VISTA-CT

USER MANUAL

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VISTA-CT
User's Manual
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Note: Information contained in this manual is subject to change without notice. Every effort has been made to insure that the material herein is correct and complete but GE Healthcare cannot guarantee that this document is free of errors or omissions.

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WARNINGS

EMERGENCY STOP—Should an emergency arise and the animal scanning bed needs to be stopped instantly or the unit completely powered down, **PUSH THE MASTER SYSTEM ON/OFF BUTTON AT THE REAR OF THE SCANNER ENCLOSURE TO "OFF".** THIS ACTION WILL IMMEDIATELY STOP THE BED MOTOR, TURN OFF THE HIGH VOLTAGE TO THE DETECTOR ARRAY AND ELECTRONICS AND DISABLE ANY FURTHER ACTIONS UNTIL THE SYSTEM IS RESET.

BED MOVEMENTS—FINGERS, etc. When moving the animal scanning bed take care to insure that fingers, coat tails, sleeves and other objects are not near, or in, the mechanisms that moves the animal scanning bed horizontally. Fingers or objects caught between the moving parts and the end-stops of the bed or vertical bed support could be injured. or damaged. Never try to stop bed movement by hand, always use the hand controller.

BED MOVEMENTS—DAMAGE TO GANTRY. As the animal bed is being inserted into the gantry aperture MAKE CERTAIN by eye that the BED, THE SUBJECT AND ANY ATTACHED DEVICES will actually pass into the aperture without hitting the edge of the aperture or the transmission annulus if in place. Injury to the animal or damage to the gantry could result if the animal or ancillary equipment are allowed to collide with the gantry.

FLUIDS SPILLED ONTO THE GANTRY TABLE—Should any fluids, e.g. water, urine, etc., be spilled onto the surface of the gantry tabletop, IMMEDIATELY WIPE THE FLUID UP WITH A SPONGE OR OTHER ABSORBENT MATERIAL. If fluids have dripped through the slot under the bed, carefully and SLOWLY remove the tray underneath the slot (and below the tabletop), taking care not to spill any fluid into the electronics below. Decontaminate and dry before replacing under the table top.

RADIOACTIVE SPILLS OR CONTAMINATION OF THE BED OR INSIDE OF GANTRY APERTURE—If a radioactive fluid, e.g. radioactive urine or blood, is spilled onto the animal imaging bed or onto the cylindrical surface inside the imaging aperture, this radioactivity must be removed at the first convenient opportunity and before the next imaging study. Contamination of the imaging bed can be removed most easily by dismounting the imaging bed and washing the bed with a suitable cleaner while drying with an absorbent towel. The aperture is protected by a plastic cylindrical insert that can be removed and cleaned in a similar way. Note that this sleeve must be replaced before the next imaging study since it protects the detector array from physical damage and from fluids leaks. Before the bed or sleeve is placed back in the scanner's field-of-view, these parts should be cleaned until no contamination of either bed or sleeve can be detected with a G-M counter.

HIGH VOLTAGE— Do not remove the gantry or enclosure covers for any reason. Circuit boards on the detector array (inside the gantry cover and normally invisible to the User) carry high voltage and serious injury can result if touched. Do not remove the covers on any of the electronics boxes within the gantry enclosure. Devices

within these boxes utilize high current and serious injury can result if touched. Only qualified VISTA-CT service personnel should access parts within the gantry cover or within the gantry enclosure. Removal of any external cover by unauthorized personnel voids the warranty.

MOVING VISTA-CT TO ANOTHER LOCATION—VISTA-CT consists of a number of electronic components that are sensitive to physical shock. If VISTA-CT is to be moved to another location, unlock the wheels and roll the gantry enclosure SLOWLY and deliberately to avoid any jarring shocks such as can occur when crossing building expansion joints often found in corridors, or across the gap between building floor and elevator floor if VISTA-CT is moved into an elevator. Rough treatment can seriously damage internal components and common sense and patience when moving VISTA-CT should be exercised. You should consult the sections on “Siting” and “Pre-Installation” in the Appendix to determine if the site to which the scanner is being moved meets the required evnironmental conditions needed for proper operation of the scanner.

PRECAUTIONS DURING OPERATION

IDENTIFY THE SYSTEM ON/OFF SWITCH AND OTHER HARDWARE ELEMENTS OF VISTA-CT BEFORE USING THE SYSTEM.

DO NOT TURN VISTA-CT OFF UNLESS ABSOLUTELY ESSENTIAL—Under normal conditions, VISTA-CT should be left fully powered at all times. If you have found VISTA-CT fully powered, use the "hot start" procedures described in a later section to begin imaging. If you have found VISTA-CT powered down, follow the "cold start" procedures described in a later section before you begin imaging. After a cold start, VISTA-CT should be allowed to warm up for 48 hours before imaging is attempted and several diagnostic tests should be run to make sure that VISTA-CT is still properly calibrated.

STARTING VISTA-CT AFTER A POWER FAILURE—If electrical power to VISTA-CT is interrupted and the system shuts down, push the main ON/OFF switch at the back of the enclosure to the OFF position. When power is restored, push the switch back to the ON position. This action will engage an automatic restart procedure. During this procedure, which takes about 2 minutes to run to completion, NO COMMANDS SHOULD BE ISSUED TO THE SCANNER THROUGH THE WORKSTATION. (See APPENDIX D—"starting/stopping the data acquisition computer" for further details).

AVOID PLACING HIGH ACTIVITY RADIOACTIVE SOURCES NEAR THE VISTA GANTRY DURING IMAGING—VISTA is reasonably well-shielded against radiation emanating from sources directly in front, or directly behind, the VISTA gantry but **VISTA is completely UNSHIELDED from sources located at the sides or on the top of the gantry**. Accordingly , the enclosure tabletop and the top of the gantry cover should never be used to store radioactive material nor should radioactive sources of any strength EVER be placed at the sides or on top of the gantry cover during imaging. To do so will severely comprised the performance of VISTA and render the acquired data useless. CHECK FOR AND REMOVE all radioactive source from the vicinity of VISTA, e.g. empty injection syringes, empty injection bottles, swabs made radioactive during injection, etc. before beginning any imaging study.

CENTER THE IMAGING TARGET BOTH VERTICALLY AND AXIALLY IN THE IMAGING APERTURE BEFORE SCANNING—The sensitivity of VISTA and any other ring-type PET scanner depends strongly on the axial position of the target in the scanning field and to a lessor extent on the radial position. It is important, therefore, that the center of the imaging target, e.g. the brain, be placed as close as possible to the axial center of the scanning field using the CENTER command on the acquisition interface. In addition you should use the vertical screw mechanism to manually and visually position the animal's (horizontal) body axis along the cenral axis of the scanning field taking care that the animal and any attached equipment will pass into the imaging region without hitting the sides of the aperture (or the transmission annulus if in place).

INTRODUCTION TO VISTA-CT

Theory of Operation

VISTA scanners are manufactured in two forms, a single detector ring version (the SR for “Single Ring tomograph”) and a two ring version (or DR for “Dual Ring tomograph”). Both systems have the same transverse aperture size and field-of-view, both utilize the same high sensitivity, dual-layer phoswich PET detector technology and both possess identical functional and analytical capabilities.

The SR and DR systems differ only in the lengths of their respective axial fields-of-view: 2 cm for the SR and 4.8 cm for the DR. In this manual we will use the convention of specifying SR parameters in parentheses if different from the DR. A parameter quoted in the text without any distinction as to type indicates that the parameter is the same for both scanners.

The VISTA detector array consists of 36 (18, SR) detector modules arranged around a circle such that the face-to-face diameter of the ring is 11.8 cm. Each detector module is placed in time coincidence with the 14 (7) opposite modules to give an effective transverse field-of-view of 6.7 cm and an axial field-of-view of 4.8-cm (2-cm). Each detector module consists of an 13 x 13 array of 1.45 mm square by 15 mm long “phoswich” elements optically isolated from each other by reflective material. Each phoswich element, in turn, is comprised of two different scintillator crystals, a 1.45 mm square x 7 mm long LYSO crystal and 1.45 mm square x 8 mm long GSO crystal, optically glued together end-to-end to form a single 15 mm long segment. The GSO end of the 13 x 13 array is optically glued to the face of a Hamamatsu R8520-C12 position-sensitive photomultiplier tube (PSPMT).

In operation, light from a scintillation event in the (front) LYSO layer passes through the GSO layer onto the photocathode of the PSPMT and is detected. Similarly, scintillation light from an event in a GSO (back) crystal passes back and forth from the LYSO and GSO layers and ultimately falls on the PSPMT where it is detected. This process is enhanced by inserting each phoswich element into a 13 x 13 matrix of highly reflective material which improves direction of scintillation light onto the PSPMT while optically isolating each phoswich element from its neighbors.

This use of dual-layer phoswich detector modules is a central and important feature of the VISTA design. Conventional small ring diameter scanners suffer from the "depth-of-interaction" (DOI) effect, a parallax phenomenon that causes (radial) spatial resolution to degrade with increasing radial distance from the center of the field-of-view (FOV) of the scanner. While this effect can be reduced by increasing ring diameter or decreasing crystal thickness, this strategy will also reduce sensitivity by moving the detectors further from the animal or reducing absorption of annihilation radiation. The VISTA design side-steps this problem by allowing a two-level estimate of the depth at which an annihilation photon in absorbed in the phoswich crystal element, either in the LYSO portion of the element or in the GSO portion. Knowledge of this depth, even to this relatively crude level of accuracy, substantially reduces the DOI effect for VISTA while preserving sensitivity compared to other scanners of similar ring diameter but without this capability.

The method used to determine whether the scintillation event occurs in the LYSO or GSO portions of the phoswich exploits the difference between scintillators in their light decay time. Since LYSO and GSO possess different light decay times (40 ns for LYSO and 60 ns for GSO) the event may be assigned to the proper layer, or depth, by knowing the light decay time for that event.

The dual-layer phoswich arrays allow three types of coincidence interactions to be recorded, LYSO to LYSO, LYSO to GSO and GSO to GSO, for a total of approximately 28.8 million (7.2 million)) valid coincidence lines passing through the 6.7 cm diameter x 4.8-cm (2-cm) deep FOV. These data are sorted into 61 (25) 2D sinograms with the 3D FORE algorithm and reconstructed with either 2D filtered backprojection or 2D OSEM into 61 (25) transverse section images that span the axial FOV.

Specifications, Performance Characteristics and Capabilities

Specifications

Detector modules
Type of modules = dual layer phoswich- front layer= LYSO, back layer = GSO
Crystal dimensions = 1.45 mm x 1.45 mm x 7 mm LYSO, 1.45 mm x 1.45 mm x 8 mm GSO
Light decay time = 40 ns, LYSO and 60 ns GSO
Crystal arrays = square 13 x 13 – 20 mm x 20 mm outside dimensions
Pitch = 1.55 mm
Phototubes = Hamamatsu R8520-C12

System
Number of detector modules = 36 (18)
Number of phoswich elements = 6084 (3042)
Total number of crystals = 12,168 (6084)
Ring diameter = 11.8 cm
Gantry aperture = 8 cm
Axial field-of-view = 4.8 cm (2.0 cm)
Effective transaxial field-of-view = 6.7 cm
Normalization/transmission source: Ge-68 filled annulus – 500-600 microCuries nominal starting activity; half-life = 275 days
Overall dimensions = 121 cm wide x 151 cm high x 82 cm deep
= 47.75” wide x 59.5 “ high x 32. 0” deep
Estimated weight = 450 pounds
Power = 120 V AC, < 20 amps

Data Sets
Acquisition mode = 3D (only)
Total number of lines-of-response = 28.8 M (7.2 M)
Number of 2D sinograms = 61 (25)
2D sinogram size = 175 spatial samples x 128 angles
2D dataset size = 5.4 Mbytes (2.2 Mbytes)
Sampling distance = 0.775 mm

Bed/Laser
Two low absorption carbon fiber beds provided: rat or mouse
Computer controlled axial centering of imaging target following laser identification of target outside gantry
Hand controller for manual bed movement/laser on/off

Performance Characteristics*

Absolute central point source sensitivity (250-700 keV window):
4.0% DR
1.9% SR
Reconstructed central (radial) spatial resolution: 1.5 mm (FBP/ramp filter)
Off-axis spatial resolution = <1.8 mm @ 1.0 cm, <2.2 mm @ 2.0 cm (FBP/ramp)
Average energy resolution = 30% LYSO layer, 30% GSO layer, 30% system
Scatter fraction-mouse-sized object, energy window 250-700 keV: 27% (20%)
Scatter fraction-rat-sized object, energy window 250-700 keV: 37% (28%)
Coincidence timing windows:
±2.5 ns (LYSO/LYSO)
±3.5 ns (LYSO/GSO)
±5.0 ns (GSO/GSO)
Coincidence timing resolution approximately half of these values
Peak NEC rates (250-700 keV energy window):
Mouse phantom (3 cm diameter cylinder 7.5 cm long) =126 kcps@ 12.2 µCi/cc
Rat phantom (5 cm diameter cylinder 15 cm long) = 77 kcps@ 3.7 µCi/cc
*all values ± 10%

Features/Capabilities
Real-time 2D persistence projection imaging of field-of-view during scanning
Laser positioning of animal with automatic insertion into central FOV

Data acquisition modes:
Static imaging: acquire single data set from a time-stationary tracer distribution
Fixed frame length dynamic imaging: acquire data sets from dynamically varying tracer distributions using fixed frame durations
Variable frame duration dynamic imaging: acquire data sets from dynamically varying tracer distributions using variable frame durations
List mode: acquire data in List mode; allows post–acquisition frame formatting
Whole-body imaging: acquire static image data from several consecutive bed positions and automatically merge into a single whole-body image
Transmission imaging: acquire a transmission data set of an object using the Ge-68 source transmission source
Blank imaging: acquire a data set using the Ge-68 transmission source used both for detector normalization and as the “blank scan” for attenuation correction

Image Reconstruction:
Convert all 3D data sets to 2D sinograms with the FORE algorithm
Reconstruct 2D sinograms with 2D FBP or 2D OSEM
Correct reconstructions of all data types for randoms, scatter and attenuation

Visualization and Analysis:
View all data types and apply various analysis tools

Injected Activity Recommendations for VISTA

Like any small animal PET scanner, VISTA has a useful linear operating range for radioactivity placed in the imaging volume. The activity values quoted below are approximate and you should perform your own experiments to make sure you are operating within this range, particularly if you plan to use the scanner in unusual ways or with "non-traditional" isotopes.

You can make such measurements by using the START/STOP data acquisition interface (see page 34) to monitor the system dead time when experimental quantities of activity are placed in the field of view. The "dead time" value reported on this menu can tell you whether this amount of activity is excessive and hence likely to be outside the linear range. Generally speaking, dead time should not exceed 30% at any time during a study and the activity should be reduced until this condition is met.

For the VISTA DR and SR machines, this linear operating range is (*approximately*) 1 - 400 microCuries of F-18 equivalent activity within the axial field-of-view. If quantitative accuracy is critical throughout an experiment, this range cannot be exceeded at any time during the study period. Given this value, **VISTA studies can be carried out successfully with good statistical accuracy in 30 gram mice using about 400 microCuries of F-18 labeled compounds and about 1-1.3 mCi of F-18 labeled compounds in 350 gram rats.** Maximum injected amounts in any given study depend on many factors such as the fraction of the animal's length that is actually in the axial FOV, the temporal and spatial behavior of the compound under study and so on. Nonetheless, these amounts represent typical maximum activities for F-18 labeled compounds, e.g. FDG, that distribute themselves throughout the body with moderate increases in organ concentration above a uniform body average. You should not attempt to perform studies with amounts of activity significantly above these values unless you have determined that the amount of activity actually in the field of view of the scanner will not exceed 400 microCuries of F-18 equivalent activity. This maximum activity corresponds to the peak NEC rates for the VISTA DR and SR scanner and also corresponds to the point at which system dead time becomes dominant and further increases in activity actually reduce count rate throughput.

These recommendations are based on F-18 equivalent amounts of activity (a pure positron emitter) and must be modified if using other, or "non-traditional", isotopes that are not pure positron emitters and/or that emit gamma radiation in coincidence with positrons. For example, Cu-64 is a positron emitter but in only 20% of disintegrations does Cu-64 emit a positron. In this case, if no other conditions were operative, you could (should) administer up to 5 times more Cu-64 activity (100% F-18/20% Cu-64 = 5) than F-18 to obtain the same flux of annihilation gamma rays onto the VISTA detector array. Isotopes like I-124 not only emit positrons in only a fraction of disintegrations, but also emits a host of coincident gamma rays that accompany every disintegration. In this case, an extra flux of (useless) coincidence events are present that are not present with isotopes that emit only positrons and the amount of activity injected must be scaled downward somewhat to compensate for this effect

which contributes to the system dead time. On the other hand, like Cu-64, the amount of I-124 must be increased because of fractional positron emission compared to F-18.

These and similar effects should be considered when embarking on a new study when trying to establish the proper amount of tracer to inject. In all of these cases, “scatter correction” should be selected in the reconstruction menu since the algorithm that corrects for scatter is also effective in removing the approximately uniform background caused by these coincident gamma events, the Lu-176 background, etc.

GETTING STARTED

MAJOR SYSTEM COMPONENTS

VISTA-CT consists of five major subassemblies: a gantry, an enclosure upon which the gantry sits, an animal scanning bed that moves along a slot in the scanner tabletop, a hand controller for bed movement and a separate operator workstation. The animal bed assembly, the vertical bed movement mechanism and the gantry aperture are shown in **Figure 1**.

Gantry –The detector array and associated electronics are located inside the gantry enclosure. At the center of the gantry is the imaging aperture into which the object to be imaged is inserted. Mounted on the front of the gantry and above the aperture is a housing containing a laser that, when activated with the hand controller, projects a cross-hair onto any object placed on the imaging bed.

Enclosure—The gantry sits on a table that forms the top of an enclosure resting on lockable wheels. All cables (power, cables to operator console, etc.) emerge from the rear of the scanner at the center-bottom of this enclosure. The enclosure contains the power supplies for all sub-systems, the data acquisition system and the bed motor and motor driver controls.

Figure 1. Animal bed, vertical bed movement mechanism and gantry aperture.

Animal scanning bed—A drive is mounted under the tabletop that moves the animal imaging bed into and out of the gantry aperture. Two removable beds of different widths are provided, one for mice and a larger one for rats.

Vertical movement of the bed is controlled manually by a hand-operated screw drive (**Figure 1**).

Figure 2. Hand controller.

Hand Controller-- Horizontal movement of the bed is controlled manually with the small hand-held controller unit connected to, and normally "parked" on, one side of the gantry (**Figure 2**). The bed will move continuously in the indicated direction as long as the corresponding button is held down. If the button is momentarily depressed and released, the bed will move in or out in a small step,

A button on this same controller also turns the alignment laser on or off. When the laser is turned on a timer is started that will turn the laser off after about one minute of operation. Hitting the laser "on" button will turn the laser back on and restart the timer. Pushing the button while the laser is "on" will turn it off. The hand controller can be located on either side of the enclosure simply by unplugging the controller from one side of the gantry and plugging it in on the opposite side.

Operator Console—A separate movable stand with keyboard, system monitor and processing computer comprise the User console or Workstation. The heigth of the tabletop on which the monitor and keyboard sit can be adjusted up or down to allow standing or seated operation of VISTA-CT. The operator console can be positioned on either side of VISTA-CT for convenience.

Figure 3. Rear of VISTA-CT scanner. Main ON/OFF switch is the large RED switch on the left.

SWITCHES/CONNECTORS

Master ON/OFF switch—All power to the VISTA gantry passes through the master ON/OFF switch located at the rear of the enclosure (large red switch at the left in **Figure 3**). This switch should normally always be in the ON position. If it is necessary to shut the system down immediately in an emergency, move this switch to the OFF position. All power to the gantry/enclosure will be interrupted. The workstation is not powered from the gantry and will remain powered even when the scanner itself is shut off.

Additional switches and connectors are also shown in **Figure 3** that are for **SERVICE USE ONLY**. When configured properly for a particular User site, the USER INTERFACE connector and the INTRANET connector allow remote access to both the User workstation and the data acquisition computer inside the VISTA-CT enclosure. If these connections are active, most service problems can be efficiently diagnosed remotely and new software quickly installed without a physical visit by service personnel.

The buttons and connectors on the right side of **Figure 3** allow service personnel on-site access to the data acquisition computer with connectors for keyboard, mouse and display. ON/OFF and RESET switches control the data acquisition computer

while the LEDs on the right show the status of this computer (left to right): power, hard disk (HD read/write), NIC1, NIC2.

Cold Start Procedure

If you find that VISTA-CT is completely "off", first go around to the rear of the gantry enclosure and make sure that the main power plug is inserted into an appropriate and active 120 VAC, 20 amp outlet. Also check at the rear to make sure that the two internet connections have been made (if available) and that the cable from the enclosure to the operator console is connected. Inspect the cables that interlink the console, keyboard and monitor to insure they are properly connected. Since the User workstation is not powered from the VISTA scanner itself, check to make sure that the workstation is also connected to a power outlet. Power up the workstation computer as you would any other PC. If power-up is successful, the VISTA-CT logo and the Login menu should appear on the workstation display.

To turn the VISTA scanner on, move the switch at the left-rear of the enclosure to the ON position. Note that the system WILL NOT immediately restart. Instead, an internal timer will begin turning sub-system on in a pre-programmed sequence that will insure proper operation and communication between all internal components. This pre-programmed start-up procedure takes approximately 120 seconds to complete and you must not enter any commands or take any other actions, e.g. recycling the on/off switch again, attempting to move the imaging bed, etc., until startup is complete.

After such a "cold start" the system should be allowed 48 hours to warm-up before starting routine imaging since previously stored calibration tables could be rendered invalid by a shutdown. However, immediately after a cold start a short imaging test should be run in order to determine if the scanner restarted properly. In order to verify a successful restart, you should image a "warm" cylinder phantom and verify that transverse images of this source are free of any gross streaking artifacts that might indicated dropout of one or more detector modules from the VISTA detector aray. If this test suggests detector dropout, you should initiate the data acquisition system reset procedure described above. If this test indicates that the data acquisition system restarted properly, you should perform, at a minimum, the "hot start" test procedures described below before imaging animals.

Animal studies should not be performed after a COLD START until at least these verification procedures have been carried out and all functional capabilities of VISTA-CT demonstrated by actual operation of the system.

Hot Start Procedure

Under normal operating conditions, VISTA-CT will be left ON and the internal electronics will be stable. In this state VISTA-CT is available for immediate use. If the system has been used successfully in the last few days, VISTA-CT will likely be operating properly. If not, it is prudent to perform at least a minimal set of tests to insure that the system is truly operational before undertaking animal imaging studies. VISTA-CT is a complex instrument that can potentially fail to operate properly in ways

that are not immediately obvious to the User. Accordingly, a few simple tests have been devised to “capture” most, but not all, of these failures and make them known to the User.

LYSO count rate test—The lutetium in the LYSO crystals contains a small amount of radioactive Lu-176 that emits beta particles and gamma rays. This small amount of contaminant gives rise to an intrinsic “singles” rate in each detector module and to an intrinsic true coincidence rate between detector modules (due to beta particle interactions in one detector module and detection of the coincident gamma ray in another opposing module). This effect can be used to monitor the stability of VISTA over time since the rate at which these events occur is constant (the half-life of Lu-176, the contaminant, is 30 billion years). Thus simply activating a static collection with no sources present and observing the data acquisition “status” panel on the monitor will give an apparent coincidence (and singles) rate that, if the system is stable, should be essentially the same from day to day. When VISTA is properly calibrated this intrinsic coincidence rate is around 550 cps (230 cps) but the exact values are machine-dependent. Significant departures from this counting rate probably indicate electronics drift in one or more system components. If so, VISTA should be re-tuned so that this typical inherent true coincidence rate is restored.

Line source imaging test—A “cool” 1.2 mm ID line source of F-18 (about 100 microCuries total) should be taped to the imaging bed and placed in the imaging aperture such that the line spans the length of the bore and is coincident with the scanner axis. A static data collection should be initiated for at least 10 minutes, reconstructed with FBP and displayed. Each slice should be carefully examined for artifacts such as streaks, circles, arcs, etc. If none are present, the system is probably usable. If obvious artifacts are present, the system is probably out of calibration and must be retuned. Because only a limited part of the field-of-view is examined with this test, this test can miss defective detector modules or drifts in the placement of certain regions-of-interest used to calibrate the system. A better system test is the “Cylinder” test below.

Cylinder imaging test—A better alternative to the line source test is to image a cylinder (about 3 cm diameter x 6 cm length) for 60 minutes that contains about 400 microCuries of F-18 total. After FBP reconstruction, the image stack should be free of streak, ring or arc artifacts and the activity in the interior of the cylinder should appear to vary smoothly across the cylinder diameter. If artifacts or widely varying changes in image brightness within or along the cylinder are present, the system must be re-tuned. If no such artifacts are detected, the system is probably usable. This test should probably be performed daily regardless of previous system use just to be sure that ensuing animal studies will yield valid measurements. This particular measurement is also required to obtain the relationship between cps per cc seen by VISTA and the actual nanoCuries per cc measured by taking an aliquot from the cylinder and counting it in a well counter.

Logging on to VISTA-CT

--User Name and Password

When VISTA-CT is in an “idle” state awaiting a User, the VISTA-CT User Interface should appear as in **Figure 4**. If you already have an existing User name and Password these data should be entered in the Log-In window shown in Figure **5**. Pressing **Login** will then allow access all VISTA-CT functions

Figure 4. VISTA-CT log-in interface.

If a new User is going to work with VISTA-CT for the first time it will be necessary to create a new account by clicking on the **Add new User** button shown in **Figure 5**.

Figure 5. Login window.

The new User should enter (and remember) a User name and a Password in the **Add User** panel shown in **Figure 6**. The User name can only contain letters, numbers and "_", and must begin with a letter. The length is limited to 16 characters. Passwords should also be chosen free of special characters. A password that is unacceptable to the system will generate an error message until an acceptable form is entered.

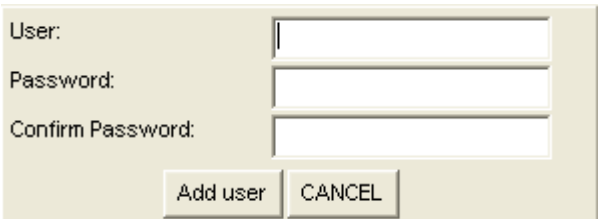


Figure 6. Add new User window.

--VISTA-CT file-naming conventions

In order to use VISTA-CT to acquire, reconstruct, display and analyze image data, the files generated during these processes must be consistently identified to the User interface (and the User). Accordingly, certain naming conventions that allow VISTA-CT, rather than you, to do most of the file bookkeeping chores have been created to keep track of raw, reconstructed and analyzed data files. The easiest way to see how this is done is to look, for example, at the data PET acquisition menu (**Figure 7**) for acquiring a STATIC emission image (although we are skipping ahead somewhat).

VISTA-CT files are comprised of an unchangeable "base name" to which is appended a string of characters that describe the study. The base name has the form "**USERS\xxxxxx\IMAGES**……." where "xxxxxx " is always the User's logon name and "……." represents additional characters that depend on study type. This form of file name will appear automatically with every file.

When a new Study Directory is to be created, the User selects "New" in the Study Parameters box and types in the new Study Directory name for that acquisition series. If that name were RATE, for example, the characters that follow the last backslash might be for PET acquired data, "RATE_13Feb07_Acq018.acq". Here the

Study Directory name is RATE, the date of the study is 13 February, 2007, this particular STATIC (designated by Acq) data acquisition is the 18th acquisition in this directory and the extension ".acq" indicates that the file is the acquisition parameter file. This text file contains vital information about the scan that is required by the image reconstruction, such as the number of "raw" data files of the scan (extension ".tru").

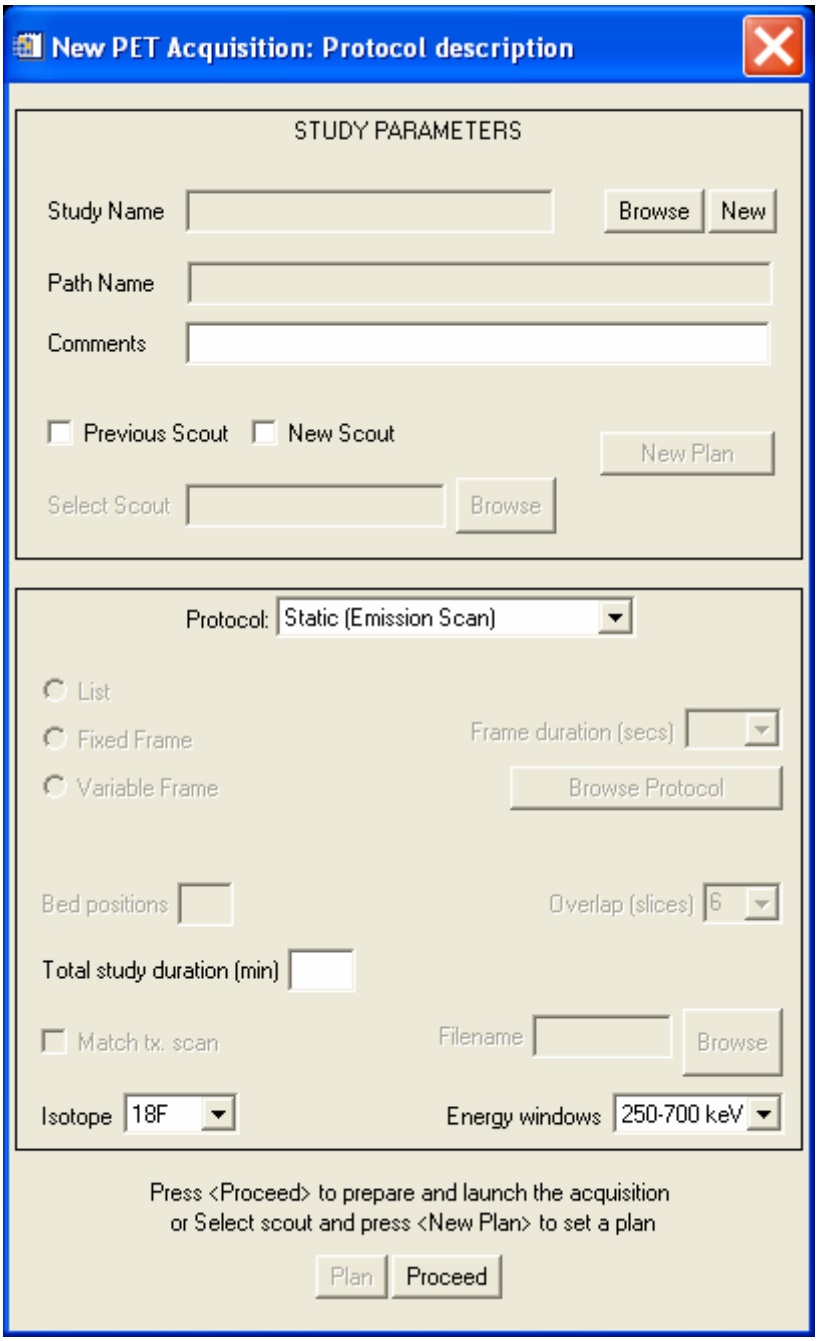


Figure 7. Static data PET acquisition panel.

The complete name of this particular study for User “Robert” is :

Users\Robert\IMAGES\RATE\RATE_13Feb07_Acq018.acq

Other PET study types, e.g. dynamic studies, whole-body studies, etc., will have DYN_Acq or WB_Acq designators in the Acq position but the acquisition parameter files regardless of scan type all end with “.acq”. The number of raw data (“.tru”) files depends on the details of the scan, such as number of bed positions or time frames.

The next step is to reconstruct these raw data files into images. To do so, simply enter the proper acquisition file name into the appropriate reconstruction window and initiate reconstruction. After reconstruction, the reconstructed image file has the same name but with the extension “.acq” replaced by the new designation “.hdr & .img” (“.hdr” and “.img” refer to “header” and to “image”, respectively). You need only know that these designations represent reconstructed and viewable image files.

If you wish to view the reconstructed images, you need only paste the appropriate “.hdr” file into the “selection” window on the visualization panel and initiate display.

In reference to CT studies, the explanation is similar but acquisition parameter files will have extension “act” and raw data files, extension “ctf”.

This process is easier done than explained so you should experiment with this naming process to see how it works.

VISTA-CT MAIN MENU ITEMS

VISTA-CT MAIN INTERFACE

When you have logged onto VISTA-CT, a menu bar appears at the upper left of the VISTA-CT main interface screen (**Figure 8**) which contains five items: e

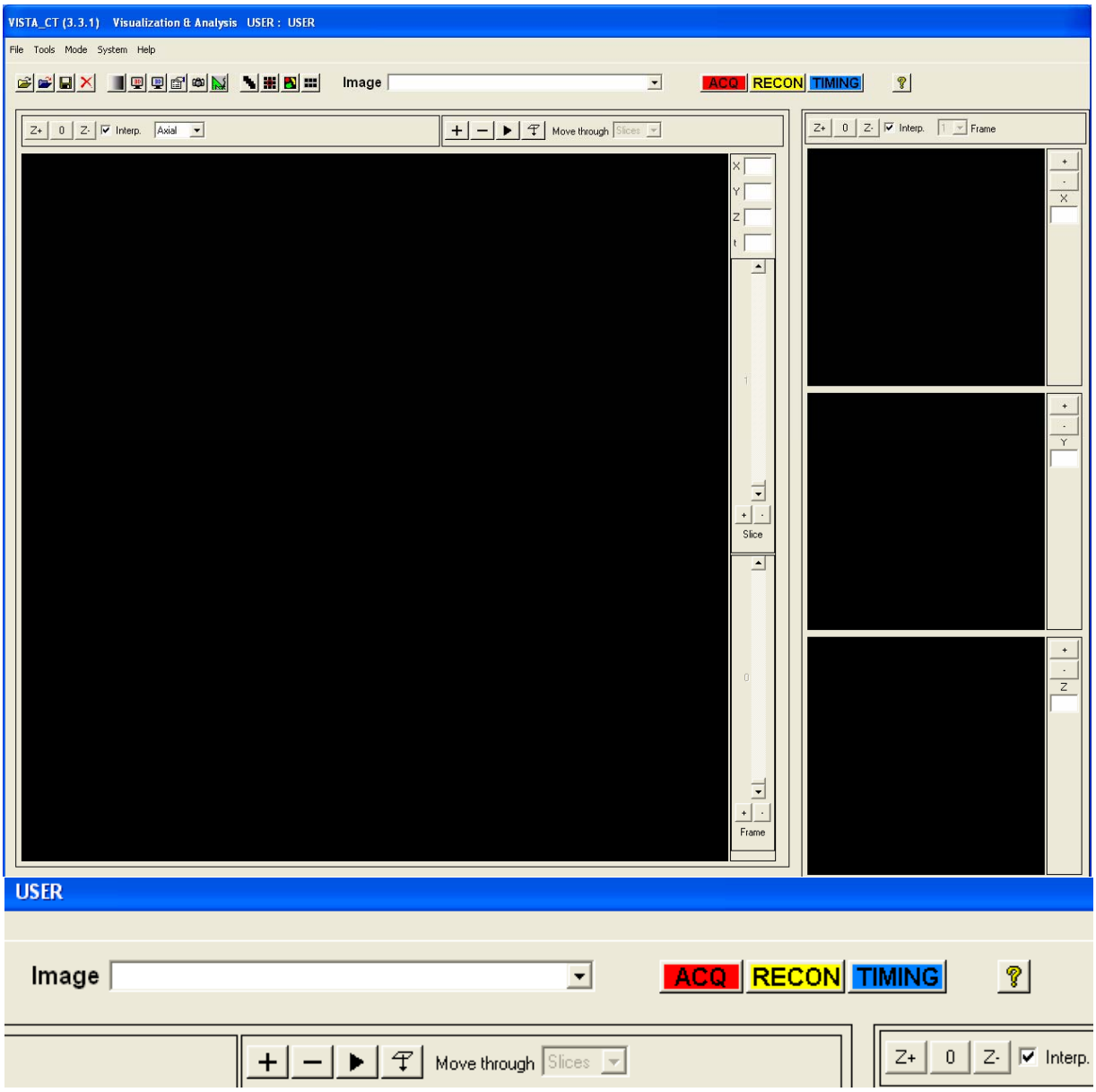


Figure 8. Main VISTA-CT interface (with a detail of the toolbar).

Menu Bar items--

FILE: This menu contains file management tools, e.g. open, import, etc.
TOOLS: This menu contains tools for image manipulation and analysis.
MODE: This menu contains different image display options.
SYSTEM: The following options are available from this drop-down menu:

- **New Acquisition**: Opens another drop-down menu that allows the User to select the type of data acquisition, i.e. PET or CT. Whether the User selects **PET** option or **CT** option, floating PET interface or CT interface, respectively, will be open. In any of these interfaces, acquisition parameters can be fixed and afterwards, the acquisition can be started.
- **Reconstruction**: Allows the User to select a reconstruction method according to the type of acquisition.
- **Timing Options:** Allows the User to select timing parameters for certain data types.
- **Configuration**: basic VISTA-CT configuration parameters and User/password management (available only to privileged User).

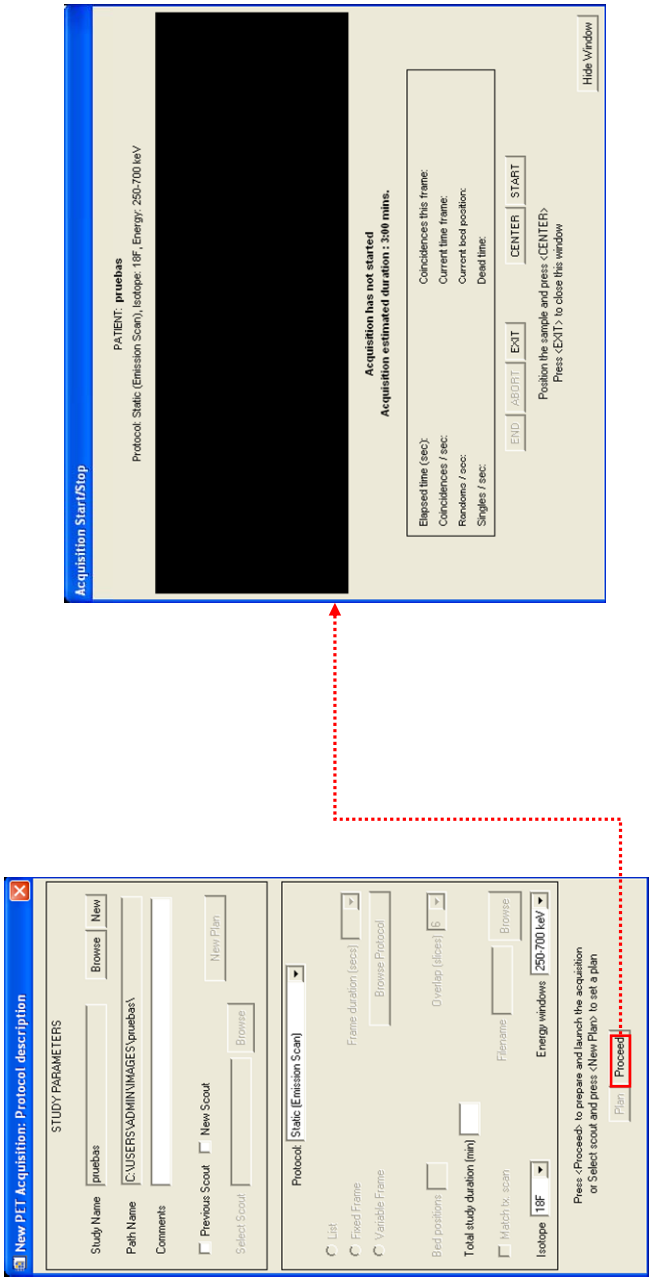
HELP: This manual and other information.

A number of icon "buttons" are also visible across the top of the main interface screen. Holding the arrow cursor on one of these icons for a few seconds will cause the function of that icon to be displayed. These buttons allow you to rapidly jump from one place in the User interface to another, bypassing otherwise intermediate steps. Three of these buttons labeled "**ACQ**", "**RECON**" and "**TIMING**" are particularly important (toolbar detail in **Figure 8**). When the User presses **ACQ** button, a menu with the same options as **New Acquisition** (Menu Bar) has got plus **Close** option to close this menu will be shown. If the button that the User presses is **RECON** or **TIMING**, the menu will have the same options as **Reconstruction** and **Timing Options**, respectively plus **Close**.

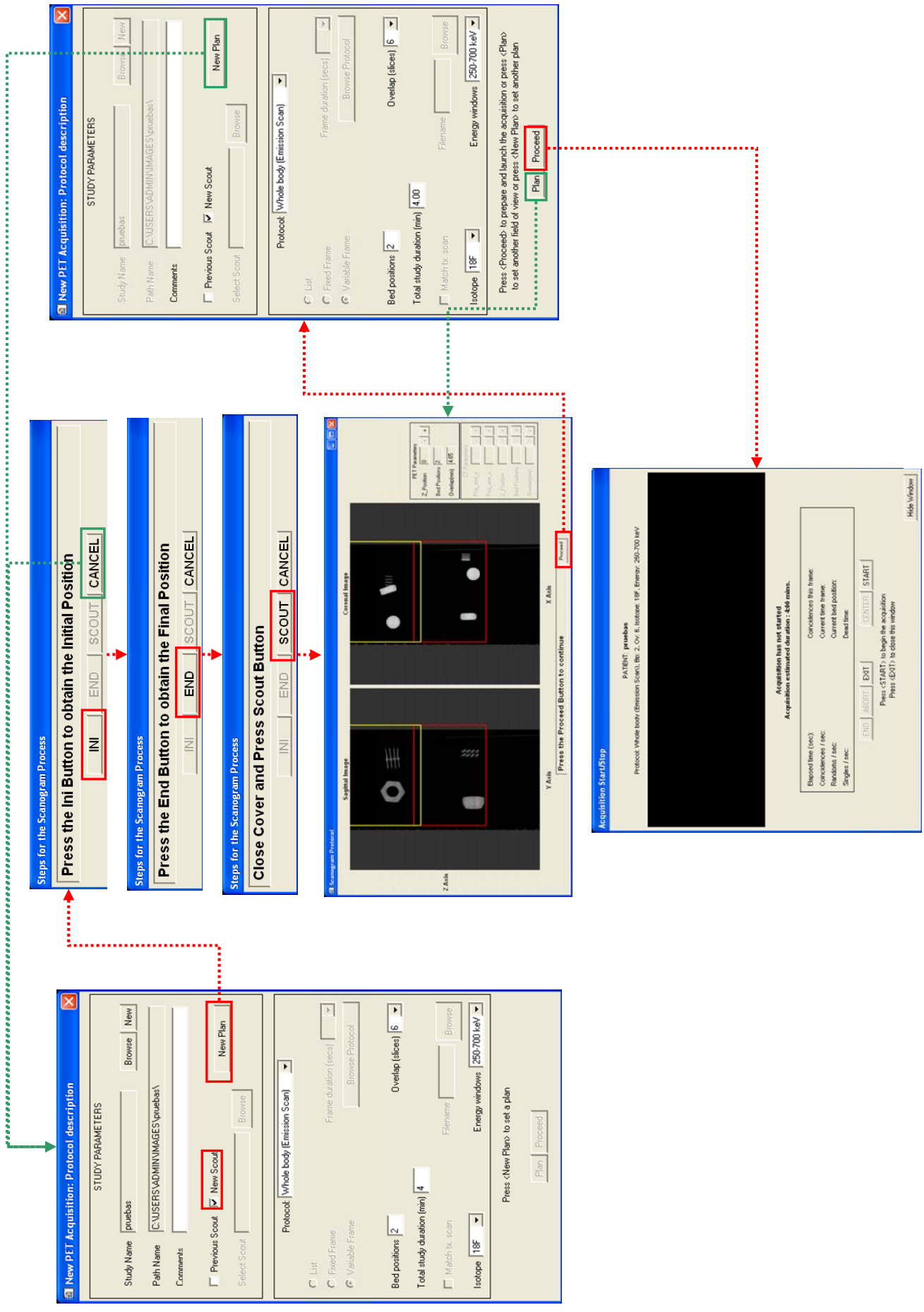
ACQUISITION

ACQUISITION WORK FLOW

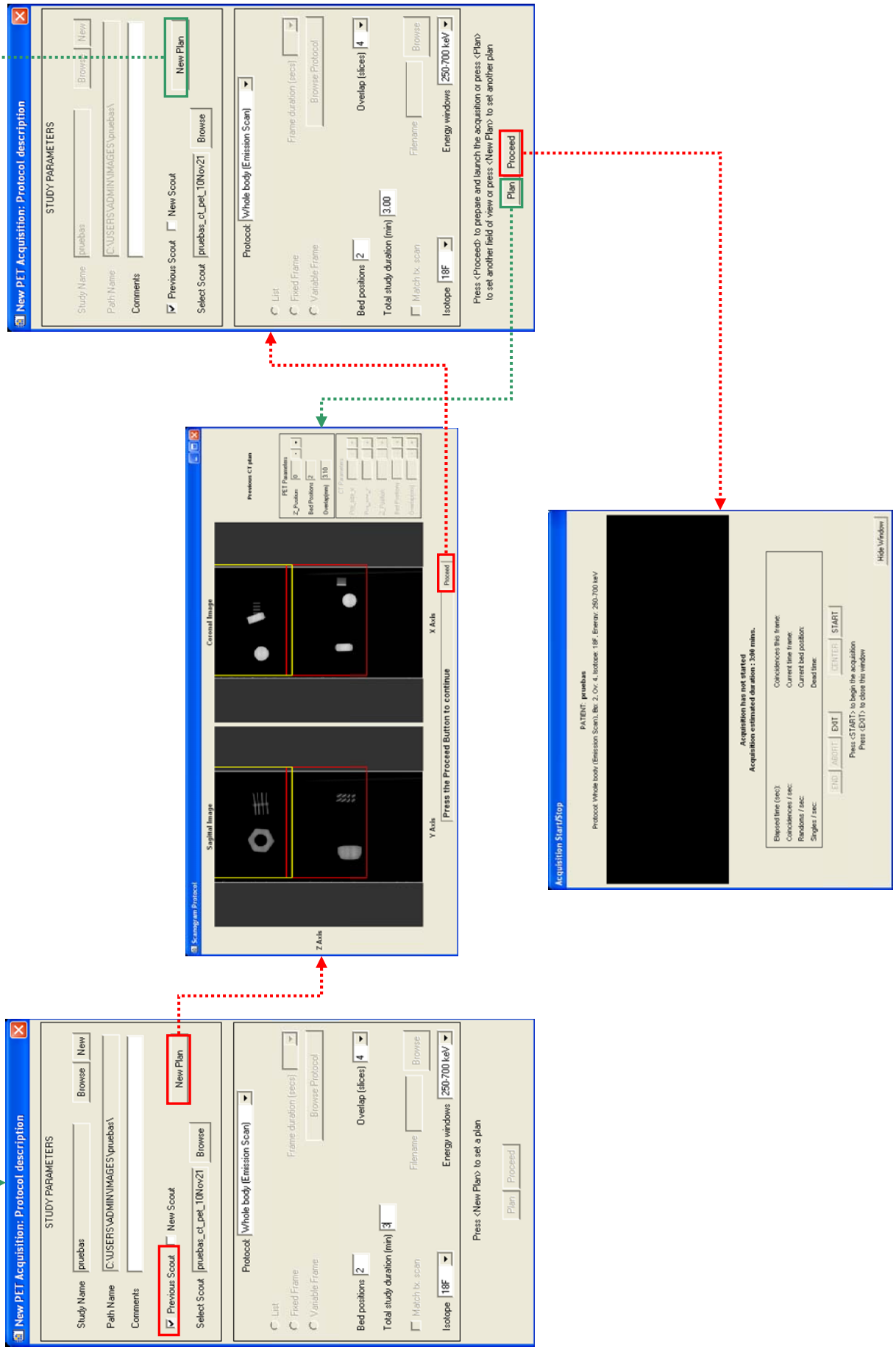
PET's Work Flow with Manual Center



PET's Work Flow with New Scout

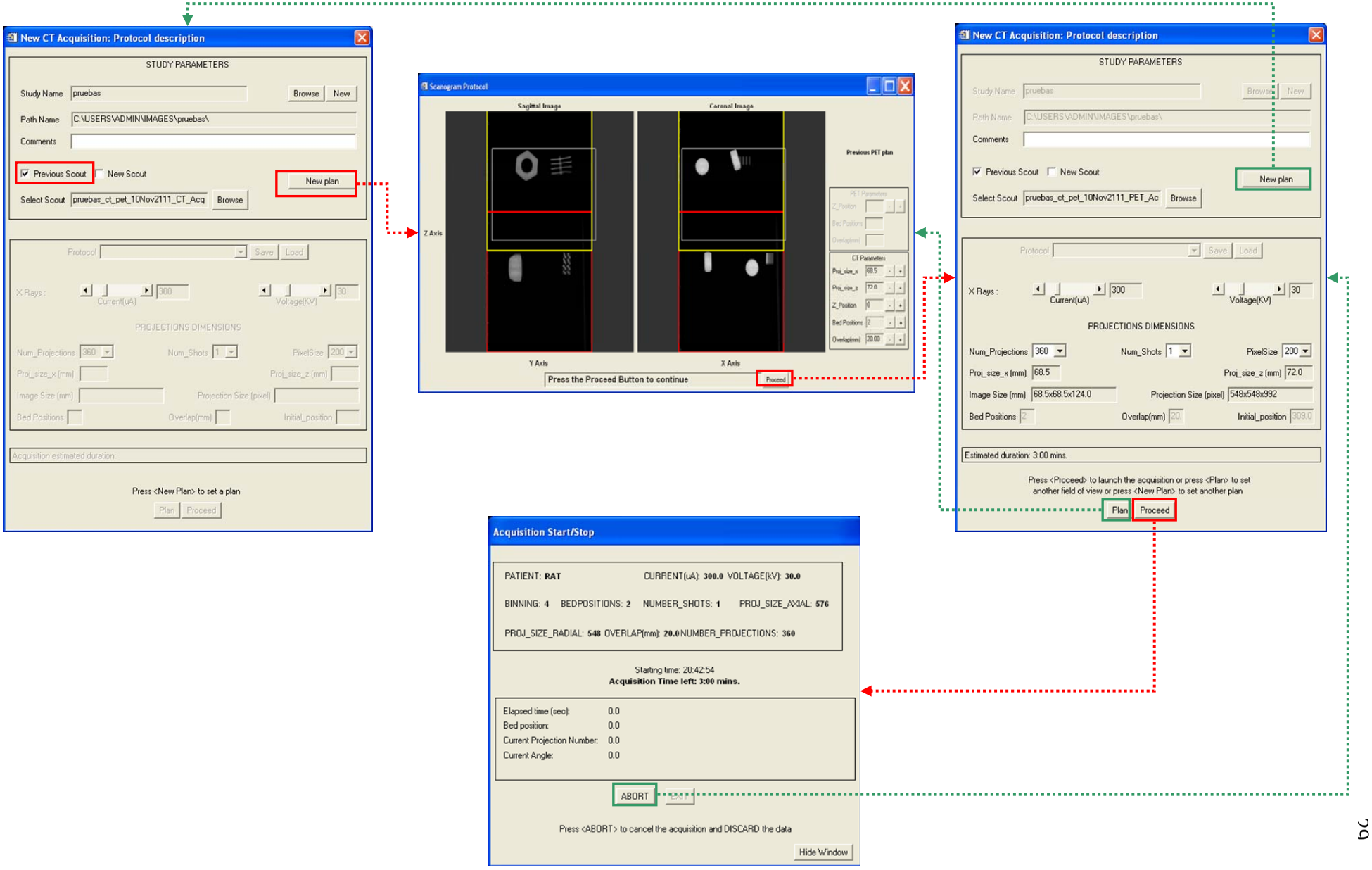


PET's Work Flow with Previous Scout



CT's Work Flow with New Scout

CT's Work Flow with Previous Scout



PET ACQUISITION

When the **PET** option (**New Acquisition,** System, or **ACQ**, toolbar) is selected, data PET acquisition is selected and the “New PET Acquisition” panel appears (**Figure 9**). This panel is divided into two parts, the upper part to entry name of study and select option of making a plan, and a bottom part to specify the type of protocol (and necessary parameters).

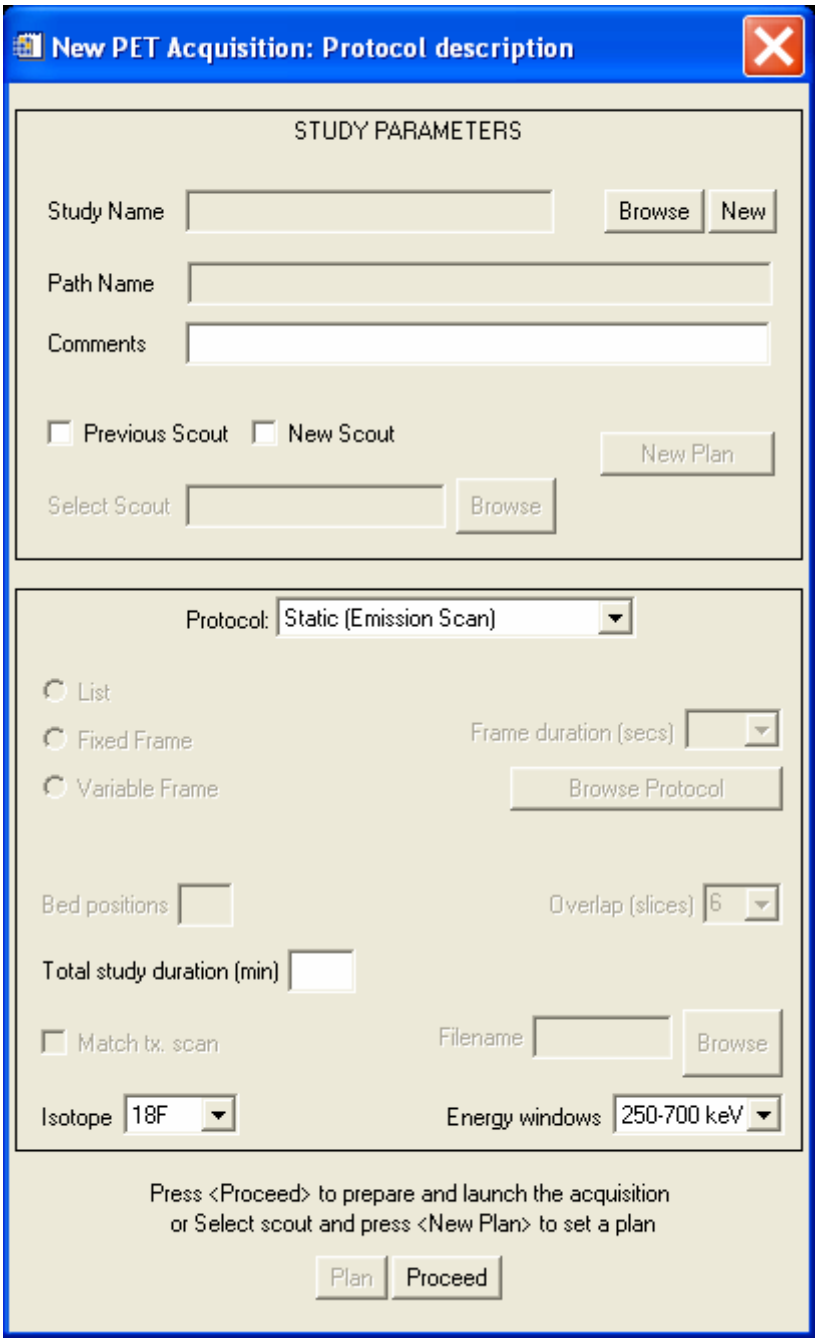


Figure 9. New PET Acquisition interface.

NEW PET ACQUISITION INTERFACE

Study Name (directory)**—** By pressing the “Browse” button, the User can bring up the menu of existing study directories. Single clicking on the identified directory name and pressing “OK” will write that name into the “Study Name” window of this panel. If a new study directory name is desired, press “New” and type in the desired name (“File name” field) and press “OK”.

Path Name— Full path where study files will be saved. Note that last directory of “Path Name” is the “Study Name”.

Comments— Additional free form text can be entered in this window. For example, you might enter the name of the radiopharmaceutical, the amount injected, the weight of the animal, etc. to help uniquely identify the study in retrospect. This field is not necessary to fill in.

Previous Scout— If the User check this box, text field labeled “Select Scout” and “New Plan” and “Browse” buttons will be sensitive meanwhile “Proceed” button will be insensitive. This option lets the User plan an acquisition from a previous acquisition, PET or CT, so the User will select the limits of the acquisition on sagittal and coronal images of a previous scanogram in next window.

New Scout— If the User check this box, “New Plan” button will be sensitive meanwhile “Proceed” button will be insensitive. This option lets the User plan an acquisition from a new scanogram.

Select Scout— By pressing the Browse button, The User can bring up the menu of previous plans. Single clicking on the identified plan name (extension “plan”) and pressing “Open” will write that name into the “Select Scout” window of this panel. The User can know if the previous plan was a PET or CT acquisition looking at plan name (letters between underscores just before number of acquisition). For example, the following plan “RATE_13Feb2007_PET_Acq018.plan” was a PET acquisition and “RATE_13Feb2007_CT_Acq019.plan”, a CT acquisition.

New Plan— By pressing this button, this window will be hidden and a new scanogram will be launched or a window with a previous scanogram will be shown. After the User presses “Proceed” button of Scanogram window, “Protocol description” window will be shown again.

Protocol— Pressing the button in the “**Protocol**” window produces a drop-down list with the following types of data acquisition:

Static (Emission Scan)— This option shown in **Figure 9** is intended for imaging tracer distributions that do not change significantly with time, e.g. the brain distribution of FDG after 30 minutes. A single 3D data set spanning the axial FOV can be reconstructed from acquisitions of this type.

Fixed Frame Dynamic (Emission Scan)— This option **(Figure 10)** is intended for imaging tracer distributions that are changing in time, e.g. transport of tracer through the brain, heart, kidneys, etc. Select the desired fixed frame duration from the drop-down menu. All time frames in a "fixed frame" study will be of this selected length.

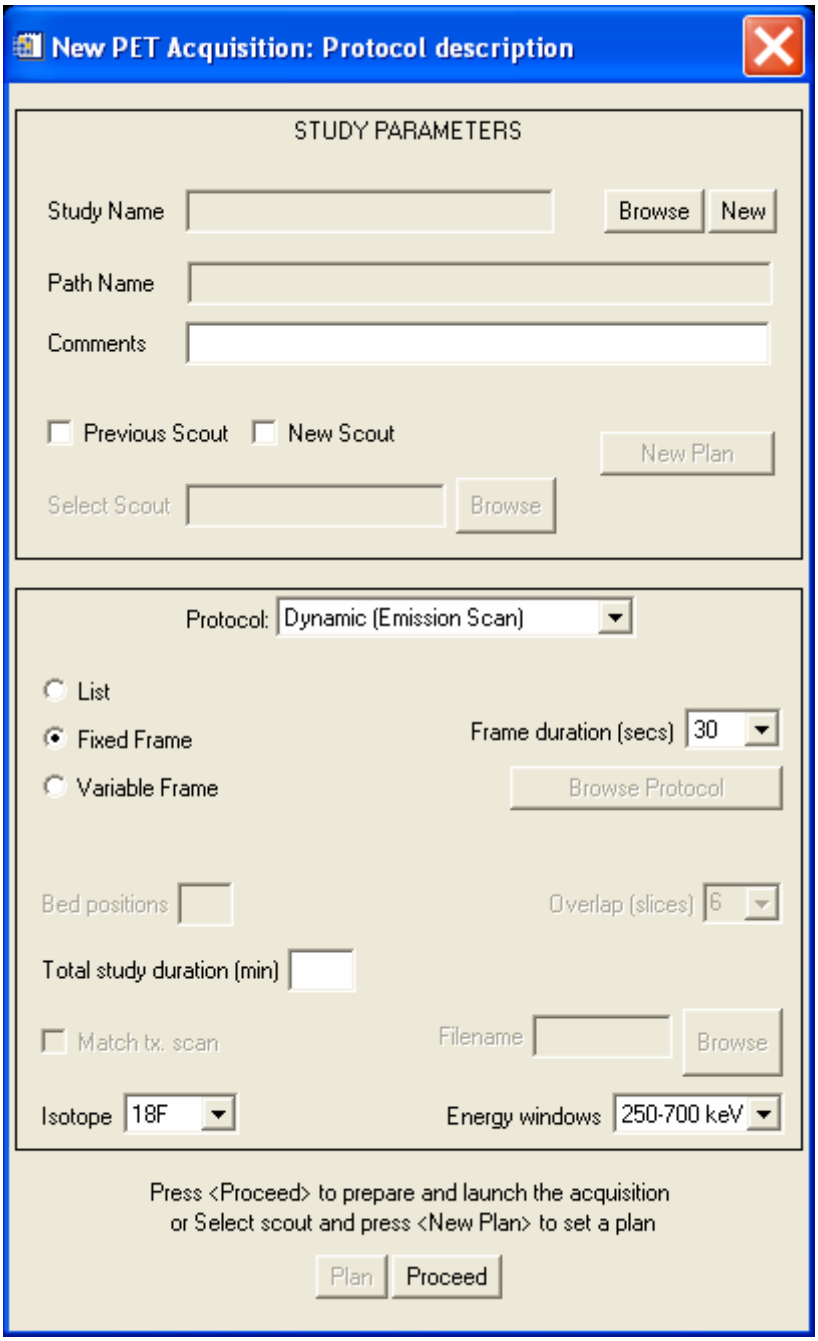


Figure 10. Fixed frame duration dynamic scan menu.

Variable Frame Dynamic (Emission Scan)— This option (**Figure 11**) is intended for imaging tracer distributions whose time variation in the target region is highly variable, e.g. a rapid change in heart activity after a bolus injection followed by a slow variation in heart activity over a much longer period.

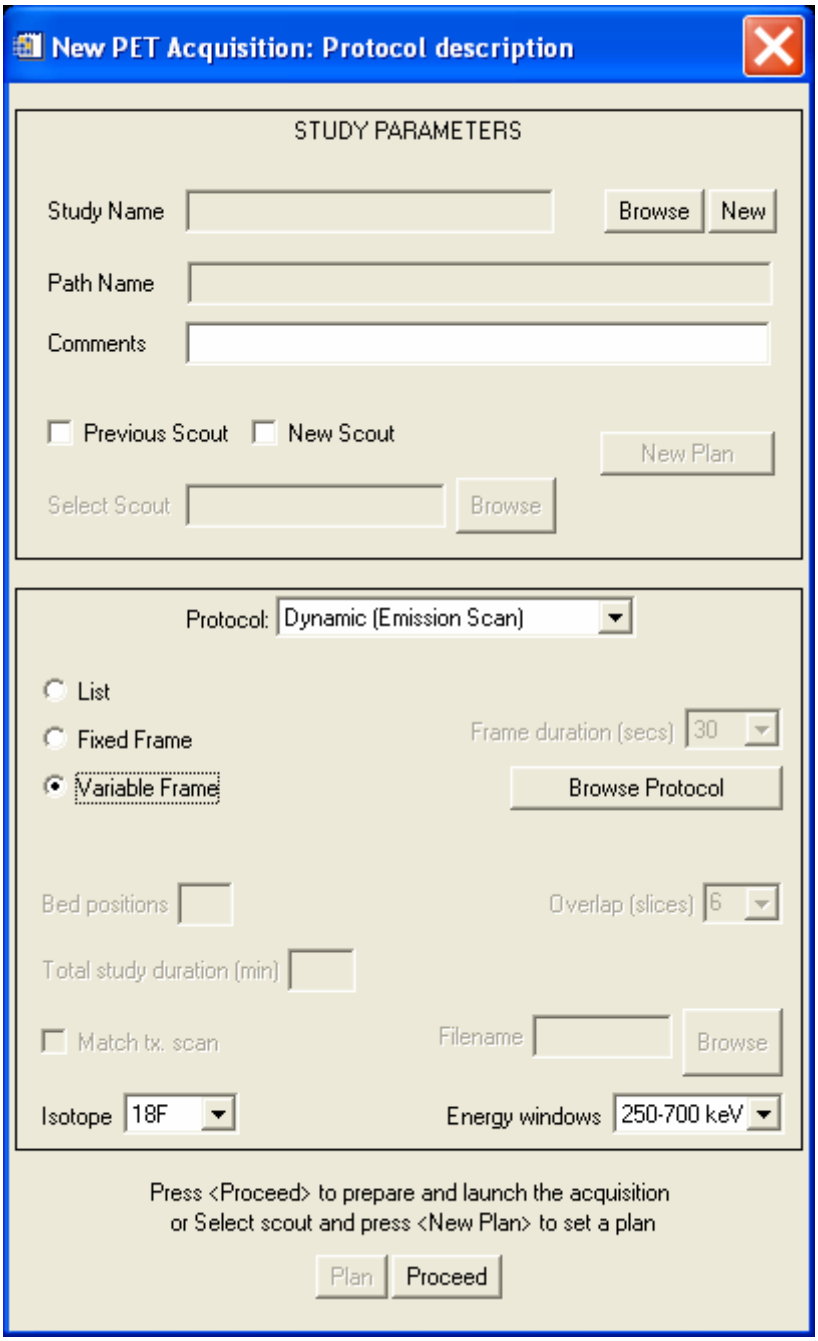


Figure 11. Variable frame duration dynamic scan menu.

In order to use this feature, you must first define a custom variable frame rate protocol with the desired frame durations. This “DEFINE VARIABLE FRAME

LENGTH PROTOCOL" procedure is accessed by pressing the "TIMING" button on the Main VISTA-CT Interface (see **TIMING** in Table of Contents). When the "VARIABLE FRAME" button is pushed on the NEW ACQUISITION menu, a list of these previously user-defined protocol names (extension "vdy") can be accessed with the BROWSE function that will load that protocol. The subsequent variable frame study will be executed with the frame durations contained in that protocol.

List Mode— If you do not wish to specify a fixed or variable frame data acquisition in advance, you may select the LIST mode option shown in **Figure 11**. LIST mode acquires the data generated by VISTA-CT but not in a specific temporal format. You can reframe or reformat the same List mode data set non-destructively with different frame durations. You can, for example, create two dynamic image sequences from the same data set that differ in their respective frame durations. After a LIST mode data set is acquired you must format these data before image reconstruction into an image sequence with known frame durations. This formatting operation is accomplished using the "LIST Mode Formatting" menu item accessible through the "TIMING" icon on the Main VISTA-CT Interface.

Whole-body (Emission Scan)— This option (**Figure 12**) is intended for imaging static tracer distributions throughout the whole body. Enter the number of bed positions needed to span the length of the animal you wish to image (usually 3 or less for the DT, 6 or less for the ST) and the number of overlap slices (to improve statistical precision across the joint between bed positions). Unless otherwise specified, the bed will advance with the specified default values.

If the emission scan will have more than one bed position and is to be corrected for attenuation using a transmission scan acquired immediately prior to the emission scan, check the box labeled "Match tx. scan" (see multi-bed position transmission scanning). After checking the box, select a file (extension "acq") pressing the "Browse" button of the same row as "Match tx. Scan". The box does not have to be checked if only a single bed position is required.

When initiated, whole-body imaging occurs under computer control until complete. A contiguous whole-body image will be reconstructed automatically from this acquisition type.

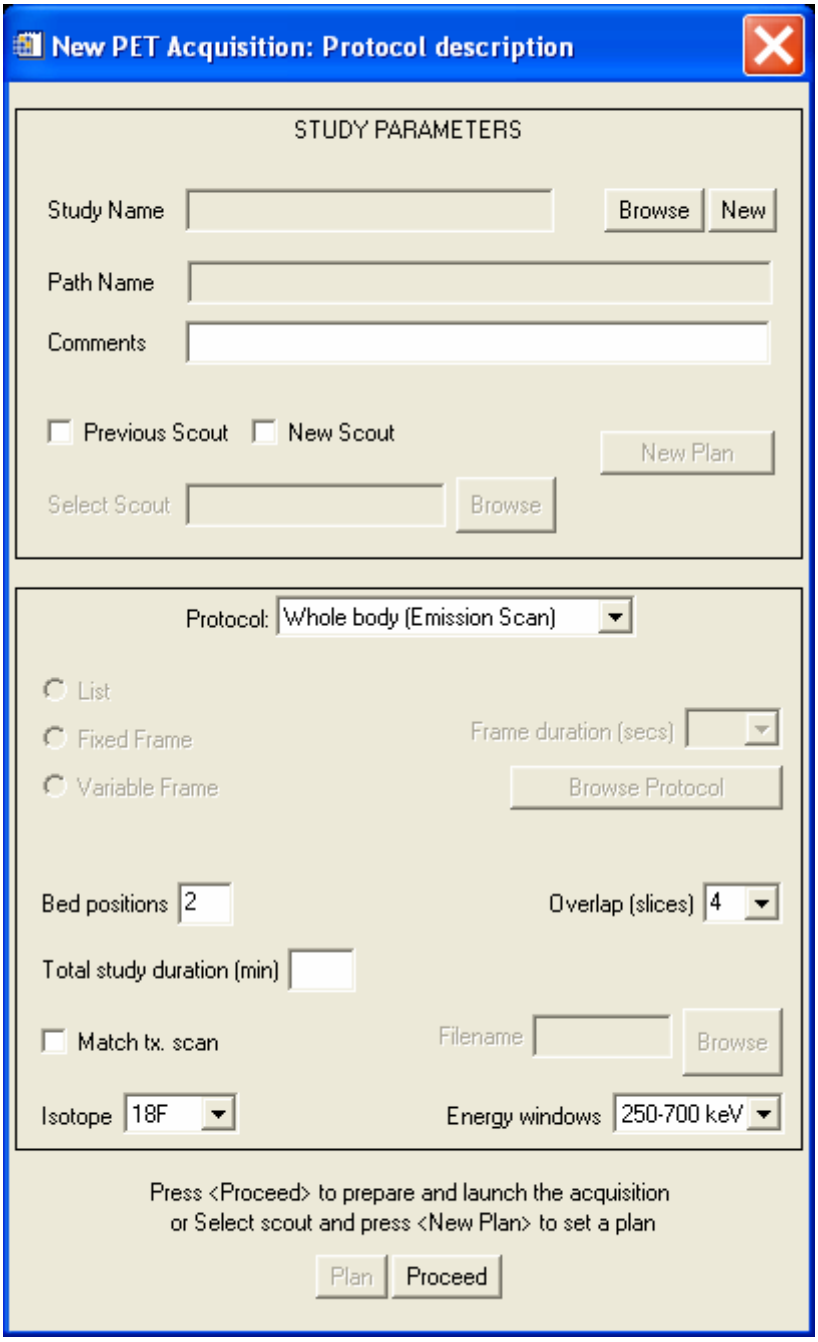


Figure 12. Whole-body (Emission Scan) interface.

Transmission Scan (Single Bed Position)— With the animal positioned in the scanning field, **AND BEFORE ADMINISTRATION OF ANY RADIO-PHARMACEUTICAL**, insert the Ge-68 transmission annulus into the aperture with the insertion tool to surround the animal. Select the Transmission Scan acquisition mode (**Figure 13**) and after filling out the appropriate menu items, begin the scan. When a Ge-68 annulus is new, a Transmission scan of 30-60 minutes is usually required to obtain adequate statistical precision for attenuation correction.

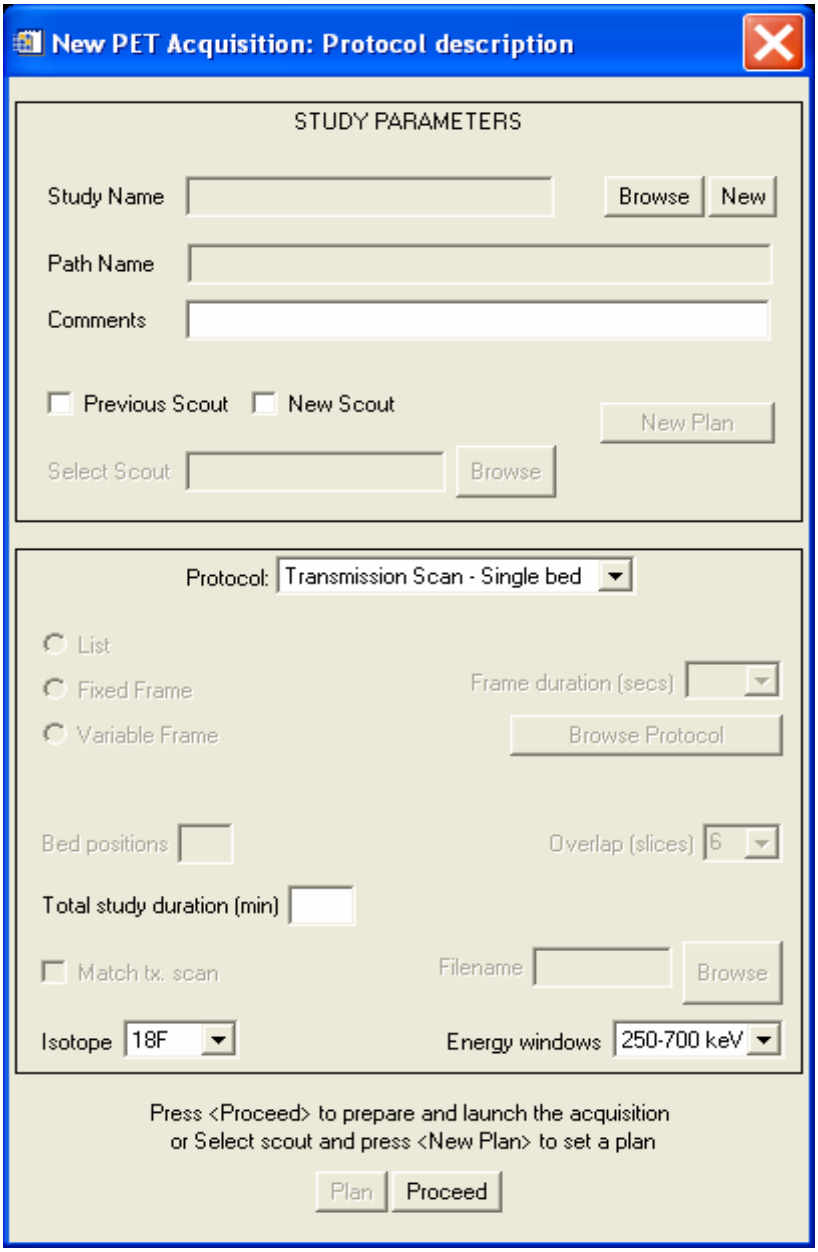


Figure 13. Transmission scan (single bed position) interface.

Transmission Scan (Multiple Bed Positions)—With the animal positioned in the scanning field **AND BEFORE ADMINISTRATION OF ANY RADIOPHARMACEUTICAL** insert the Ge-68 transmission annulus into the aperture using the annulus insertion tool to center the annulus axially and around the animal. Select the Multiple Bed Position acquisition mode (**Figure 14**), fill in the required menu items and initiate the scan.

Transmission data must be acquired for each corresponding emission bed position if the entire emission data set is to be corrected for attenuation using the Ge-68 source. For example, if a whole body emission scan is performed with four bed positions, four transmission scans must also be performed with the same overlap parameter,

number of bed positions and in the same bed positions. Each of these scans must possess sufficient counts to yield an accurate attenuation correction for each bed position, i.e. 30-60 minutes per bed position x number of bed positions = total scan duration.

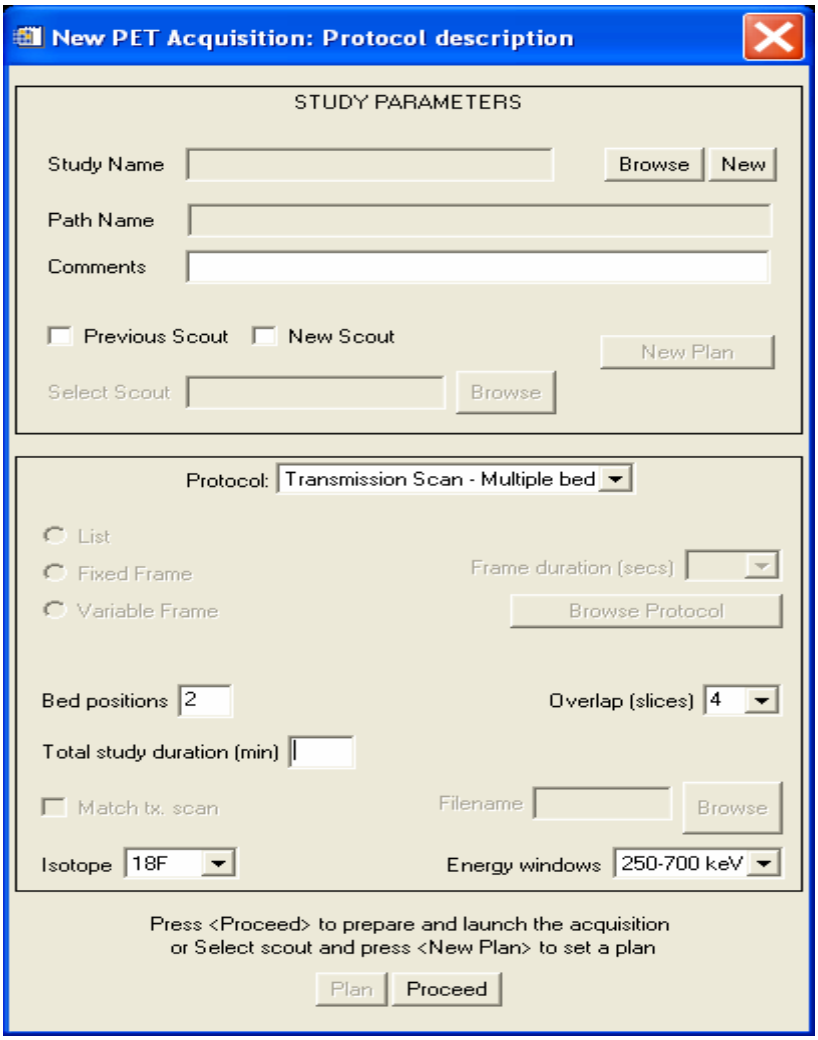


Figure 14. Transmission scan (multiple bed position) interface.

Blank Scan— "BLANK" scans serve two important purposes on the VISTA scanner: first, Blank scans are needed for periodic calibration of the system and, second, the most recent of these Blank scans is used as the Blank scan for attenuation correction of emission studies. With this scheme it is not necessary to acquire a Blank scan for attenuation correction of an emission study since a Blank scan with excellent statistical properties will already exist from the prior system calibration.

A Blank scan (**Figure 15**) must be acquired with no objects, including the animal bed, in the field-of-view. With the field-of-view empty, slide the Ge-68 annulus into the aperture from the rear of the scanner using the provided cylindrical centering tool to axially center the annulus. A Blank scan for every energy window should be run long enough to reduce statistical error in the calibration routine (also called "Normalization"

in a later section) to an absolute minimum since the quality of all subsequent images created by VISTA-CT depends strongly on this parameter. Recommended BLANK imaging times for each energy window are shown below. Note that the lengths of these scans depend on the age of the annulus after its calibration date.

100-700 keV energy window: 12 hours (17 hrs*) (21 hrs**)
250-700 keV energy window: 18 hours (25 hrs*) (31 hrs**)
400-700 keV energy window: 36 hours (50 hrs*) (63 hrs**)

*90-180 days after the annulus calibration date
**180-270 days after the annulus calibration date

It is important to remember that the Blank scan that is collected applies only to studies having the same energy window and Blank scans must be acquired for all three energy windows if VISTA-CT is to work properly with all three windows. When setting up a BLANK scan, the User must also select the "Ge-68" option from the Isotope menu.

The critical role played by Blank scans in calibrating the VISTA-CT system is described in detail in the "Normalization" section of this Manual (see Table of Contents) and includes a description of how a fictitious user named "QC" (for "quality control") is created to manage Blank scans acquired over time.

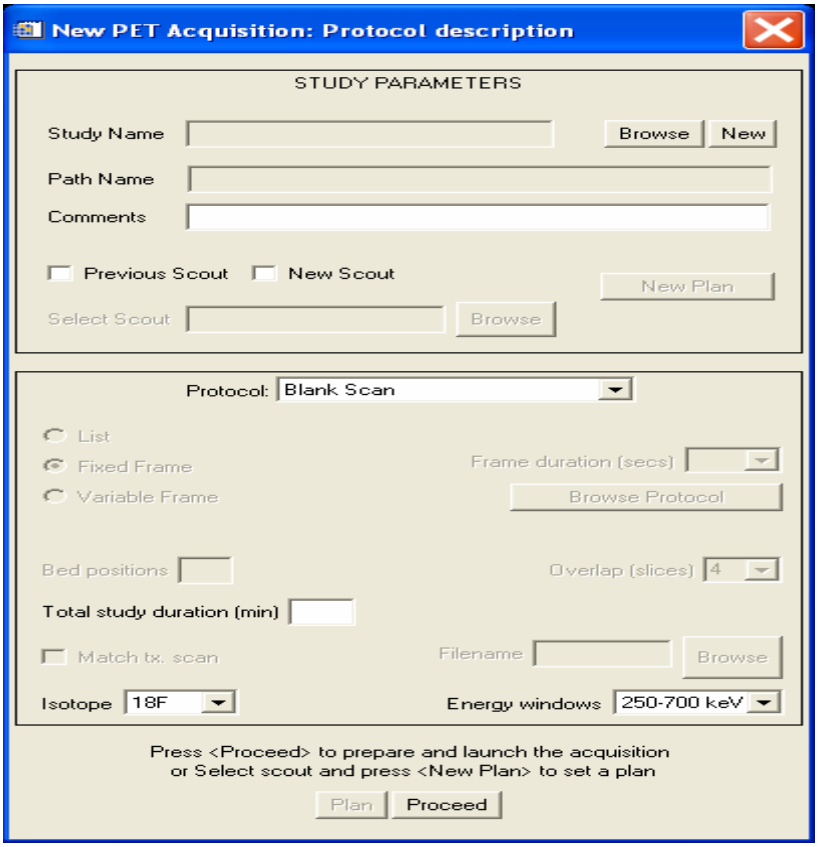


Figure 15. Blank scan interface.

Whole-body Dynamic (Emission Scan)— This option (**Figure 16**) mixes whole body and imaging tracer distributions whose time variation in the target region is highly variable.

As “Whole-body (Emission Scan)”, this protocol requires that the animal be re-positioned in exactly the same bed positions for emission imaging as for the previous transmission scans. In order to do so, check the box labeled “Match tx. scan” and then enter the WB Dynamic transmission scan filename (extension “acq”) in the “Filename” window when it becomes active. Doing so “tells” the Whole Body Dynamic (Emission Scan) acquisition protocol to access the bed position data recorded during the “Transmission Scan (Multiple Bed Positions)” and to use these same bed positions for the WB Dynamic emission study (and all other parameters as well).

The User must first define a custom variable frame rate protocol for Whole_Body Dynamic with the desired frame durations. This “DEFINE DYNAMIC WHOLE BODY PROTOCOL” procedure is accessed by pressing the “TIMING” button on the Main VISTA-CT Interface (see **TIMING** in Table of Contents). When the “VARIABLE FRAME” button is pushed on the NEW ACQUISITION menu, a list of these previously user-defined protocol names (extension “wdy”) can be accessed with the BROWSE function that will load that protocol. The subsequent variable frame study will be executed with the frame durations contained in that protocol.

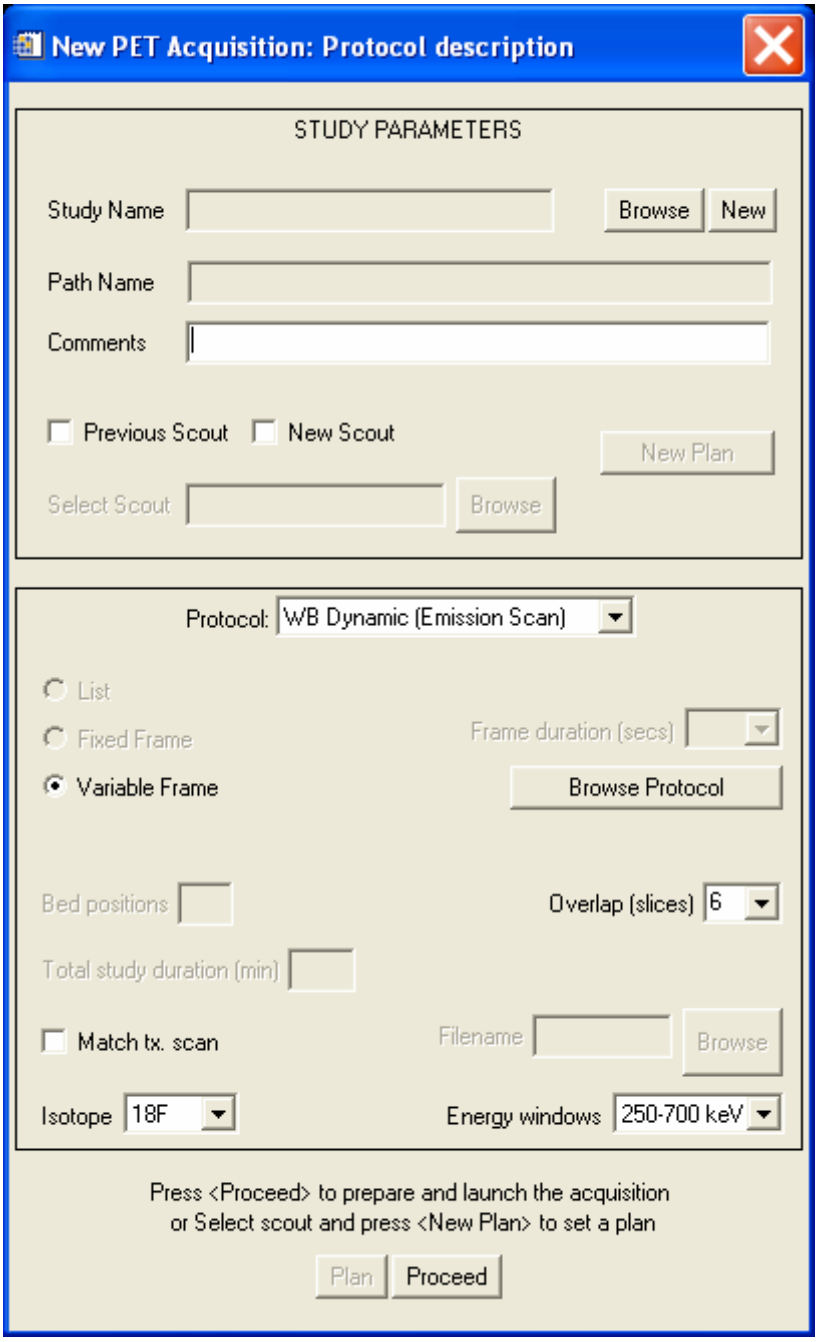


Figure 16. Whole Body (Emission Scan) interface.

Isotope— Clicking on this selection will produce a drop-down menu of isotope selections (**Figure 17**). Pick the isotope you are using for the study. Time-activity curves generated from a data set will be corrected for the radioactive decay of the isotope selected from this menu. These decay corrections are made relative to the time that the data collection started, i.e. for the elapsed time after the collection was initiated.

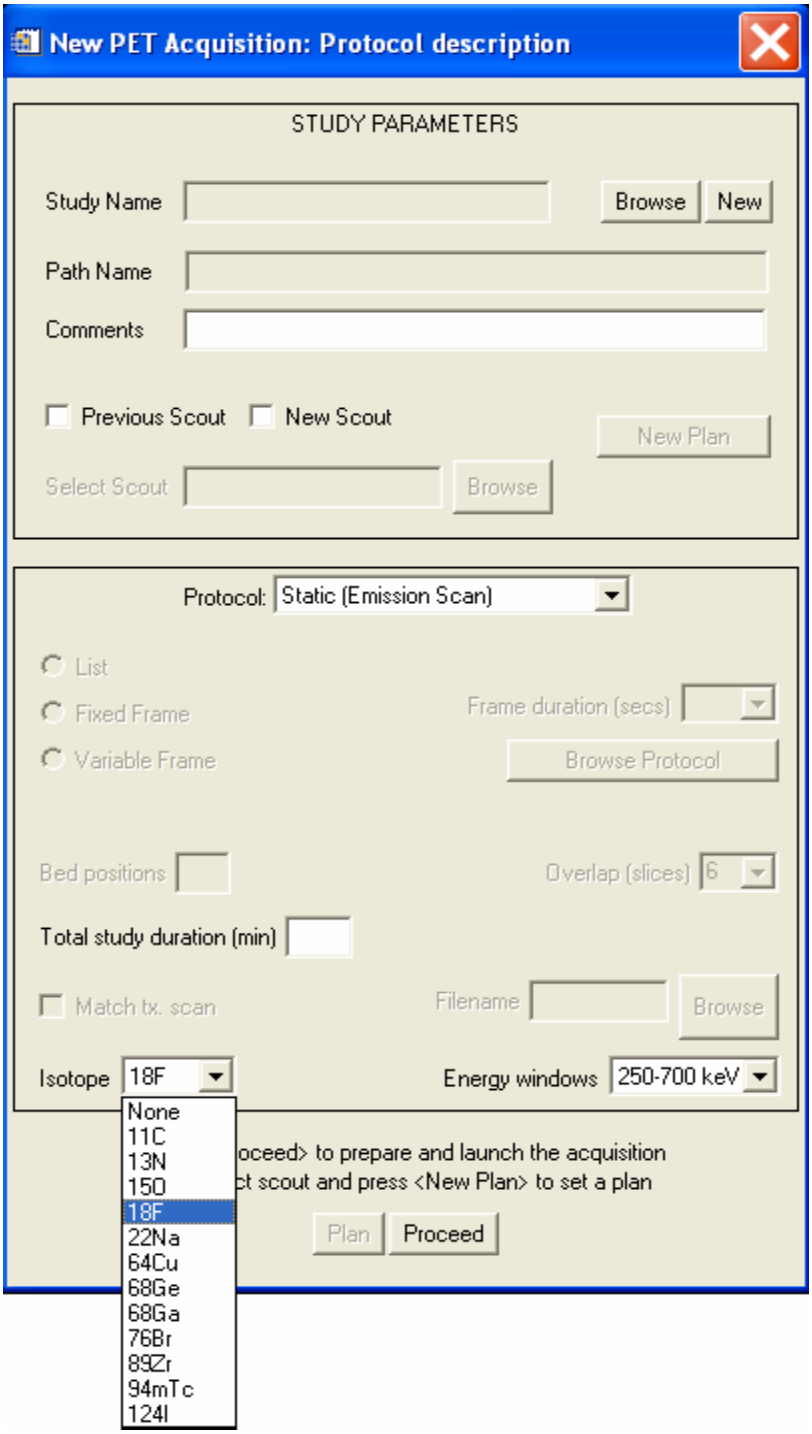


Figure 17. Drop-down menu for correction of radioactive decay.

Study duration—Enter the **total** imaging time for the study regardless of type. The total length of a dynamic study is the duration of each frame times the number of frames. The total length of a whole-body scan is the dwell time per bed position times the number of bed positions.

Energy window— Three options are available in the drop-down menu shown in **Figure 18** for the range of absorbed photon energies declared to represent valid coincidence events. The default range is 250-700 keV, a window that gives medium sensitivity (4.0% DT, 2% ST) and moderate scatter rejection. The narrowest range (400-700 keV) has the lowest sensitivity (2% DT) but better scatter rejection. The widest range (100-700 keV) has the highest sensitivity (6% DT, 2.6% ST) but poorer scatter rejection.

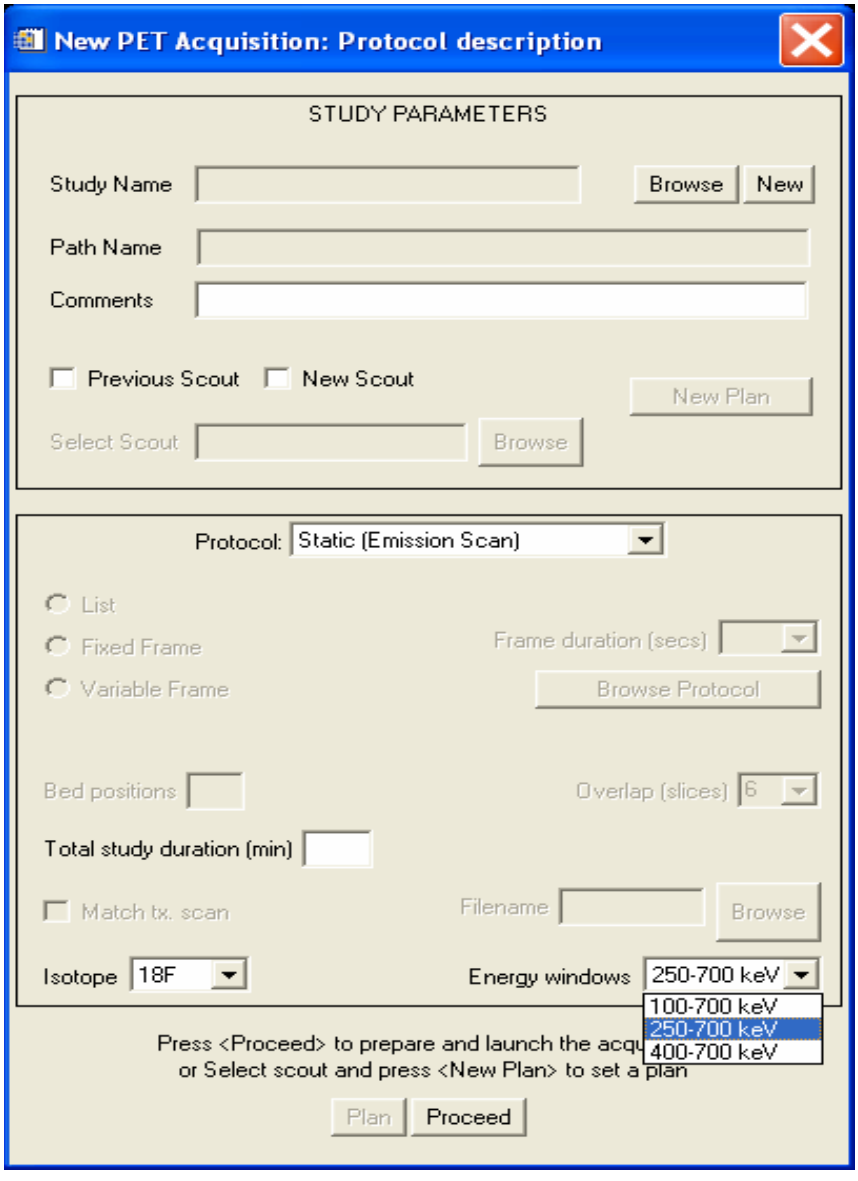


Figure 18. Acquisition interface illustrating drop-down energy menu.

Plan— This button is sensitive when the User has made a plan, ie. he/she has selected the limits of the acquisition on Coronal and Sagittal images of a scanogram. Pressing this button causes to go back to the made plan.

Proceed—Pressing this button causes VISTA-CT to accept all entries in the New PET Acquisition panel and move to the next panel in the data acquisition process shown in **Figure 19**. This panel shows the progress of the data acquisition and reports important attributes of the ongoing data collection, e.g. coincidence rate, etc. The study name, type of acquisition, the isotope and the energy window are also displayed along the top of this panel.

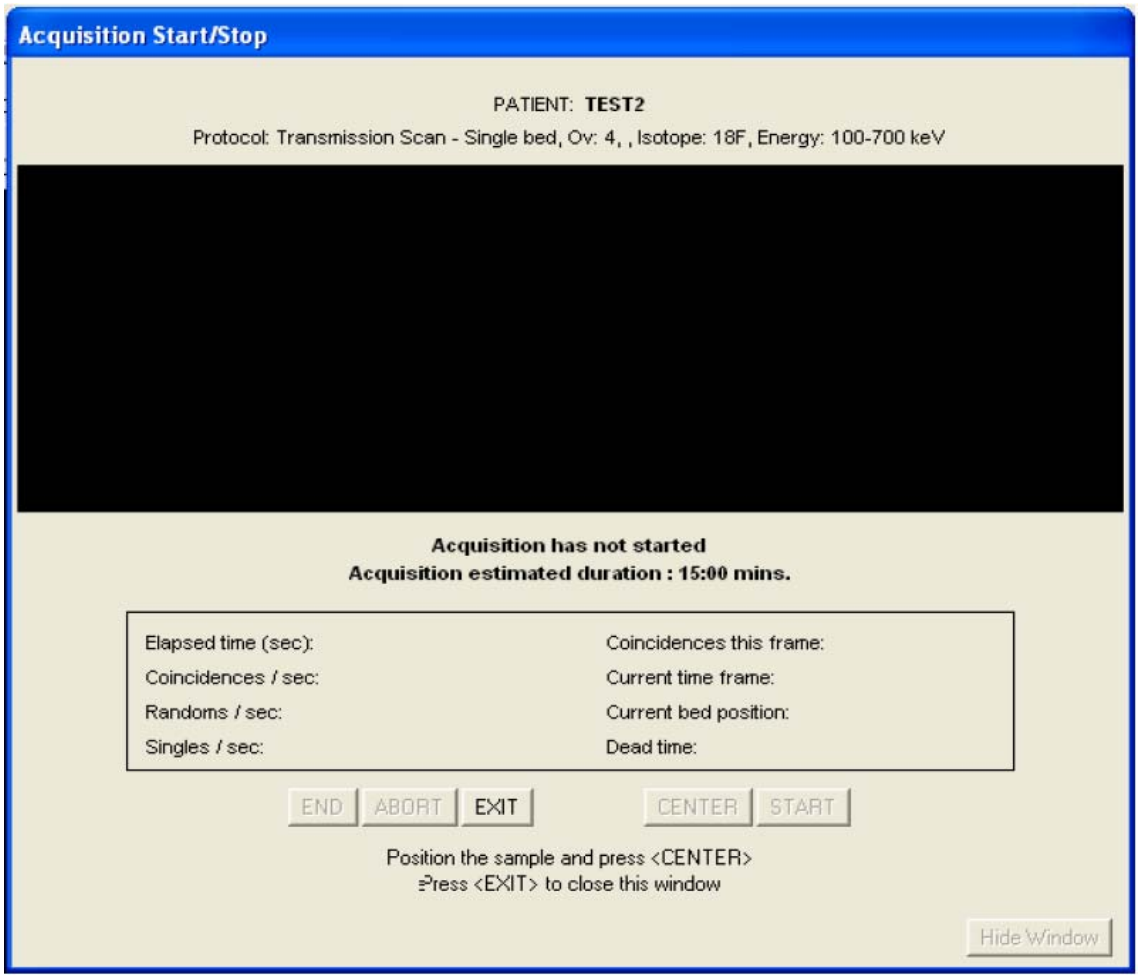


Figure 19. Acquisition Start/Stop interface

Close (System Menu)— Pressing this button deletes the New PET Acquisition panel, current plan (if it applies) and all entries.

After pressing “New Plan” button with “New Scout” box selected, the window which will be shown is that whose title is “Steps for the Scanogram Process” (Figure 20).

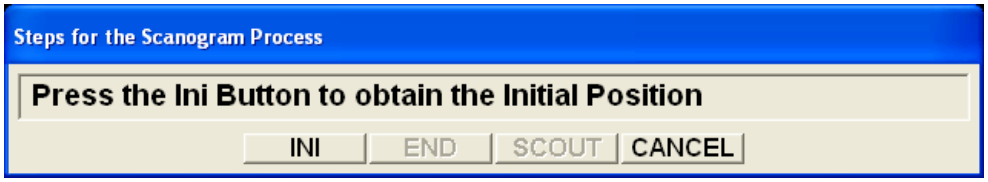


Figure 20. Steps for the Scanogram Process interface.

STEPS FOR THE SCANOGRAM PROCESS INTERFACE

Ini— Prior to press the “Ini” button, the User moves the bed to its initial position and, then, the User will press “Ini” button. Note that using laser beam is a better way to fix this position.

End— Prior to press the “End” button, the User moves the bed to its end position and, then, the User will press “End” button. Note that using laser beam is a better way to fix this position. If the User doesn´t move the bed after pressing “Ini” button, the size of the scanogram will be one single bed. If the distance between initial and end position isn´t a whole multiple of CT bed size, the size of the scanogram will increase up to the distance is a whole multiple.

Scout— If the User press this button, the acquisition of the scanogram will be launched. While the acquisition is carrying out, X-Rays notice will be ON.

Cancel— Except while the acquisition is carrying out, if the User presses “Cancel” button, this window will be deleted and “New PET Acquisition” panel will be shown.

After pressing “New Plan” button with “Previous Scout” box selected or finishing scanogram acquisition, the window which will be shown is that whose title is “Scanogram Protocol” (Figure 21).

SCANOGRAM PROTOCOL INTERFACE

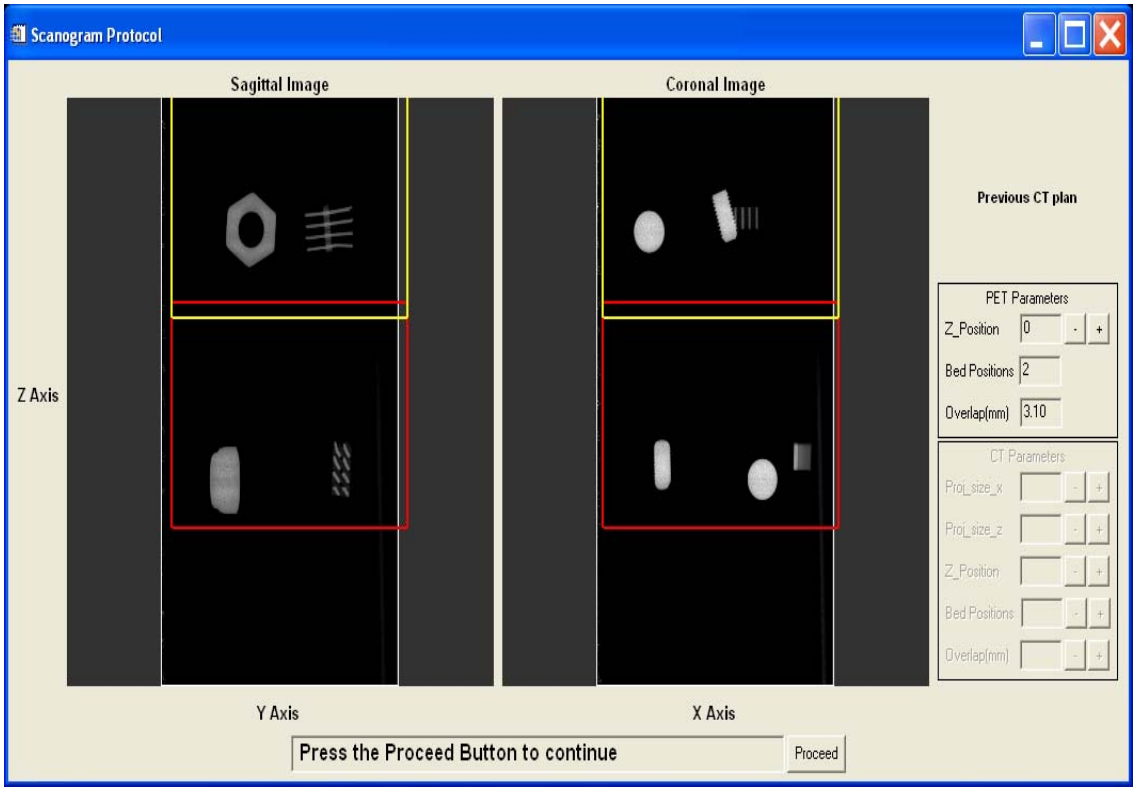


Figure 21. Scanogram Protocol interface for PET acquisition (with a previous CT plan).

PET Parameters— The User can modify the following parameters when he/she desires to acquire PET data. Thus, the User can select what he/she wants to acquire.

Z_position— Pressing Plus or Minus buttons, the User moves the bed position along axial axis.

Bed Positions— This text field shows the number of beds of the acquisition. The User can just modify this parameter in the “New PET Acquisition” window. Each bed will be shown with a different colour. For example, in Figure 21, first bed is represented as a yellow rectangle and second bed, as a red rectangle.

Overlap— This text field shows the overlap in mm among beds. The User can just modify this parameter in the “New PET Acquisition” window.

Proceed— Pressing this button will close this window and will show “New PET Acquisition” window if PET acquisition is or “NEW CT Acquisition” if CT acquisition.

If the User has selected a previous plan, the type of plan will be shown in the right upper corner. For example, in Figure 21 the previous plan was a CT plan. In addition, the limits of this previous plan will be shown (grey lines).

ACQUISITION START/STOP INTERFACE

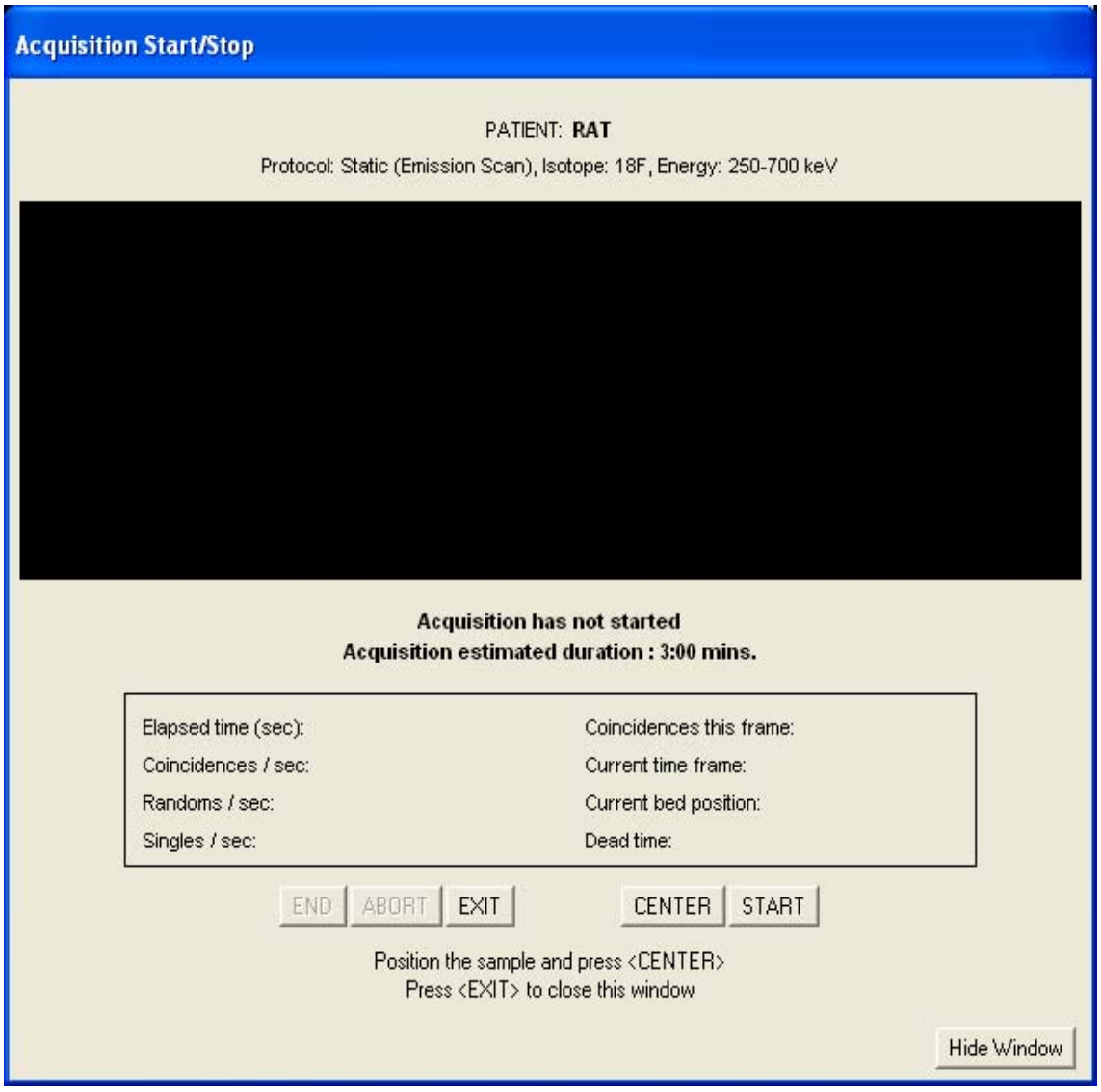


Figure 22. Acquisition Start/Stop interface.

Note that the “Center” button will be sensitive just when the User make a PET acquisition without a plan.

When a positron-emitting object appears in the field-of-view after the CENTER button is pressed, the top portion of this panel will display an axial “persistence” projection image of the field-of-view as if you were looking down through the top of the gantry at the animal lying on the imaging bed. This image is a “projection” in the same way

that a chest x-ray is a projection of the chest onto a piece of film or that a gamma camera image is a planar representation of activity in the field-of-view. The third, or depth, dimension in these images is collapsed onto a plane and lost but the distribution of activity in the two-dimensional plane is acquired at much higher sensitivity than a tomographic image. This persistence image is continually refreshed at 10 second intervals allowing changes on this time scale to be visualized.

Note that this image is intended primarily as a Quality Control aid. The way that this image is formed causes the appearance of an object to be dependent on the thickness of the object, the distribution of tracer in the animal and on the vertical position of the object in the field of view. As a result, you should regard this persistence image as a relatively crude representation of the actual tracer distribution.

By way of example, the image shown in **Figure 22** is that of a rat head containing F-18 FDG. The animal's nose is at the top of the image, the Harderian glands are the bright spots left and right and the brain is the larger, diffuse structure towards the bottom of the image. While anatomical detail is relatively poor in this image, it is clear that the brain is within the axial FOV and that the animal is correctly positioned for imaging the head and brain (one of the purposes of this kind of display). More generally, this persistence image can be used to guarantee that any pre-labeled organ is in the FOV before imaging.

The status of the data acquisition process is updated on the panel below the persistence image. Elapsed time, coincidence rate, singles rate, randoms rate, total coincidences in the current frame, current time frame number (if dynamic study), current bed position number (if whole body scan) are all shown during data acquisition. The time-of-day of the start of acquisition and the estimated time to completion are also shown.

When this panel first appears, CENTER, START and EXIT are active but are shown as inactive in **Figure 22**. At this point you should place the animal on the imaging bed, move the animal forward with the hand controller until the laser illuminator is directly over the center of the imaging target and then click on CENTER. With this command, VISTA-CT automatically moves the animal forward into the aperture to place the laser-designated target point exactly at the center of the axial field-of-view. This action will also initiate the persistence image acquisition.

Before initiating bed movement you should make certain that the animal or imaging target is **vertically** centered in the aperture using the manual screw drive and that the animal or any attached equipment will actually pass into the aperture without hitting the gantry. Remember that if a transmission study is also to be done, the animal and bed must also pass through the transmission annulus when it is positioned in the aperture. If you are unsure this will happen, it may be useful to manually drive the animal into the aperture with the transmission annulus in place before starting imaging to make sure the animal and bed won't hit the annulus.

Once the animal has been inserted properly using the CENTER command, hitting the START button will initiate the acquisition and the status panel will appear as in **Figure**

22. After 10-15 seconds the status panel will begin to update as data are accumulated. When the START button is pressed, the current active buttons are turned off and the END and ABORT buttons become active as shown in **Figure 22**. The acquisition will continue uninterrupted until the stop conditions are reached. The status panel will then signal that the acquisition is done at which point you can press the active EXIT button to store the acquired data and return to the main menu.

If something goes wrong during an already started acquisition, e.g. the animal moves, etc., you may stop the acquisition in one of two ways (**Figure 22**). First, you can END the acquisition. If END is selected, the acquisition terminates and all data acquired to that point are saved. If ABORT is selected, data acquisition ends but the file is deleted and the data discarded. These two modes give you the option of saving a study that is almost finished when something goes wrong or throwing away a study that is made truly useless by some misadventure, e.g. animal movement early in a study compared to animal movement during the last frame of a two-hour study.

As suggested earlier, you can use these same features to center a pre-labeled organ in the axial FOV. If after CENTERing the axial position of the organ appears incorrect by inspection of the persistence image, you can press ABORT and repeat the CENTERing procedure accounting for the change you wish to make in the axial position of the organ. Once satisfied that this position is correct, you can START the data acquisition.

CT ACQUISITION

When the **CT** option (**New Acquisition,** System, or **ACQ**, toolbar) is selected, data CT acquisition is selected and the "New CT Acquisition" panel appears (**Figure 23**). This panel is divided into two parts, the upper part to entry name of study and select option of making a plan, and a bottom part to specify the type of protocol (and necessary parameters).

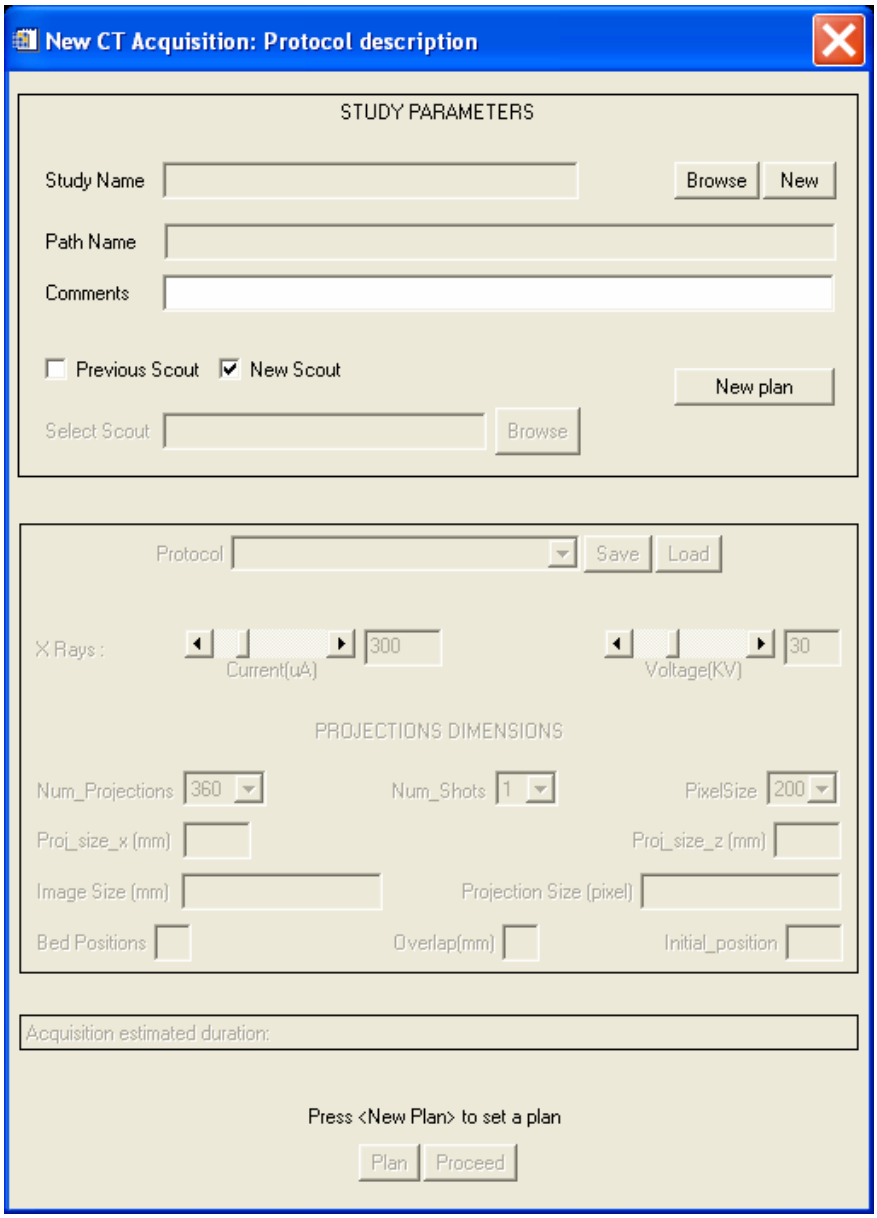


Figure 23. New CT Acquisition interface.

As the upper part of “New PET Acquisition” and “New CT Acquisition” are equal, these fields won´t be explained next.

NEW CT ACQUISITION INTERFACE

Study Name— See “New PET Acquisition” Interface.

Path Name— See “New PET Acquisition” Interface.

Comments— See “New PET Acquisition” Interface.

Previous Scout— See “New PET Acquisition” Interface.

New Scout— See “New PET Acquisition” Interface”.

Note that when “Previous Scout” is checked, “New Scout” isn´t and the opposite way. The “Proceed” button won´t be sensitive unless the User make a plan.

Select Scout— See “New PET Acquisition” Interface.

New Plan— See “New PET Acquisition” Interface.

Protocol— This option isn´t available in this version.

X-Rays— The User can select the current and voltage of X-Rays through these sliders after the plan is made.

Projections dimensions— The User can select number of projections (droplist ***“Num_Projections”***), number of shots (***“Num_shots”***) and pixel size (***“Pixelsize”***) after the plan is made. In addition, the size of a single bed in axial axis (text field “**Proj_size_z**”) and in the other axis (text field “**Proj_size_x**”) in mm, the total size of the acquisition in mm (text field “**Image Size**”) and in pixels (text field “**Projection Size**”), the number of beds (text field “**Bed Positions**”), the overlap between beds in mm (text field “**Overlap**”) and the initial position of the study (text field “**Initial_position**”) will be shown after the plan is made.

The possible values of “**Num_Projections**” are 360, 720 and 1080; “**Num_shots**”, 1,2,4,8,16 and 32 (although possible values depend on value of “Num_projections”) and “**PixelSize**”, 50, 100 and 200.

Acquisition estimation duration— This label shows an estimation of the acquisition duration after the plan is made.

Plan— See “New PET Acquisition” Interface.

Proceed— When the User press this button, the CT acquisition is launched, "New CT Acquisition" interface is hidden and "Acquisition Start/Stop" interface is shown. This button is sensitive when the plan is made.

After pressing "New Plan" button with "New Scout" box selected, the window which will be shown is that whose title is "Steps for the Scanogram Process" (see PET Acquisition).

If the User presses "New Plan" button with "Previous Scout" box selected or finishing scanogram acquisition, the window which will be shown is that whose title is "Scanogram Protocol" (Figure 24).

SCANOGRAM PROTOCOL INTERFACE

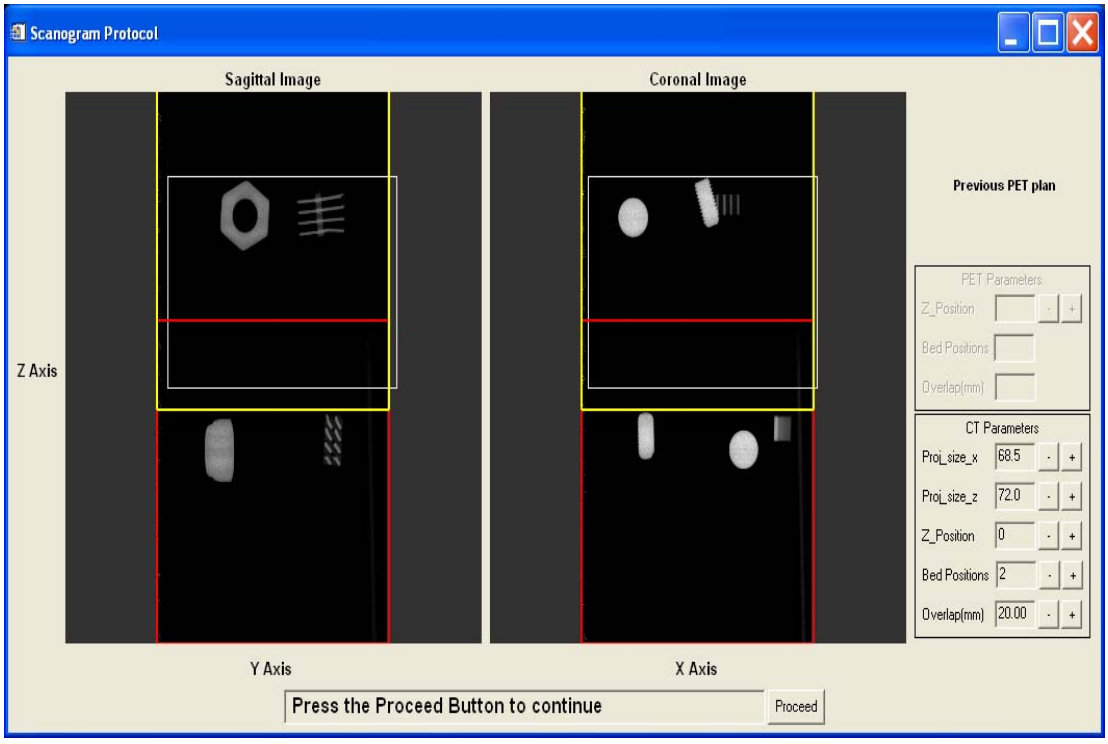


Figure 24. Scanogram Protocol interface for CT acquisition (with a previous PET plan).

CT Parameters— The User can modify the following parameters pressing minus or plus buttons when he/she desires to acquire CT data. Thus, the User can select what he/she wants to acquire.

Proj_size_x— This field shows the size in mm of a single bed along X or Y axes.

Proj_size_z— Size in mm of a single bed along axial axis.

Z_position— Pressing Plus or Minus buttons, the User moves the bed position along axial axis.

Bed Positions— This text field shows the number of beds of the acquisition. Each bed will be shown with a different colour. For example, in Figure 24, first bed is represented as a yellow rectangle and second bed, as a red rectangle.

Overlap— Overlap in mm among beds.

Proceed— See PET Acquisition.

If the User has selected a previous plan, the type of plan will be shown in the right upper corner. For example, in Figure 24 the previous plan was a PET plan. In addition, the limits of this previous plan will be shown (grey lines).

ACQUISITION START/STOP INTERFACE

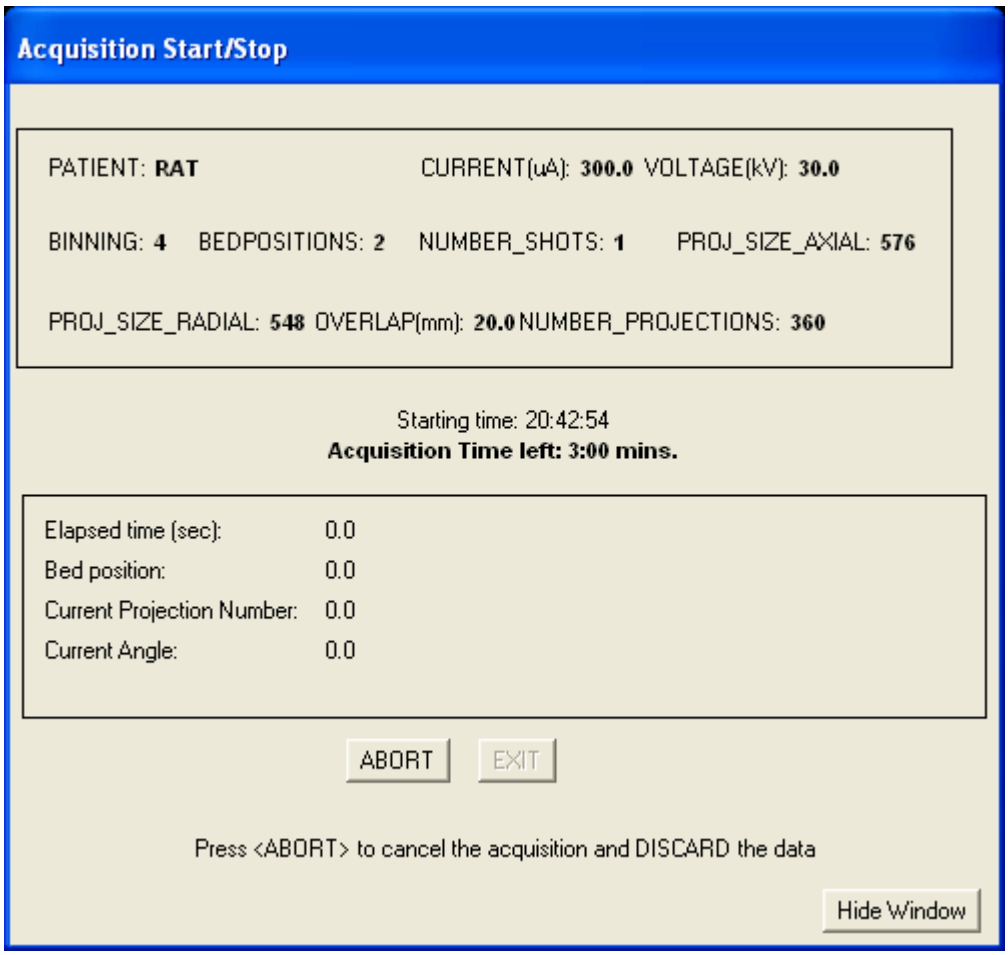


Figure 25. Acquisition Start/Stop interface for CT Acquisition.

Figure 25 shows Acquisition Start/Stop interface for CT Acquisition. In the upper part, the User can see the acquisition parameters: name of the study (**PATIENT**), current and voltage of X-Rays (**CURRENT** and **VOLTAGE**, respectively), the value of the binning chosen (**BINNING**), the number of beds (**BEDPOSITIONS**), the number of shots (**NUMBER_SHOTS**), the size of a single bed in pixels (**PROJ_SIZE_AXIAL** for size along axial axis and **PROJ_SIZE_RADIAL** for size along X or Y axes), the value of overlap in mm (**OVERLAP**) and the number of projections (**NUMBER_PROJECTIONS**).

In the middle of the panel, **Starting time** and **Acquisition Time left** (after finishing Calibrating Images) are shown.

In the bottom part of the panel, the User can see the current values of **Elapsed time** in sec, **Bed Position**, **Projection Number** and **Angle.**

While the acquisition is carrying out, X-Rays notice will be ON.

Abort— Pressing this button will cancel the acquisition. After several seconds, “Exit” button will be sensitive.

Exit— If the User presses this button, Acquisition Start/Stop Interface will be deleted, showing “New CT Acquisition” interface if the User has pressed “Abort” button or VISTA-CT main interface screen if the acquisition has finished without any problems.

Hide Window— While the acquisition is carrying out, the User can continue with other tasks after pressing this button. To go back to this panel, press **CT** option in **New Acquisition** (System) or in **ACQ** (toolbar).

If during the acquisition, an error happens, the acquisition will be aborted, an error message will be shown and after pressing “OK”, “New CT Acquisition” interface will be shown.

RECONSTRUCTION

PET RECONSTRUCTION

If the “Reconstruction” option in the drop-down “System” menu is selected or the “**RECON**’ button pressed on the Main Interface, two-dimensional filtered backprojection (**2D FBP)** and two-dimensional ordered subset expectation maximization (**2D OSEM)** become available for image reconstruction after pressing **PET** or **PET_RECON** option, respectively. Both of these reconstruction algorithms operate on 2D sinograms created with the **FORE** algorithm (Fourier RE-binning algorithm) from the 3D data sets acquired by VISTA-CT. This algorithm permits the optimal amount of 3D data to be used in the reconstructions. Direct user access to these sinograms is described in Appendix E.

2D FBP reconstruction—Local 2D FBP reconstruction (**Figure 26**) is initiated by selecting “BROWSE” and entering

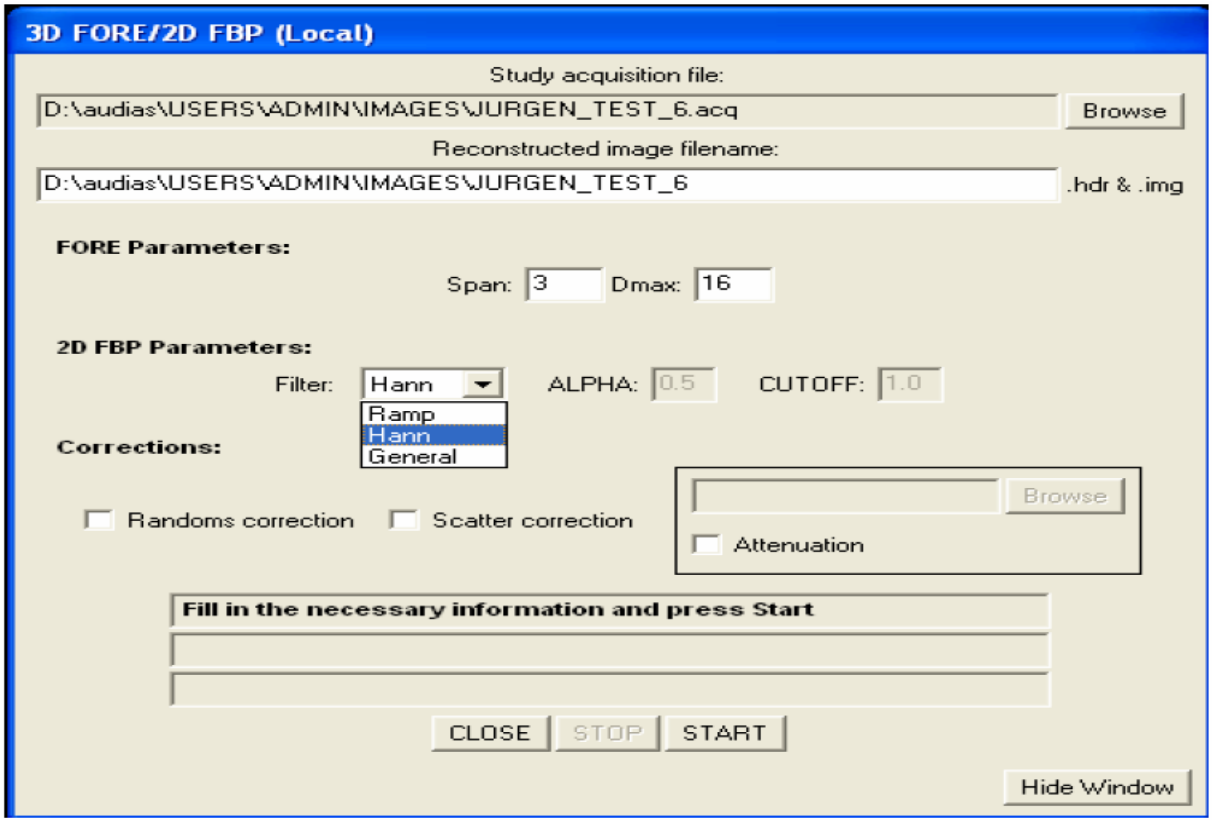


Figure 26. 3D FORE/2D FBP reconstruction menu.

the desired “.acq” filename into the Study acquisition file box. This action will automatically create a Reconstructed image filename by replacing the “.acq”

extension with the ".hdr & .img" suffix indicating that the output file is now a reconstructed image sequence rather than raw data.

Dmax (Ring Difference**)—**The VISTA detector array consists of "rings" of scintillation crystals and it is coincidences between adjacent rings that allow 3D data to be acquired. Dmax is defined as the maximum number of rings that are allowed to be in coincidence with one another. For example, the VISTA DT has 32 effective rings so that the maximum ring difference, N, is 31, i.e. 32 – 1 = 31, one ring in coincidence with the 31 other rings. A ring difference less than 31 will limit the range of coincidence lines to a smaller number but with less steep lines-of-response. Image data acquired with the VISTA DT can be reconstructed only if $N \geq 10$ and in the range $10 \leq N \leq 31$ (16 is the recommended default ring difference for the DT). The VISTA ST will accept ring difference values in the range $0 \leq N \leq 12$ since there are 13 rings of scintillators. The default ring difference for the ST is 12 since the axial field-of-view is less than the DT and none of the 3D lines-of-response are particularly "steep".

Since FBP reconstruction starts with 2D sinograms created with the FORE algorithm, you must enter values for Span and Dmax that control the FORE re-binning process.

While it might seem that one would always want the largest ring difference (to use the most 3D data), a price is paid for accepting all coincidence lines. As the "steepness" of the lines-of-response in the axial direction increases, axial "blurring" of objects in the field of view becomes more pronounced. As a result, for 3D machines with a large axial field-of-view, some upper limit less than the maximum ring difference must be selected unless axial resolution is unimportant in the study at hand. The default values for Dmax that appear when the RECON menus is selected are reasonable compromises between these choices.

Span—Span refers to the degree of axial angular compression of lines-of-response. Larger values for span will combine a greater axial angular range of lines-of-response and, ultimately, increase axial blurring. The default value for span that appears in the interface is a good choice for most imaging studies.

FBP Filter--Once the file names have been established, you may select the kind of filter to be used in the reconstruction (Ramp, Hanning,…) and the properties of that particular filter (Alpha and Cutoff). Default values are supplied for each of these parameters that under most circumstance give reasonable reconstructions.

2D OSEM reconstruction-- As with FBP, you must identify the .acq file to be reconstructed and select the FORE parameters described above in the 2D OSEM menu shown in **Figure 20**. Once the FORE parameters have been selected, you can choose the number of subsets into which the calculation is divided and the number of approximating iterations. The default values supplied on the 2D OSEM menu (DT values in Figure 27) will give reasonable (and rapid) results for most studies but you should experiment with these values to ascertain the consequences of using different values.

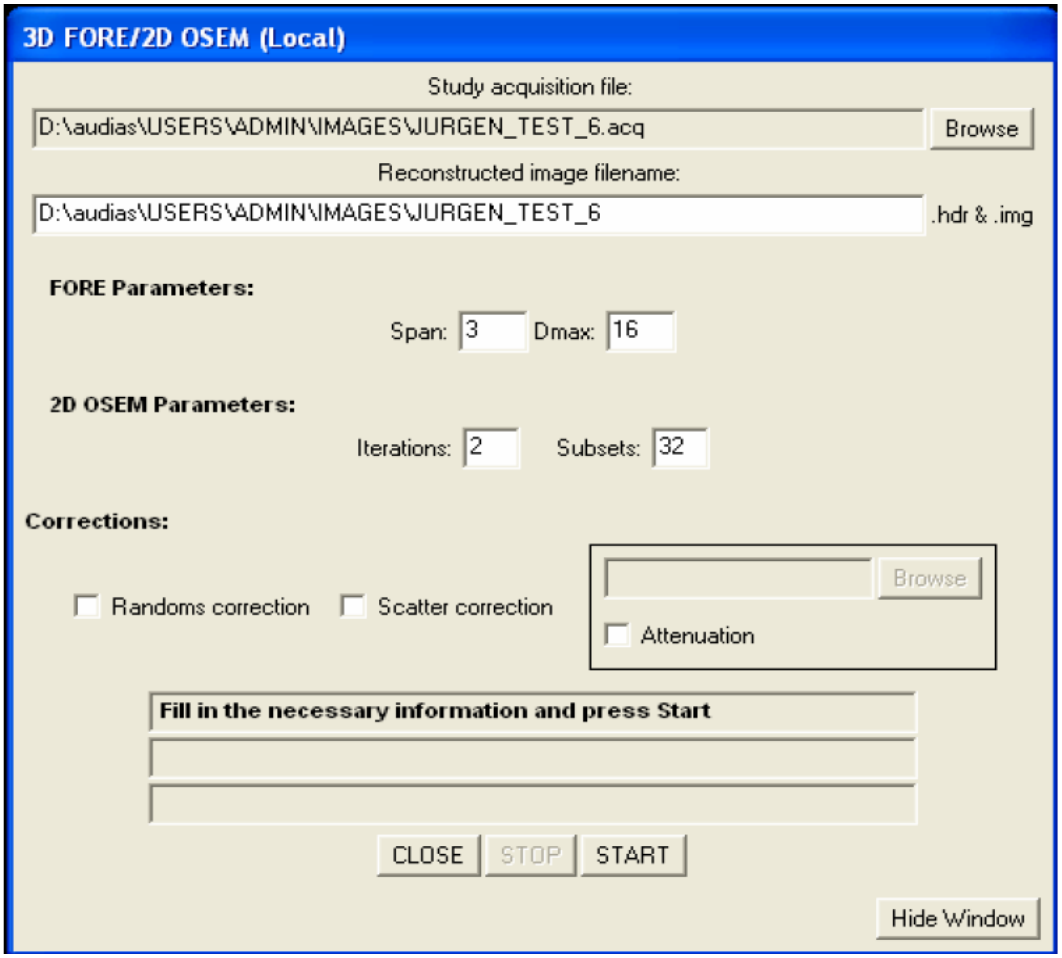


Figure 27. 3D FORE/2D OSEM reconstruction menu.

Filtered backprojection is a fast, analytical method for reconstructing an object from its projections and runs rapidly on the VISTA-CT workstation (approximately 90 seconds for a reconstruction of 61 slices including FORE). Given this reconstruction speed, FBP can serve not only as a final reconstruction method, but also as a QC procedure to check the validity of any given data acquisition when a study is finished. On the other hand, 2D OSEM gives the option of invoking "resolution recovery" but at the expense of an increased reconstruction time (albeit not a large increase: <3 mintues/61 slice data set including FORE). This difference in reconstruction times suggests a strategy where FBP is used primarily for quality control at the end of each data acquisition but where OSEM is used for final image reconstruction when there is little or no time pressure for machine access, e.g. overnight. This difference is particularly acute if the 3D OSEM (remote) option is available since reconstruction times with this algorithm are far greater than with either method provided "locally" on the VISTA-CT workstation. It should also be borne in mind that image reconstruction and data acquisition can proceed simultaneously on the VISTA scanner since image reconstruction is carried out on the VISTA-CT workstation while data acquisition is controlled by a separate data acquisition computer. Note also that 2D OSEM is

implemented on the VISTA-CT workstation and that resolution recovery occurs only in the transverse plane, not in the axial direction.

Corrections—
Three additional buttons are provided under “corrections” that allow you to choose which corrections are applied during the reconstruction process. In “real” imaging studies implementing these corrections can add unacceptable statistical “noise” to the reconstructed images or add significantly to the computational time or to the length of the imaging study itself, e.g. added time to perform the transmission scans. Scatter and attenuation in mouse-sized objects, for example, are not large effects and it is sometimes possible to ignore these corrections, which if applied, might increase image noise and the length of the scanning session without improving (or actually decreasing) quantitative accuracy. As a result, you have the option of using or ignoring these corrections as conditions permit.

Randoms correction and scatter correction are independent processes that can be invoked individually or together for any data set. You can simply check one or both of these boxes and the identified correction(s) will be made. Attenuation correction, on the other hand, requires: (1) a pre-existing transmission scan acquired immediately before the corresponding emission scan, (2) correction for scatter and (3), if needed, correction for randoms (recommended). That is, if you wish to correct an emission data set for attenuation, the scatter and attenuation boxes must be checked (and the Randoms box also for consistency). If Attenuation correction is checked and the Scatter correction box is not, or if there is no previously acquired transmission scan, reconstruction will not be permitted. Correction for attenuation proceeds by first correcting the 2D FORE sinograms for random coincidences, then for scatter and finally for attenuation. It is not possible to apply an attenuation correction without first correcting for scatter since attenuation correction of sinograms that contain scatter will lead to quantitatively inaccurate reconstructions.

Randoms Correction—Selection of this item will cause the reconstructed images to be corrected for random coincidences. A computational method is used to make this correction, rather than “delayed coincidence”, that uses the measured singles rate on each crystal and the coincidence timing window for a given crystal pair (line-of-response or LOR) to calculate the random coincidence rate for that LOR. This calculated number of random events for each LOR is subtracted from the number of events recorded for that LOR to obtain a randoms-free measurement of coincidence rate along that LOR. This random coincidences correction is applied to all LORs and removed from the data before image reconstruction.

Scatter Correction—Scatter in small laboratory animals, e.g. rats and mice, while a smaller effect than in humans subjects, still represents a significant fraction of the total events detected by most small animal PET scanners. Scatter fractions for rodent-sized test objects range from about 15% (mice) to 45% (rats) depending on instrument and energy window. The amount of scatter actually acquired during data acquisition can be substantially reduced by choosing a narrow energy window for a study, e.g. 400-700 keV, rather than the usual “default’ window of 250-750 keV, but at the expense of substantially reduced sensitivity. Conversely, a wider energy window,

100-700 keV, will exhibit higher sensitivity so that smaller amounts of tracer can be administered while preserving count rate (important when imaging brain receptor ligands) but at the potential expense of quantitative accuracy. There is no hard and fast rule about how these energy window should be set so you should experiment with different energy windows with and without applying the scatter correction routine described below.

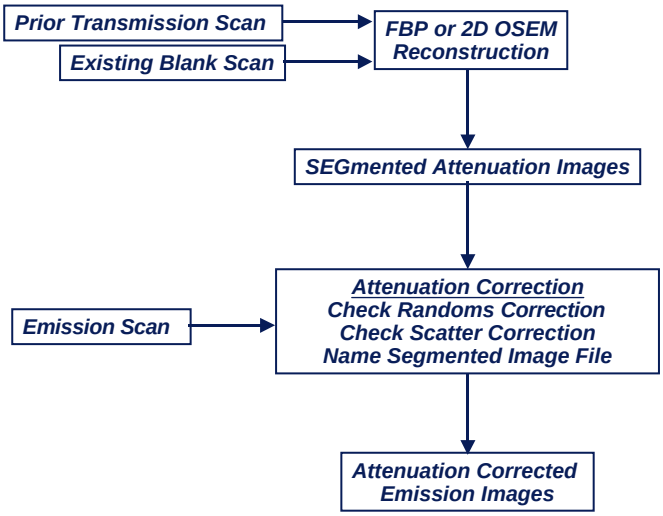
Scatter correction is applied to the FORE sinograms before reconstruction with either FBP or OSEM. Here, the count profile in each line of a sinogram is fit with a straight line that uses only points in the profile near the edges of the field-of-view for the fit, i.e. ignores the counts actually in the object. The counts represented by this best fit line are then subtracted from the count profile to remove the scatter contribution. This process is repeated for each line in the sinogram, for all 61 (25) sinograms (slices) in each data acquisition and for all data acquisitions over time (dynamic scans) or space (whole-body scans). It is useful to note that this method provides a first order correction not only for scatter but also for the LSO background present in the scanner and for multiple gamma ray coincidences that occur when imaging certain “non-traditional” radionuclides such as I-124. The supplied scatter correction can be used effectively in all of these circumstances and is recommended for routine use.

Attenuation Correction—If an emission scan has been immediately preceded by a transmission scan, the emission scan can be corrected for attenuation. First, you must submit the transmission scan to either the FBP or 2D OSEM menus as a regular .acq study where the entries in both menus are made to be identical to those that will be used to reconstruct the emission scan. These transmission data are then reconstructed into CT-like images with the selected algorithm that portray the distribution of attenuating material within the field-of-view. The User can (and should) view these attenuation images before applying the correction (using the Visualization and Analysis tools) to insure that the image data have been properly segmented. After creation, the names of these CT-like images will contain the abbreviation _seg to help identify them as different from regular emission images.

These images are calculated by first locating the most recent Blank scan (done automatically), dividing this scan by the acquired transmission scan and then computing and displaying the logarithm of these ratios. These images are segmented by setting all values greater than a predetermined threshold to unity and all values below the threshold to zero. The effect of this segmentation is to retain points in the images where attenuation is appreciable. These images in transaxial view appear to the eye to be cross sectional images of the solid objects within the field-of-view, e.g., the animal, the bed.

These segmented images are then retroprojected into count profiles for all projection angles in each slice. A sum along a projection line through the object at a given projection angle is proportional to the thickness of the object along that projection line at that angle. These thickness estimates are then used to calculate an attenuation correction factor for every projection line in a count profile assuming a water attenuation coefficient at 511 keV. This correction factor is then used to scale the

counts in the randoms and scatter-corrected count profile in the same slice and at the same projection angle to correct for events lost due to attenuation. This process is repeated for each projection line in a count profile, for all count profiles in a slice and for all slices in the data acquisition. The sequence of events required to obtain attenuation corrected emission images is schematically illustrated in the drawing below.



This method of correcting for attenuation possesses several virtues. First, because the correction is not a “measured” attenuation correction that uses the counts actually acquired during the transmission and blank scans to make the correction, this method does not directly propagate statistical “noise” into the corrected emission images. A major deficiency of attenuation correction methods that depend on radioisotope transmission sources is that such corrections are “noisy” often to the point where the improvement in quantitative accuracy from the correction is offset by the introduction of statistical noise.

Statistical noise does, however, indirectly influence the accuracy of the segmentation process so it is still necessary to “smooth” the acquired transmission data prior to segmentation. If the attenuation images are created with FBP, you should select a HANN filter for reconstruction to smooth these data. If you choose 2D OSEM, you should choose one iteration for reconstruction rather than the default value to achieve the same effect.

Finally, it should be borne in mind that this attenuation correction method assumes that the attenuation coefficient of matter within the field-of-view is water-like so that regions with differing, non-zero attenuation coefficients will not appear different from one another. While a uniform attenuation coefficient is clearly an assumption, it is a plausible assumption since small animals are comprised mostly of soft tissue along almost any given projection line.

Normalization using the FBP reconstruction menu-- You will need to perform one or more **BLANK** scans with the Ge-68 annulus either after a shutdown of the system, or periodically, in order to maintain good system calibration. The purpose of these scans is to define calibration factors that are used to normalize each line-of-response to the same apparent sensitivity for each energy window. Since there are a very large number of these lines, these scans of the Ge-68 annulus must each be carried out for extended periods, e.g. 12 hours on more. Once these data sets are acquired, one for each energy window, the sensitivity correction factors for each crystal pair are re-calculated and stored as a new look-up table that will be used until the next update.

To use this feature, an “artificial” user named “QC” (for “quality control”) initiates a very long **BLANK** data collection through the New Acquisition Protocol interface. This user name “QC” is reserved exclusively for this normalization procedure and should never be used for any other data collection.

When this collection is done, user QC selects the 3D FORE/2D FBP menu in **Figure 26**, supplies the study acquisition filename and starts the “reconstruction”. Since, however, this file was generated by user QC, the data will not be reconstructed. Instead, when this computation is complete, a new table of normalization factors will be created that replaces the old table and that will be used from then on until replaced by data from the next **BLANK** (normalization) scan. These normalization factors do not depend on the other items listed in the menu and only a “Study acquisition file” name must be entered. When the “START” button is pushed, the other entries are ignored. Note that no output is produced during calculation of these normalization factors: the process simply runs to completion and STOPs.

CT RECONSTRUCTION

If the “Reconstruction” option in the drop-down “System” menu is selected or the “**RECON**’ button pressed on the Main Interface and then, the User presses **CT** or **CT_RECON** option, respectively, the Reconstruction Interface will be shown (Figure 28).

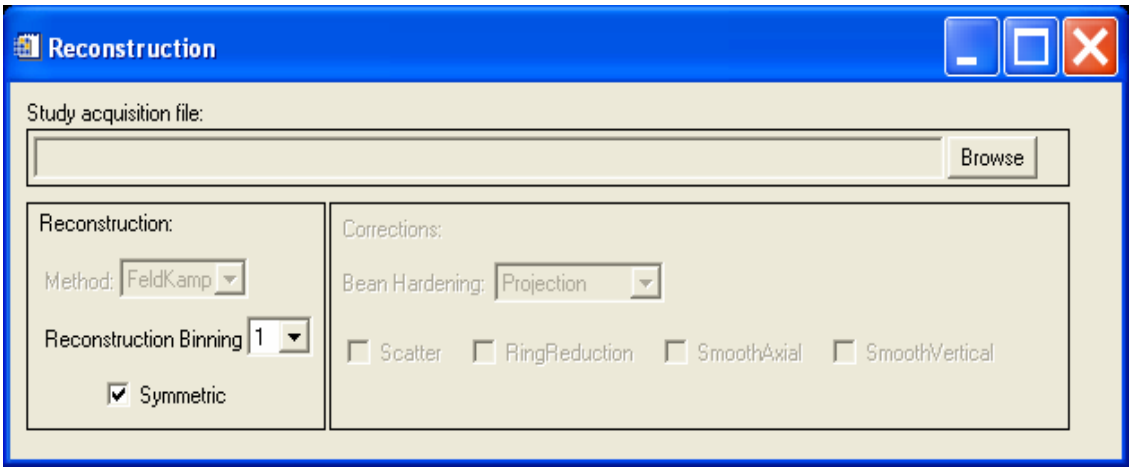


Figure 28. Reconstruction Interface (CT).

Pressing **Browse** button, the User can select an acquisition parameter file (extension “act”) to reconstruct the image acquired previously. After this action, the Reconstruct interface will look as Figure 29 if the number of beds of acquisition was greater than one and as Figure 30 if the acquisition was of a single bed.

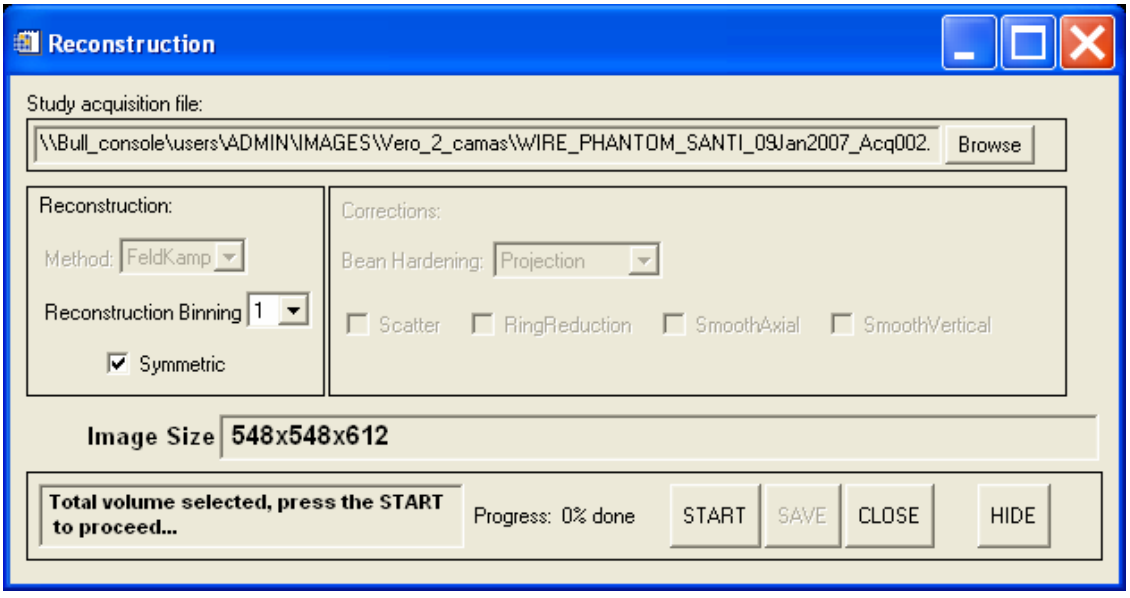


Figure 29. Reconstruction Interface (CT, multiple beds).

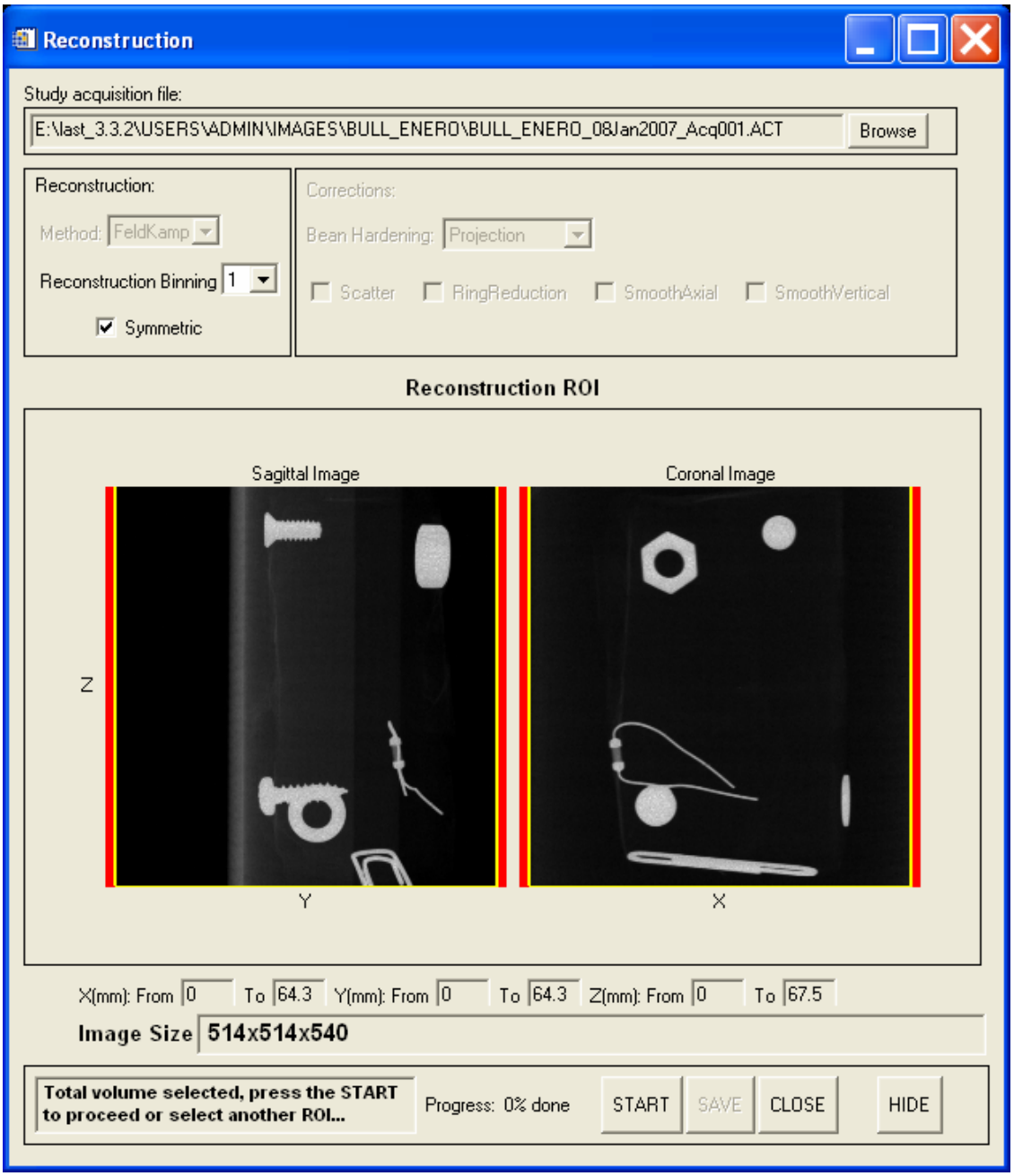


Figure 30. Reconstruction Interface (CT, a single bed).

The difference between Figure 29 and Figure 30 is that the User can see two images (Sagittal and Coronal Images) of the image that he/she desires to reconstruct. In addition, just in acquisitions of a single bed, the User can select a ROI of the image. To do this, the User places the mouse on any of the images (Sagittal or Coronal), presses left button and without releasing (a yellow rectangle, which represents the selected ROI, will be shown), moves the mouse to the right position (Figure 31).

Text fields **X(mm)**, **Y(mm)** and **Z(mm)** will shown the limits of the image which will be reconstructed and **Image Size**, the size of the final image in pixels.

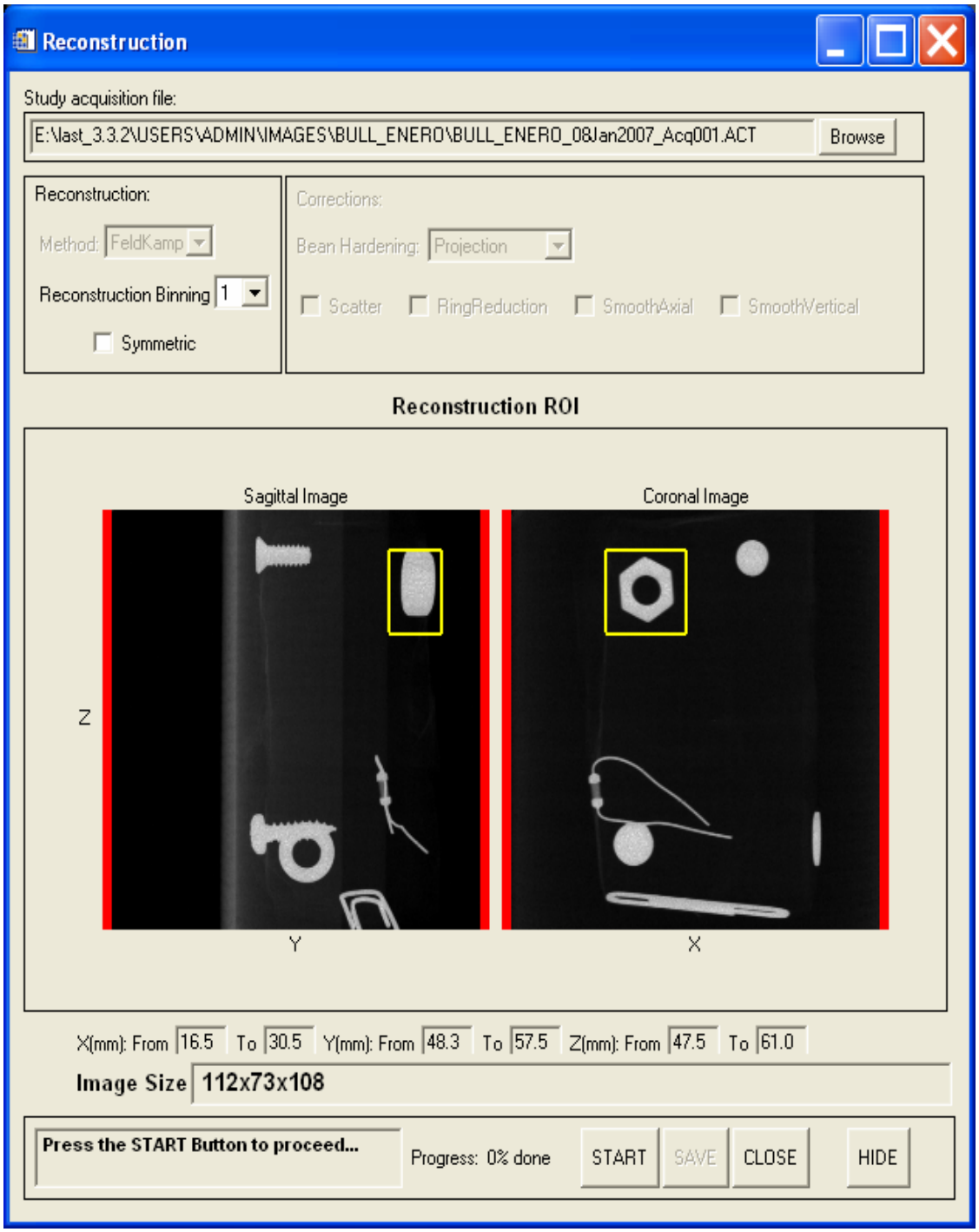


Figure 31. ROI selected.

There are several options which aren´t available in this version: **Method** of reconstruction, **Corrections** (Bean Hardening, Scatter, Ring Reduction, SmoothAxial and SmoothVertical).

The binning of the reconstruction can be modified through **Reconstruction Binning** droplist (possible values: 1, 2, 4, 8 and 16). Increasing binning will reduce reconstruction process duration, size of final image but will make worse spatial resolution of the image.

If the User checks **Symmetric**, the ROI will be symmetric along axial axis regarding the center of the two images (Sagittal and Coronal), so the ROI's in both images will be the same (Figure 32).

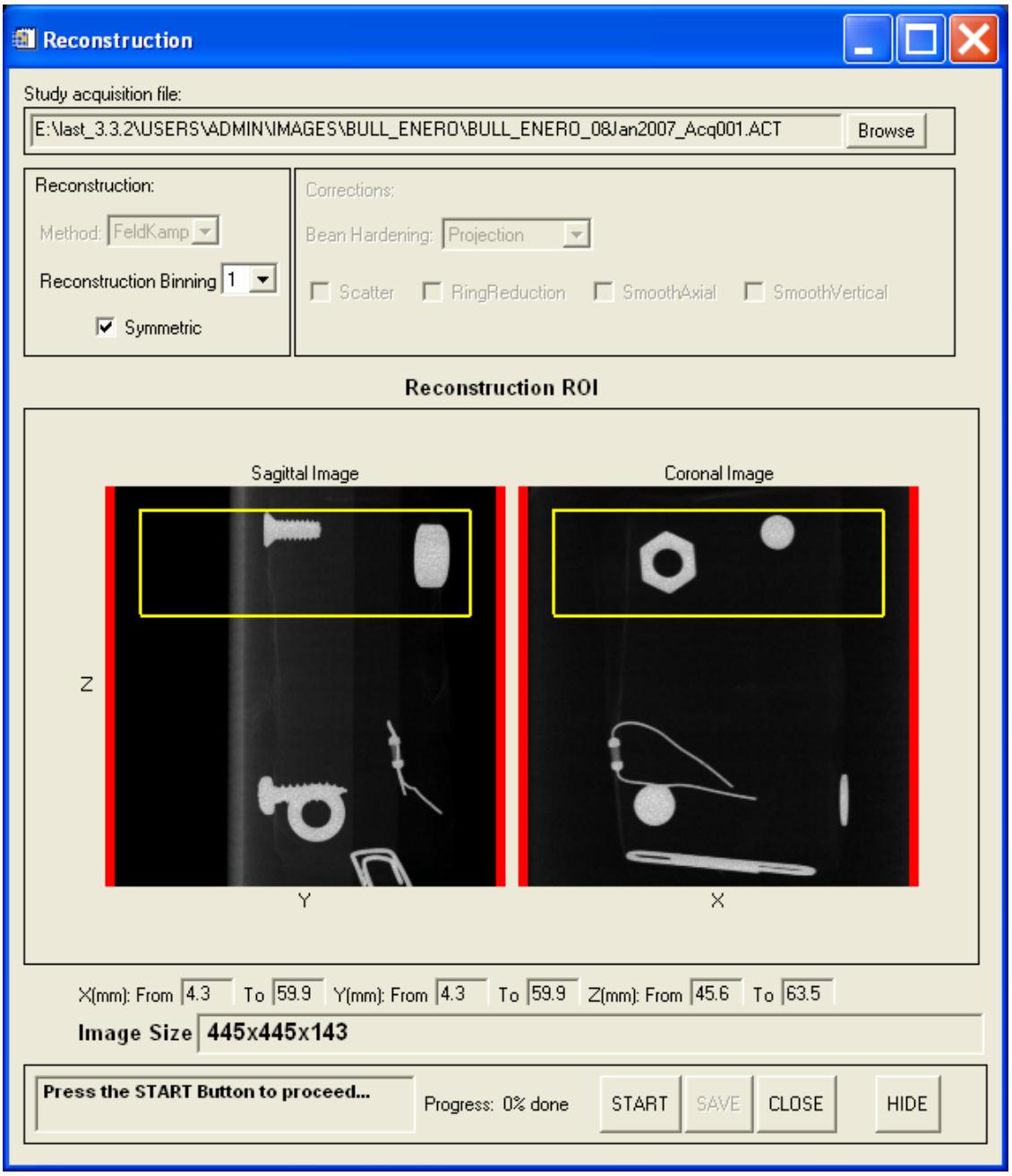


Figure 32. Symmetric option.

To start the reconstruction, press "**Start**" button. The percentage of reconstruction progress will be shown next **Start** button (Figure 33).

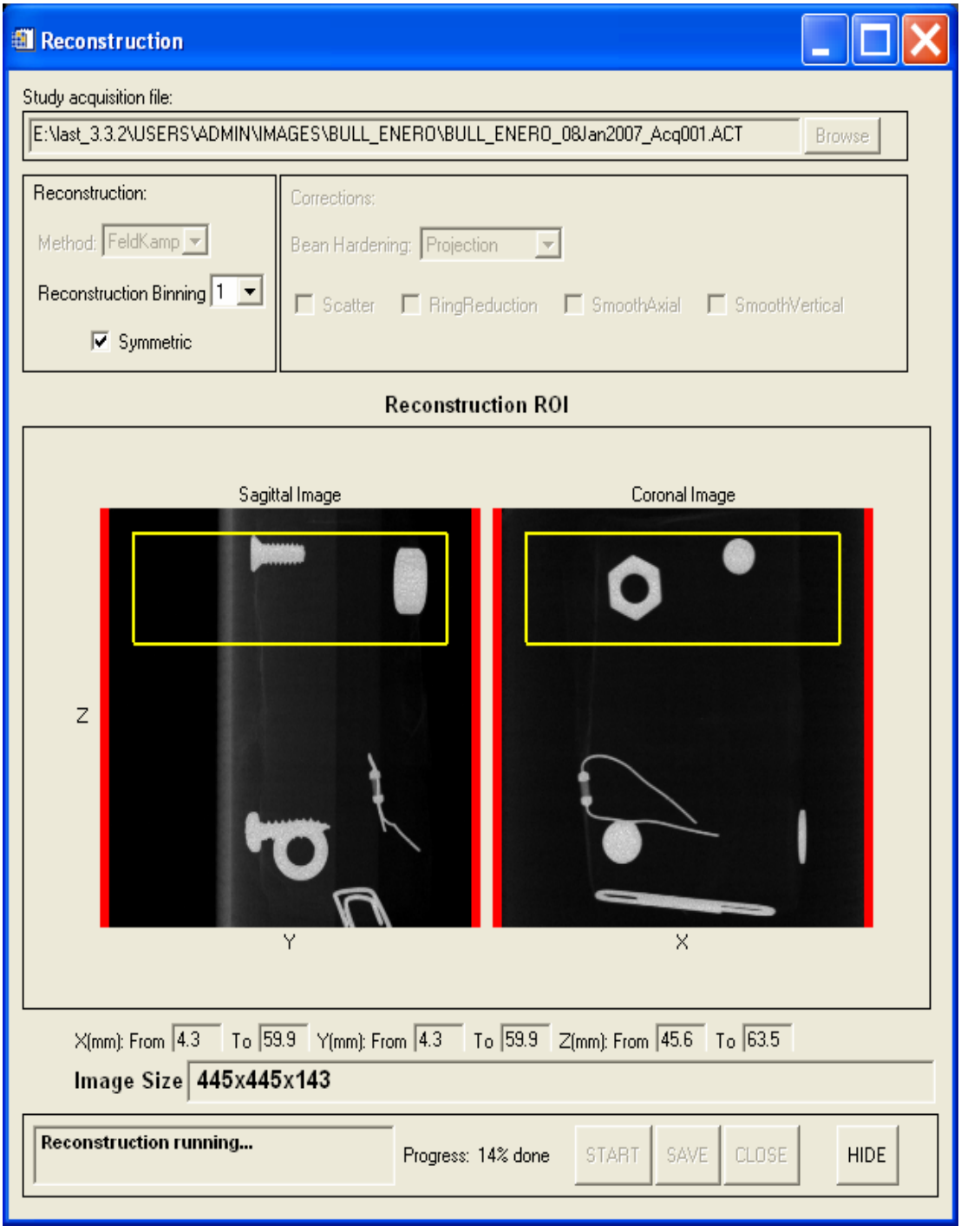


Figure 33. Reconstruction in progress.

While the acquisition is carrying out, the User cannot abort the process but can continue with other tasks after pressing "**Hide**" button. To go back to this panel, press **CT** option in **Reconstruction** (System) or **CT_RECON** option in **RECON** (toolbar).

When the reconstruction has finished, the image will be shown in VISTA-CT main interface (Figure 34) and the User can save by pressing "**Save**" button or "**Save**" option of menu "**File**' (VISTA-CT main interface). If the User doesn´t save the image, it will be lost. This is another difference with PET reconstruction where the image is saved automatically but the User doesn´t select image name as in CT reconstruction.

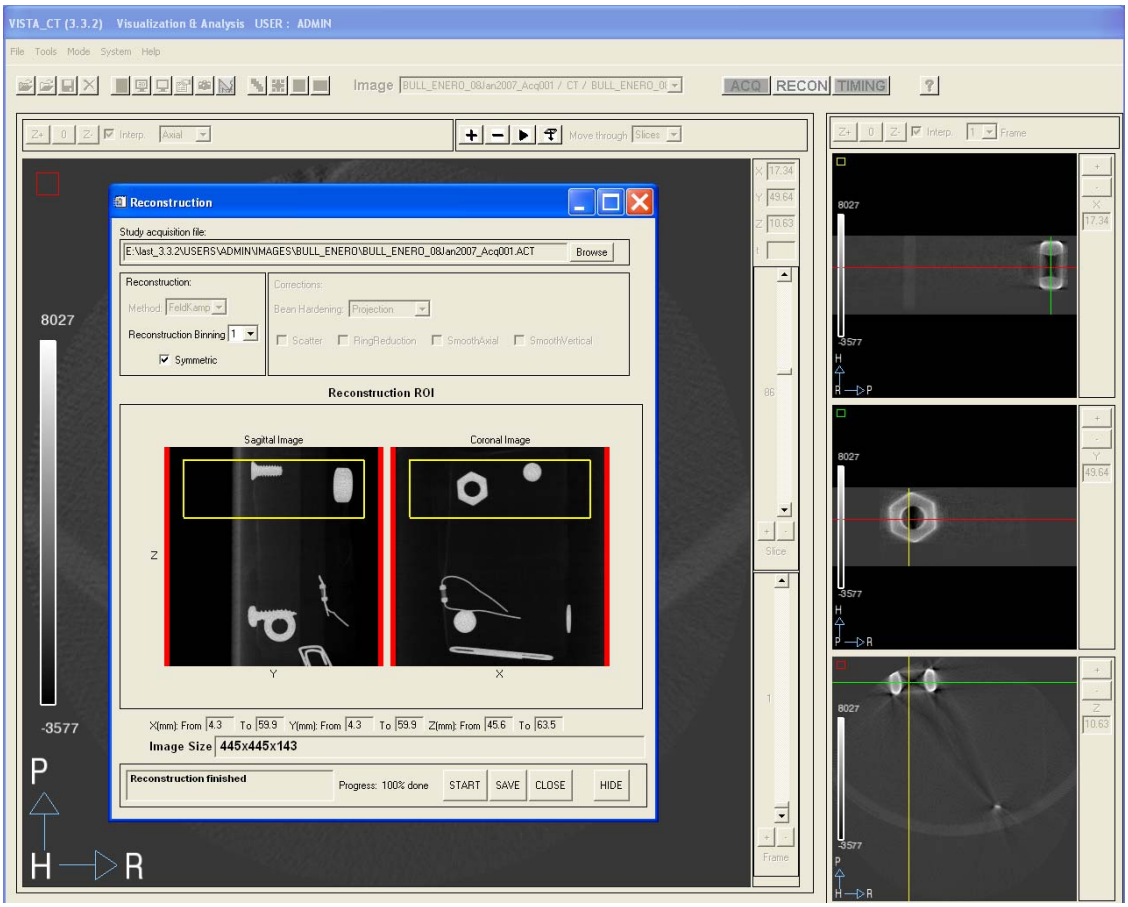


Figure 34. Reconstruction finished.

To close this interface, press '**Close**' button.

TIMING

In addition to ACQ and RECON, **TIMING**, can also be selected from the Main VISTA-CT Interface that produces the menu shown in **Figure 21**.

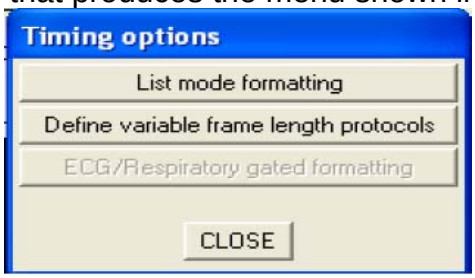


Figure 21. TIMING options available through the Main VISTA-CT Interface.

The purpose of these timing options is to allow you to retrospectively reformat LIST mode data sets into sequences having User defined frame durations and to define protocols that allow variable frame rate dynamic studies to be acquired according to your specifications.

LIST mode formatting—When this item is selected from the "options" menu in **Figure 21**, the screen shown in **Figure 22** appears. The User identifies the List mode data set with the BROWSE function but the output filename continues to have the appended ".acq" designation. This output data set is still in .acq form since LIST mode reformatting only transforms the data set into raw data blocks with USER specified durations. Once this sorting operation is completed, the reformatted raw data set can be submitted for **RECON** with any of the available methods.

Figure 22 shows the List mode reformatting menu after the User has selected the List mode data set to be reformatted, the output file name has been created and the User has selected an already existing dynamic protocol for formatting (named "Rat-Brain…) from the protocol name file. The BROWSE functions are inactive showing that the algorithm is running and that at this moment, about one-third of the data have been processed. When reformatting is complete, the CLOSE button becomes active and the User can leave this menu to continue processing this data set.

If there were no pre-existing protocol with the variable frame durations needed by the User, the User would first select "Define variable frame length protocols" from the menu shown in **Figure 21**. This selection yields the menu shown in **Figure 23**.

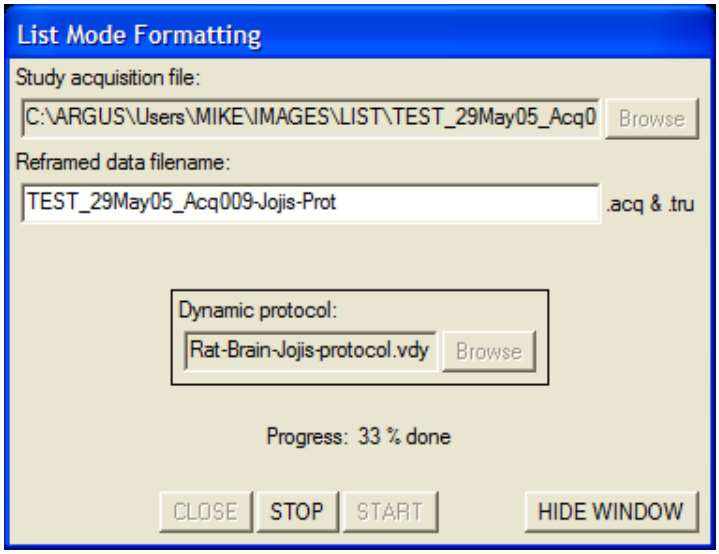


Figure 22. List Mode Formatting menu.

Define Variable Frame Length Protocols—If this item is selected from the TIMING menu, first enter a descriptive name for the variable frame length protocol about to be created.

Since these protocols can be easily retrieved by name, they should be given names that are associated with the study type and investigator (for example) that are easily remembered and/or recognized.

The procedure for filling out the protocol "form" is illustrated in **Figure 23**. You can define up to 9 different time "blocks" where each block can contain a different number of frames with a given (but different) frame duration. In the example shown in **Figure 23**, 6 has been entered for the number of frames in time block #2 and 30 seconds for the length of each of these frames. This means that after 120 seconds (after completing acquisitions directed by time block #1), a series of 6 consecutive frames will be acquired, each 30 seconds long. At the end of this interval (300 seconds after the start of the study= 120 + 180 seconds), control will pass to the third time block and so on until all filled-in time blocks have been exhausted.

For convenience, the total amount of time spent in each time block is shown at the right of the menu and is continually updated as you fill in the numbers. The sum of these times, the "total study duration" is shown at the bottom of the form and is the time required to execute the entire protocol. This feature, which is also continually updated with each new entry, is useful in that you can experiment with different time entries in each block and use this sum to insure that the total study duration is not excessive.

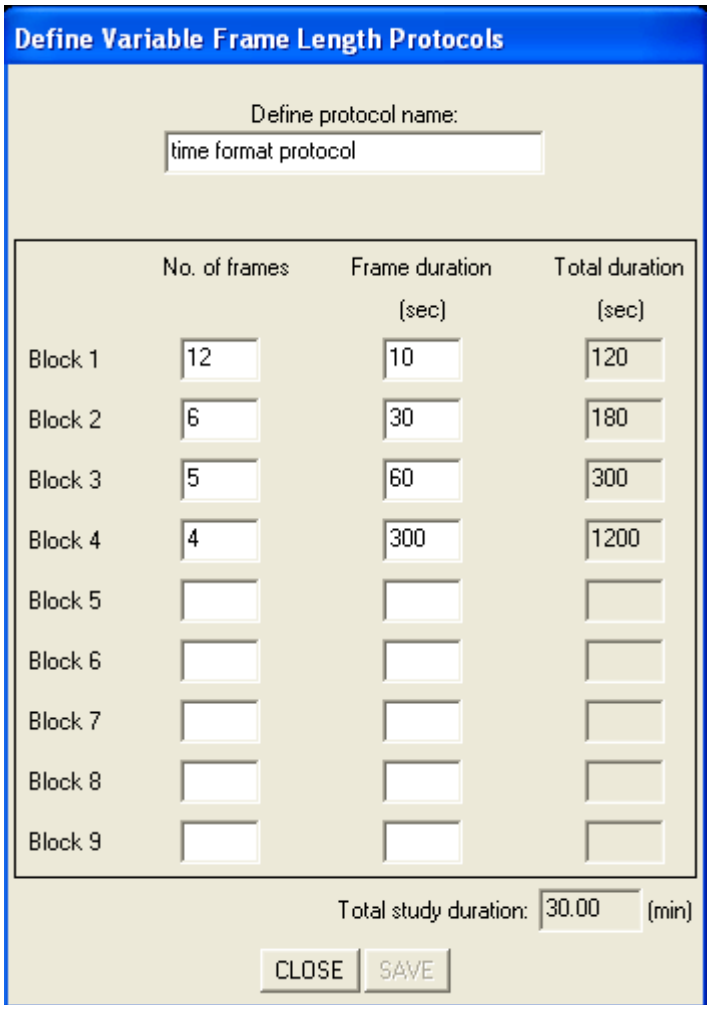


Figure 23. Define Variable Frame Length Protocols menu.

Protocols defined in this way can be “called” from the New Acquisition menu to guide a variable frame rate acquisition or, as shown here, called to guide reformatting of LIST mode data prior to reconstruction.

VISUALIZATION AND ANALYSIS

After a raw data set is reconstructed, you can utilize the **File, Tools** and **Mode** items in the VISTA-CT toolbar to analyze and display these images.

File menu

Image input/output:

Clicking on **File** will produce a drop-down menu with Open, Import, Close, View, Save, Save As, Close All and LogOut.

Clicking on Open will allow the User to select the file for display. Image files are always opened with ***File->Open*** button. The opened image file will be written to the *image stack*, that is the group of images that are loaded from VISTA-CT (maximum 15 images).

The ***File->View*** button is used to select which image from the stack is on display.

Any image from the image stack can be closed using ***File->Close*** button, selecting the right image from the button list.

The ***File->Close All*** button is used to close all the images that have been opened. The ***File->LogOut*** button allows the user to finish the session.

The ***File->Import*** button is used to open images that have been stored in other formats, such as DICOM or RAW.

When ***File->Import->DICOM*** button is pressed, the user is prompted to select a single image from the folder where the whole DICOM image series is stored. The system will search for all the images belonging to the same series and load them in the image stack. When ***File->Import->RAW*** button is pressed, the window displayed in Figure XXX will appear.

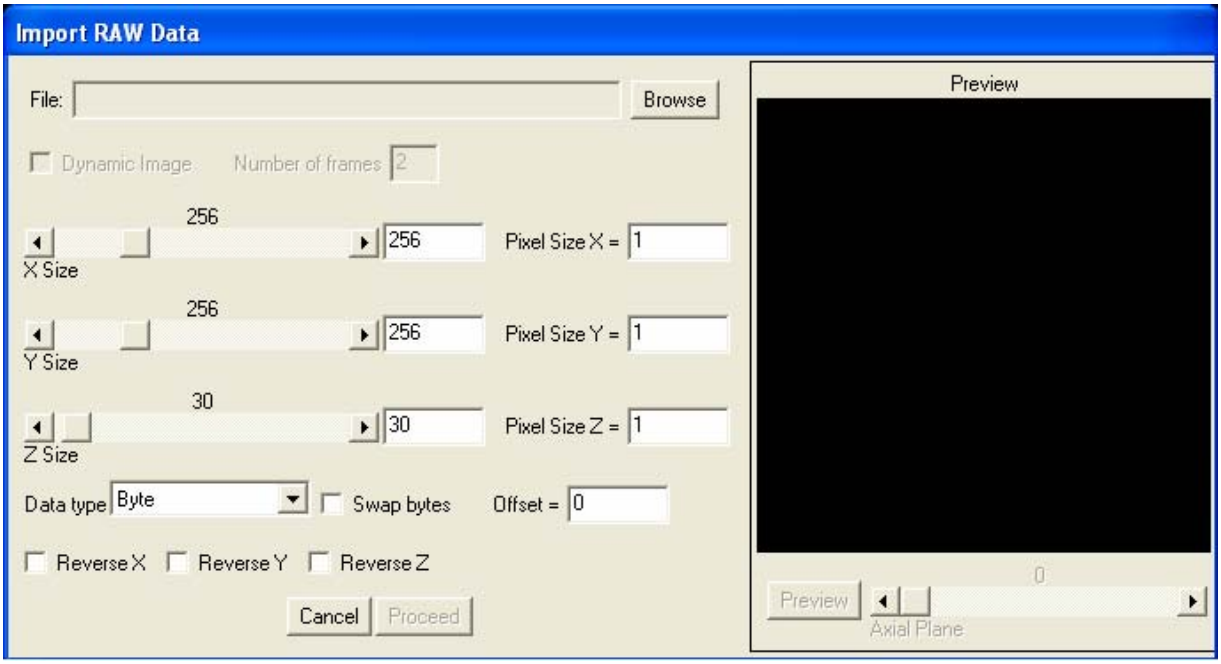


Figure XXX. Import RAW data menu.

RAW images are those stored in a single file that only contains pixel values. In order to properly read a RAW file, the user must select the image file using Browse button and insert the X, Y and Z image dimensions in xsize, ysize, zsize fields. Pixel values data type, byte-swapping option, byte offset or pixel sizes must be also selected. Preview button allows displaying how the image 2D slices will be read using those user defined values. PROCEED button will finally load the resulting image in the stack.

DICOM--The “Save As” item in the File menu allows reconstructed images to be exported in **DICOM** format (**Figure 25)** by selecting the **File->Save As...->DICOM** path.

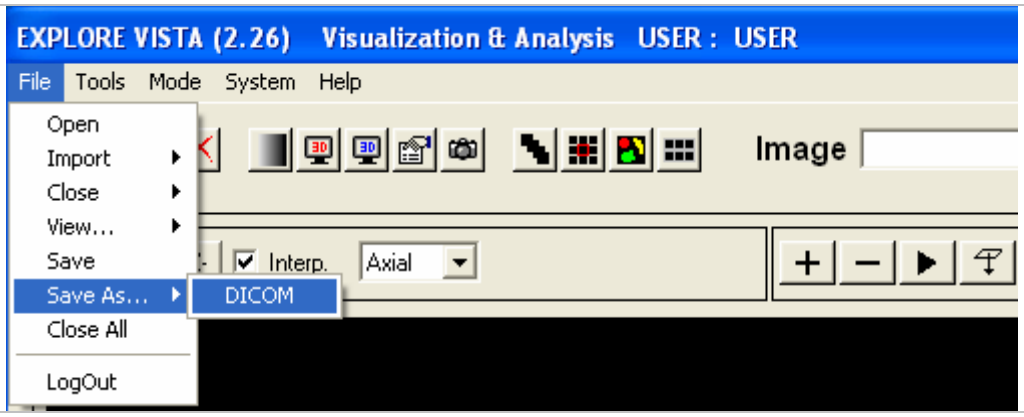


Figure 24. Exporting to DICOM.

When this option is selected, you must create a folder in which to save the images and a name for the images in that folder. All these files will have the extension **.dcm** added to the name and these will be appended with 000, 001, 002, ..., 060 to distinguish images from one another.

Once a file is selected with Open from the File menu, it is immediately loaded and displayed to the User on the screen shown in **Figure 21** in the default “Stack” mode. There are **four** different visualization modes inside the Analysis & Visualization Interface: Stack, Montage, Dual View and Analysis. You can switch freely between different modes at any time using the Mode menu and icon combinations that are always present.

The following features are common to all the Analysis & Visualization modes.

Tools menu

Window / Level—This button opens a floating interface to manipulate the brightness (level), contrast (window) and color palette of the displayed image.

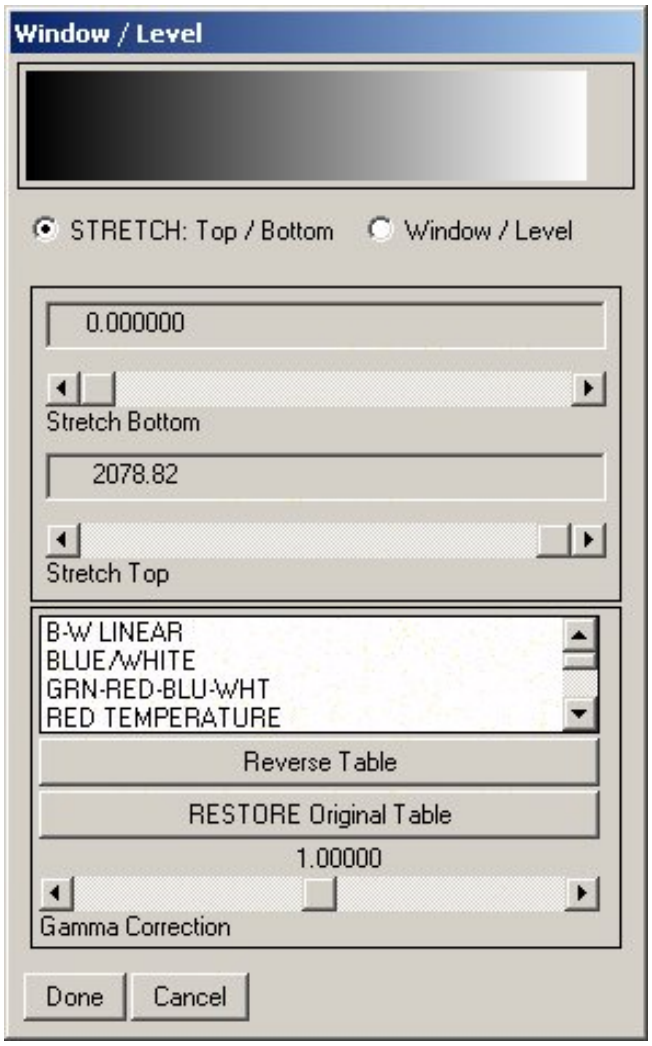


Figure XXX. New Figure Window / Level.

Volume Rendering Tool— Pressing the RENDER button allows creation of a three-dimensional representation of a two-dimensional image stack. The rendering "quality" and type can be selected. The difference among the three quality options is the size of the rendering window (the size of the volume to be rendered) and consequently the rendering quality and time needed to render. Rendering type can also be selected. In **Figure 25**, for example, the User has selected type "MIP" or "maximum intensity projection" as the rendering algorithm.

The render manipulation is similar to the animation interface. Every time a rendering is created, the previous version is deleted from memory. The tools described above

are available in all modes. Details for every mode are explained in the following pages. The resulting render can be saved as a standard AVI movie using SAVE button. If *select AVI options* is checked, the user will be prompted to select the quality of the film and the compression method used when creating the movie file.

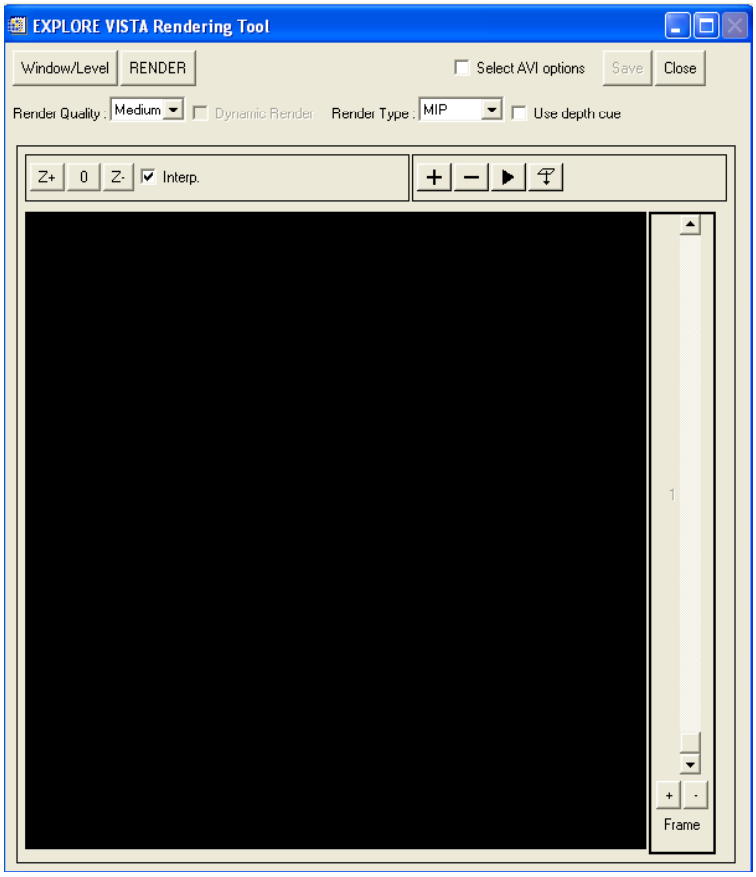


Figure 25. Rendering tool.

Interactive Render.- The Interactive Render button opens a floating interface where a three-dimensional representation of the currently displayed image created. Unlike the volume rendering tool, the image can be freely rotated by moving the mouse with the left button pressed. The rotation can also be restricted to one axis. The rendering quality and type, zoom, image interpolation and window/level settings can be modified. The render window and the tri-planar viewer are synchronized, and OV axes can be displayed on the render.

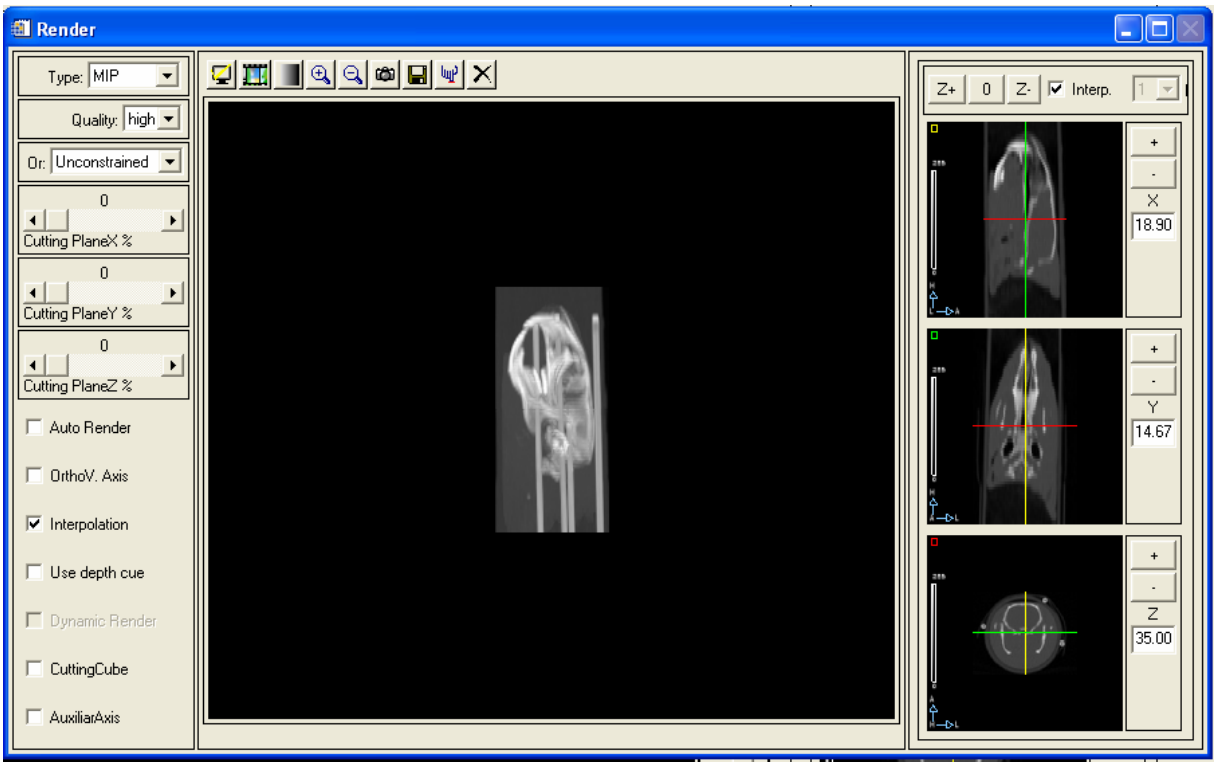


Figure XXX. New Figure Interactive Render.

Interactive render tool allows creating movies of the rotating render by clicking on Cine button (New Figure). The rotation axes, total rotation, angle step and total number of projections can be selected, and pressing CONTINUE button the movie will be rendered. The result is displayed in the same interface as in the standard render tool (New Figure), and can be saved form there.

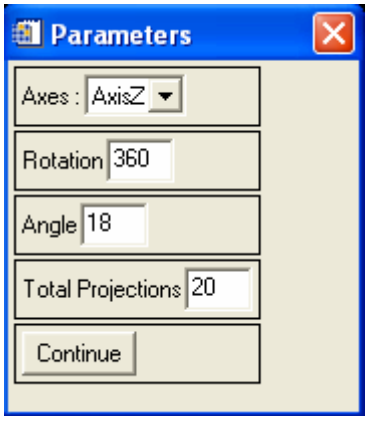


Figure XXX. New Figure.

Reformat.- The Reformat button opens a floating interface that allows the user to apply different geometrical transformations (translation, rotation, scale, affine, mirror) to the image currently displayed. PREVIEW button shows the result of the transformation in the OV, while PROCEED finally reformats the image according to the selected transformation parameters. Interpolation type (Trilinear or Nearest Neighbor), background pixel value and output sizes can also be modified.

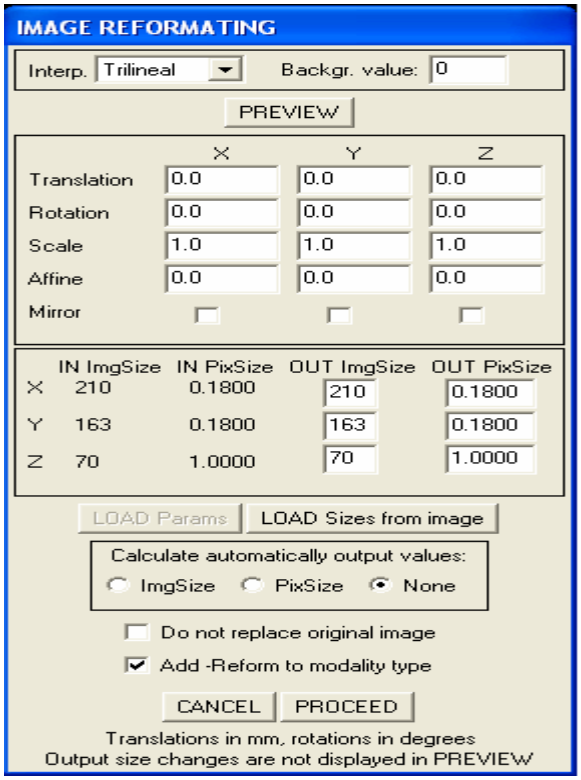


Figure XXX. New Figure Reformat.

Image Info.- The ImageInfo button opens a floating interface where image information is displayed. The image information is classified into six groups:

-Patient: patient demographic info (id, sex, age..).
-ImgData: features related to how image values are represented.
-ImgInfo: general information about the image.
-StudyInfo: properties related to the study.
-SerInfo: properties related to the image series.
-FrameInfo: temporal information only displayed for dynamic studies.

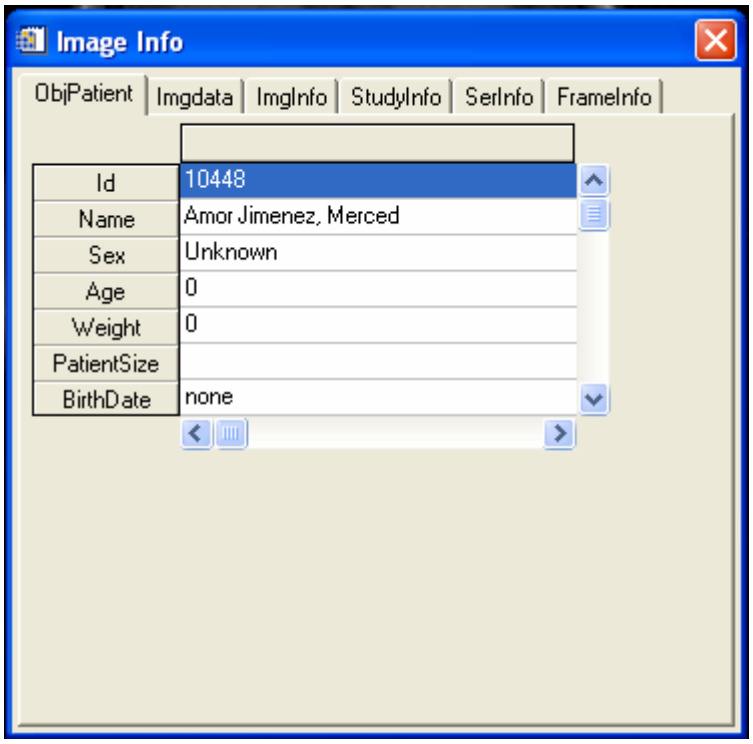


Figure XXX. New Figure Image Info.

Snapshot.- This tool allows the user to capture one of the current image views and save the contents to a TIFF (Tagged Image File Format) file. The picture filename must be selected using BROWSE button. The capture will be saved when EXPORT FILE button is pressed.

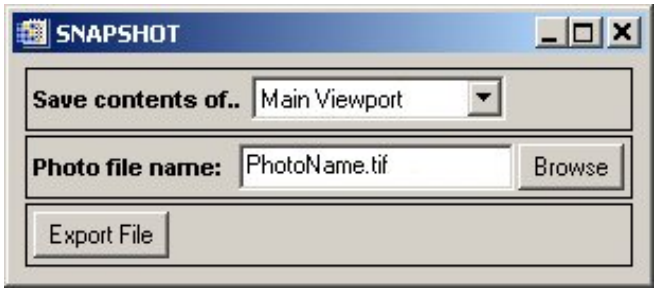


Figure XXX. New Figure SnapShot.

Stack Mode:

In this mode image "slices" (slice = anatomical image) are displayed on a single window and also on the tri- planar viewer (called Ortho Viewer or OV) shown in **Figure 26**. You can freely navigate through the 3D images in the OV by clicking on any of the three views. Buttons in the main window **(Figure 27)** allow the image to be zoomed (+Z larger, 0 none, -Z smaller) and to change the view (**Axial, Coronal** or **Sagittal**). If the displayed study is dynamic, the **Frame** slider will also become active allowing you to move from one anatomical data set to the next through time (frame = moment in time).

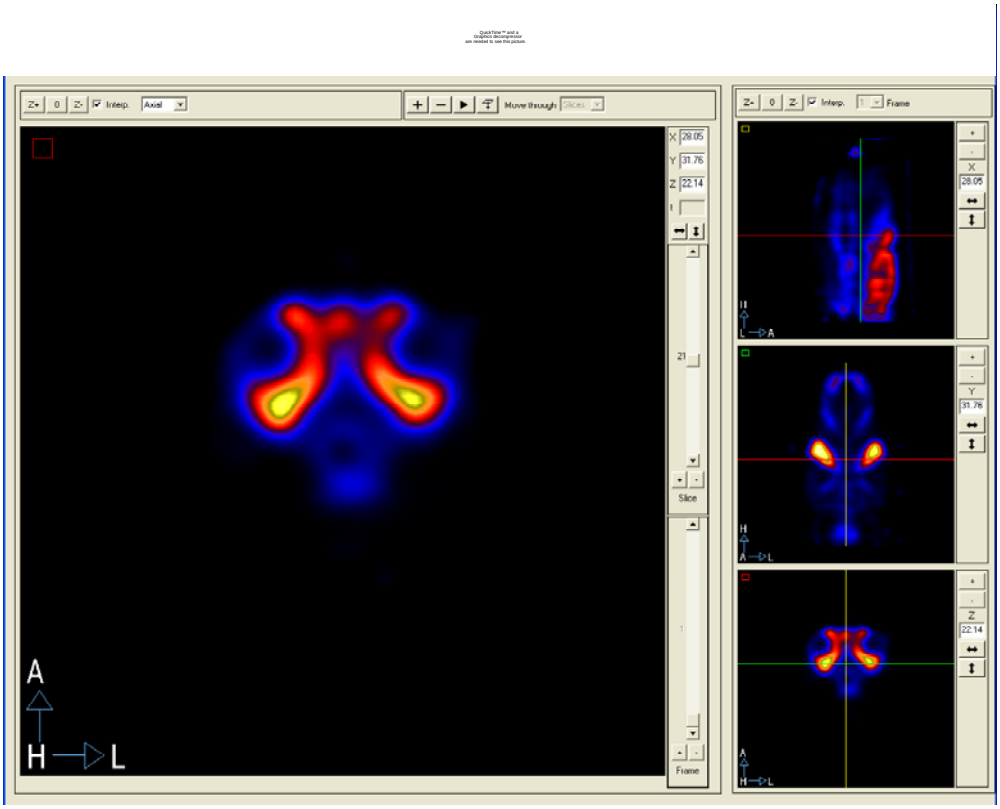


Figure 26. Stack Mode

Figure 27. Visualization controls for zoom, interpolation and current view.

A Cine display of all slices or frames can be played or stopped (right arrowhead) and its speed can be increased (**+**) or decreased (**-**) with the controls shown in **Figure 28**. Both main and OV viewing tools have zoom controls (**Z+** bigger, **0** none, **Z-** smaller) and image interpolation-**Interp.**

Figure 28. Cine tools.

You can also move through the slices (or frames for dynamic images) using the down arrow icon shown in **Figure 28**.

Montage Mode:

In this mode **(Figure 29)** there is an OV on the right of the interface. On the left all the slices are displayed in a single window. This window has Zoom and

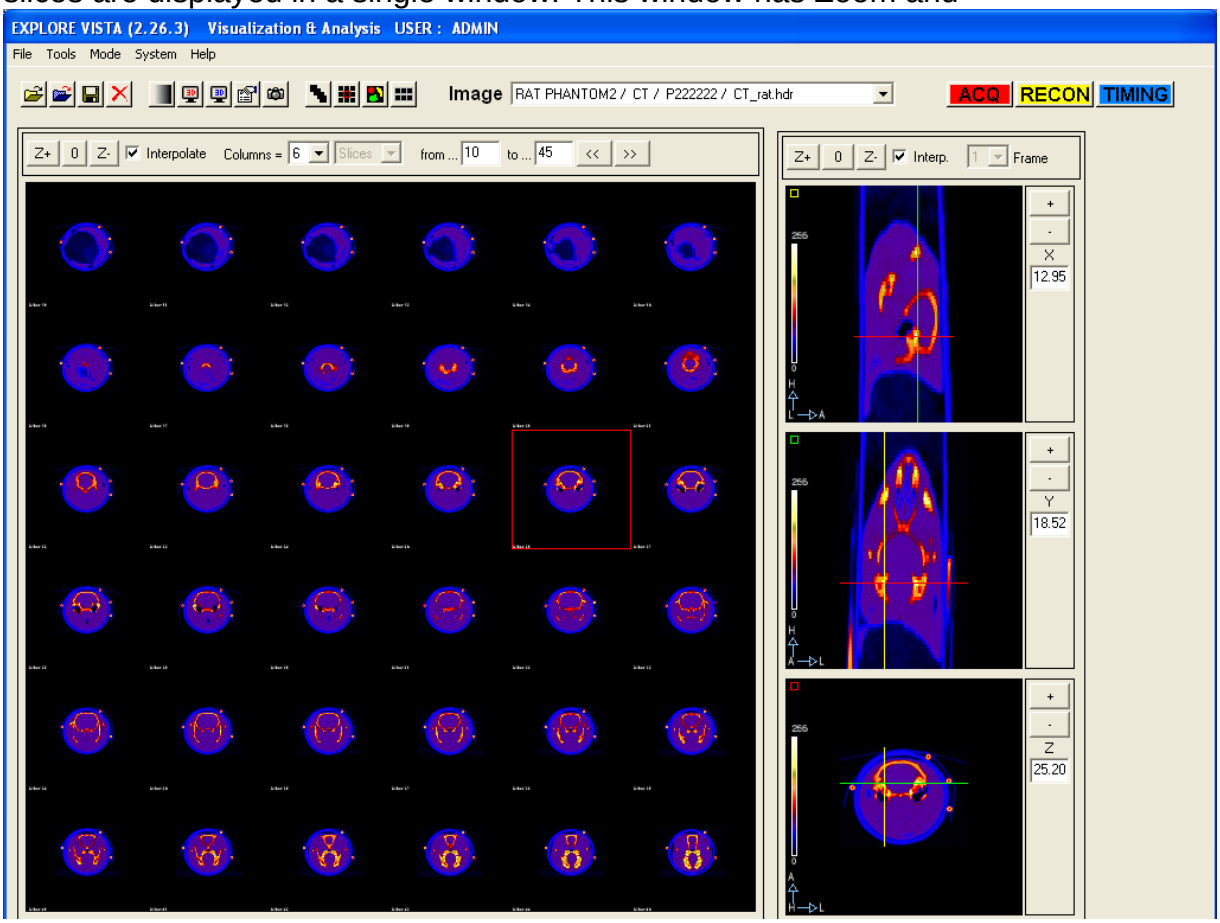


Figure 29. Montage Mode showing anatomical slices through object

an Interpolation option and controls that allow the layout of image columns on the display to be modified by the User (visible just above the Montage display). A droplist allows you to switch the main viewing window from displaying multiple anatomical **slices** (**Figure 29**) to displaying a sequence of dynamical **frames** (same anatomical slice over time) like those shown in (**Figure 30**).

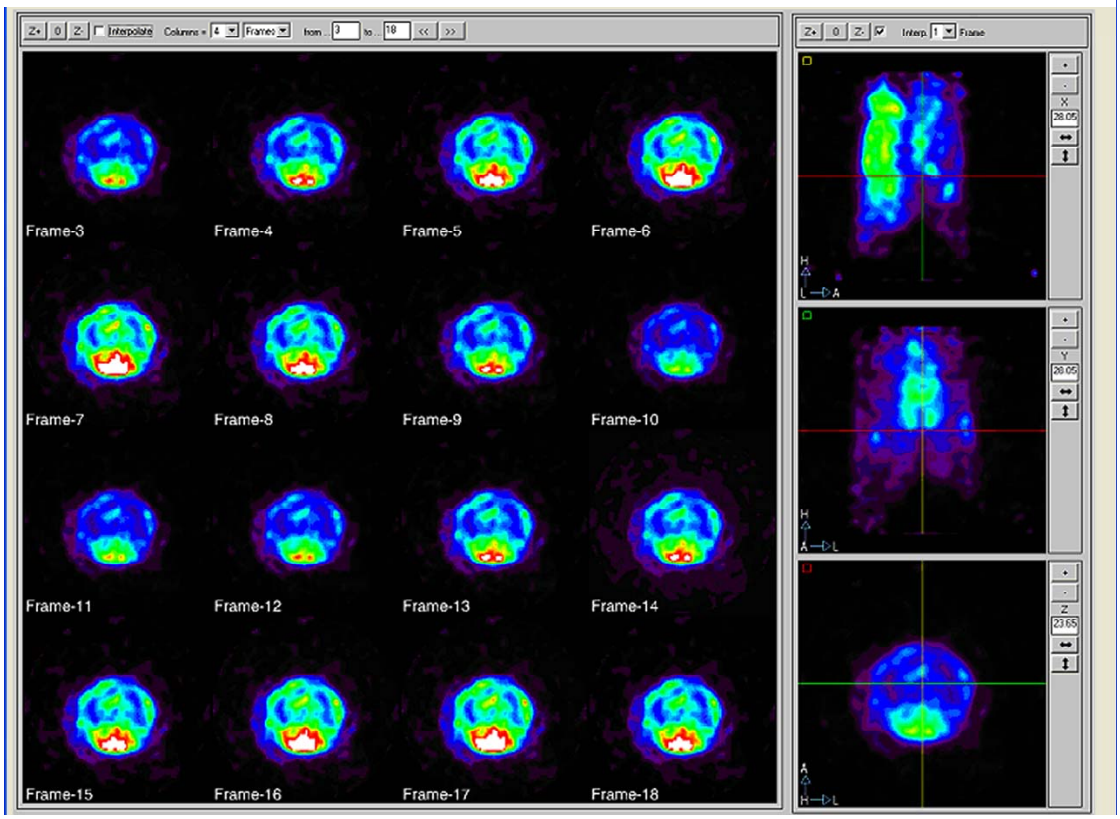


Figure 30. Montage mode used to display a sequence of dynamic frames.

Registration Mode:

This mode has two tri-planar ortho-viewers, OV1 and OV2 **(Figure 31),** to display simultaneously two sets of image data. In this mode the buttons inside the File and Tools menus are duplicated allowing you to interact with each tri-planar viewer independently. Dynamic images can also be displayed and the current frame can be selected using the frame droplist.

Registration Tools are also available and include:
Markers registration-- This registration method requires you to introduce at least three correspondent positions in both image sets and then calculates the transformation matrix.

MI registration--Using this procedure, the transformation matrix is calculated automatically with almost no User interaction.

Join/Unjoin 3D viewers--When both images are registered, the 3D viewers can be joined. The axes will be updated at the same time in both.

Fused display--This button starts the fusion interface that creates a new image combining information from both registered images.

Arithmetics.- This button opens a floating interface that allows different arithmetic operations between the two images. Both images can be combined using different operators (add, subtract, multiply, divide, raise to the power of a number), and every image can also be modified with a scalar value (maximum, mean value of the image or a scalar introduced by the user). DO IT button will calculate the result and display it in the selected OV.

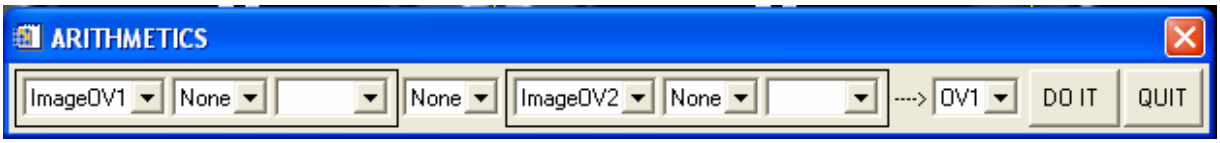


Figure XXX. New Figure Arithmetic.

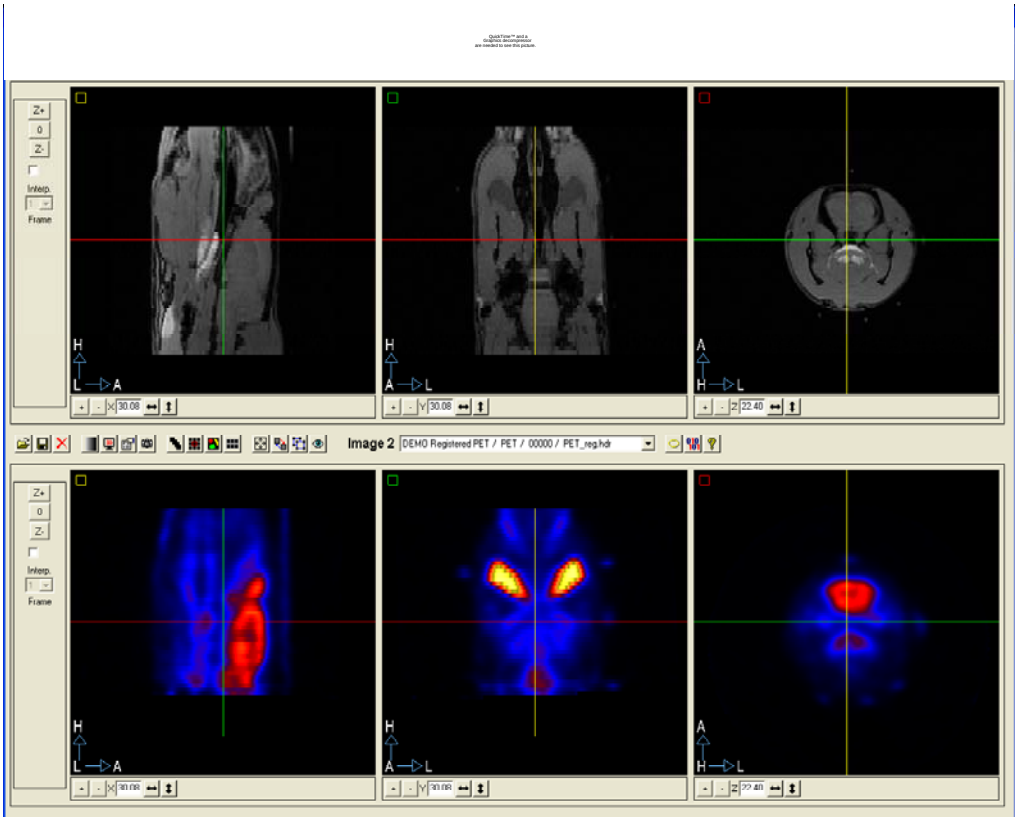


Figure 31. Dual View Mode

Each OV contains three cursors that can be moved by dragging or simply by moving the mouse icon to a point in an image and clicking. With this action, the cross-hairs in the active image will be immediately re-located to the same mouse icon position in both upper and lower image displays. In this way, a location identified in one image set can be transferred to the second set.

Although the Dual Viewer can be used to view any two sets of image data, the Dual View mode is primarily intended for comparing two spatially registered data sets. If, for example, a spatially registered CT data set is displayed in OV1 and the corresponding PET study in OV2, the anatomical information in the CT study can be used to help identify the location of concentrations of activity in the PET study.

Analysis Mode:

The **Analysis** main interface is similar to **Stack** mode. The procedure to segment and analyze one or several regions proceeds by clicking on the **Analysis** button **(Figure 32).** Two floating interfaces will appear over the main screen: **ROIs** (Regions-Of-Interest) and **SEGMENTATION TOOL**. The **SEGMENTATION TOOL** handles the selection of segmentation methods whereas the rest of functions are controlled by the **ROI** interface.

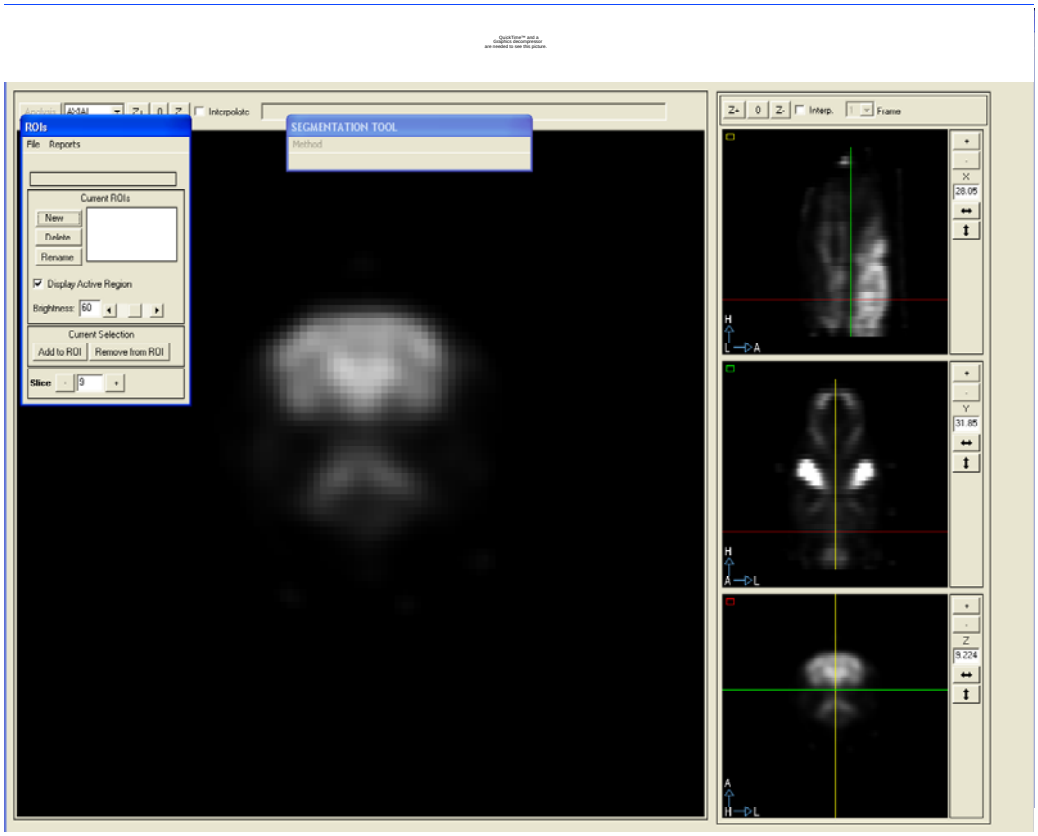


Figure 32. Segmentation floating windows over VISTA-CT Analysis Mode

How to begin a segmentation session:

Before beginning a segmentation, a new region-of-interest ***must first be named*** by pressing the **New** button in the **ROI** floating interface, and typing the name of one or more ROIs (spaces allowed). Only after naming these new ROIs should the desired segmentation method (**MANUAL, REGION GROWING**, …) be selected from the Method section of the **SEGMENTATION TOOL** floating interface. Click **NONE** if you are not proceeding with the segmentation now, or **QUIT** to close the Analysis module (this will delete from memory the ROIs not stored on disk).

Segmentation is performed slice-by-slice, building up a 3D region (ROI) by using one of the three different methods available: **MANUAL**, **REGION GROWING**, and **THRESHOLD**. Only in **THRESHOLD** and **REGION GROWING** is the User allowed to extend the segmentation of the current slice to the whole stack of image slices. Segmentation masks (up to nine ROIs) associated with the image are stored in a separate file for later retrieval, editing or quantification.

Segmentation methods:

MANUAL: When Manual is selected the floating interface shown in **Figure 33**. will appear.

Figure 33. Segmentation Tool interface with manual method selected

This segmentation method allows a freehand ***closed*** contour to be drawn around the desired region with the mouse. Begin by clicking the **DRAW** button to activate the "draw' function. Then position the mouse cursor at the starting point of the contour. If you click the mouse, move the cursor and left-click again, a straight line will automatically be drawn that connects the last endpoint with the current point. Alternatively, you may hold down the left mouse button and draw a continuous, freehand contour around the region as shown in **Figure 34**. In either of the modes, a right click on the mouse ***must*** be used to close the contour. Clicking the **CLEAR** button will erase the draft contour.

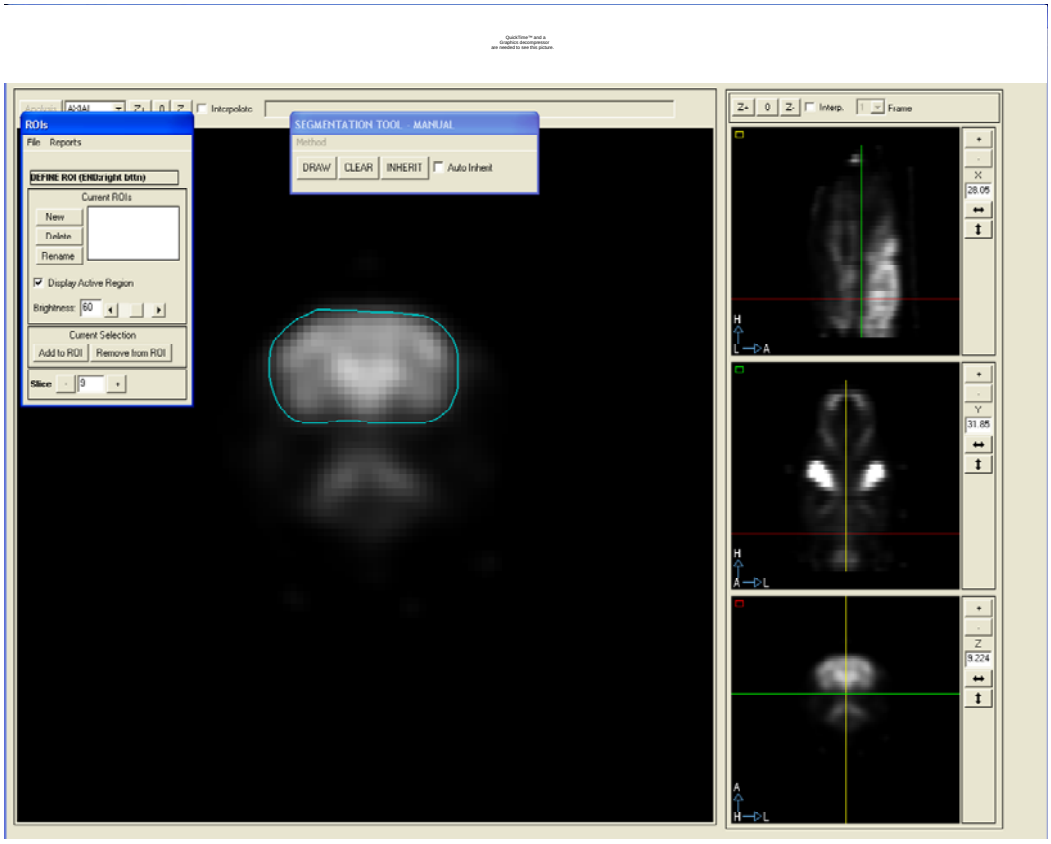


Figure 34. Freehand contour drawn on a slice using manual segmentation

Once the contour is closed, the **Add to ROI** button ***must*** be pressed to save the ROI and assign it the name that is currently active in the ROI window. When this button is pressed, a color will fill in the ROI indicating a successful save and name assignment **(Figure 35).** The same contour can also be included in another ROI by selecting it from the list and clicking again on **Add to ROI.**

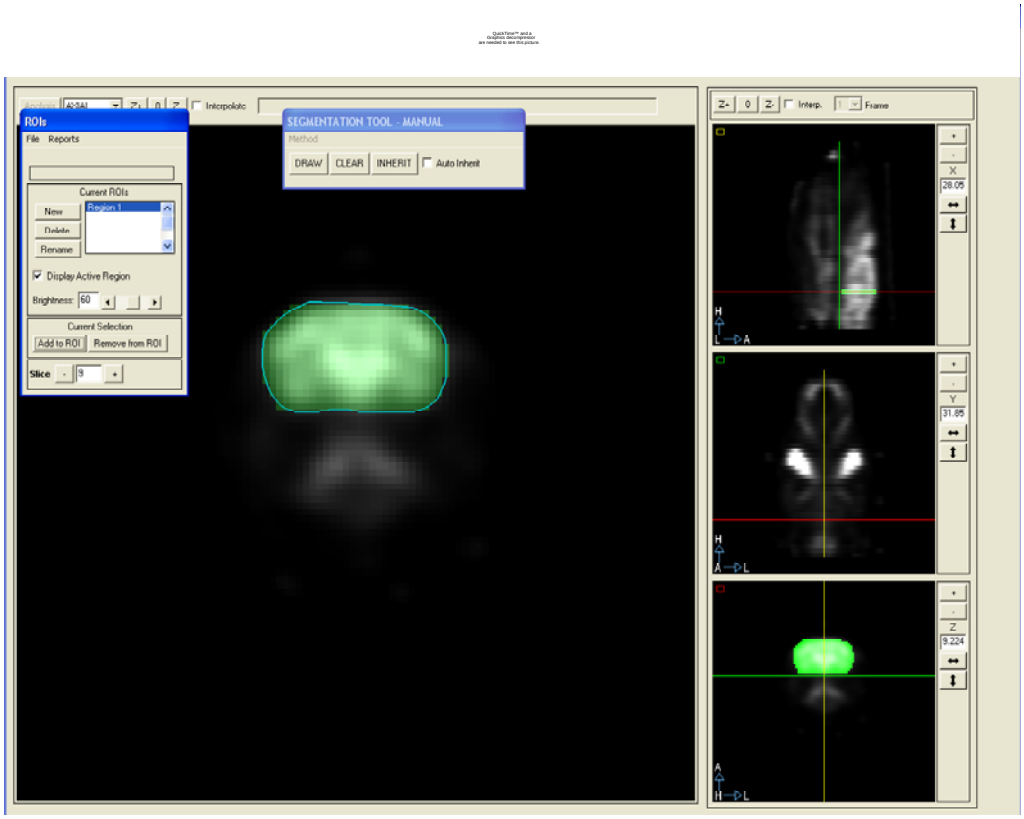


Figure 35. Filled-in freehand contour assigned the name “region1”

The same ROI may be added to other slices by clicking on Slice + or – to move up and down through the image stack. A dotted duplicate of the previous slice contour will then be shown on the new slice **(Figure 36).** If the **INHERIT** button is then pressed, this dotted version of the contour will be copied (***no editing allowed***) onto the new image. Activating the **auto Inherit** check box will keep the contour active throughout the image stack.

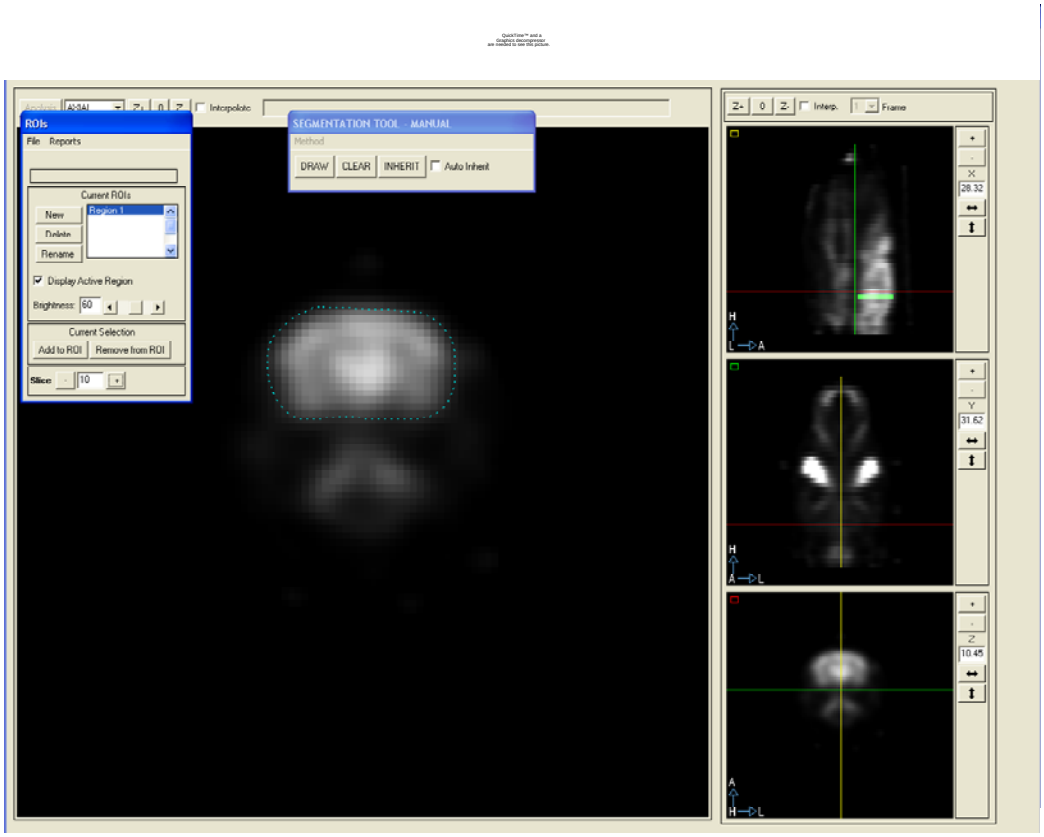


Figure 36. Dotted contour that can be copied using **inherit** button

THRESHOLDING: The floating interface in **Figure 37** will appear when this method is selected.

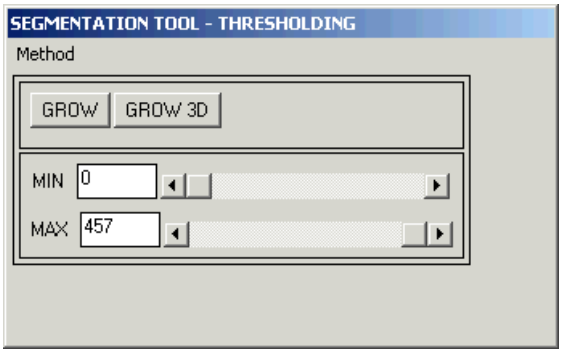


Figure 37. Segmentation Tool interface with thresholding method selected.

With this segmentation method, an ROI can be created by selecting all slice pixels within a specific range of gray levels. Typing a value in the **MIN** or **MAX** text window or using the slider bar will set the range extremes. Clicking the **GROW** button will create a draft region for the current slice colored in pale blue (**Figure 38**), whereas

the **GROW 3D** button will extend the segmentation through the whole image stack. The User can modify the selected range of gray level interactively, till the desired region is obtained. As in the other segmentation modes, clicking the **Add to ROI** button will save the ROI and its name for the current slice.

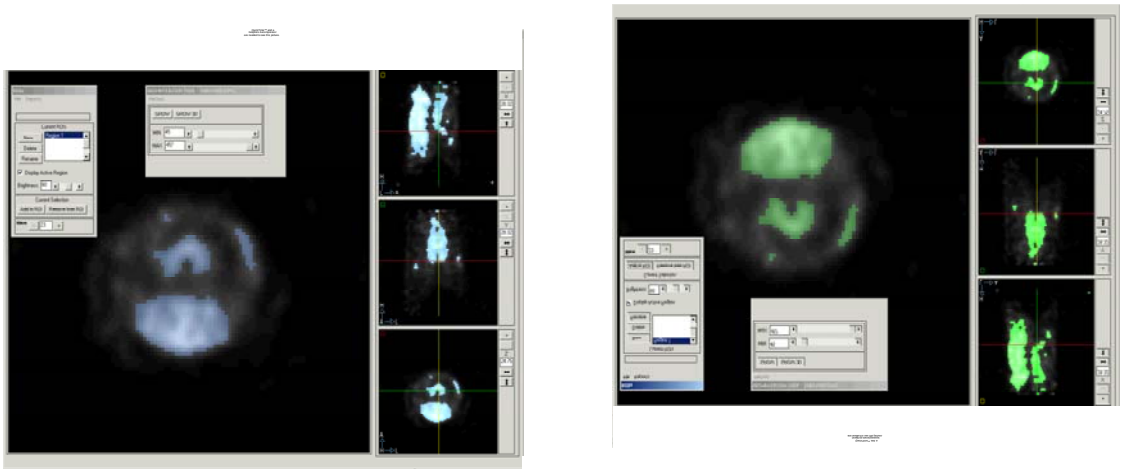


Figure 38. Draft selection created using **THRESHOLD** method and **GROW3D** appears in pale blue (left) until the User presses **Add to ROI** button (right)

REGION GROWING: The floating interface shown in **Figure 39** will appear when this method is selected.

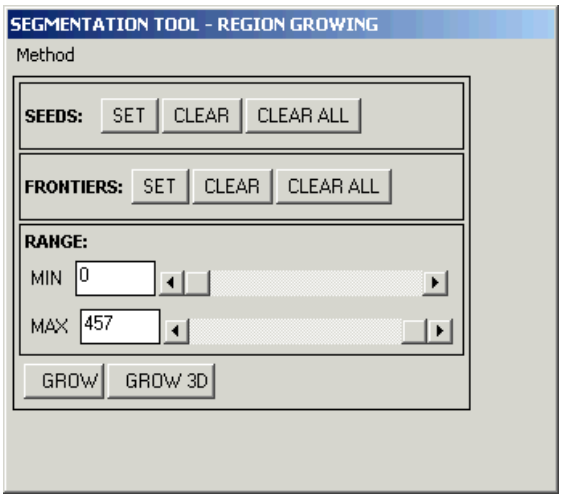


Figure 39. Segmentation Tool interface with region growing method selected

This segmentation mode is an advanced version of the **THRESHOLD** mode with an added pixel connectivity criterion. This mode groups pixels which are next to each other and that also share a similar gray level. You must set the range of gray levels

and also a seed point upon which the connectivity criteria is built. The segmentation begins by clicking the **SET** button in the **SEEDS** menu. This will set a seed point at the cursor position when the left mouse button is clicked, and a seed icon will appear. Then, clicking the **GROW** button or modifying the gray level range will create a draft region colored in pale blue. Multiple seeds can be set to add other portions of the image within the desired gray level range that are not connected (i.e. the left and right parts of bilateral structures). Seeds can be added or removed with the **SET** or **CLEAR** buttons on the **SEEDS** menu. The connectivity criteria can be intentionally interrupted in a specific area using the **FRONTIERS** tool, which allows you to draw breaking lines. Clicking the **SET** button will activate the left mouse button to draw frontier lines on the screen. Clicking the right mouse button ends the frontier line. As with the seeds, more than one frontier can be set. Frontiers can be set or removed at cursor position with the **SET** or **CLEAR** buttons on the **SEEDS** menu.

Typing a value in the **MIN** or **MAX** text window or using the slider bar sets the range extremes. Clicking the **GROW** button will create a draft region for the current slice colored in blue. The User can modify the selected range of gray level interactively until the desired region is obtained. As in the other segmentation modes, clicking the **Add** button will create permanently save the ROI for the current slice with the current **Region name**. Clicking the **GROW 3D** button will extend the segmentation through the whole image stack (**Figure 40**).

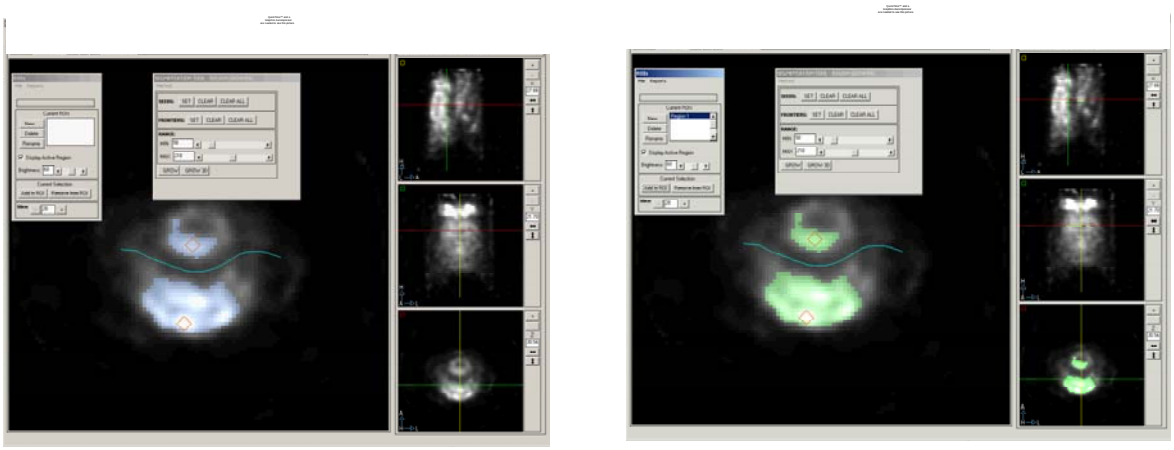


Figure 40. Draft ROIs created using the **Region growing** method for two different seeds (pale blue - left) and after the User presses the **Add to ROI** button (right), adding it to any existing region.

ROI statistics:

Information about every ROI can be obtained with the Tools->Statistics option. After selecting this option, a floating interface will appear **(Figure 41)** that displays measurements made on the pixels within the selected ROI, e.g. volume, mean gray level…). If a dynamic image is being analyzed, a frame slider will allow the User to select the frame from which the statistics are calculated. If the selected ROI is changed or updated, the statistics window will be automatically refreshed.

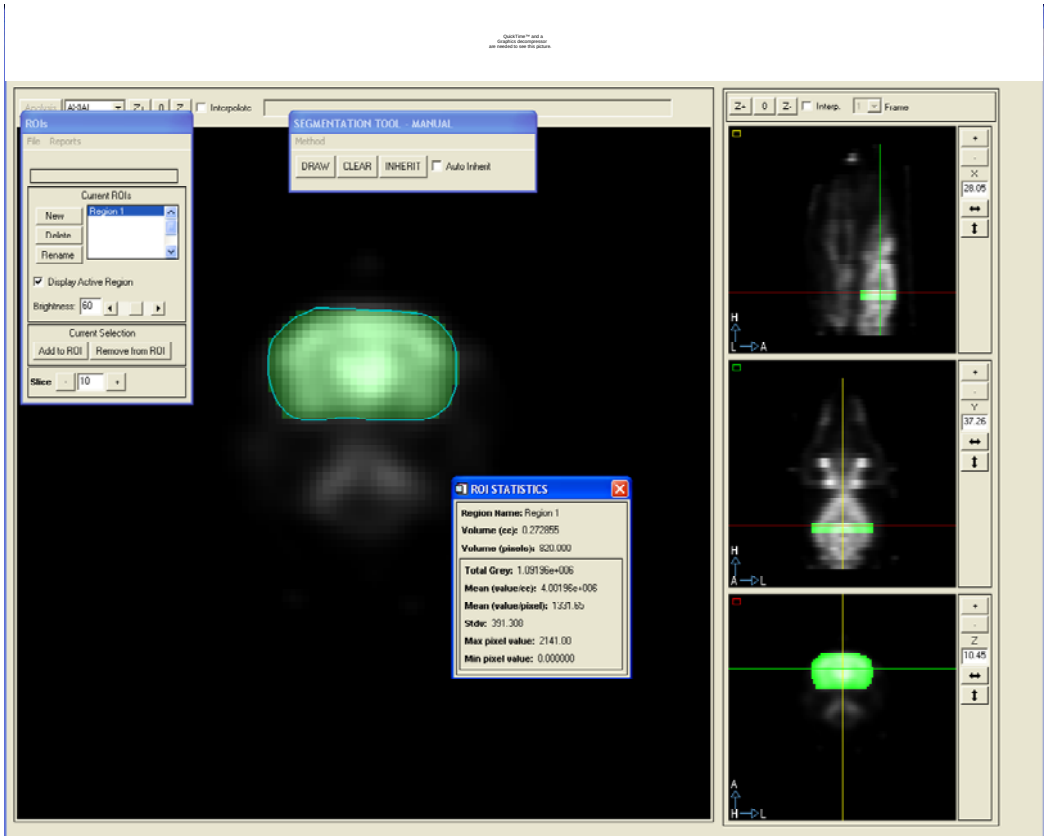


Figure 41. Statistics window shows information from the selected ROI.

Time-activity curves:

Time-activity (or Time) curves can be generated for a dynamic image sequence by selecting the **Tools->Time Curve** option **(Figure 42).**

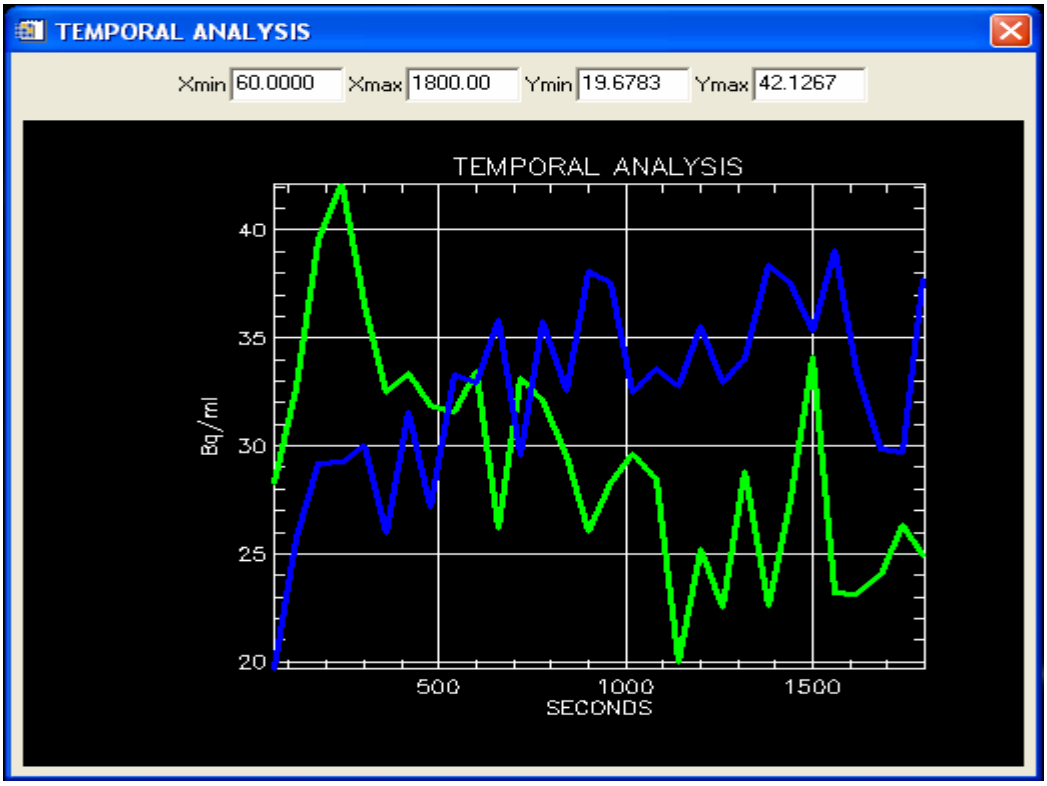


Figure 42. Time-activity curve created by applying a pre-defined ROI to a dynamic image sequence with the Temporal Analysis tool.

If more than one ROI is active when this tool is selected, all of the time-activity curves will be plotted on the same graph. Scaling of these curves is determined by the minimum and maximum values contained in the time-activity curves so that these graphs will not necessarily have a zero ordinate value.

APPENDIX

A. SITING

The following items are the responsibility of the User.

SITING
MAGNETIC FIELDS--Scanner must be outside the 5 gauss line (sphere) of any nearby MRI scanner or NMR spectrometer and ideally outside the 2 gauss line. Care must be taken to insure that the scanner is not under or above these kinds of devices as well as next to these devices. This warning is not based on measured effects but on precautions typically taken with such potentially interfering devices.

RADIATION--The VISTA-CT machine should be operated in a space in which the ambient ionizing radiation field from sources other than the imaging subject will never exceed twice the natural background radiation level during active imaging including those times when stored radioactive sources are present and when nearby radiation emitting devices are operating. The User should establish that this condition exists at the installation site by monitoring the selected area with a G-M survey meter for an extended period prior to delivery and installation of the system. "Ambient radiation level" is defined as the level measured when all radioactive sources are removed from the imaging area and all nearby artificial sources of ionizing radiation are "off".

RADIATION SHIELDING--VISTA scanners are unshielded from the sides in order to reduce the weight and control the weight distribution of the gantry. As a result, radioactive sources of any kind must not be located in such a way as to irradiate the scanner from either side, the top or the bottom. The scanners are shielded only to reduce the intensity of radiation originating from a region in the front or rear of the gantry and to some extent from portions of the scanning subject that are outside the field of view. Accordingly, the scanner must not be located next to, above or below a radiopharmacy, near a patient waiting area where patients might contain radioactive tracer or near radioactive animals that might be caged near the scanner. No radioactive material other than that in the scanning subject should be near the scanner during imaging and no material should ever be placed or stored on or around the scanning gantry, e.g. full or empty dose syringes, waste cans for radioactive material, the Ge-68 annulus, etc. These precautions apply to any kind of ionizing radiation field that might impinge on the scanner including those from nearby X-ray emitting devices, e.g. CT scanners, X-ray machines, etc., even if these devices are not in the same room.

OTHER NEARBY PET OR SPECT SCANNERS-- If two or more VISTA scanners are operating in the same general area, these machines must be located such that radiation from an animal, dose syringe, radioactive tubing, etc. at one machine does not significantly irradiate the second machine, particularly from the sides, during actual imaging. Accordingly, two nearby VISTA scanners should be physically separated from one another to the maximum possible extent and oriented such that the fronts or backs of the machines are opposite one another, i.e at opposite corners of a room facing one another. These guidelines are the minimum needed to allow the

scanners to operate. No shielding can compensate for large amounts of positron-emitting material brought near the gantry of any scanner during imaging so it is the User's responsibility to insure that this never happens during imaging. It is also possible that an animal in one machine could contain enough activity to interfere with imaging on the other even during normal imaging depending on the amount of activity, the distance between the scanners and the orientation of the scanner with respect to each other. Should this occur the User would have to introduce additional shielding at an appropriate place to reduce the radiation field incident on the second machine.

The User should be aware that radiation shielding provided in most single photon imaging systems is insufficient to protect these devices against high energy positron annihilation radiation. If a SPECT or other kind of single photon scanner is to be operated in the vicinity of a VISTA-CT machine, particular care should be taken to prevent irradiation of the single photon machine with even modestly intense radiation fields from positron emitting animals, syringes, etc. Thin layers of lead that are highly effective against gamma radiation from common single photon isotopes, e.g. 140 keV gamma rays from Tc-99m, are essentially transparent to 511 keV radiation so that the performance of nearby single photon devices can be more easily compromised. Keeping positron sources inside thick Pb containers, heavily sheilding pump-driven injection devices, timing studies to minimize cross-contamination, etc. are among the various strategies that can be used to reduce across machine effects. The User should expose any nearby single photon scanner to realistic amounts of positron-emitting sources while monitoring the performance of the single photon scanner to determine the effectiveness of any of these strategies.

Similarly, the User should expose the VISTA scanner to realistic levels of single photon tracers used in single photon imaging studies while monitoring the performance of the VISTA-CT machine. Although the front and back shields on the VISTA scanner are sufficient to totally absorb direct radiation from a low energy single photon source, scatter from very high activity single photon sources, e.g. 12-20 mCi doses of Tc-99m, can reach the VISTA detector array through the unshielded sides or scatter off the VISTA-CT aperture into the detector array. Again, the User should experiment with doses, locations and prevention strategies until any deleterious cross-machine effects are eliminated.

SPECIAL CONDITIONS—VISTA-CT, like any other device dependent on electrical power, should be sited in such a way as to avoid the possibility of water damage from overhead plumbing or piping in the imaging area. The User should inspect the ceiling area above the imaging room and place the scanner where it is not underneath points where leaks might likely occur.

ENVIRONMENTAL CONDITIONS—VISTA-CT must be operated under the following conditions: humidity--< 50% relative, temperature--< 72 degrees F, power—20 amp/120V AC, weight—floor capable of supporting 100 pounds/sq. ft, dimensions—1.3 m (wide) x 1.3 m (deep) x 1.5 m (high), HVAC to remove heat dissipation of 1500 watts.

B. PRE-INSTALLATION

POWER SUPPLY STABILITY AND CONTINUITY—VISTA-CT requires a stable and continuously available supply of electrical power to insure reliable operation. The User must purchase a "UPS" (uninterruptable power supply) that can supply electrical power to the VISTA-CT machine during short power failures and that can prevent line voltage fluctuations and power surges during normal operation. This UPS should be able to support VISTA-CT for a minimum of 20 minutes at 1500 Watts without house power. Two UPSs can be used if a single UPS with this rating cannot be found, one to power the VISTA scanner itself and the second to power the workstation. Any UPS must also have the capability of being monitored from a distance through a serial port and, if possible, an internet connection.

INTERNET CONNECTIONS—The User is strongly advised to install two internet connections in the imaging room and to obtain two static IP addresses so that the scanner and workstation can be interrogated remotely over the internet for QC and diagnostic purposes. Such connections can greatly speed installation of new software and facilitate timely diagnosis/correction of any problems that might arise with the scanner.

C. Ge-68 ANNULUS TRANSMISSION/CALIBRATION SOURCE

The User must purchase an appropriate Ge-68 annulus (SR or DR versions) from Isotope Products and have this sealed source on hand at the time of delivery of the scanner. It is the User's responsibility to pay for this phantom, to have the required licenses to order and take receipt of this radioactive object and to store and handle this phantom in a manner in accord with state and/or federal regulations. The User is responsible for maintaining the currency of Ge-68 phantoms and agrees to purchase such phantoms at approximately one year intervals to keep the strength of this source high enough for timely calibration and transmission imaging.

Ge-68 annulus handling and radiation field:
Transmission imaging and calibration procedures require use a Ge-68 filled plastic annulus that fits closely into the aperture of the VISTA scanners. The dimensions of this annulus have been chosen such that the annular volume containing the positron emitter Ge-68 just spans the axial field-of-view of the scanner when the annulus is properly positioned in the aperture. The annulus is slid or pushed into the aperture *from the rear* of the scanner with an insertion tool specific for that scanner type (single ring or dual ring). When fully inserted, the tool positions the active annular volume of Ge-68 exactly in the center of the axial field of view.

These annuli are radioactive and contain about 500-600 microCuries of Ge-68 at the time of delivery from Isotope Products to a customer. The actual radioactivity content and the calibration date are written on the outside of each annulus. With this half-life these sources must typically be replaced every 12 months or so if enough activity is to be present to efficiently perform both normalization and transmission imaging of small animals (the other use of this source).

Ge-68 is a pure positron emitter with a half-life of approximately 275 days and is uniformly distributed in an epoxy resin within the active volume of the annulus. Care should be taken to store this source in a thick-walled Pb container surrounding the source on all sides including top and bottom. In addition, care must be taken not to physically damage the annulus by rough treatment. Fracturing an annulus could potentially contaminate a laboratory for an extended period of time or force an expensive decontamination of the accident site. More importantly, cracking or opening the annulus in any way could also potentially contaminate workers in violation of radiation safety regulations and likely put in jeopardy the radioactivity license held by the customer. These sealed sources should be safely stored until use, transported quickly and securely to the scanner, inserted into the rear quickly but carefully with the insertion tool and then removed with equal care when the source is no longer needed and returned to its shielded storage box.

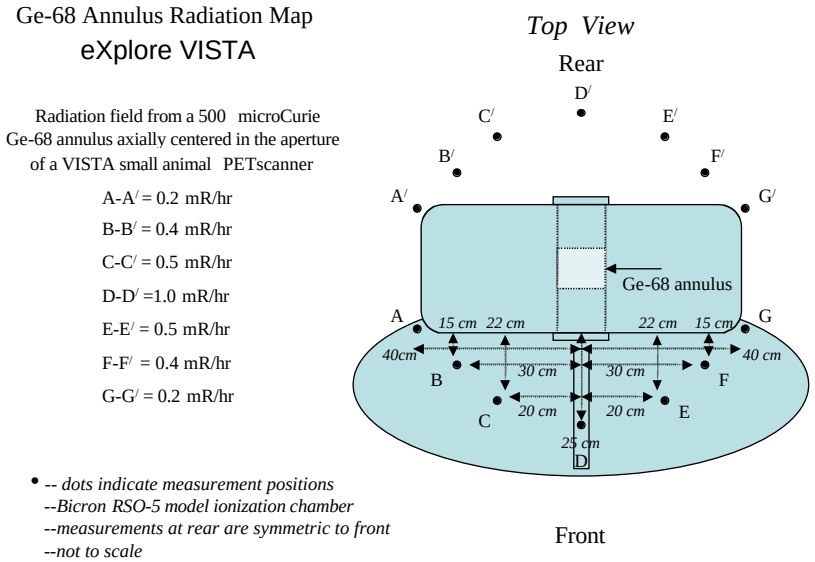


Figure 43. Exposure rates (mR/hr) from a 500 microCurie Ge-68 annulus centered in the axial field-of-view of a VISTA dual ring (DR) tomograph. Exposure rates for the VISTA SR scanner may differ somewhat from these values because of differences in geometry and internal shielding.

When the source is in the scanner, an easily seen sign should be posted (taped) to the scanner gantry that says **"Radioactive Ge-68 Source in Aperture-Maintain Distance!".** It is not easy to see that an annulus is actually inside the aperture and individuals who come by, or stand near the scanner, may not know it is present. The sign is required to keep radiation exposure to these individual to a minimum and to make all parties aware of the fact that the source is in use and not in its storage container. The exposure levels at various locations around a VISTA DR scanner with an annulus in place are shown in **Figure 43** above.

D. STARTING/STOPPING THE DATA ACQUISITION COMPUTER

Normally, a Main Power Switch restart of the VISTA scanner will automatically bring the workstation and the data acquisition computer to full operation. In the rare event that the data acquisition computer (DAQ) fails to start, you can start this computer manually. Conversely, if you wish to turn VISTA-CT completely off, you can perform an orderly shutdown of the data acquisition computer that will leave the system in a secure state.

STARTING--If the scanner appears to be ON but unresponsive to commands to initate data acqusitions, go around to the rear of the machine and determine if the data acquisiton computer POWER light (or any of the LEDs) is ON (see **Figure 44**). If these lights are off, you can initiate the IPMI software procedure described below to start the data acquisition computer from the Workstation.

How to use the IPMI software:

1. Open the *IPMI View* application in the user interface.

Figure 44.

2. Press double click on the configured connection as is shown in the **Figure 45**.

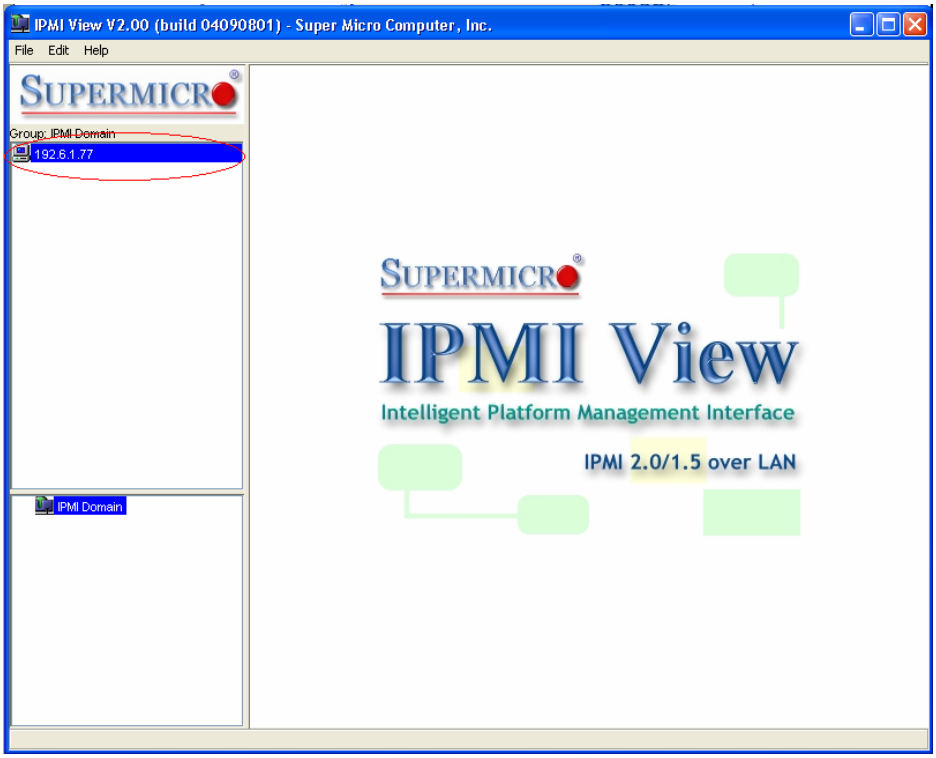


Figure 45.

Log in using user *ADMIN* and password *ADMIN* (set by default). If the connection is successful a message of CONNECTED will appear as shown in **Figure 46**.

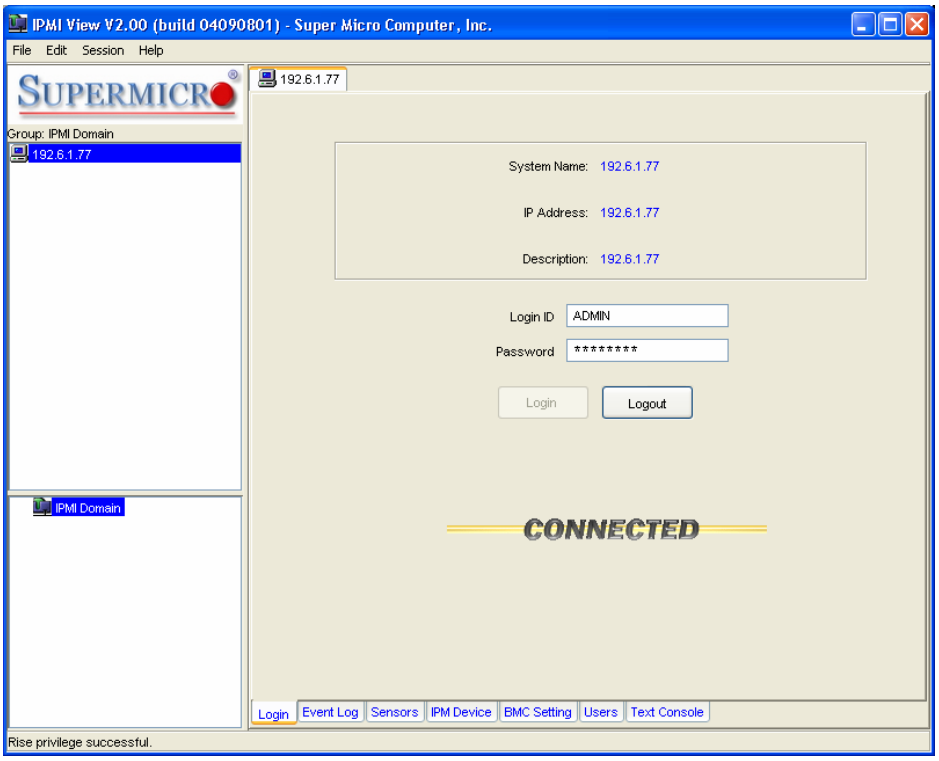


Figure 46.

3. There will be some tabs below where you can find all the functionality of this application. In the *IPMI Device* can be found some buttons to power on, power off and reset the server.

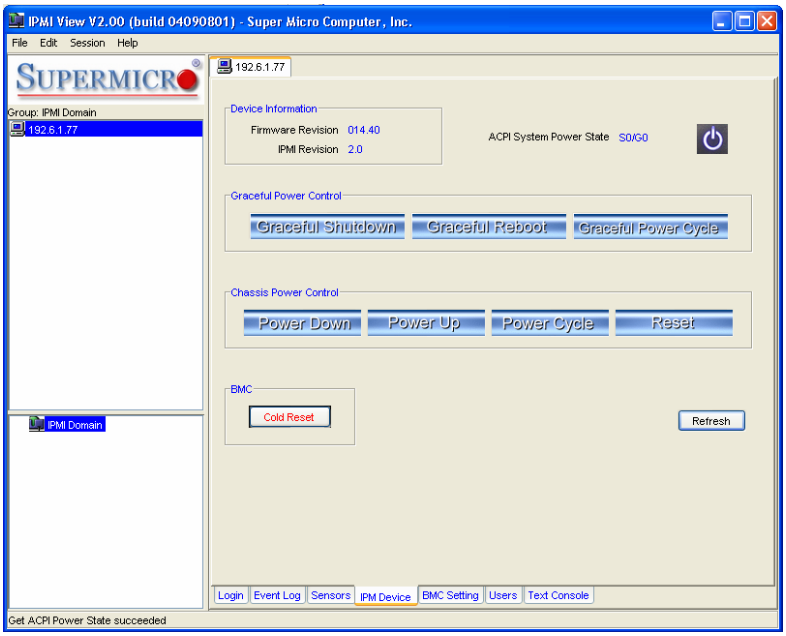


Figure 47.

STOPPING—Occasionally, you may wish to turn VISTA-CT off, e.g. move it to a new location, change power outlets, etc. If so, the IPMI procedure described above should FIRST BE USED TO SHUT DOWN THE DATA ACQUISITION COMPUTER prior to un-powering the scanner. Although protections exist against unplanned shutdowns that might damage operating hard drives, use of this IPMI shutdown procedure will guarantee the integrity of the DAQ for the next start-up. While the scanner can be shut down simply by pushing the Main ON/OFF button to OFF, and can be re-started by pushing this same button to ON, this procedure runs the small risk of damaging hard drives that are in operation when the switch is moved to OFF. The IPMI procedure avoids this risk and is recommended whenever you purposefully shut the system down.

E. USER ACCESS TO FORE SINOGRAMS

VISTA-CT can produce fully reconstructed and corrected images that should be sufficient for most experimental studies. However, some users may wish to manipulate VISTA data prior to reconstruction with available VISTA software and instead use their own reconstruction or pre-reconstruction processing methods, e.g. different methods of scatter correction, etc.

Because of the way data are acquired with VISTA, the best (and only) place for the user to access these data is at the end of the Fourier RE-binning process where the acquired 3D data are transformed into 2D sinograms, one for each slice. Because most users will never need access to these sinograms, and hence do not need the extra burden of recording and moving these sinograms around on a routine basis, access to FORE sinograms is provided only if the user so wishes.

To gain access, the user creates a text file in the directory shown:

C:\FORE\keep_sino.text

The user then simply enters a “Y” (for “yes”) in this file as the first and only element in the file and saves the file. As the form of this statement implies, this command tells VISTA-CT to “keep” the FORE “sinograms” from then on rather than deleting them after reconstruction.

After the user take this action, the FORE sinograms for every reconstruction will be saved and will be accessible to the user in a form that can be viewed with VISTA-CT software like any other image or can be retrieved for data processing purposes. The sinogram filenames will have the form:

… username_25June05_acq003_sino .img & .hdr

This example output is from the third (003) acquisition by “username” on 25 June 2005 and is a **sino**gram file, that can be viewed and manipulated like any other .img & .hdr images.

The user can turn off this process simply by opening the sino.text file, deleting the character “Y” and saving this file. FORE sinograms will be not be saved from then on.

F. SOFTWARE OPTIONS

ECG/Respiratory Gated Formatting—This capability, not supplied as part of the standard VISTA-CT software package, is available as an option (see **Figure 21**) and is accessed with the **TIMING** button on the Main VISTA-CT Interface. This item allows you to create a single, average cardiac or respiratory cycle from many such cycles. This procedure is also known as “signal averaging” and requires a physiological marker that occurs at the same moment in time during a heartbeat or a breath and that can be used to align each single cycle to a common starting point before averaging. The logical steps required to produce such an average cycle are shown in **Figure 48**.

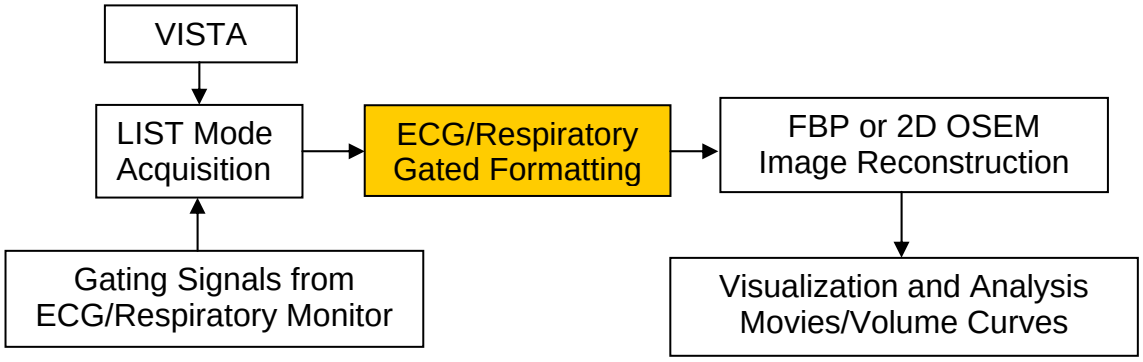


Figure 48.

The reasons that this is a useful strategy when attempting to visualize a periodic or near-periodic phenomenon is that the amount of data acquired during a single heartbeat (for example) is insufficient to allow a meaningful tomographic representation of cardiac volume variations during a cycle. Average cardiac cycle length in awake mice, for example, is of the order of 100 msec and if this cycle were further subdivided into say 10 increments of 10 msec each during which myocardial movement was to be visualized, virtually no data would be acquired during each interval. An attempt to reconstruct a dynamic data set with 10 msec frame durations would yield a uselessly “noisy” set of images. In contrast, gating of these same data to create an average cardiac cycle could improve the number of counts per frame by factors easily in excess of 1000 and yield statistically “smooth” images at apparently high temporal resolution.

A gated study requires a timing signal that occurs at the same moment in each cycle. In the case of the heart, the example used here for illustrative purpose, that signal is usually the time of occurrence of the R-wave in the animal’s externally monitored ECG signal. A variety of commercial ECG-gating devices are capable of detecting this signal and will output a TTL-compatible trigger signal when it occurs. Such

gating devices, cardiac or respiratory, are not included in this VISTA-CT option and you are responsible for providing the input trigger signals in TTL format. Pin assignments for the VISTA-CT input connector are provided at the time the gating option is purchased.

VISTA scanners have a multi-pin input connector on the side of the enclosure that will accept TTL signals from up to four independent gating devices at the same time. Note, however, that no provision is made in the sorting software to allow logical ANDs or Ors of these signals and only one gating channel can be processed at a time. That is, while both a respiratory signal and an ECG R-wave signal can be acquired by VISTA simultaneously, and this same data set sorted into gated respiratory and into gated ECG images, these data cannot be sorted into a data set where conditions have been placed on both signals simultaneously, e.g. use only data from cardiac cycles that occur midway through a respiratory cycle.

A gated study begins by connecting the trigger output of the gating device to the VISTA-CT physiological input connector. Once the animal is correctly positioned in the

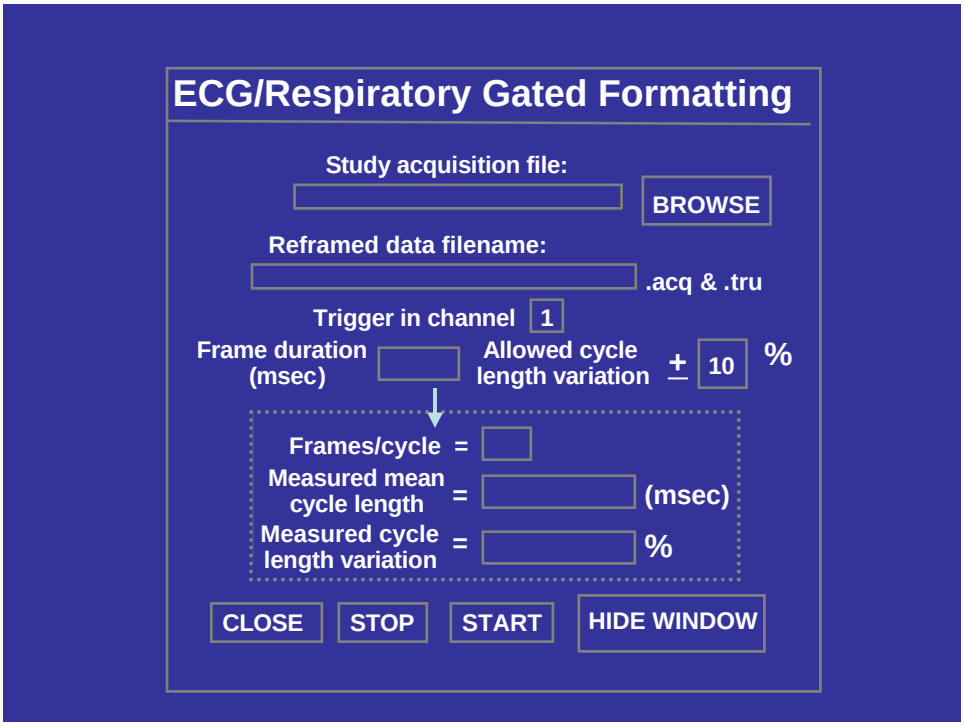


Figure 49. ECG/Respiratory Gated Formatting menu.

field-of-view and the tracer administered, a **LIST** mode acquisition is started through the **New Acquisition** menu. Upon completion of this collection, the ECG/Respiratory option shown in **Figure 22** is selected from the **TIMING** menu.

This step transforms the acquired gated LIST mode data set into a consecutive sequence of raw data blocks that appear to be raw data from a dynamic study of known frame lengths (and, hence, able to be reconstructed into images).

You first identify the LIST mode data set by filename (**Figure 49**) and VISTA-CT appends the .acq suffix to the output filename indicating that the output data set is still in raw form. When this window opens, only the upper portion of the window is visible and the portion of the window inside the dotted box cannot be seen. You then enter the channel number in which the gate signal of interest occurs (1, 2, 3, or 4), specify the duration of each frame in the gated sequence(e.g. 10 msec if a cardiac study in mice) and specify the allowable range of cycle length fluctuations permitted in the data used to create the average cycle. Hit “START” and the sorting process begins.

When the formatting routine has finished, the items inside the dotted box in **Figure 49** are displayed. These data should be recorded for future reference. Sorting will give rise to a number of data blocks equal to the number of frames per cycle and will display the conditions found while creating these data blocks, i.e. mean cycle length, measured cycle length variation (standard deviation of cycle length/mean cycle length), as well as the values entered for frame duration and percent allowed variation in cycle length.

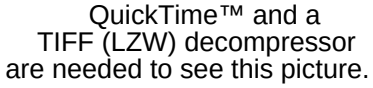
These data are now in a form where they can be reconstructed into images using the provided reconstruction methods. The User identifies the filename output by the ECG/Respiratory sorting routine to the selected reconstruction menu and initiates the reconstruction.

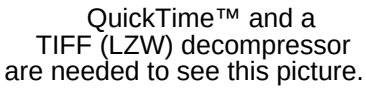
After reconstruction, these images can be manipulated with the Visualization and Analysis tools in much the same way that a dynamic studies can be displayed. If, for example, the image sequence represents cardiac motion by virtue of labelling the blood pool with an appropriate tracer, these data can be displayed in “cine-loop” movie format. This simple visual technique, used routinely in human cardiac studies, is an extremely effective way of detecting subtle differences in regional myocardial wall movement. Similarly, the time variation of ventricular volume (and ventricular pump function) can be quantified by plotting time-activity curves over the ventricular chambers with the tools provided in the VISTA-CT Analysis software package.

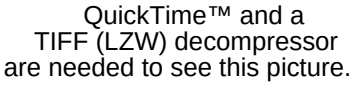
Bear in mind when specifiying frame duration in the Formatting menu that the number of frames requested for the average cycle (mean cycle length/frame duration) will be equal to the number of data sets that must be reconstructed with FBP, OSEM or other algorithms. In the example cited above, a 100 msec long cycle was divided into 10 time frames. Each of these 10 frames must be reconstructed individually and if a FBP reconstruction takes 90 seconds, ten will take 900 seconds or about 15 minutes. Reconstruction times will be greater still with 2D OSEM so some thought should be given to trading temporal resolution against reconstruction time when entering frame duration for gated studies.

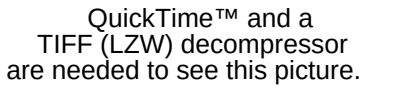
3D OSEM IMAGE RECONSTRUCTION—Another option available with VISTA-CT scanners is image reconstruction with a 3D OSEM resolution recovery algorithm.

This option requires an external computer cluster as well as the OSEM codes tailored to the geometry of the VISTA scanners (SR and DR versions are different). Installation of the cluster and algorithm are performed by service personnel and the details of this process are provided at the time of installation. Performance characteristics of this algorithm are available on request. Menus from the 3D OSEM interface are included on the following pages primarily to illustrate the interactions required to initiate reconstruction on the cluster from the VISTA-CT workstation.


QuickTime™ and a
TIFF (LZW) decompressor
are needed to see this picture.


QuickTime™ and a
TIFF (LZW) decompressor
are needed to see this picture.


QuickTime™ and a
TIFF (LZW) decompressor
are needed to see this picture.


QuickTime™ and a
TIFF (LZW) decompressor
are needed to see this picture.