrum consists of 256 points, one for each of the 256 chemical shift or rank images stored in a probe-P image. Each spectrum covers the range from 4.30 to 0.49 PPM.

⇨ Under **Set Y Unit** you have the option of choosing **absolute**, **relative, percentage,** or **shape comparison**. For probe-P data display, always select **absolute** which plots the actual pixel values for each point. The other choices are meaningless for spectral data.

⇨ **List Values** or **Spectrum**: Toggles between the spectrum display, and the display of a scrollable list of signal intensities (Figure 7) for each point in the spectrum.

⇨ **Histogram**: Displays a histogram of the data in an ROI. This selection is only available if an ROI has been placed on the images. If selected, the shortcut menu is reduced to three selections, **Spectrum**, **List Values**, and **Save View** as shown in Figure 13, and the shortcut menu is limited to three selections until you select the **Spectrum** display again.

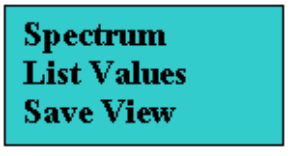


Figure 13: Spectral grid viewport menu if **Histogram** is selected.

⇨ **Show dev.** or **Hide dev.**: Shows or hides the deviation or measure of variability of the plotted data.

Section 5 - The Metabolite Image or Lower Left (LL) Viewport

Average or Ratio metabolite maps corresponding to the protocols selected with **[Get Protocol]** or **[Function]** are displayed and manipulated in the lower left (LL) viewport. In the metabolite image viewport, the prescribed PRESS voxel is overlaid (the voxel is outlined in white) on the map as shown in Figure 14.

The metabolite maps are a combination of spatial and spectral signal intensity information. The maps are derived from the CSI rank images that can be viewed individually in gray scale in the chemical shift viewport. Average maps are created by combining/averaging several contiguous CSI images. The contiguous regions (see Table 1) correspond to the locations of the metabolite resonances or peaks.

Metabolite	*Image range*	*PPM*
Choline	images 64..74	3.24 +/- 0.08 ppm
Creatine	images 78..88	3.02 +/- 0.08 ppm
N-Acetyl	images 143..154	2.02 +/- 0.08 ppm
Lactate and Lipid	images 183..222	0.9..1.5
Startup	images 50..200	3.5-1.33
Composite	images 64..222	0.9..3.32 ppm

Table 1

Ratio maps are a simple extension of the average technique in which two different, contiguous sets of CSI rank images are separately combined, and then the two combined images are divided to produce a ratio map. In essence, a map corresponds to the spatial distribution of the signal intensity of a region of a spectrum, or of the ratio of signal intensities in two regions of a spectrum.

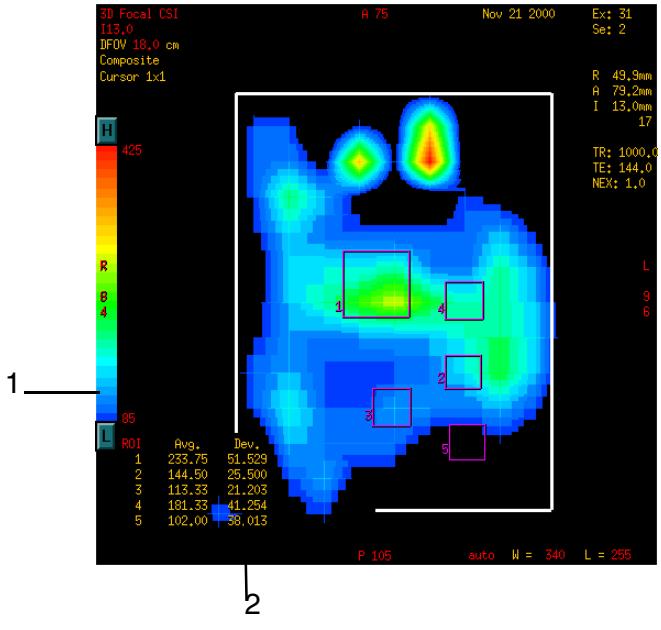


Figure 14: Metabolite image viewport display.

A numeric list of information appropriate to the current metabolite map or ratio map for each ROI is displayed on this viewport. The default location of the list is at the bottom left of the viewport. Click and drag the ROI text

to move the listed information to another area of the viewport. In the example (Figure 14), ratios from five ROIs are listed. The “Dev.” column (2) displays the standard deviation of the selected metabolite. Depending on the metabolite chosen instead of “Dev.” a “%” column appears showing the relation of the individual ROI ratio values to the 100% value assigned to the active (green) ROI. The ratio for the active, fifth ROI is listed as 1082.2 (the actual value is 1.0822 which is scaled by 1000). The ratio for the fourth ROI is listed as 1555.5 which is 43% greater than the ratio from the active ROI.

Depending on the metabolite chosen instead of a “%” column you may be given a “Dev.” column displaying the standard deviation.

You can adjust the window width and level of the map by clicking and dragging the middle mouse, or by clicking on the active annotations at the bottom left of the viewport – “W = 340” or “L = 255” in Figure 14. The range of the colorscale (1) at the left edge of the viewport is related to the window width (W) and window level (L) as

colorscale maximum = W + L/2,

and

colorscale minimum = W – L/2.

You can adjust the colorscale maximum and minimum by clicking on the numbers at the top and bottom of the colorscale; 425 and 85 in Figure 14. If you select **[H]** at the top of the colorscale, those pixels in the map with an intensity larger than the maximum colorscale intensity are colored black. If you select **[L]** at the bottom of the colorscale, those pixels with an intensity less than the minimum colorscale intensity are colored blue. The **[H]** selection allows you to quickly see the maximum areas on any map.

If you change the display in the metabolite image viewport, e.g., if you zoom on the image or adjust the window width or level, the same changes or selections will be applied to the metabolite map overlaid on the LR reference viewport.

The Metabolite Image Viewport Menu: To access this menu, right-click in the viewport. The default shortcut menu contains four toggle selections – **No smooth/Smooth**, **Show/Hide grid** , **Hide/Show Press ROI**, and **Show/Hide SAT bands**. Once an ROI, any other graphic object, or annotation has been placed on the viewport, an additional toggle item is added, **Hide graphics** and **Show graphics** is added to the menu. Menu options selected in this viewport that affect the display of the map in the metabolite image viewport have the same effect on the map overlaid on the reference viewport. The contents of the menu are:

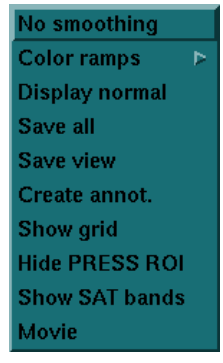
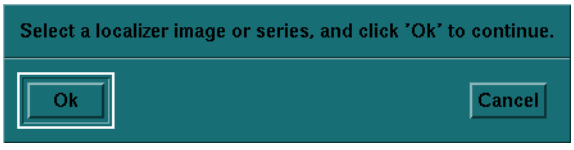


Figure 15: Metabolite image viewport menus.

Section 6 - The Reference (with Localizer Overlay) or Lower Right (LR) Viewport

Initially the display in the reference viewport consists of a metabolite map at a 50% transparency level overlaid on the localizer image currently displayed in the chemical shift viewport with the prescribed PRESS voxel outlined by a white line (Figure 1). When the display tool is launched a dialog box appears asking you to select a localizer image, highlight the localizer

series from the browser, the default is image three of the selected series.



This localizer reference image is displayed in the reference viewport, as shown in Figure 16.

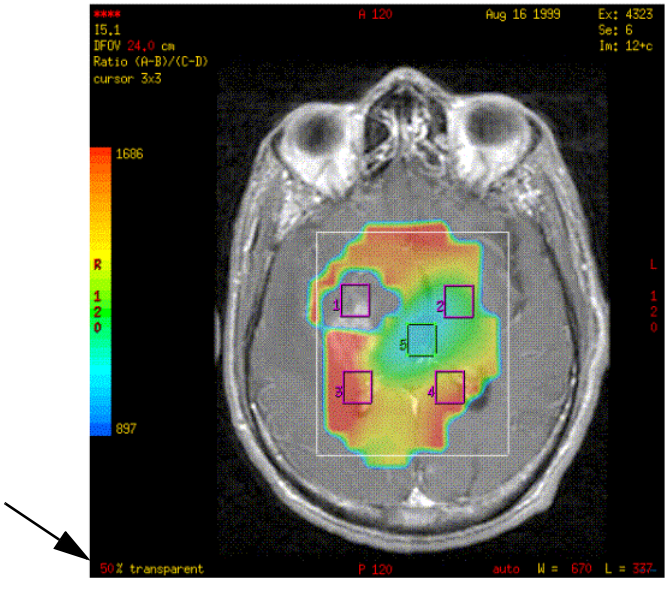


Figure 16: Reference viewport display with reference image.

You can adjust the transparency of the overlay by clicking on the 50% transparent (arrow) active annotation. You can adjust the window width and level of the localizer image by clicking and dragging the middle mouse.

The Reference Viewport Menu: The default shortcut menu contains 10 selections. These selections are accessed with a right-click in the viewport. Once an ROI, any other graphic object, or annotation has been placed on the viewport, other menu options appear.

The contents of menu are:

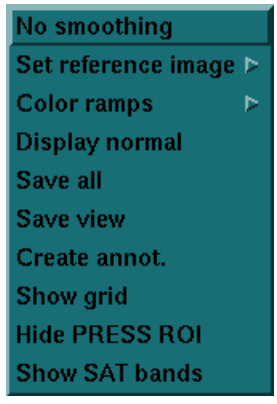


Figure 17: Reference viewport menus.

⇨ **Set Reference Image** to display a selected image, or the original, default display. The shortcut options are **original** and **selection**.

The selection properties are:

⇨ The default display in this viewport is a metabolite map at a 50% transparency level overlaid on the default image of the localizer series that you selected. Use **Set reference image** to display an image from a selected series, or the original CSI image with smoothing.

- If you select **original,** the smoothed CSI image appears with a metabolite map overlay.
- If you select **selection**, the localizer (selected) series, image three appears with a metabolite map overlay.

Section 7 - The Function Parameters Window

Function

Selecting a protocol from the **[Function]** menu on the command window, a Function parameters window appears as shown in Figure 18. No input lines are displayed on these windows and the selected protocols cannot be modified.

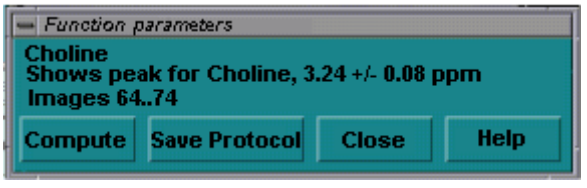


Figure 18: When choline is selected from the Function menu, the Function parameters window appears.

Get Protocol

Selecting a protocol from the **[Get Protocol]** menu on the command window, a Function parameters window, specific to the protocol, is displayed. Windows similar to those seen in Figures 19 and 20 appear. You can modify these windows, although the startup and composite windows cannot be modified. The Function parameters window for the Average metabolite maps of N-acetyl, choline, creatine, and lactate-lipid regions is fairly simple, with one input parameter line that defines the metabolite region and combining method (Figure 19).

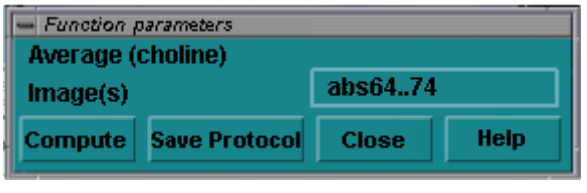


Figure 19: Function parameters window for the Average (choline) protocol.

If you select one of the Ratio (A-B)/(C-D) map protocols from the **[Get Protocol]** menu, a more complex window (Figure 20), is displayed. For the

pre-defined choline/creatine and N-acetyl/choline ratio protocols, four of the 6 input parameter lines are used to define 2 spectral regions, a threshold factor, and a scale factor.

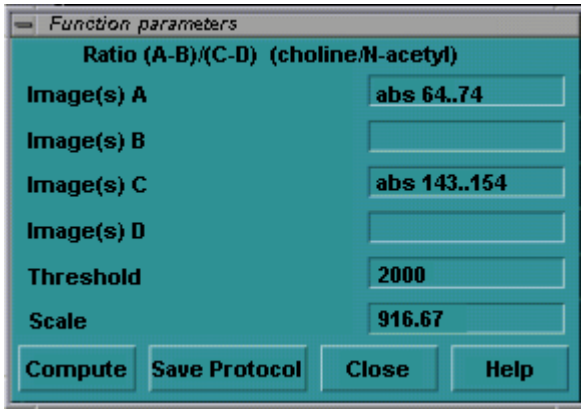


Figure 20: Function parameters window for the Ratio (choline/N-acetyl) protocol.

Both Average and Ratio (A-B)/(C-D) Function parameters windows contain four (4) selectable buttons. The four buttons shown in Figure 19 or 20 are labeled; **[Compute]**, **[Save Protocol]**, **[Close]**, and **[Help]**. Typically, you will only use **[Close]** to close the window.

⇨ **[Help]** enlarges the Function parameters window to include an explanation of the protocol, simple algorithmic information, and definitions of the parameters.

⇨ Changes made to the parameters in the input parameters fields are invoked by selecting **[Compute]**. Whenever you select **[Compute]** the protocol title on the Function parameters window, the metabolite image viewport, and the reference viewport is changed to the generic Average or Ratio (A-B)/(C-D).

⇨ To save the changes for future use, select **[Save Protocol]**. Enter the name of the new protocol in the field. Selecting **[OK]** creates and saves the new protocol.

- Selecting **[Cancel]** leaves the Save protocol window without creating the new protocol. User

created protocols can be deleted at any time by selecting **[Del. Protocol]** on the command window and drag to the protocol to delete.

⇨ Select **[Close]** to close the window.

The Function parameters window for the Ratio (A-B)/(C-D) (choline/N-acetyl) protocol displayed in Figure 20 is the basis for all of the spectroscopy Function parameters windows. The Average (choline) example in Figure 19 is a simplified version of the ratio window.

In addition to the four selectable buttons, the window has six input parameter fields:

⇨ The first four fields, labeled **Image(s) A**, **Image(s) B**, **Image(s) C**, and **Image(s) D**, specify an image or a range of images used in the protocol calculations. The values returned by the pre-defined protocols are the scaled values of A, or A/C. It is possible to return the values of A, A – B, A/C, (A – B)/C, or (A – B)/(C – D), depending on which input parameter fields are left empty. For example, to return the simple ratio A/C, the B and D input parameter fields are left empty as shown in Figure 20. Clearly the Image(s) A input parameter field can not be empty.

⇨ The fifth field specifies a pixel value **Threshold** used to suppress background noise or spurious signals. The threshold value is compared to the value of the denominator C or (C – D); whenever the denominator is less than the threshold value, the ratio is set to zero, and appears as a black pixel in the ratio map.

⇨ The last parameter field defines a **Scale** factor. A scale factor of 1000 is recommended to minimize round-off and integer truncation artifacts. For example, a scale factor of 1000 means that ratio values like 1.432 or 0.789 are listed in the metabolite image viewport as 1432 and 789, respectively. Using a smaller scale factor, in most cases, will reduce the number of digits in the ratio. For example, scale factors of 100, 10, and 1 would scale the 1.432 value as 143, 14, and 1, respectively. Scale factors other than 1, 10, 100, or 1000 will make either visual or simple arithmetic comparisons of the spectra and ratio values difficult and are not recommended.

The general Ratio (A-B)/(C-D) algorithm uses the threshold and scale factors to return a value for each pixel in the ratio map according to the general equations:

if Threshold $\leq$ (C – D) then,

Pixel Value = Scale * (A – B) / (C – D),

or if Threshold > (C – D),

Pixel Value = 0.0 (the pixel is set to black on the ratio map).

The **Image(s)** input parameters can be a single image **N**, or a range of images **N..M**. For spectra this means either a single point, or a range of points in the spectra, respectively. There are also five, 3 letter input parameter prefixes that can be used to modify the combination of the points in the given region of the spectrum during a calculation:

- **abs N..M** – returns the average of the absolute values of the pixels in the range,
- **min N..M** – returns the minimum pixel value from the range,
- **max N..M** – returns the maximum pixel value from the range,
- **log N..M** – returns the average of the natural logarithms of the pixels in the range,

- **dev N..M** – returns the standard deviation of the pixels in the range.

The input entry fields in the pre-defined protocols for the four metabolite maps, and two metabolite ratio maps are all of the form **abs N..M**. Image or spectral regions are defined for three chemical species (N-acetyl groups, choline, and creatine), and a region containing the two chemical species lactate and lipid. The startup and composite protocols combine the signals from most of the spectral region.

The choline, creatine, and N-acetyl regions are used to define the input parameter entries for the choline/creatine, and the choline/N-acetyl ratio maps. Using the Function parameters window for the choline/N-acetyl Ratio map in Figure 20 as an example, the absolute values of the signal intensities for the chemical shift images 64 through 74 (**Image(s) A = abs 64..74**) are divided by the absolute values of the signal intensities of the chemical shift images 143 through 154 (**Image(s) C = abs 143..154**) using a threshold value of **2000**. The quotient is multiplied by the **1000** scale factor.

Note:

A scale factor should be a multiple of 10.

The ratio map for with this protocol is calculated using the equation:

Pixel value = 1000 * (abs 64..74) / (abs 143..154)

where any value of **(abs 143..154) <2000** is set to zero (0).

Hints

Using Numeric Data Lists: To insure that the numeric data from an ROI that is listed on one of the 3 image viewports is consistent and reproducible, always set the cursor size active annotation on the spectral grid viewport to read “cursor : **1** pix …” (arrow Figure 21). The cursor size is also indicated by the “cursor 3x3 …”

(circled Figure 22) annotation near the top left corner of the metabolite image and reference viewports. Using a value other than one invokes an additional pixel smoothing algorithm for the metabolite and ratio maps that varies with the cursor size.

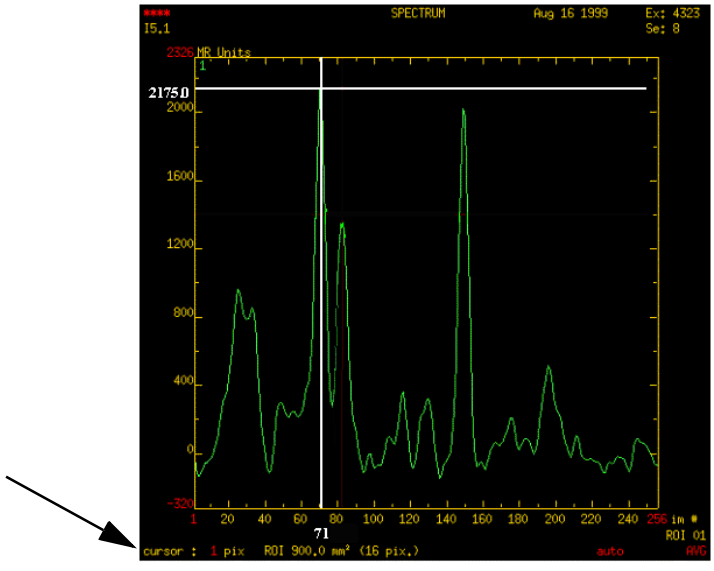


Figure 21: Solid White=choline peak maximum.

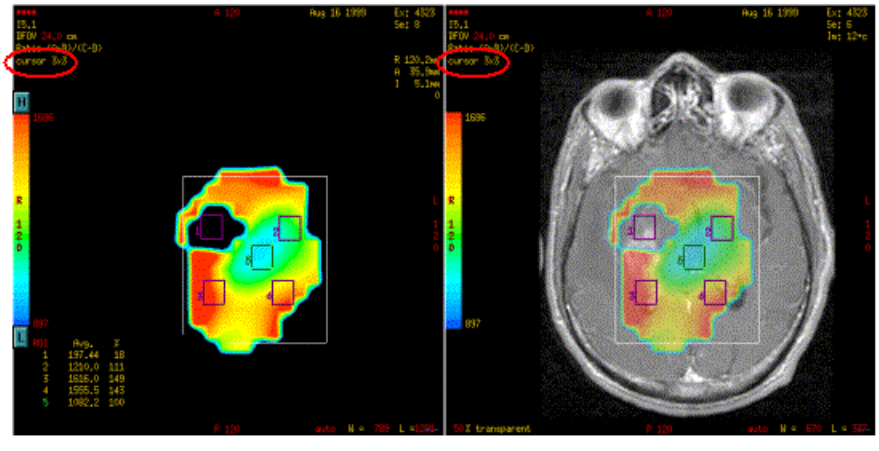


Figure 22: Metabolite image and reference viewports with nine (3x3) pixel cursor smoothing.

Metabolite and Ratio Maps with Sharp Edges: Occasionally the metabolite and ratio maps terminate with a sharp edge. The sharp edges are often an artifact of the cursor size smoothing algorithm noted just above. To avoid these artifacts always set the cursor size active annotation on the spectral grid viewport to read **"cursor : 1 pix ..."**.

Set-Up

Displaying 3D Focal CSI Images

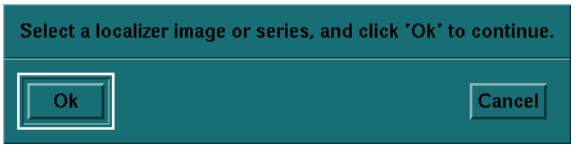
Use this procedure to display the 3D Focal CSI images that you obtained during scanning. The prerequisites for display are a valid image set of 3D Focal CSI images and a display tool such as Functool CSI or MIROI. Software versions below Functool 2.0 are not able to accomodate the 3D Focal CSI images.

(1) Select a 3D Focal CSI series from the browser.

(2) Select the display tool, **[Functool CSI]** for example, to launch the display software.

(3) A message window appears requesting selection of a localizer series or image. Select an appropriate localizer series/image from the browser and click **[ok]**. Click **[cancel]** to discontinue display.

When the display tool is launched a dialog box appears asking you to select a localizer image, highlight the localizer series from the browser, the default is image three of the selected series.



- The display tool command window appears on the left and four viewports appear to the right. The upper left (UL) viewport displays a chemical shift image, the upper right (UR) is for displaying spectra (blank until an ROI is selected), the lower left (LL) displays a metabolite map, and the lower right (LR) displays a metabolite map overlaid on a reference image.

Note:

The image in the UL, LL, and LR viewports default to the first image of the selected CSI series.

The viewports default to the reference of metabolites, you must select from the **[Get Protocol]** menu to select a different metabolite. See step 4.

(4) Select **[Get Protocol]** and drag to select a metabolite display protocol from the menu. This displays the metabolite map and the map overlay. The protocol menu provides the following metabolite map selections:

- N-acetyl
- Choline
- Composite
- Startup
- Creatine
- Lactate Lipid
- Choline/creatine
- Choline/N-acetyl

(a) If desired, a right-click in the viewport displays a shortcut menu that allows selection of saving one or all images for later viewing from the browser.

(b) You can stop here, repeat steps one through four if needed, or continue with steps five through 10 to select specific ROIs and obtain metabolite information for those areas.

(5) Select one of the following ROIs from the display tool command window.

- Select elliptical for a circular ROI.
- Select square for a square ROI.
- Select spline for a spline ROI, and draw the ROI.

The ROI is drawn on the three image viewports. You can page through the slices and place multiple ROIs on any of the slices. The ROIs will be numbered consecutively (even if ROIs are placed on multiple slices). The maximum number of ROIs on one image is 12, for more than 12 ROIs, the data is replaced for previous ROIs. For example, ROI number 13 replaces the data for ROI number one, ROI number 14 replaces the data for ROI number 2 and so on. All the ROIs are still seen on the viewport, just the data is missing. You can view the data for all the ROIs with a right-click in the UR viewport and click **List Values**.

(6) Click and drag one of the square handles to size the ROI.

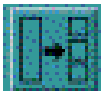
(7) Click the center of the active ROI and drag to move to desired position.

(8) Place the cursor in the spectral grid viewport and press the **Spacebar** to scale the grid to fit the viewport.

(9) To place multiple ROIs on the viewports do one of the following:

(a) Click on the ROI in the viewport to make inactive, then select the ellipse, square, or polygon/spline. Repeat as needed, remember to make the active ROI inactive.

(b) To split an ROI, select the ROI and click **[Split ROI]**.



(10)With the crosshair still remaining in the upper right viewport, right-click to view a shortcut menu. Drag to **X Unit** and select **ppm** (parts per million). This displays the ppm scale below the spectrum which designates the chemical address of each metabolite.

(11)In the upper right viewport the active annotation cursor : **#** pix should be one. To change the number (#) click, or click and drag left/right on the cursor number. Setting the value to one avoids cursor size smoothing.

Note:

At anytime you have the option to Split the ROI, or Merge the ROI by selecting the icon from the display tool command window.

Setup

Creating a Custom Protocol

As a simple example, a protocol is created to display a ratio map and ROI ratio lists that correspond to the maximum of one metabolite (choline) divided by the maximum of the another metabolite (creatine) with reasonable Scale and Threshold values.

(1) Have a valid 3D Focal CSI data set with the display tool launched.

(2) Select **[Get Protocol]**.

(3) Select a metabolite ratio protocol.

- The Function parameters window will appear.

(4) Determine the maximum for the desired metabolite peaks using the cursor in the spectral grid view. The example shown in Figure 22, the solid white lines indicate that the maximum choline signal appears at point **71**, and the dotted white lines show that the maximum creatine value occurs at point **82**. In actual practice the maximum value for the creatine peak would be determined using solid white lines too, but for illustration dotted white lines

are used to show the maximum creatine value in Figure 22.

(5) In the Image(s) A input parameter field, enter **abs 71**, the point value of the first metabolite.

(6) In the Image(s) C input parameter field, enter **abs 82**, the point value of the second metabolite.

(7) Leave the Image(s) B and Image(s) D input parameter fields empty.

(8) Change the Threshold value to an initial value of **500**.

(9) If necessary, change the Scale value to **1000**.

(10) Select **[Compute]** to compute and display the new Ratio map.

(11) Make any changes to the Threshold value required to create a pleasing ratio map, and to the Scale value to produce reasonable ratio values. For example, setting the Threshold value to 500 may produce a map with spurious signals outside of the prescribed PRESS voxel, in that case you would increase the value. If on the other hand the map is black, the threshold is too large and should be reduced.

(12) Save the new protocol by selecting **[Save Protocol]**.

(13)When prompted for the new name, enter a suitable name, for example, Cho/Cr MAX, and select **[OK]**. The new protocol will now appear on the **[Get Protocol]** menu, and can be selected until deleted.

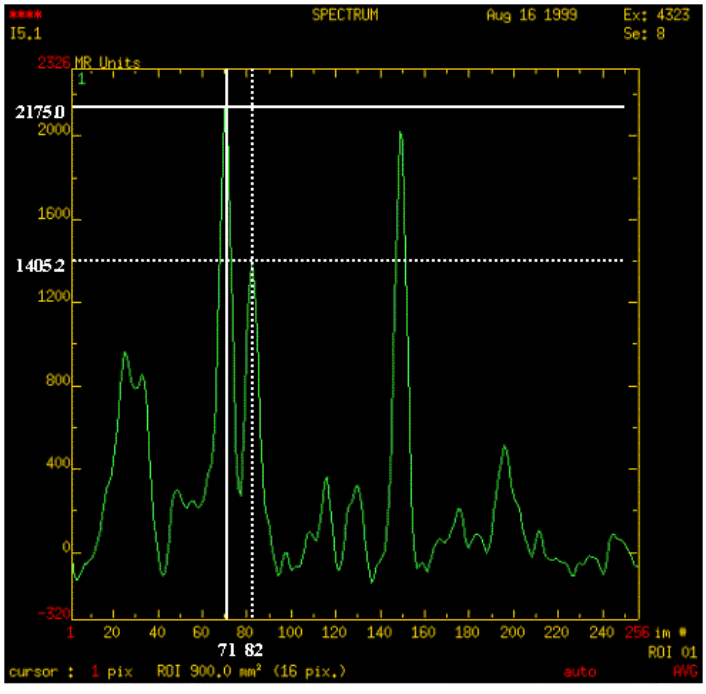


Figure 22: Spectral grid viewport. Solid White=choline peak maximum. Dotted white=creatine maximum.

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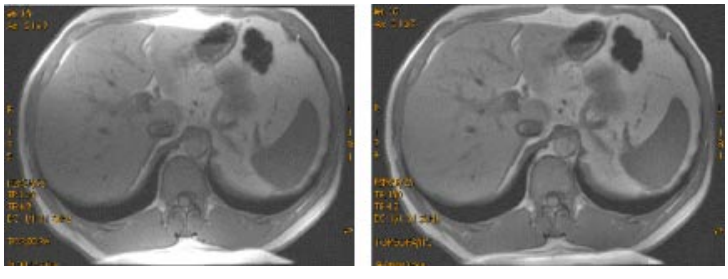
Surface Coil Intensity Correction (SCIC)

Description

An image created using a surface coil has an intensity fall-off determined by the coil properties. This intensity fall-off causes distracting artifacts and makes it difficult to film images at a single window/level setting. The Surface Coil Intensity Correction (SCIC) feature is an automatic post-processing technique that corrects the low spatial frequency intensity modulations, reduces noise, and enhaces contrast in the image. It will produce a series of filtered images with decreased intensity near the coil, reducing the areas of bright spots.

SCIC is an imaging option available for pre-configured coils. With SCIC, each scanned series produces two reconstructed series: one original and the other corrected using SCIC.

Original T1W Liver Image **SCIC Corrected Image**



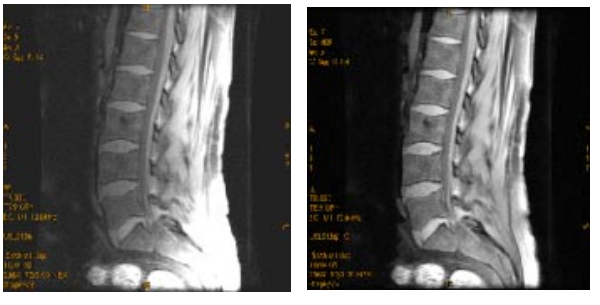
Coil Specific Selections

The SCIC imaging option is supported by all imaging planes and pulse sequences, but is only available with the coils listed in the table below. Select Surface Coil Intensity Correction on the Imaging Options screen. If you request processing for an invalid coil, the SCIC option is not available for selection.

SCIC is available with the following coils:

	1.0 and 1.5T Coils	1.0T Coils Only	1.5T Coils Only
USA Instruments CTL Spine Coil	USCTLTOP, USCS123, USCS12		
	USCTLMID, USCT234, USTL345, USTS23, USTS34		
	USCTLBOT, USTL45, USLS456, USLS56		
GE by Teledyne CTL Spine Coil	CTLTOP, CS123, CS12,		CT234
	CTLMID, TL345, TS34, TL45	TL456	TS23
	CTLBOT	LS567, LS56, LS67	LS456, LS56
Other Coils	ENDOREC		
	TORSOPA		
	PVUPPER		
	TPUPPER, TPLOWER		

Original Image **SCIC Corrected Image**



Notes

- ⇨ It is recommended to use the SCIC processed images along with the corresponding images that have not been processed with SCIC.
- ⇨ The AutoViewer will only display the non-processed images. You must go into the Display Browser to view the SCIC processed images.
- ⇨ A SCIC processed image will have SC added to the beginning of its series description.

- ⇨ The SCIC processed images are annotated with SCIC following the coil name. For example, an imaged processed with the CTL coil would be annotated CTL/SCIC.
- ⇨ A new series number will be assigned to the post-processed images. The SCIC processed series is numbered 100 more than the non-processed series. For example, if series 4 has SCIC applied, the SCIC processed series will be labeled 104.

Considerations

- ⇨ Once you select the SCIC imaging option, if you change to an unsupported coil, the SCIC option is turned off and a pop-up message appears on the prescriptions screen.
- ⇨ The SCIC option is not compatible with the Real-time option. When SCIC and Real-time are selected together, a error message will be reported when you exit the Imaging Options screen.

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Auto N-Coil

Description

Sometimes one or more elements of a multicoil array extend physically beyond the selected FOV. These outlying coil elements are often better at receiving unwanted tissue signals from outside than desired signals from inside the selected FOV. Signals from outside the FOV are often poorly controlled in the imaging process which can lead to ghosting in the phase encode direction. These ghosts, which can run across the entire phase encoding dimension of the offending receiver's image, will often lie on the anatomy of interest.

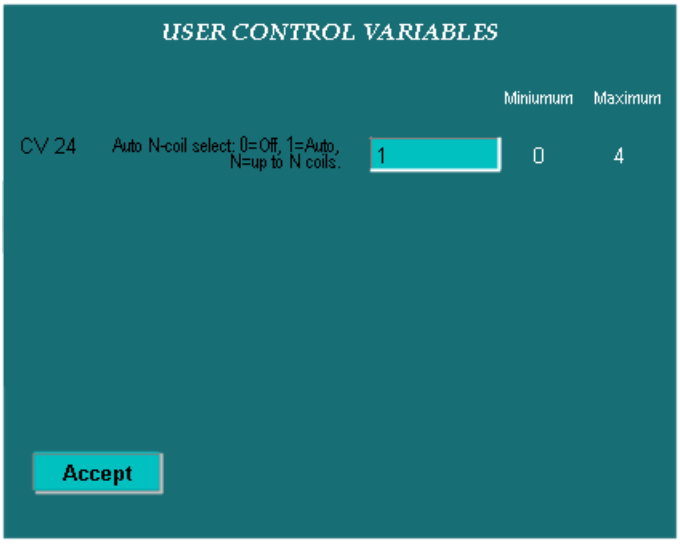
The original version of Auto N-coil reconstruction solved this problem by identifying the ghosting receivers beforehand and hardcoding these receivers in the coil configuration file. Since the ghosting depends on FOV and receiver position, N-Coil reconstruction failed to identify the ghosting receivers in the run time.

By calculating the mean for each intermediate image, the new version of Auto N-Coil identifies the right receiver's images that contain ghosting and rejects them from the final combined image. Auto N-Coil achieves this by selecting the maximum mean of the signal from each coil and calculates the threshold of each image. Only the intermediate images that are above the threshold are combined to form the final image.

Set-up

You can enable the Auto N-Coil feature by selecting the User Control Variable (CV) from the User CV page in the additional parameters of the ScanRx Desktop.

⇨ This feature is only available with Fast Spin Echo (FSE) pulse sequences.



The following table summarizes the User CVs available for Auto-N coil.

User Control Variables		
Auto N-coil	Off = 0	Select 0 if you do not want to utilize the Auto N-coil option.
	Auto = 1	The system will use the selected FOV to identify which receivers to use during reconstruction.
	2 Receivers = 2	The system will choose two receivers with the highest signal intensity to use during reconstruction.
	3 Receivers = 3	The system will choose three receivers with the highest signal to use during reconstruction.
	4 Receivers = 4	The system will reconstruct the images using all four receivers.

Guided Install for HIS/RIS DICOM Mode

Description

Selecting HIS/RIS DICOM mode requires no password to access. Configuration is restricted to HIS/RIS tab, which allows configuration of server and port setups, and to the SCP (charge codes used by the scanning facility when billing insurance) tab. The Verification tab is available to verify any changes made to HIS/RIS are legal. The Log File can also be viewed from this mode.

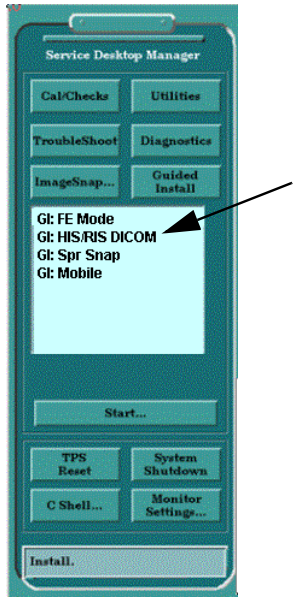
Mobile Sites can follow the same steps as fixed sites to map protocols to charge codes; be sure to check that the IP address and the port number are correct on the HIS/RIS tab.

Setup

(1) Select Service Desktop from the control panel.

(2) Select **[Guided Install]**.

(3) Select **[GI: HIS/RIS DICOM]**.



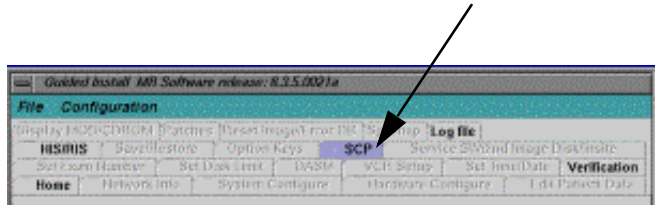
(4) Select **[Start]**.

(a) If HIS/RIS configuration has NOT been done, you would need the assistance of your facility's Information Technology department and service engineer to help setup the server and the port configurations. Continue with step 5 when the configurations have been completed.

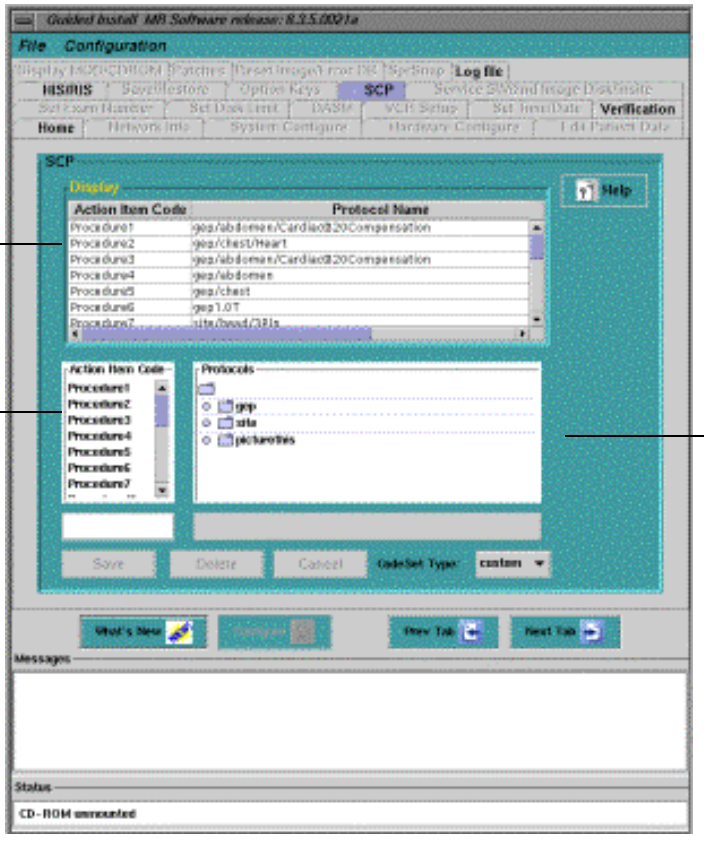
The Guided Install window will appear.

(5) Select the **SCP** tab from the top of the Guided Install window.

- The SCP tab allows you set up (map) protocols to charge codes that are used for billing insurance.



The SCP Display window will appear.



The top display box (**A**) shows the HIS/RIS Action Item Codes and the protocols linked to them. The lower two display boxes show the Action Item Codes for the system (**B**) and the system protocol (**C**) libraries.

(6) To map protocols, select the procedure number from area **A** (HIS/RIS), and type in desired code, such as CPT code.

(7) Select the procedure number from area **B,** and type in the same number (code) used in area **A**.

(8) Select the desired Protocol Library.

(9) Select the protocol to map with from area **C**.

(10) Select the desired Protocol Category.

(11) Select the desired protocol.

(12) Choose one of the following:

(a) Select **[Save]** to save the mapping of the Action Item Code with the selected protocol.

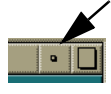
(b) Selecting **[Delete]** will remove the mapping of this protocol to the Action Item Code.

(c) Selecting **[Cancel]** will cancel the mapping process.

(d) Selecting **[Help]** from the menu at the top of the page will give you step-by-step instructions for the mapping procedure. Refer to **[Help]** when you have questions about the Guided Install.

(13) To exit the Guided Install window, in the upper left corner of the window click and drag to Exit.

- Selecting **[Close]** or clicking on the second icon to the right, closes the Utilities window and places the icon behind the desktop icons where it cannot be accessed.



Guided Install for GI Mobile Site Mode

Description

You can now enter the Mobile Site Setup window from the Service Desktop. This window allows you to configure a mobile scanner for specific sites. Once the mobile site information has been entered, it can be retrieved each time the scanner is at that location.

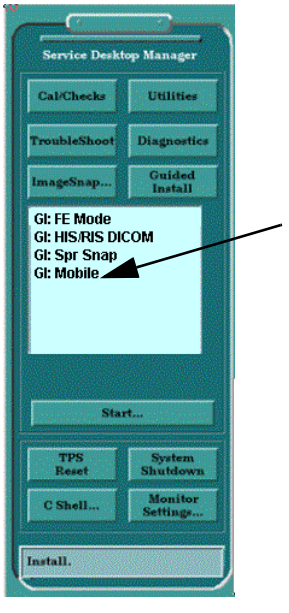
Using the SCP tab you can map protocols to charge codes used when billing insurance.

Setup

(1) Select Service Desktop from the control panel.

(2) Select **[Guided Install]**.

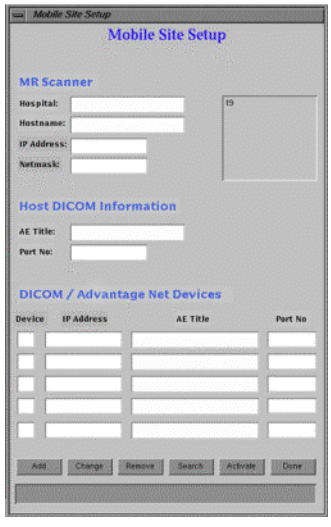
(3) Select **[GI: Mobile]**.



(4) Select **[Start]**.

(5) Enter the password in the command window. Contact your service engineer to give you this password.

The Mobile Site Setup window will appear.



(6) Select **[Add]** to start the Mobile Site Setup.

(7) Enter the information in the appropriate fields.

(a) You will need the assistance of the facility's Information Technology department and service engineer to give you information regarding IP addresses, the Netmask, AE Titles, and Port numbers.

(8) Select **[Add]** to add another site to the list.

(9) Select **[Done]** when all the sites have been entered.

Setup

To recall and activate the site use the following steps.

(1) Follow steps 1-5 from above.

(2) Highlight the site from the list (on the right side of the window).

(3) Select **[Activate]**.

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