

GAMMA MEDICA - IDEAS

Users Manual

Triumph X-SPECT[®]

Software Manual for Acquisition and
Processing of SPECT images using Triumph
X-SPECT.

USERS MANUAL

Triumph X-SPECT[®]

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Introduction

This manual describes the use of Triumph_SPECT, the software used for acquiring images in the Triumph™ instrument, and the use of the FLEX_SPECT™, which reconstructs the acquired images. This manual is intended for use in direct conjunction with Section 1 of this manual, and is not intended for use on its own. It is recommended that the reader become familiar with Section 1 prior to reading this software manual.



Figure 2.1.1 Photograph of FLEX™ Triumph™ system. Overall dimensions are approximately 90" x 58" x 48".

Nuclear (“SPECT”) and x-ray (“CT”) imaging subsystems use different acquisition and processing software loaded on the SPECT and CT PC’s, respectively. Co-registration of the CT and SPECT images are performed with separate software on the CT PC, and fused images are displayed using VIVID.

NOTE: It is strongly advised NOT to install other software onto either the SPECT or CT computers, as it may interfere with the proper functioning of the equipment.

SPECT Software

Triumph SPECT imaging package consists of two software entities: Triumph_SPECT™ for data acquisition, SPECT system maintenance/quality control, and FLEX_SPECT™ for image processing and reconstruction. Both are proprietary products of Gamma Medica Ideas and are loaded, with two short-cut icons on the SPECT PC.

User Interface:

The user interfaces for Triumph_SPECT™ and FLEX_SPECT™ are both essentially multi-tabbed, multi-tiered menu. The first tier contains icons or drop down menu bar for choosing individual applications; the second tier contains push-buttons and/or input fields for the specific operations which can be performed within that application. If the operations need to be performed serially, push-buttons and/or pop-windows are activated serially. Multiple push-buttons are activated if operations can be performed in parallel individually. The software does not allow operations to occur out of order or on non-parallel steps. Triumph_SPECT™ and FLEX_SPECT™ are independent so acquisition and processing on different set of data can be performed at the same time.

Triumph_SPECT™:

Triumph_SPECT™ is a protocol based data acquisition and database management software. It is configured to control SPECT image acquisition with Triumph gantry consisting up to four gamma cameras. From the graphical user interface, there are five categories of functionality that guide user to optimize data acquisition:

- Set-up:

Set-up window is the starting point, where users establish their database. It contains two tabs: protocol and study, which are the two indexes used in the program to manage all imaging data. Protocol defines camera and gantry settings, including collimator type, scan type, camera position, acquisition time, isotope and energy windows. Study manages experiments and patients/animals.

- Scan:

Scan window starts and stops a scan. It starts by selecting pre-defined study, patient and protocol. Scan window also has cross-action buttons allowing users to modify or create new parameters, studies and protocols.

- Calibration:

Calibration window contains control panels for three standard system maintenance procedures. Gantry calibration for mechanics, camera calibration for detector uniformity and quality control flood image acquisition tabs. In the top menu bar, there is also a tool for collimator change gantry positioning.

- Data viewer:

Data viewer window provide explore window for data base management and projection data viewing window.

- Protocol Builder:

Protocol builder window is an interactive version of the protocol set up procedure, it provide persistent camera windows linked to protocol setting function boxes for facilitate protocol establishment.

FLEX_SPECT™:

- Single Reconstruction:

Provide standard 3D OSEM reconstruction interface of a single image data;

- Batch Reconstruction:

Provide multiple input fields for imaging data to allow reconstruction performed on one set of data.

- ColorSPECT:

ColorSPECT provides list mode parsing functionality, it was wide used for dual isotope image prior to the release of Triumph_SPECT™. While multiple isotope processing has been implemented into the Triumph_SPECT and no longer needs ColorSPECT, ColorSPECT can still be used to reprocess flood data for UCT regeneration.

Chapter
2

Features of Triumph_SPECT™

To switch the mouse and keyboard control from the CT monitor to the SPECT monitor, hit the “*Scroll Lock*” key on the keyboard *twice*, and then hit enter, make sure that the mouse was not moving while switching.

Set Up Window

Set up window contains two tabs: Study and Protocol. It is activated by clicking on the “set up” icon on the top menu bar.

Study

Study window contains four sections: study list; study info, patient addition and study history:

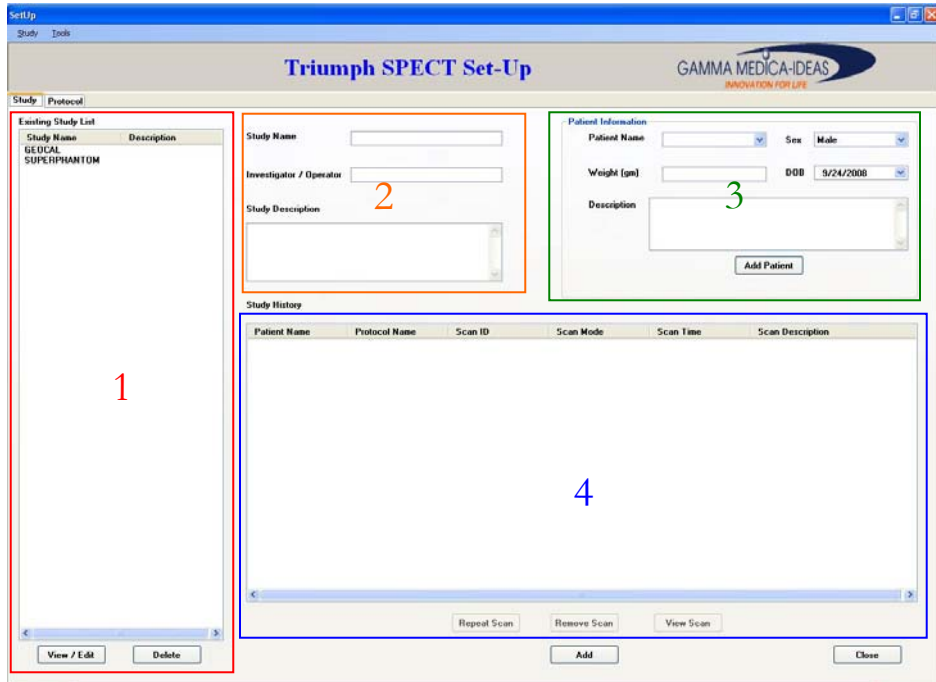


Figure 2.1.1 Protocol window

1. Study List:

This explore style window contains all established studies displayed by names. For a brand new user, this panel should be empty. Established study can be viewed, edited and deleted, with action buttons listed at the bottom of the panel.

2. Study info:

This section contains critical identifiers of a study.

Study name: Generally speaking, studies are the purpose or theme of a research project or an experiment. E.g. “whole body distribution – mAb²⁸”, “reanl clearance- folate 001”.

Investigator/Operator: Although not a mandatory field, it is encouraged to be filled to facilitate organization of studies, especially for core facility instruments.

Study Description: Free style text box for study notes, not mandatory.

3. Patient info:

Each study can be linked to multiple patients and this section is for users to fill up the patient list for the particular study.

Patient Name: under usually condition, this section is the species and strain name of the animal to be imaged. A patient for Triumph could be a mouse, rat, hamster or even a rabbit. It is recommended that the strain and/or a particular genotype be associated with the patient name, e.g. “BalbC/J #383”; “SCID_ApoE-KO#77”.

Sex: Sex of the animal, contains a drop down list of “male” (default) and “female”.

Weight: weight of the animal at time of imaging.

DOB: Date of birth of the animal, the drop down list is a calendar.

Description: Any further genetic and/or physical modification be recorded in the “description” window, e.g. “prostectamy performed 9/24/08”.

Add button: this button add the established patient into the study history list.

4. Study history:

This is not a user input section. It contains all the studies established and/or performed under this study. It is by default sorted by patient but can be resorted by clicking on the desired column. There are three interactive button that links the history page to the “scan” window which allows users to repeat the exact scan, to view the performed scan or to remove the scan.

Protocol

Protocol window contains a total of six sections, defining the acquisition condition from all necessary aspects of nuclear imaging.

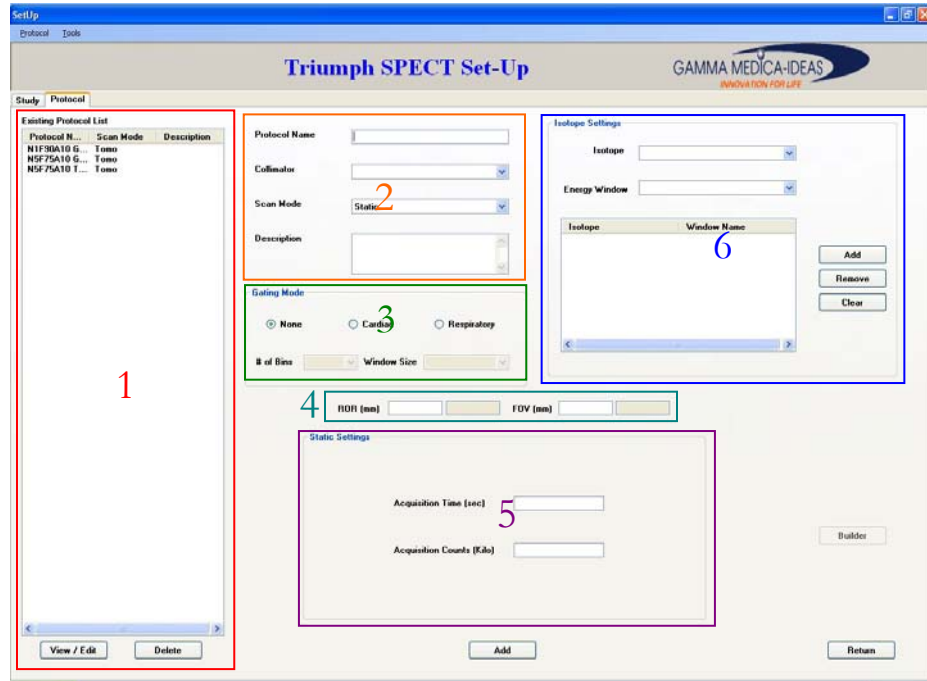


Figure 2.2.2 Protocol Set up Window

1. Protocol List

Similar to the Study window, the protocol list is an explore style window that allows you to organize, view, edit, or remove your protocols.

2. Protocol info

Protocol info panel sets the critical identifiers of the protocol. It contains three items.

Protocol Name: Although no fixed pattern, protocol name is recommended to be precise and distinct. It is recommended that the unique feature of the scan be specified in the name. E.g. whole body, close range, spiral, multipinhole, etc.

Collimator: collimator name can only be chosen from the drop-down list. Please make sure that the name be introduced in the standard training session at machine delivery. The following are names for standard delivery collimators:

N1F90A10	single pinhole collimator, 1mm aperture
N5F75A10	multipinhole collimator, mouse style, 1mm aperture
N5F65A10	multipinhole collimator, rat style, 1mm aperture
HRES	standard parallel hole collimator

Scan Mode: scan mode refers to the gantry movement for the scan. There are four types of scan mode enabled by the current release of Triumph_SPECT and they can only be chosen from the drop down list:

Static	no gantry movement, single planar image will be acquired
Dynamic	no gantry movement, multiple planar images will be acquired with a series of pre-defined time frames
Tomo	gantry will rotate 90, 180 or 360 degrees based on setting while a series of projections images will be acquired at pre-defined angle. Based on detail tomo setting, animal bed will either stay (circular) or inward at steady speed along axial direction (spiral).
Dynamic Tomo	with pre-defined time frame, a series of circular tomographic images will be acquired

3. Gating Mode

For Static and standard tomographic imaging, Triumph hardware has implemented mechanism for projection images to be parsed based on cardiac and/or respiratory rhythm, i.e. gated. Current release of Triumph_SPECT™ and FLEX_SPECT™, however, have not implemented the handling of gated data. Therefore in this release of user manual, gating mode section will not be discussed and user is to always choose “none” in this section.

4. ROR

Radius or Rotation (ROR) is the distance from the surface of the collimator to the center of rotation of the gantry. For pinhole collimators, ROR decide object magnification, geometry calibration reference, field of view and final reconstructed image size. Therefore, an ROR for a scan is very important. In terms of a protocol, however, ROR does not need to be fixed and linked to any other parameters and under many practices, turns out to be the ONLY parameter that needs change in the protocol. Therefore, the protocol set up window placed the ROR setting in an independent window. The white input field allows user to set ROR in mm for the protocol, while the grey field indicate the current ROR the gamma cameras are positioned. FOV stands for field of view, which is automatically calculated based on input ROR and should not be edited by users.

5. Scan Mode Setting

Scan mode setting is a subset, or a continuous setting window for scan mode. It defines the detail scan parameters of the particular mode. Therefore the content changes based on the which scan mode has been chosen.

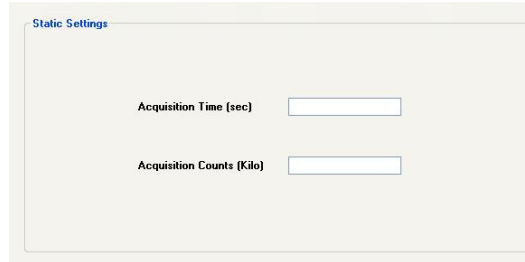


Figure 2.2.3 the Static detail setting window

Static Scan: if static scan is chose, user simply need to put in the stop condition either by time or by total final counts.

Dynamic Scan: for a dynamic planar scan, user need to define the time points and time frames in the following detail window:

- Num. Of Frames: how many planar images you wish to acquire;
- Frame duration: how long do you wish to acquire for each image;
- Interframe duration: do you wish to wait during frames and how long;
- Phases: if you wish to set different frame duration, e.g. some frames are 10 sec and some are 20 sec, these frames need to be separated into different phases.
- Pause: if checked, the program will wait user’s keyboard command to start the second phase.

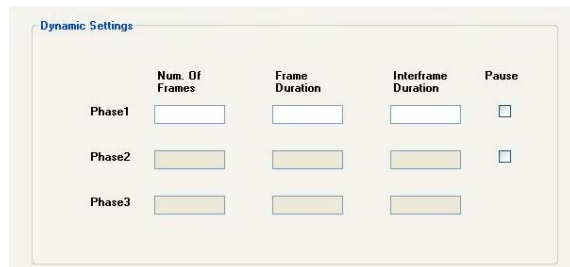


Figure 2.2.4 Dynamic scan detail setting

Tomo Scan: there are two kinds to tomo scans, the “circular” scan is the standard tomo scan and the setting window looks like this:

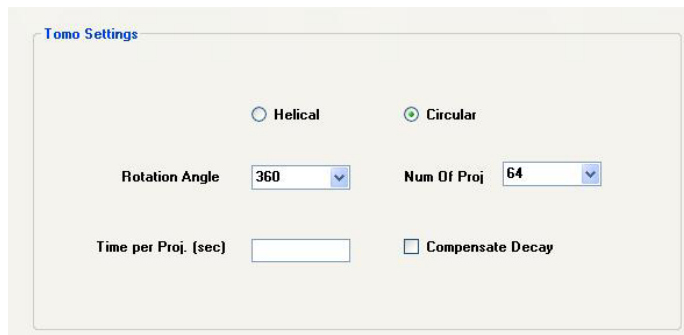


Figure 2.2.5 Tomo Scan detail setting window

- Rotation Angle: defines the distance for gantry rotation for a full tomo scan. For a single camera system, the minimum is 360°. For a 2 or 4 camera system, the minimum is 180° and 90°, respectively.
- Num of Proj: number of projections/images to acquire over the rotation angle defined. In order to object optimal sampling, it is recommended that 64 projections be acquired over 360°. i.e. for 4 cameras, 90o and 16 projection is recommended. Acquire projections more than recommended will be oversampling and unnecessary.
- Time per Proj: how long each projection should last, it is recommended that 5 sec or longer to be entered.

- Compensate Decay: if checked, time for later projection would be adjusted based on radiation decay of the isotope to match the total activity of the first acquisition.

The “Helical” scan is tomo scan with constant axial bed movement. The detail setting window is similar except that the angel of rotation is no longer changeable. To ensure adequate sampling, full round rotation has to be achieved. In addition to detail setting, manual bed positioning is needed during an actual scan, please follow the instruction in the next section when actually perform a spiral scan.

6. Isotope info

The last and also very critical parameter field for a protocol is isotope(s), more than one isotope can be added to the list, meaning more than one isotope can be imaged simultaneously. Each isotope has more than one choice of energy windows. Bigger window allows more counts to be recorded yet it risks cross-talking should another isotope is getting co-imaged. Since Triumph CZT cameras has a very sharp energy resolution: 4% at 140Kev, users are recommended to choose as narrow of a window as possible.

Isotopes can be added, edited and removed from the list.

Scan Window

Scan window has three main panels: Scan condition panel, animal status window and camera status window.

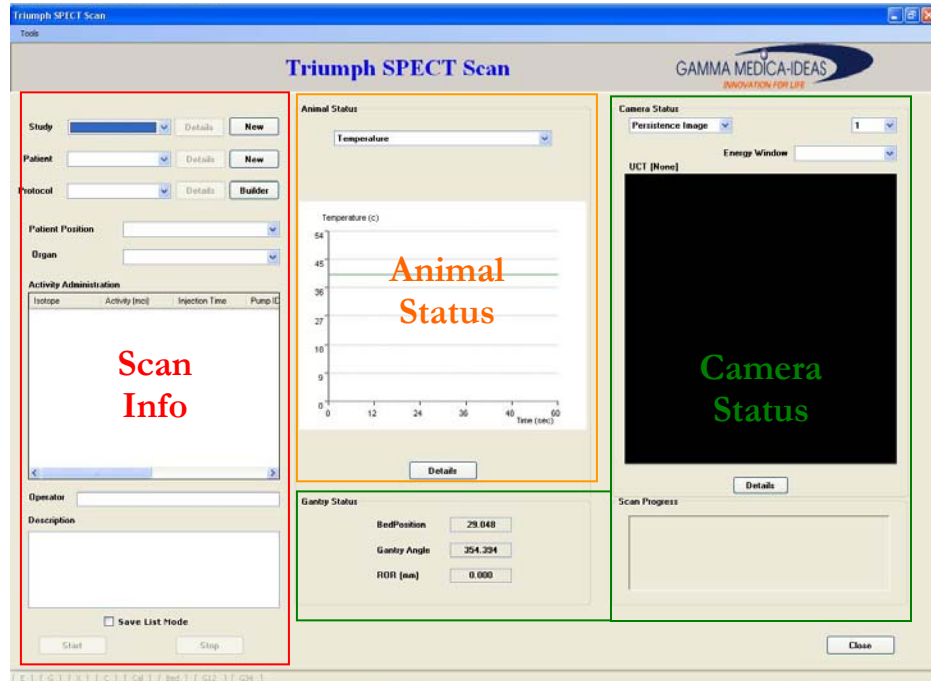






Figure 2.2.6 Scan Window

Scan Info

The main identifiers, or determinants of the scan, are the top three inputs:

- Study
- Patient
- Protocol

Therefore all there are mandatory fields to be filled in order to start a scan.

Each inputs has a drop down list , a review button  which will be activated once an item is chosen from the list, and a button for users to start one on the fly:  or . The “builder” refers to protocol builder, which will be introduced in the next section: to perform a scan.

- Patient position: choices are “prone” (*animal is faced down on the bed*) or “supine” (*animal is laid facing up*), for image orientation reference.
- Organs: the targeted organ of the image acquisition. Although in animal imaging there are usually multiple interests, there is only one organ can be physical “centered” in the FOV. This field is, similar to patient position, serve only for reference and do not orchestrate any gantry movement.
- Activity Administration: This is an additional feature that is effective only when user connect a Triumph compatible infusion pump with the gantry (*for installation instruction please reference related hardware manual*). Once properly connected, the pump will start injecting radioisotopes at a pre-time, with pre-set speed and total volume before or during image acquisition. The contents in all the columns are self-explanatory so will not be listed in this paragraph. If there is no pump connected the contents in this window will not affect any gantry function.
- Operator: an optional field for the names of investigators.
- Description: a free text field to record experimental notes.
- Save Listmode: if the toggle box is check, list mode data will be saved in addition to the normalized projection for future analysis using colorSPECT (*see FLEX_Triumph™ manual*).

Animal Status

Triumph gantry is equipped with animal monitoring sensors and, once connected to the animal with proper probes, the following animal vital signs can be monitored in real time, with or without image being acquired:

- Temperature: through a rectal probe
- Heartbeat: through 2 EKG needles
- Breathing: through an external pillow sensor

Based on the type of vital sign chosen in the top drop down list, the center

screen will display the bio-graph in real time. To view all active vital signs at one glance, click the “Detail” button under the graph and a complete animal vital status window will be presented. Note that oxygen level is also incorporated in the graph for user elected upgrade. Also both cardiac and respiratory statuses are presented in two formats: the conventional histogram and a rhythmic chart. The “clear” button will clear previous cumulation and start the charts from a fresh beginning.

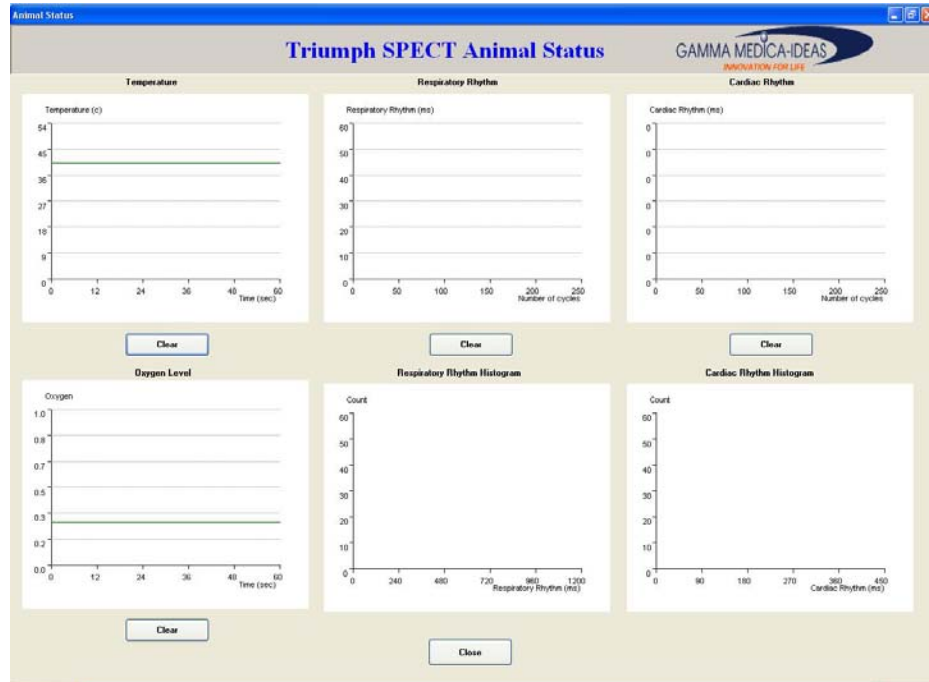


Figure 2.2.7 Complete animal vital sign status

Camera Status

- Monitor window setting: choices By selecting different input and different head , user can choose to monitor the camera by persistent image or count rate chart or any head in the system. User can also adjust energy window to see variously “filtered” image, which should help determining whether or not protocol needs to be modified.
- Monitor: Display of persistent projection images or histogram based on the input setting defined above. To monitor all input of all cameras, click on the “Detail” button, a camera detail window will appear (*see figure ###*)
- Scan Status: a message box that updates scanning progress and report errors. E.g. for dynamic scan, it reports when every frame is starting, for tomographic scan, it reports when projection is acquired.
- Gantry Status: an interactive indicator/meter of the bed position, gantry angle and the ROR.

Detail Camera Status

By clicking the “Detail” button in the “camera status” panel in the scan window, a “detail camera status” window will be invoked.

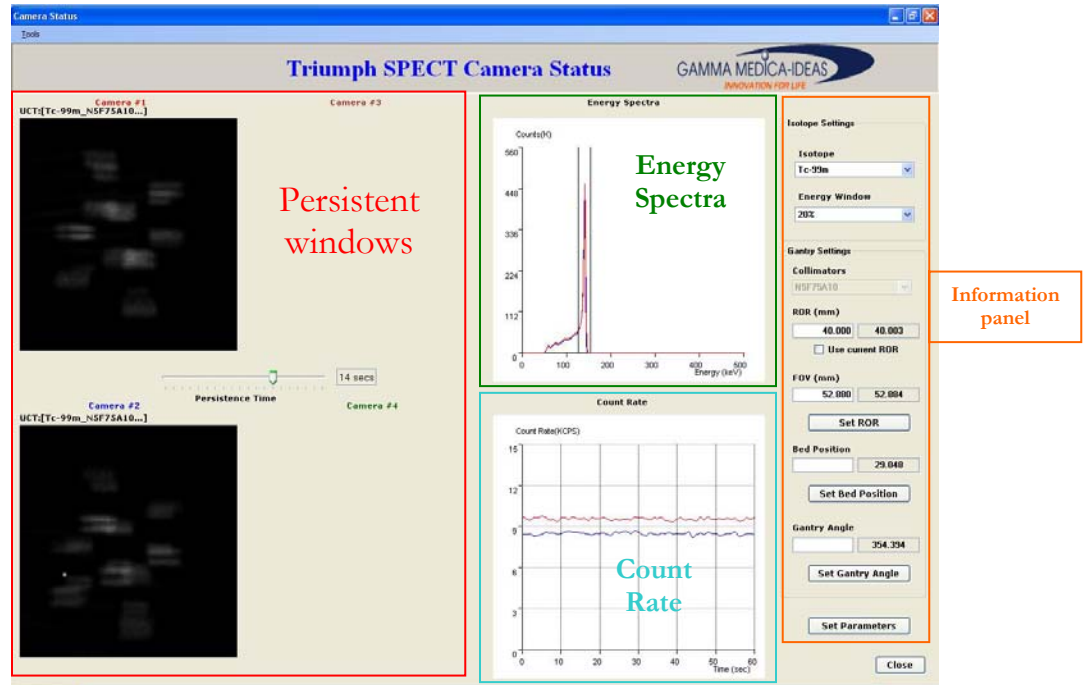


Figure 2.2.8 Detail Camera Status

- Camera Persistent Window: Display real time signal of all camera heads, the cameras heads are indicated on the top with each screen and color coded. In the middle, a scale was place to adjust the accumulation period before display. E.g. a “14 secs” scale means that all images displayed are accumulated signals for 14 seconds.
- Energy Spectra: Accumulated (all time) energy spectrum for all cameras. The colors of the lines matches the color codes of the camera head indicator in the persistent window.
- Count Rate: Real time count rate display of all camera head, “cps” stands for counts per second. Lines are color coded similarly.
- Information Panel: Detail gantry status window, during a scan, all input fields are disabled and for observation purpose only, before a scan, this panel can be used as a protocol builder, which will be introduced in a later section.

Data Viewer Window



Data viewer window will show up after user selected interested image from the data list. The viewer window contains the following panels.

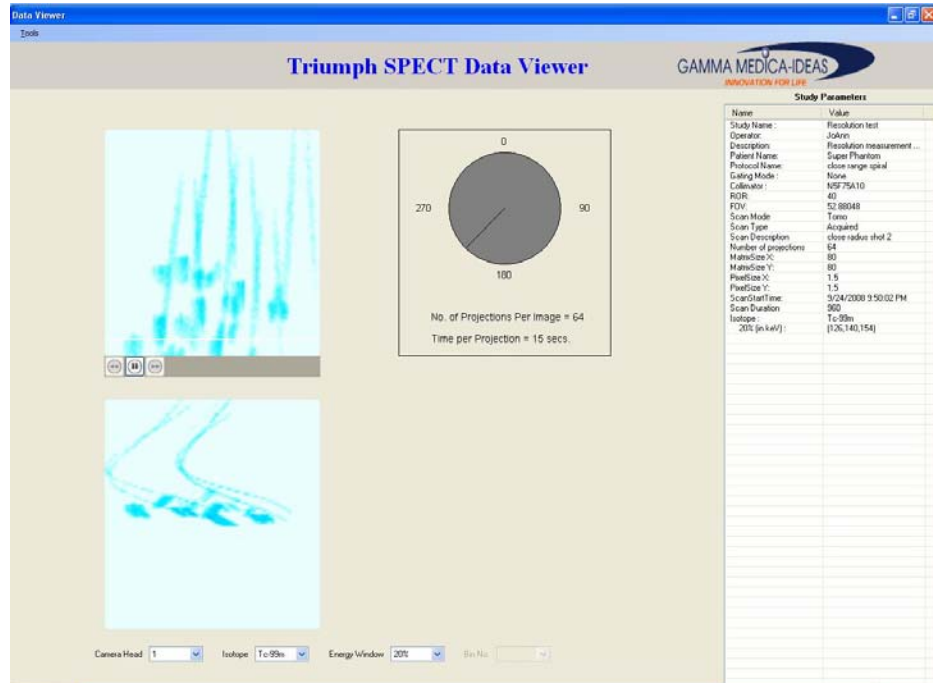


Figure 2.2.9 Data Viewer Window

- Viewer screen: The top window in the left panel continuously run through acquired projections with a chosen camera head. The play control under the screen can stop, run, pause or adjust running speed of the movie. The bottom screen shows the sinogram of a selected plane through out all the projections, the plane can be selected by dragging a white line up and down the projection window.

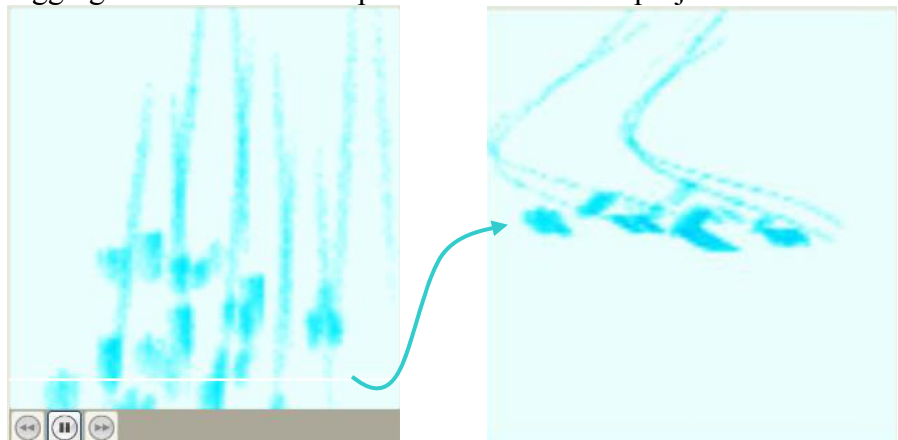
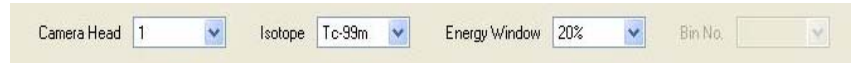


Figure 2.2.10 Projection and sinogram

- Setting control:



These drop down list allow user to choose which camera head to monitor/view and using which isotope and energy window as filter.

- The clock: The middle panel reflects the gantry angle of selected camera head corresponding to the projections on the left.
- The image information: The right panel is a data information summary.

Calibration Window



Gantry Calibration



Figure 2.2.11 Gantry Calibration window

Gantry calibration is the simplest interface of the program. It has two panels, the top panel reflects the current bed position and gantry angel for user’s reference. The lower panel is a information box that reports the start and finish of the process. The “start” button starts the calibration.

UCT (Uniformity Correction Table)

UCT window is for users to acquire isotope/energy/collimator specific flood image for camera uniformity calibration. It differed from scan window in that

1. It is only for acquiring static image.
2. A “calculation” process will be automatically following the flood image acquisition to generate UCTs for more than isotopes therefore there are additional settings that is usually not needed in regular static scan.
3. UCT calibration will have an option to be followed by a “QC” procedure so there is an additional setting to check it.

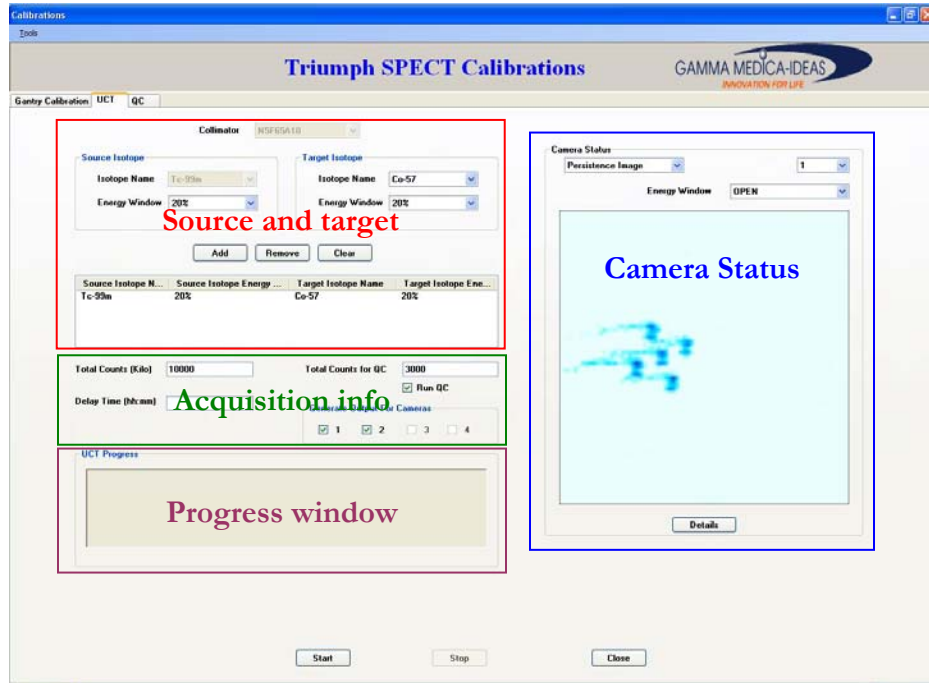


Figure 2.2.12 UCT window

- Source and Target: This is the essence of the UCT window. It defines all the identifiers of the correction table:

Collimator: the drop down list of this input field contains exactly the same list of collimators as for the protocol window.

Source Isotope: the isotope that will be used to acquire the flood image. The Energy window drop down list is unique to the selected isotope and can not be left blank.

Target Isotope: the additional isotope and energy window that this UCT could be used. This input field can not be repetitive of the source isotope for the source isotope has already been included and is not “additional”.

Action Buttons: for adding, removing target isotopes and for clearing the entire isotope list.

Isotope list: all target isotopes this UCT will be calculated for, the source will be listed by default, plus any “added” target isotopes.

- Acquisition info: This session assures the quality of the flood images in order to obtain a good UCT.

Total counts: the minimum count every camera has to obtain in order to complete image acquisition.

Delay Time: Waiting time between the “start” button is pushed to acquisition really starts. This is very helpful when prepared flood phantom is too strong (> 30kcps).

QC toggle box: Once checked, a QC procedure will automatically follow the UCT calculation, acquiring a static image with the updated UCT.

QC total counts: similar to the UCT total counts, this input field defines the minimum counts each and every camera has to obtain before calculating QC factors.

- Progress Window: Information box that reports the status of the UCT acquisition and calculation.
- Camera Status: The same camera status window as in the scan window.

QC-Quality Check

The QC window is an independent window although usually invoked after UCT is calculated. User can click to the QC tab directly and acquire flood images and have the quality factor checked.

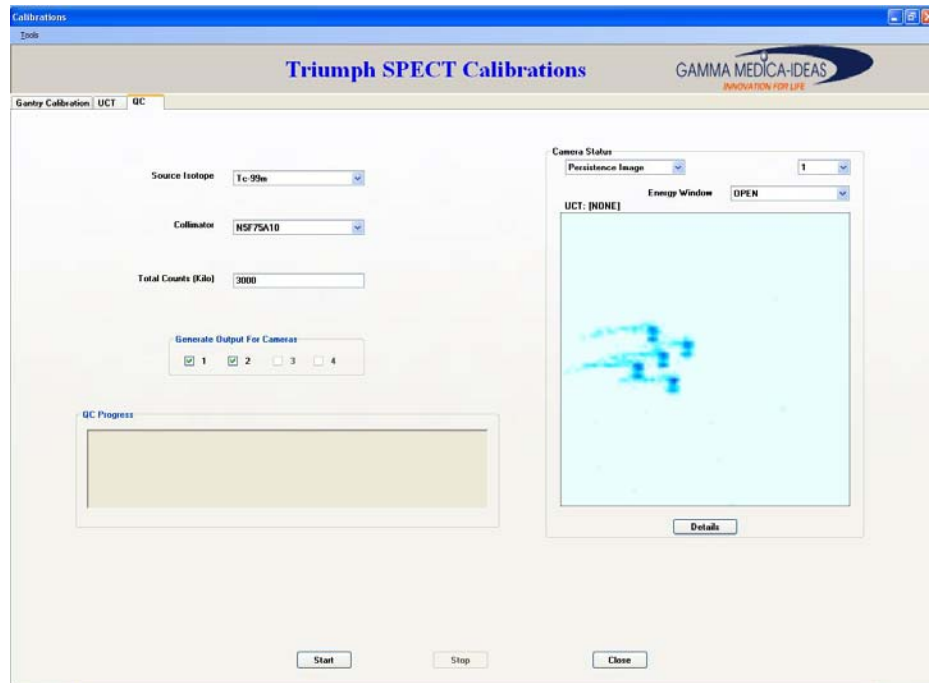


Figure 2.2.13 The QC window for calibration

Protocol Builder



To facilitate establishing a protocol, especially the right ROR, Triumph_SPECT set up has implemented an interactive “Protocol Builder”, this window can be invoked by the clicking the pencil icon in the top menu bar, or clicking the “Builder” button in the scan window, right by the “Protocol” drop down list.

The builder window looks very much like the camera detail window except the window title’s clear indication. It has persistent windows for all activated camera heads, the energy spectra and count rate window with all cameras plotted, colour coded. On the right, is the information panel user will need to fill out:

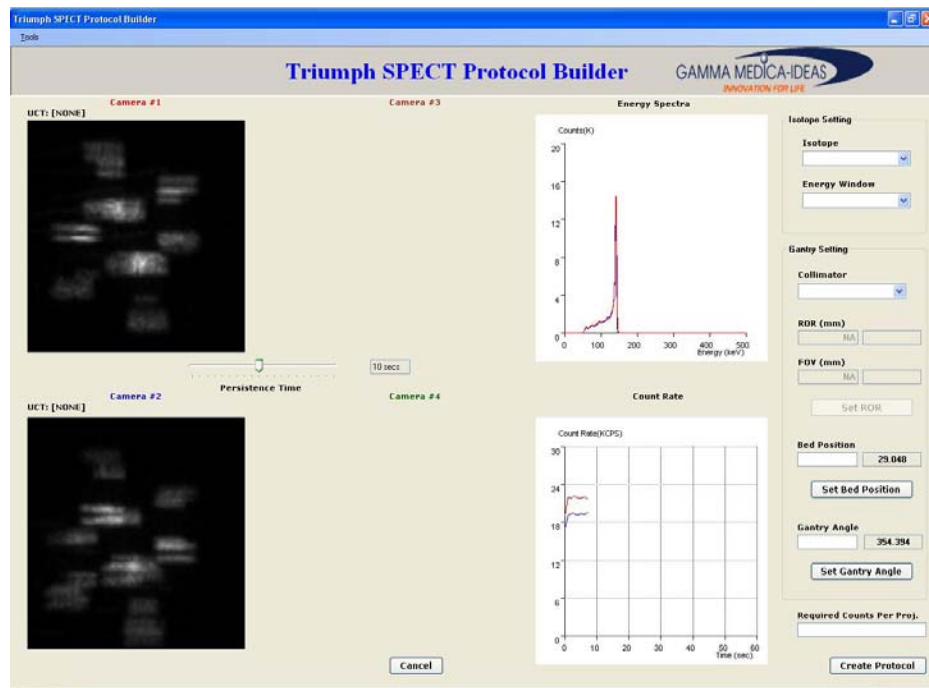


Figure 2.2.14 Protocol Builder window

Isotope Setting: Isotope and energy window, can only be input one at a time.

Gantry Setting: Collimator type needs to be put in for ROR input to be activated. After activation, user can view the current ROR in the right cell of the ROR panel. By entering numbers in the left cell and hit “set ROR” button, user can reset the camera to a new ROR and the FOV will change instantly so would the persistent window images.

Gantry Setting: Bed position and starting gantry angel can also be set in the similar way, persistent windows will change based the resetting.

Requested counts: This input field defines the desired counts per projection,

program will use this input to calculate the acquisition time needed per projection.

Data Acquisition with Triumph_SPECT™

To switch the mouse and keyboard control from the CT monitor to the SPECT monitor, hit the “*Scroll Lock*” key on the keyboard *twice*, and then hit enter, make sure that the mouse was not moving while switching.

To Start the Connection

Before starting the acquisition software, a communication needs to be activated between the SPECT PC and the camera read out board, DDROB. To do this, open the DOS command window on the SPECT PC by right clicking on the “Start” button at the bottom left corner of the screen and choose “All Programs” → “run”:

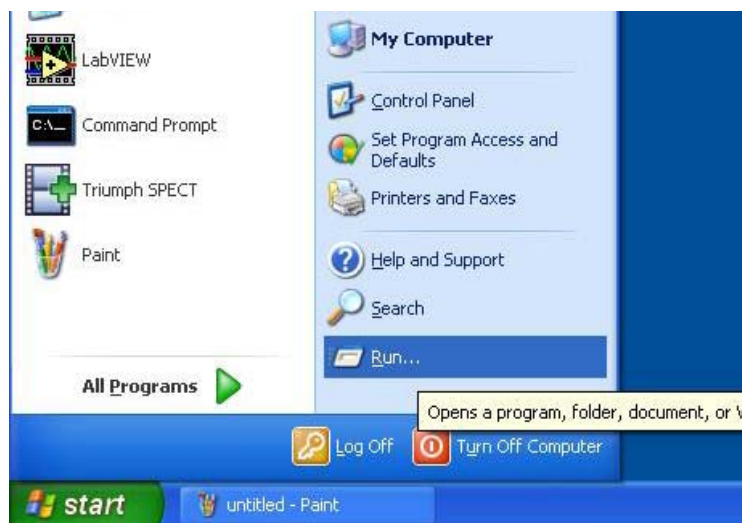


Figure 2.3.1 Invoking the command window

When prompted, type in “cmd” and hit OK, the command window will open.

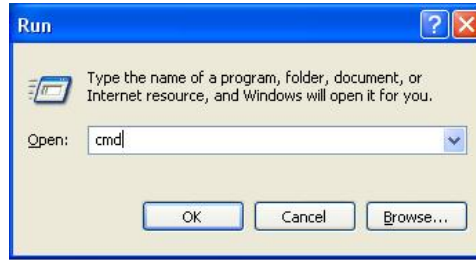


Figure 2.3.2 Invoking the command window

In the command window, type “telnet 10.1.1.10” to start the communication with the DDROB.

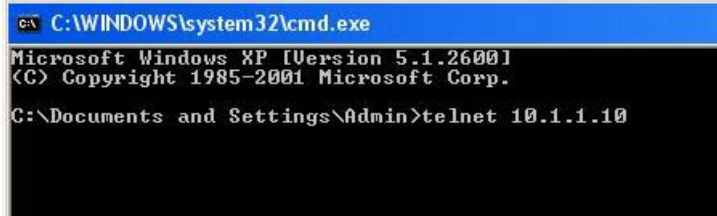


Figure 2.3.3 Telnet to DDROB

User will be asked for username and password, which are “root” and “ideas”, respectively. Password entry will not be shown on the screen. After entering the password, hit “return” key. The cursor will move down and connection will established. There will not be and message occuring on the DOS window indicating the established connection. Please proceed to open the acquisition window.

To Start the Program



The “Triumph_SPECT” shortcut icon can be found on the desktop of the SPECT PC, double click on it and an inquiry window will open to ask for system configuration.



Figure 2.3.4 Triumph_SPECT initial window: camera setting

Usually for a single head system, only Camera 1 can be checked, i.e. Camera 2-4 toggle boxes are inactivated. For a 2 head system, Camera 1 and 2 will be active, yet user can choose only to use one head. Similarly, for a 4 head system, all toggles are active and user can choose any configuration. Check

all the heads you want to use then click “OK”.

NOTE: This is the only time the program asks for camera settings, should user decided to change camera heading, e.g. active the second head, the only way is to exit and restart Triumph_SPECT. There is no need to re-establish the telnet connection for this purpose.

In a few seconds, the Triumph_SPECT™ will open, by default, “Scan” window will be presented to you. If you have already established your studies and protocols for your experiment, please go ahead to “open and scan window” section. If this is the first time you use your machine, please take some time to build your protocol and study libraries.

To Set up a Scan



Build or modify a Study

To build a study, click the “set up” icon on the top menu bar of the software, and the set up window will replace the default window, with “study” tab at the front. The “Add” button at the bottom indicates that this is the time for you to generate a new study.

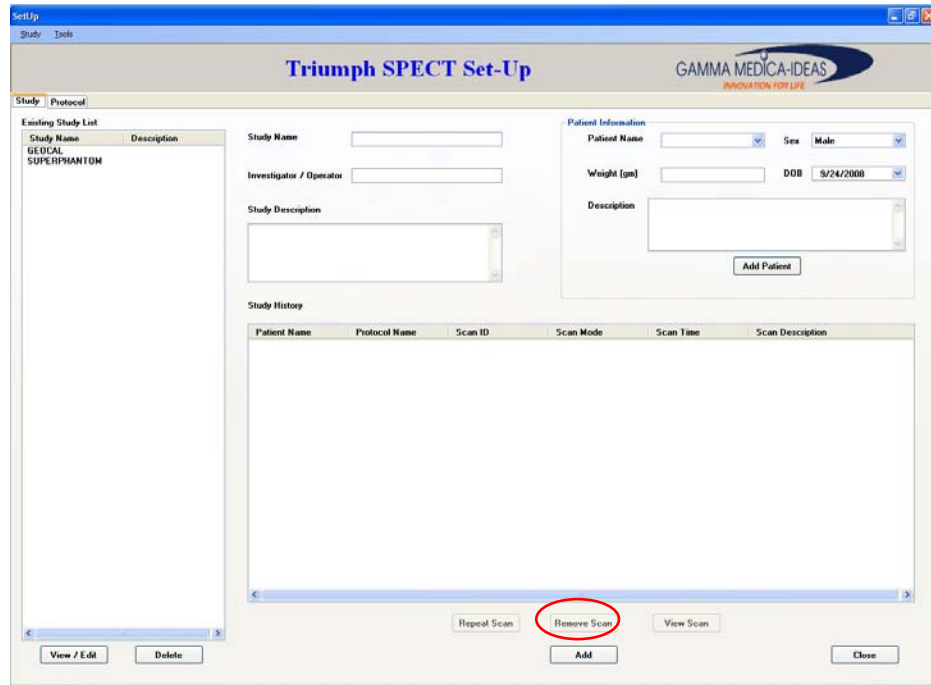


Figure 2.3.5 the original “study” window

Being as specific as possible, please enter the “Study name”, “operator” and a short, description of the study. In the example shown below, a standard scan to determine the system spatial resolution is established.

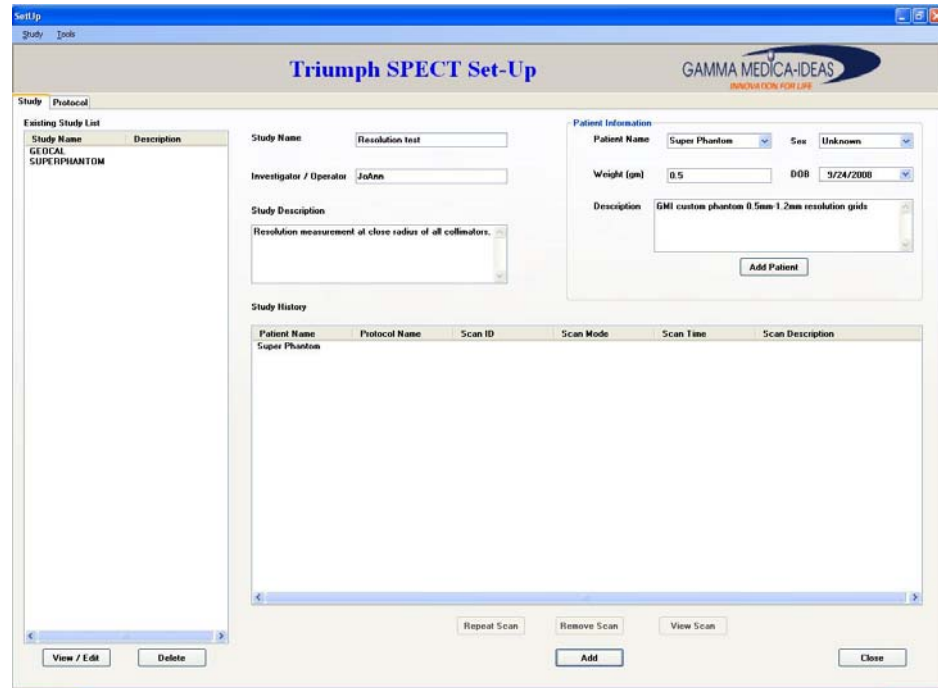


Figure 2.3.6 A study ready to “Add”

The study window usually is not complete without a “patient” established, since an experiment without a mouse or rat could not be done. Therefore, a patient set up window is co-resided in the study set up window. Do your best to fill in all the information as complete and possible for future reference (*for suggestions please reference the feature introduction in the previous chapter*). Upon finish, click the “Add Patient” button, the patient will show up in the “Study History” window.

Upon finish of all the inputs of study and patient, click the “Add button” at the very bottom of the screen, the study will show up in the left window study list, and the right panel will be ready for you to generate another study.

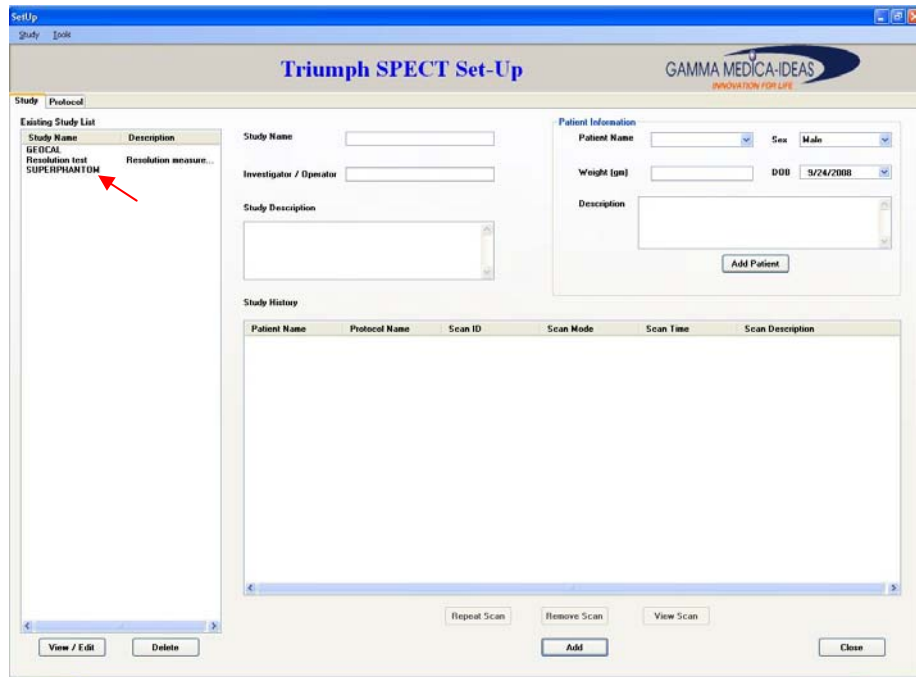


Figure 2.3.7 A study “Added” to the lists

To modify a study, select the study name in the list and click on the “View/Eidt” button at the left bottom, an editing window will be presented.

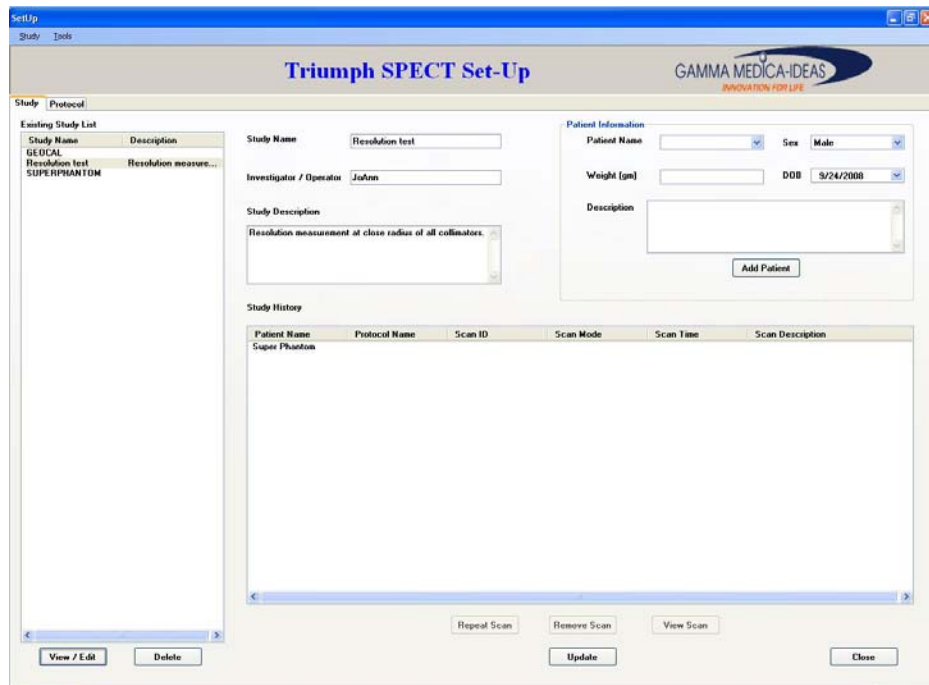


Figure 2.3.8 To edit an existing study

In this window, all aspect of the study can be changed and additional patient can be added to the list. Upon finish, click the “Update” button, and all the modification will be made to the study upon users confirm.

NOTE: Patient can not be deleted unless the entire study is “deleted” from the list! So please be careful not to make unnecessary mistypes;
NOTE: “Add” and “Update” should serve as a good indication whether you are adding or changing studies.

Build a Protocol

To build an imaging protocol, click on the “Protocol” tab in the set up window to bring the protocol page into the front.

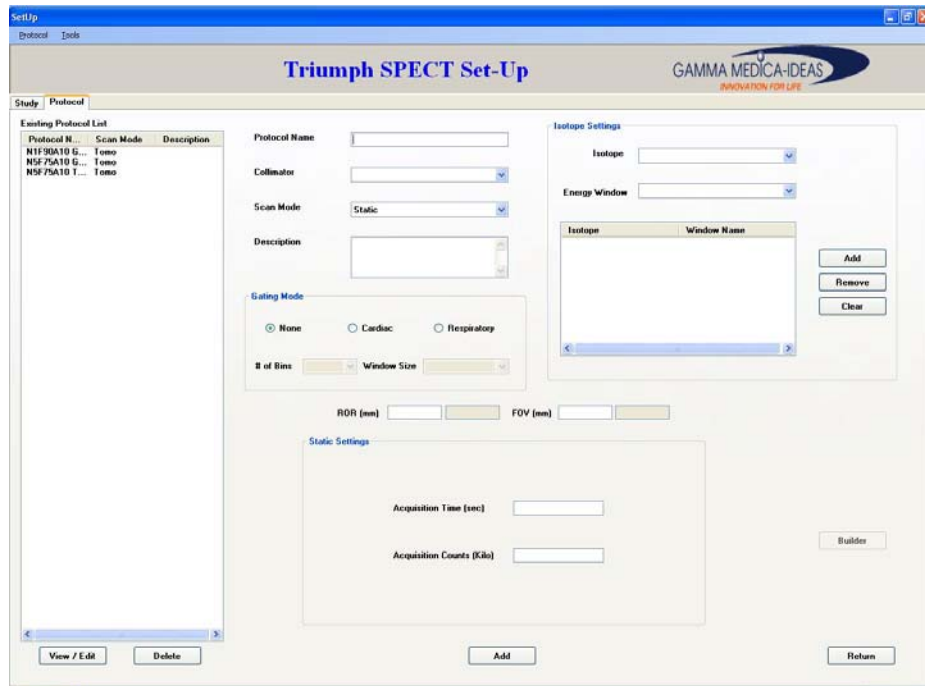


Figure 2.3.9 Original Protocol window

To create a protocol, work from “Protocol Name” input field and down wards to fill in all information regarding the system setting, note that the detail setting window at the bottom will change according the “Scan Mode” selected. So please select the “Scan mode” before trying to fill in any details.

NOTE: Radius or Rotation (ROR) can always be modified later using the “protocol builder” (see later section). So a “guessed one” or a “ball park” usually is good enough to start.

Like “Patient” to “Study”, protocol is not finished until isotope(s) are chosen. So after the camera settings, please put in all the isotopes and the energy window of choice into the isotope set up window and click “Add”. In the example, a protocol was established to acquire tomographic image of a high resolution phantom at a very

close ROR with a multipinhole collimator using Technicium 20% window. The simplest mode of tomo was selected, meaning only circular mode but a full round of rotation.

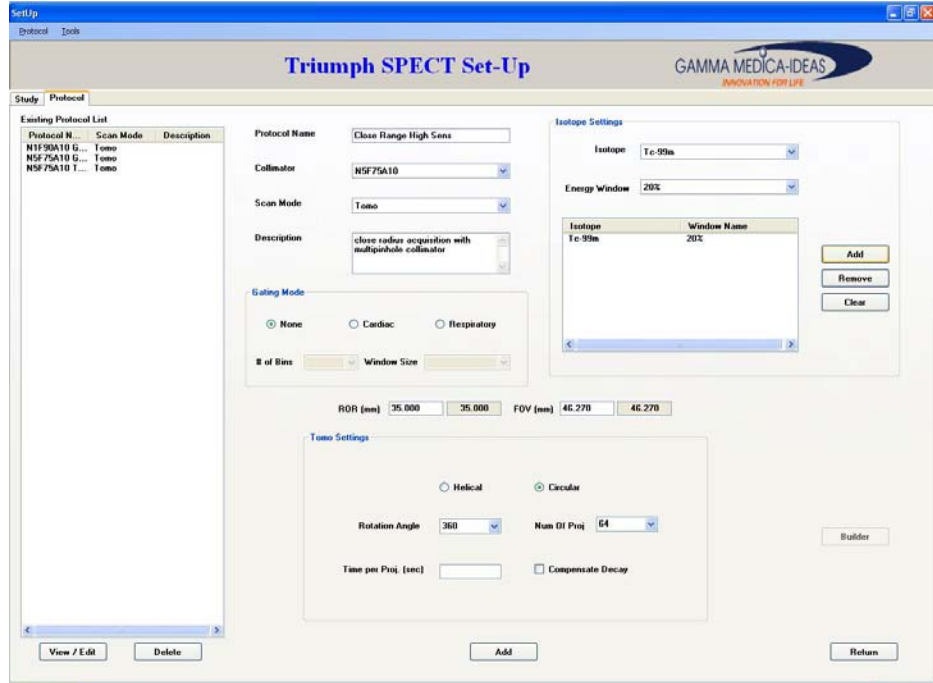


Figure 2.3 10 A protocol ready to “Add”

Similarly, “Add” button will add the protocol to the left window’s list and make the right window ready for another addition. To modify the existing protocol, select the protocol and click “View/Edit” button.

NOTE: Unlike the Patients, isotopes from a protocol can be removed by clicking the “Remove” button or even the entire list can be “cleared”. So be careful during setting to avoid accidental deletion.

Build a Protocol Using Protocol Builder



To invoke the protocol builder, click into the scan window, and the right of the “Protocol” input field, click on “Builder”.



Figure 2.3.11 To invoke a Protocol Builder

Fill in all the information on the information panel. For

ROR, bed position and gantry angle, use the hand controller to move the cameras and pick the position as you like.

Note: Gantry angle should be kept as default to assure optimal rotation unless for static scan

After all parameters have been determined. Enter the “requested counts” for program to calculate acquisition time.

Note: Requested counts should be serve as reference. In the actual protocol user should double check the acquisition time.

When all things are set, click “Create protocol”, the window will return to protocol set up for user to “Add” protocols.

To Perform a Scan - Tomographic

Open the Scan Window 

After all the studies and protocols are built, you are ready to start a scan:

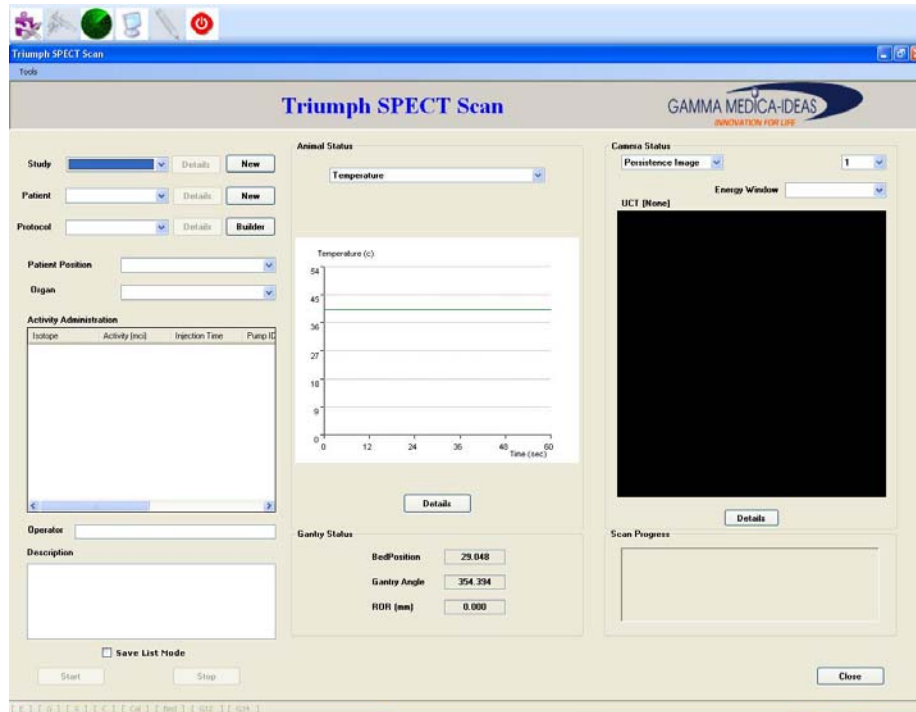


Figure 2.3.12 Default Scan Window

To start a scan, click the “Scan” icon and go into the scan window. In the left panel, from top to bottom, please select the study, patient, and protocol you

would like for your scan. . In this section the most common scan, a circular tomographic scan will be used. To start the scan, click on the “scan” icon to the top menu bar and the default scan window should be presented. After selection, the “detail” button will be activated and, upon clicking, you can review all the important features of that particular study, patient and protocol.

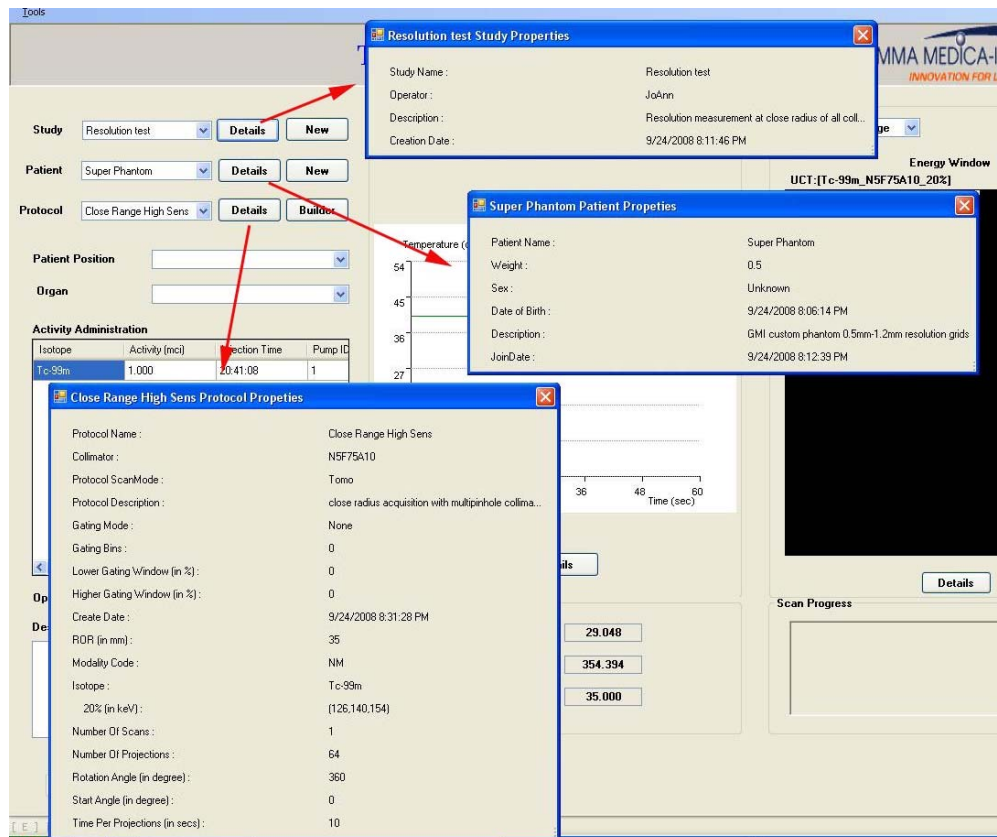


Figure 2.3.14 Details overview of Study, Patient and Protocol in the scan window.

Although not encouraged, it is possible to generate a new study, a new patient for this study or a brand new protocol on the spot. By clicking the “new” button or the “Builder” button, related set-up window will be invoked for you to generate new items for your libraries. Upon close of the set up, new items will be added to the related list, which you will be able to see when pulling the drop down list again. Select the item you want and continue with your inputs.

“Patient position” and “Organ” are not mandatory fields but it is encouraged to be filled for the completeness of the database.

“Activity Administration” only needs to be modified when an injection pump is attached to the system and users intend to activate during image acquisition. By default, one injection activity will always be filled in, but it will not affect any imaging acquisition if there is no pump connected.

“Operator” and “Description” are also optional fields but it is recommended that they be filled for the completeness of the project.

By default, “List Mode Data” are not checked hence not saved, for it consumes relatively large memories. Under the circumstance when users wants to reprocess the data under a different energy window/new isotope, partial time span, or for camera uniformity/pixel correction, list mode data can be saved by checking the toggle.

Position the animal by hand

At any time during the Triumph_SPECT™ operation, animal or imaging objects can be positioned into the gantry by using the hand controller to move the patient bed out to the front deck. Please reference Triumph manual section 1: operation manual, to perform this operation. Remember that for animal bed to move all the way to the front, no imaging module, i.e. cameras, x-ray tube and detectors, can be anywhere in the gantry (off limit switch). When in doubt, push all the “out” buttons on the hand controller to make sure.

The following picture shows the animal positioned, secured and connected to the gantry gas anesthesia system.

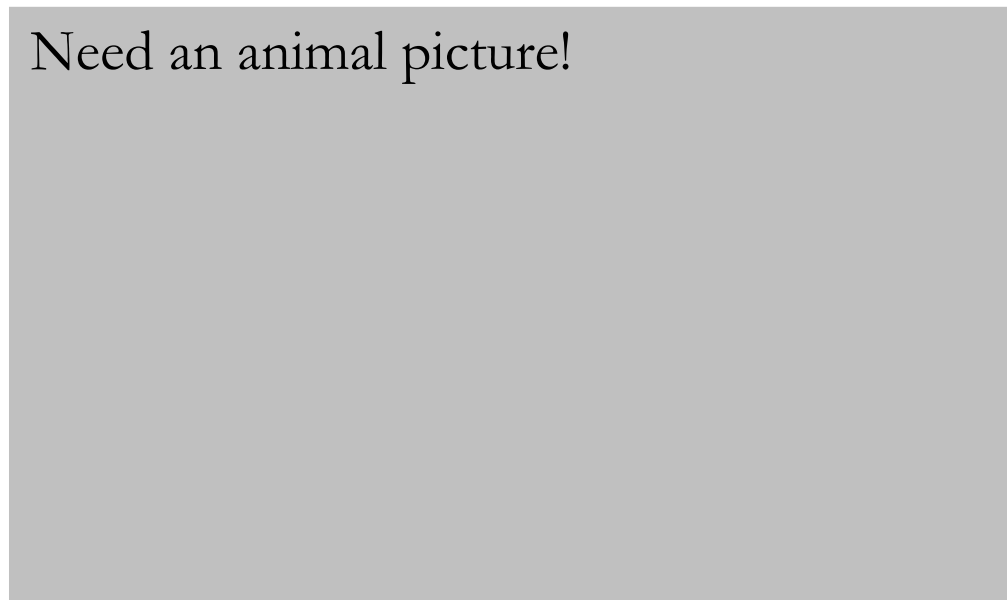


Figure 2.3.15 Animal positioned and ready to be imaged

Alternatively, the bed can also be sent out by the “protocol builder” bed setting function. Please reference later section on how to do it.

NOTE: At this point the scan can start! The following instructions on how to fine tuning the animal position in gantry are optional! Automatic centering of the target of interest is provided by the scanning procedure.

When the animal or object is sent into the gantry, you will gain you first glance at the object you want to image on the right panel of the scan window.

At this point, you can either click the “start” button on the scan window, or use the hand controller to fine position your animals and/or have a thorough check of your position. Please reference the section 1 of this manual for detail hand controller movement to:

1. *Move in and out the patient bed;*
2. *Move up and down the patient bed;*
3. *Move left and right the patient bed;*
4. *Move in and out the gamma cameras;*
5. *Rotate the gantry.*

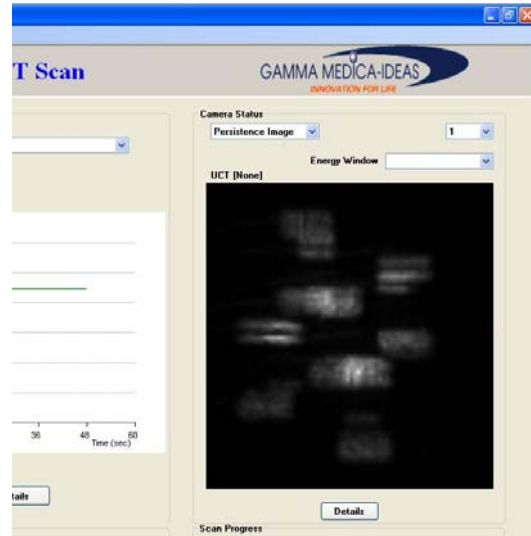


Figure 2.3.16 Instant images after object positioning.

In addition, user can choose to view different head, view energy window, choose different energy window or click “Details” to see all camera heads. Please reference the chapter 2 of this section of manual for detail introduction of all the features in this “viewer” window operation. In this paragraph, only basic function is cover to enable user to start the scan.

Start the Sacn - Automatic and affine positioning

After all the information in put into the left panel, and the animal secured on the bed at the front deck, you can click the “start” button to start scan preparation. Upon pushing “start”, first step for automatic targeting will be presented:

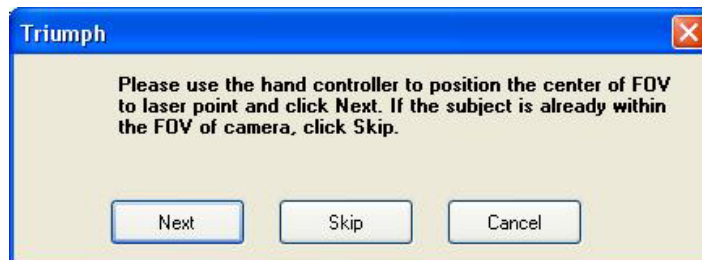


Figure 2.3.17 step 1 of scan: position the target of interest.

If you have already positioned the animal into the gantry and you are satisfied with its position, click on skip. Otherwise, use the handcontroller and move the animal bed towards the front gantry entrance where the “guiding lasers” are positioned (*to activate the laser, click the right buttons on the hand controller, please reference the operator’s manual for detail*). By moving the bed in and out, up and down left and right, try your best to position the target of interest and the laser center. Then click “next” in the message window. “Skip” or “Next”, step 2 will be presented.

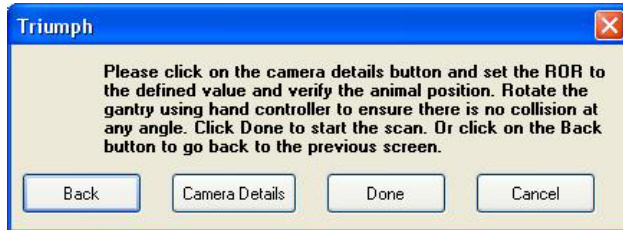


Figure 2.3.18 Scan step 2: refine the ROR

If you have positioned your camera and you are sure that the ROR matches your protocol, click “Done” directly. Otherwise, click “Camera Details”. The camera detail window will be presented, showing persistent images of all activated cameras.

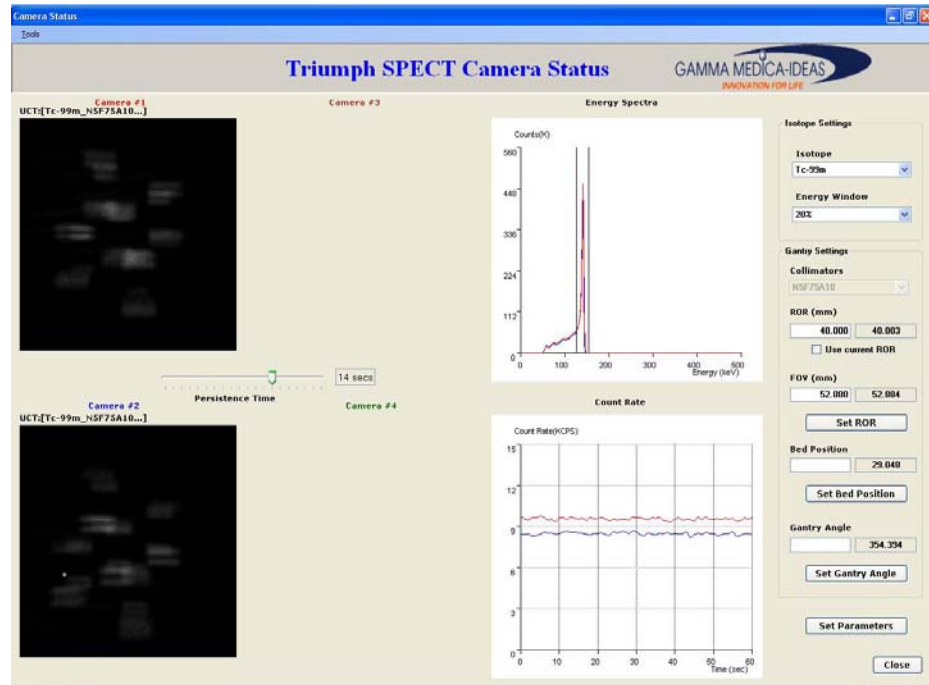


Figure 2.3.19 Camera Detail Window

In this window, set the ROR (FOV will automatically determined based on the set ROR), bed position and even gantry angle to better fit the protocol.

If you realize that the ROR you set for the protocol was unreal, use hand controller to move to a satisfying ROR and check the toggle box by the “Use the current ROR” text.

If you wish to modify yet again the protocol, click the “Set Parameters” button at the bottom, the parameter window will pop up, allowing you to change (OK) or reset to original (Reset).

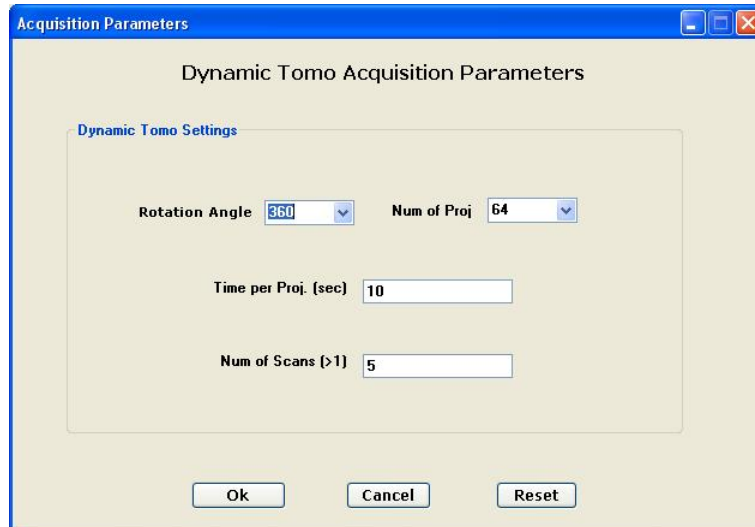


Figure 2.3.20 Change parameters in the camera detail window

After setting all the parameters, close the camera detail window will bring users back to the step 2 message window. This time, click “Done”. The Scan will officially start.

The gantry will first position the gamma cameras to the pre-defined ROR, then rewind to pre-defined starting position. Then the scan will start.

During scanning, user can monitoring the progress by the following marks on the scan window:

- A. The Progress bar;
- B. The information window, usually summarizing after each projection;
- C. The estimated time passed and time left;
- D. The persistent window.
- E. Animal status (please reference chapter 2 for more details)

NOTE: Circulated with red circle in the image, the total counts acquired in each projection is shown after each projection is acquired.

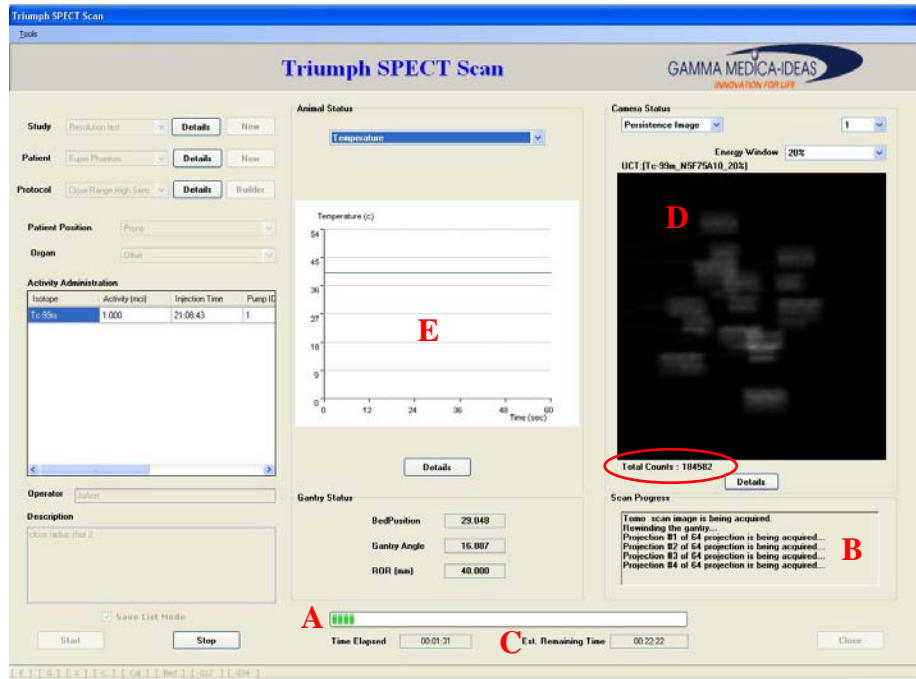


Figure 2.3.21 Scan in process

To perform other type of scan

Static Scan

Static scan is an acquisition of a 2D gamma image. To perform a static scan, simply build a protocol with the “static” selected in the scan mode section, then fill in the needed setting parameter in the bottom window.

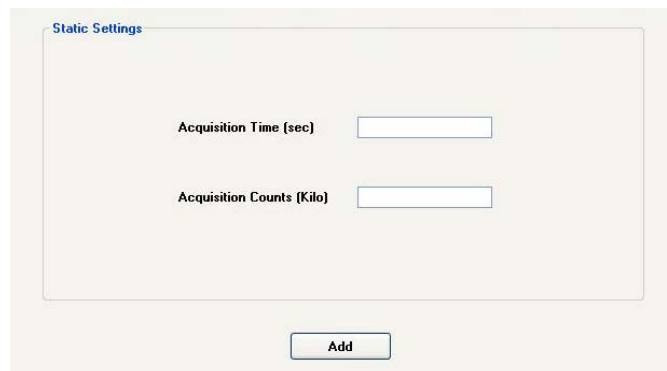


Figure 2.3.22 Static scan settings

When perform the scan, choose the static protocol. Animal positioning and scan manual operation are the same as for the tomo scan.

Dynamic Scan

Dynamic Static scan is an acquisition of a series of 2D gamma images for a pre-set time point and time span. To perform a dynamic static scan, build a protocol with the “Dynamic” selected in the scan mode section, then fill in the needed setting parameter in the detail setting window (*please reference the feature introduction in the previous section*). The Phase 2 will be activated once phase 1 is all filled.

After the parameter is set, the dynamic scan can be performed in the scan window in the similar way as the static scan. If “Pause” is enabled, a “check point” window will appear in between phases, awaiting user’s keyboard action.

Tomographic Spiral Scan

To perform a spiral scan, “Helical” instead of “Circular” mode needs to be selected in the “Tomo settings” during protocol set up. After “Helical” is selected, the window will be formatted to remove the “Rotation Angle” for it will be automatically established.

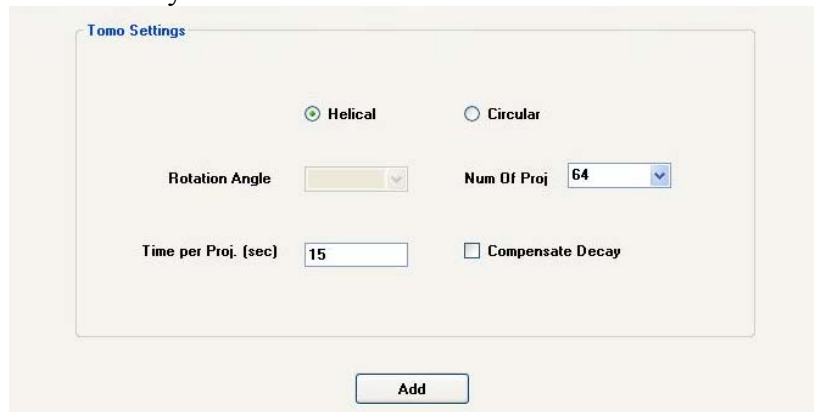


Figure 2.3.23 spiral scan setting

When performing a spiral scan, select the spiral scan protocol in the scan window, position the animal/object onto the bed in the front deck, then click on “start” button, a different positioning guide will show up:

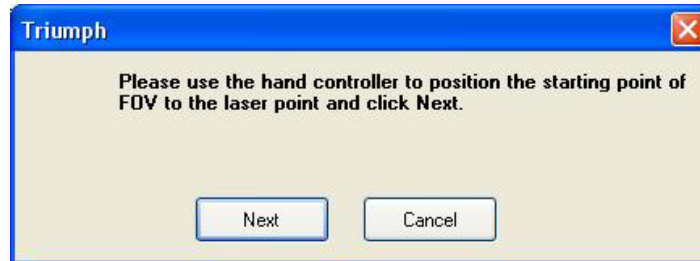


Figure 2.3.24 Step 1 message for spiral scan

At the request, use the hand controller to move the bed so the starting position is aligned with the front entrance laser, then hit “Next”. The second request will show up, asking for where it ends.

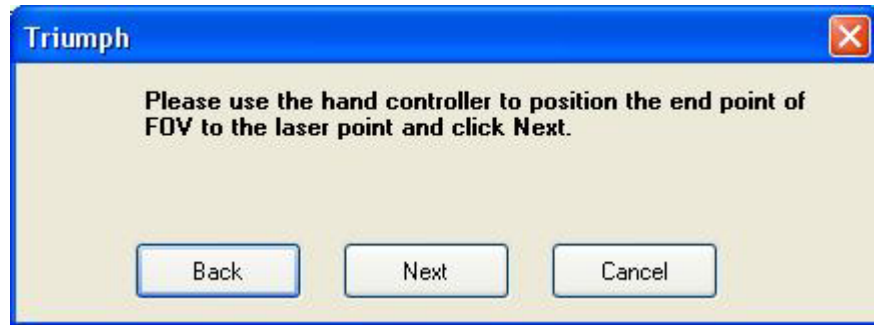


Figure 2.3.25 Step 2 message for spiral scan

At the request, user can use the hand controller to define the end point, alternatively, “Back” button can be hit should user wish to change the starting point. Upon setting the end point, hit “Next”. The regular message box for “Camera Details” will be presented. User should follow similar routine to fine position the object, except **do not worry about the bed position, it won’t matter!**

After all the parameters are set, and user clicks “Done”, the scan will start, the gantry will first move the animal bed to the point so the “start” point will be at the center of the FOV, then the cameras will be moved to ROR, then gantry will rewind to fixed starting angle. All progresses can be monitored in the same way.

NOTE: The bed only moves inward! Therefore, the “starting” position should always be bigger than the ending position! Otherwise, movements will be all wrongfully operated.

NOTE: The moving step is calculated based on the total moving distance defined by user and a hard coded rule to cover the entire FOV within 180° of gantry rotation.

Dynamic Tomo Scan

To perform a dynamic tomo scan, the “Dynamic Tomo” should be selected during protocol set up. The respective setting window will appear in the protocol window bottom panel:

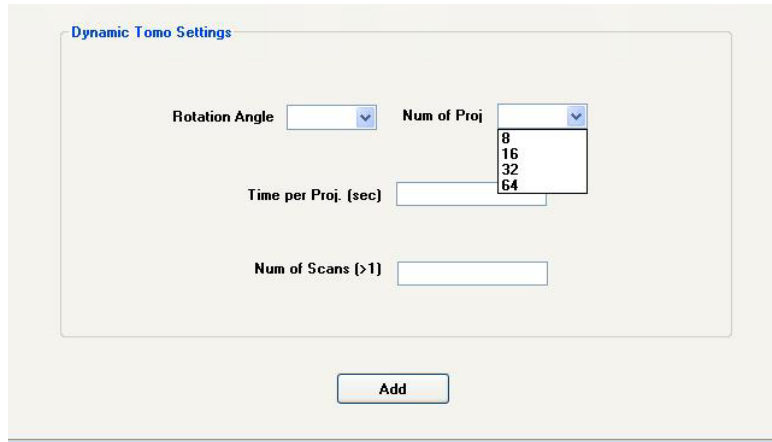


Figure 2.3.26 Dynamic tomo setting

Comparing with the standard tomo window, the choice of “Helical” vs “Circular” is removed as the dynamic scan can not be performed with helical mode. In addition, one more input field is needed: how many frames to be performed.

After setting up the protocol, all scan operation of Dynamic scan is the same as the standard tomo scan.

NOTE: There is no phases! Dynamic tomo scan can only be performed with fixed rate (time per projection).

Cardiac or Respiratory Gated Scan

At this release, Cardiac or respiratory gated scan has not been enabled.

After a Scan

At this release, Acquisition using Triumph_SPECT™, reconstruction using FLEX_SPECT™, and image display and analysis using VIVID™ are independent and unlinked. Therefore, the acquisition, all projection images can only be qualitatively viewed the Triumph_SPECT™ data viewer window. For reconstruction or further processing and analysis, projection data need to be “exported” to a common folder on the PC which is accessible by other software.

Data Viewing



To view acquired data, click on the “Data Viewer” icon on the top menu bar, the image database will be presented to you.

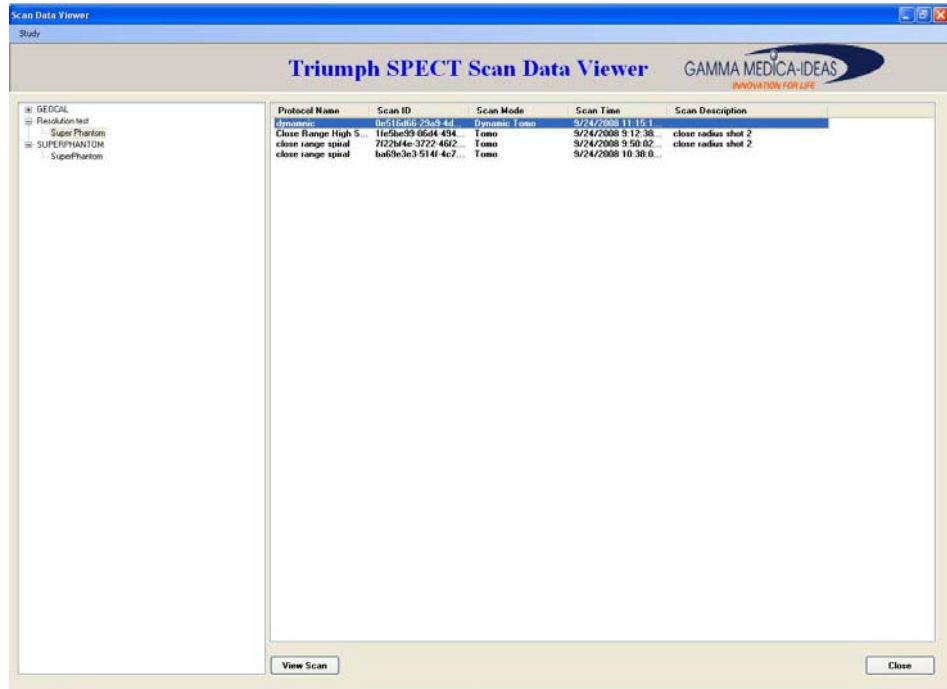


Figure 2.3.27 Image Database in the data viewer

To view, select the study in the left the window and the particular scan in the right, then click “View Scan” button. The chose scan will be presented. *For detail contents in the window please reference the previous section.*

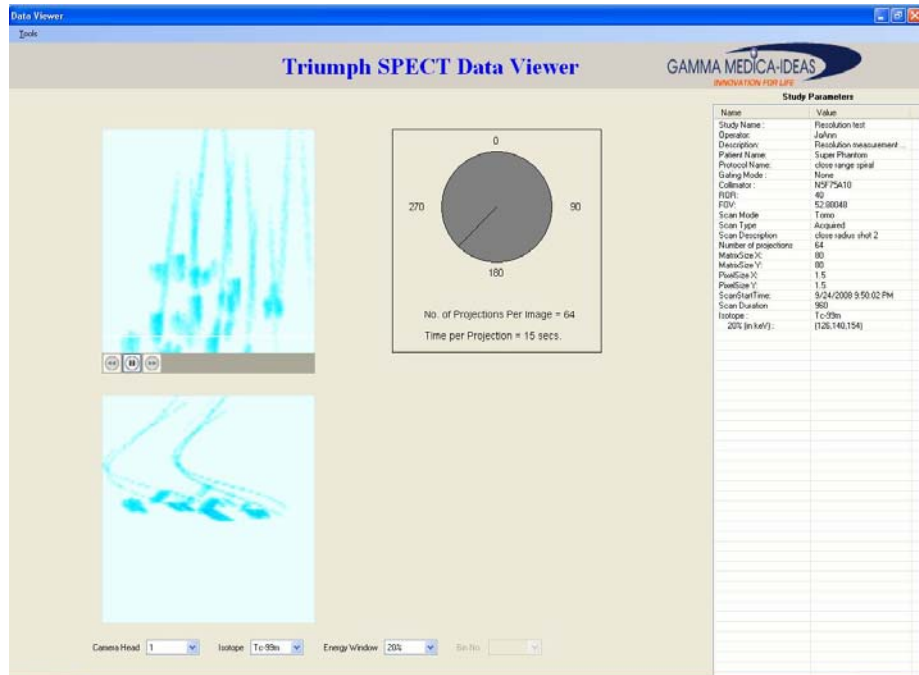


Figure 2.3.28 Data Viewing Window, the red arrow points to the play control bar.

Data Import and Export

Projection data are exported and imported through the data viewer window. To export data as standard interfile, select the targeted scans from the right window, then go to the top menu bar and select Study → Export → Interfile.

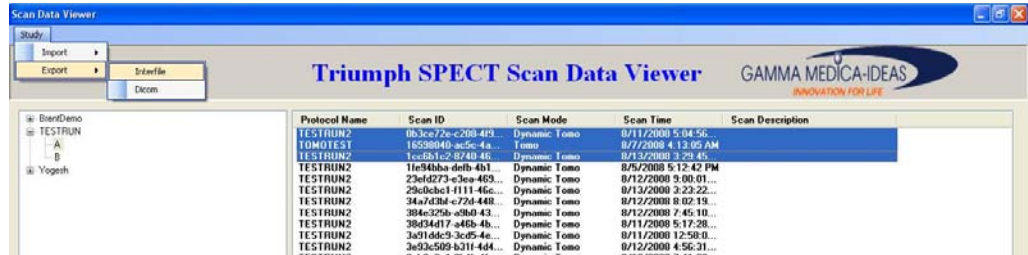


Figure 2.3.29 Export data

Upon selection, a message box will show up asking user to verify the destination of the exported file. By default, the data are stored in C:\Interfile directory. If user would like to choose a different data path, click on the path box on the right and define a directory.

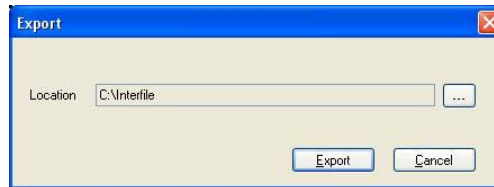


Figure 2.3.30 Select destination of data export

After data path selection, click “Export”, the selected data will be automatically converted to the two file (.img and .hdr) interfile format and stored in pre-defined data folder.

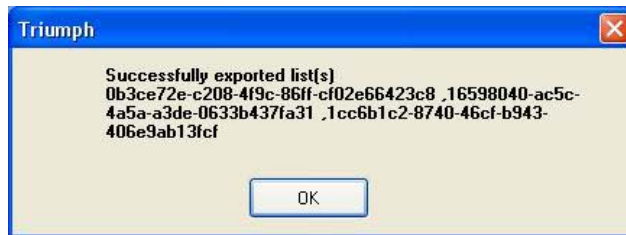


Figure 2.3.31 Notice for successful data export

NOTE: The exported data file names are results of Triumph_SPECT internal database tracking logic. After export, user can change the file name to their liking, as long as the corresponding “data path” in the .hdr file is changed accordingly also.

In similar way, standard interfiles can also be imported into the database.

Service and Maintenance - Calibration



Change a Collimator

Collimator exchange in Triumph gantry requires gantry rotates to specific angle so that the targeted camera head is positioned at proper height at the service door. To automatically perform this rotation, Triumph_SPECT™ implemented a “collimator exchange” routine. Click into the “calibration” (icon shown above) window and on the top menu bar select “Tool” → “Change Collimator” and follow the instructions.

Gantry Calibration

To ensure accurate gantry rotation and limit switch sensing, “Gantry calibration” needs to be performed on a monthly basis or anytime when the gantry was powered down. To perform gantry calibration, click into the calibration window, the default window should be gantry calibration tab. Click on start, the gantry will automatically run all the modules to their limit switches and start calibration process.

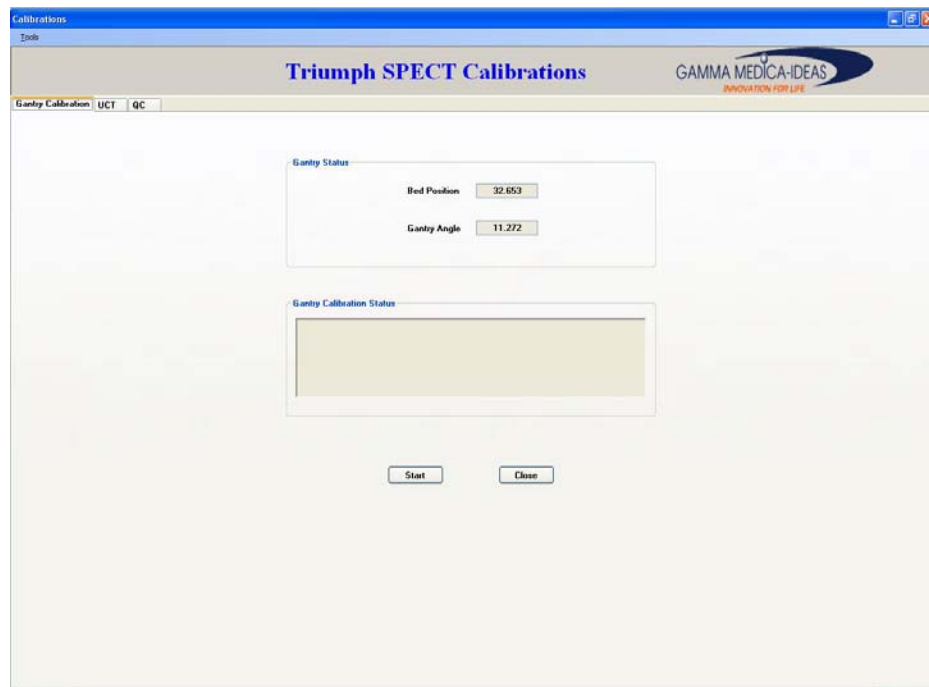


Figure 2.3.32 Gantry calibration window

Upon finish a “gantry is calibrated successfully” message will show up in the information box.

NOTE: Please remember your camera setting prior to the gantry calibration, for modules will NOT be returned after calibration. All modules need to be repositioned.

Camera Calibration – UCT and QC

The UCTs (Uniformity Correction Tables) of the gamma cameras must be updated on a regular basis due to a small amount of drift that occurs within the electronics over time. To calibrate the cameras, a planar image of a uniform flood source must be acquired. The calibration is source- and collimator-specific, so there must be a calibration file for each isotope and energy window. While all SynapSPECT use an intrinsic image (i.e. an image acquired with a point source without collimators), single pinhole and parallel hole SPECT require extrinsic images (i.e. images taken with flood phantom with the exact collimator). Once the necessary images have been acquired, a UCT will be automatically generated. After the UCT has been generated, a QC will run to ensure proper functioning of each camera.

Uniform sources for UCT calibration

SynapSPECT requires an image without the collimators, therefore, a $\sim 10\mu\text{Ci}$ point source (e.g. a 10λ liquid at the bottom of an Eppendorf tube or in a syringe) would be enough. Position the eppendorf tube on a regular mouse bed and send into the gantry and have the cameras midway, or adjust so that the average count rate could around 5000-8000 cps.

To acquire extrinsic images, a liquid flood phantom is needed. GM-I provides a 2"x2" flood phantom for single pinhole collimators and a 5"x5" phantom for all parallel hole collimators. Total activities in the phantom must be adjusted based on the count rate to achieve the most efficient and effective calibration. Usually, 10mCi of Tc99m for single pinhole (2"x2") and 5mCi for parallel (5"x5") is recommended. Due to the shape of the flood phantom, extrinsic UCT can only be done one pair of cameras at a time. To position the phantom, use the supplied "phantom holder" instead of animal bed (please refer to the operator's manual) and have the cameras as close to the phantom as possible, centered well.

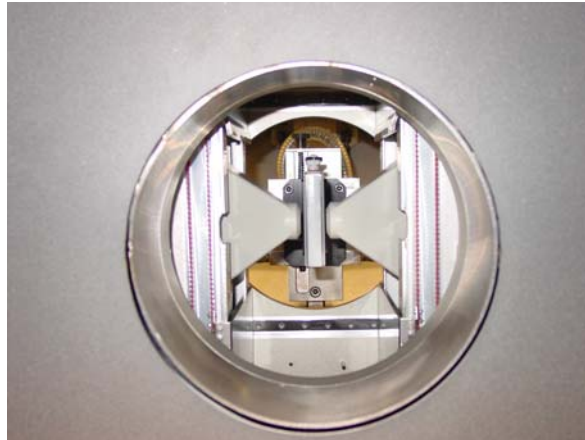


Figure 2.3.33 Flood image acquisition for UCT. The cameras are in service position, closing in on the flood phantom.

Procedure for UCT calibration

To run UCT, click into the calibration window and select “UCT” tab. In the window, from left to right fill in all information asked. With the following guidelines:

1. Source isotope is the isotope used during UCT flood acquisition;
2. Target isotope is the “additional” isotopes with similar energy peak profile. E.g I^{123} and Co^{57} can both be the target isotope of Tc^{99m} .
3. Total count value is recommended to be at least 10000 kilo for UCT and 3000 kilo for QC.

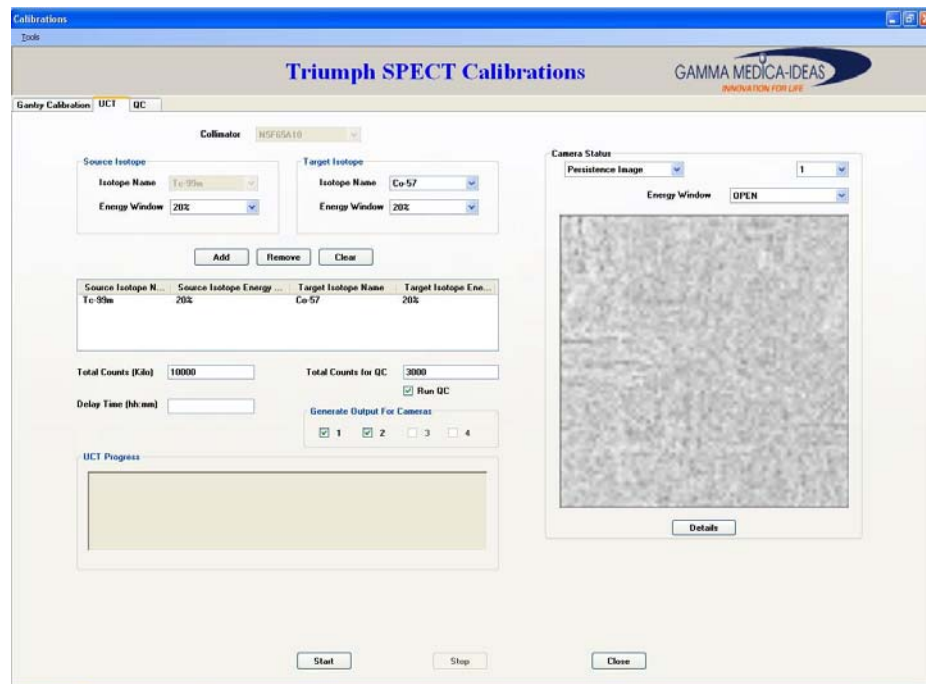


Figure 2.3.34 UCT window

After proper parameter input and proper source positioning, click start to start acquiring the flood image. UCT will run automatically after the acquisition. UCT is recommended to be recalculated at least every month for electronics do shift with time which will affect pixel response to signals.

If the QC tab is checked, UCT will be followed by a QC acquisition and noise calculation if the “run QC” is checked.

QC can be run independently anytime users want to check if the camera uniformity is still good. Unlike UCT, QC should be done more frequently, preferably every other week during a constant use of the system. To run QC, prepare source isotopes in a similar way as for the UCT, then click directly into the QC tab in the calibration window.

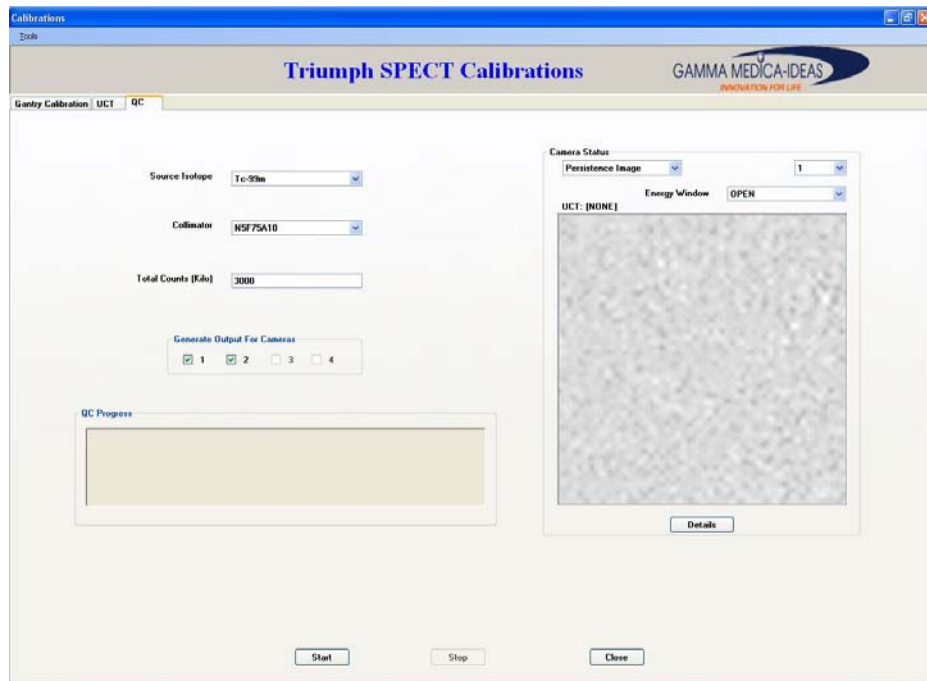


Figure 2.3.35 QC window

After putting in necessary information and positioning the source and cameras, click “Start”, the program will perform a standard “static” acquisition and calculate whole FOV uniformity quality factor: “standard deviation” over “mean” pixel values.

Error Messages and Troubleshooting

This section will highlight some of the many check point message boxes that should guide users away from mistakes and to proper next steps.

Gantry Connection Error



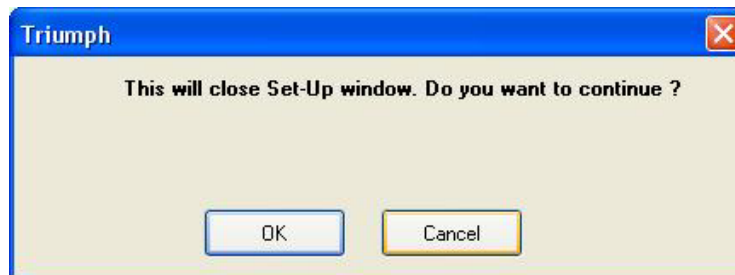
Most commonly, user would get this message, when trying to start Triumph_SPECT™ without switching the gantry control to “SPECT” computer on the hand controller. User can choose “Ignore” if only want to view or export data.

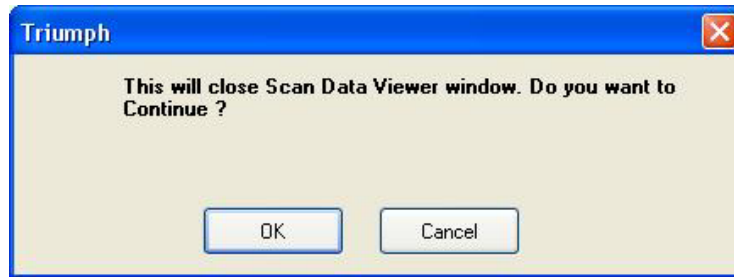
Program Connection Error



This message will show up if the gantry is not connected to the computer or if the DDROB is not communicating with the program. Check if the hand controller is switched, and if the “telnet” process has been completed.

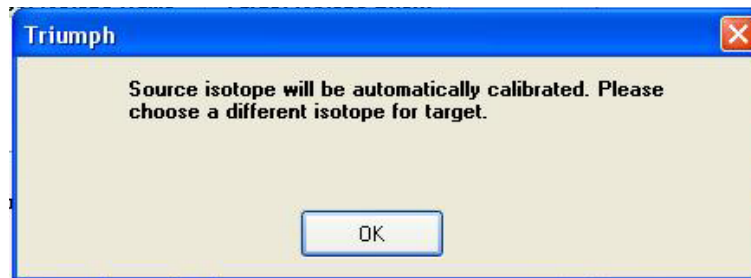
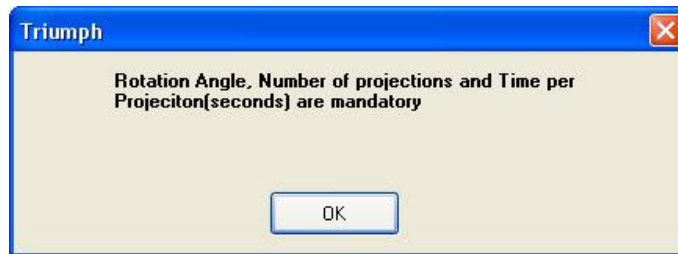
Warning upon an exiting action





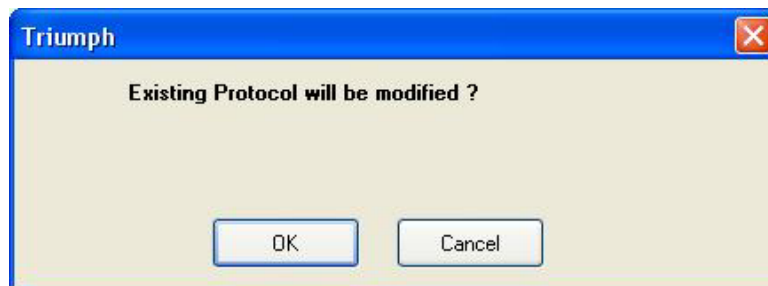
These messages will show up every time user click a “close” button or hit the cross symbol of a window. This is to prevent accidental keyboard stricks.

Warning for missing information



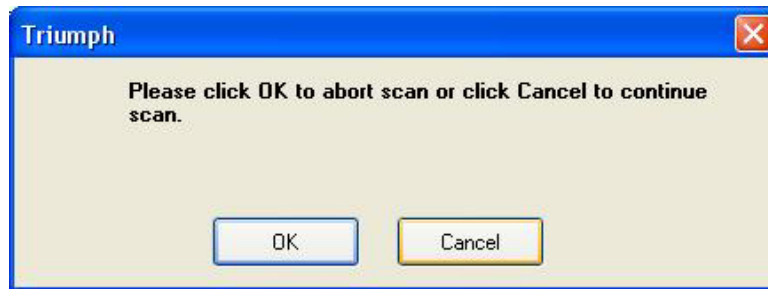
These type of messages will inform user what is missing or incorrectly put during a set up process, these messages is imbedded in all set up windows, scan windows and calibration windows.

Warning for modification



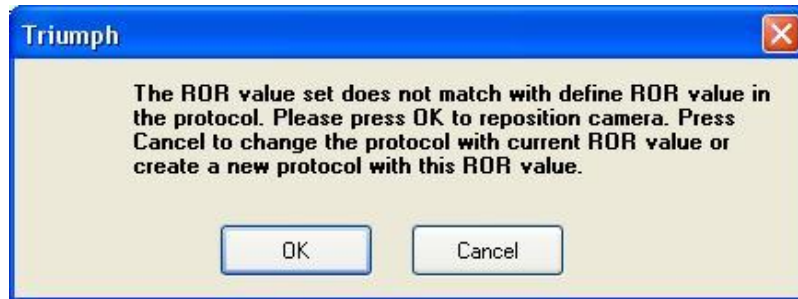
Whenever a protocol or a study has been modified and user struck the “Update” button, the message will appear for user to confirm purposeful action.

Confirmation on exiting action



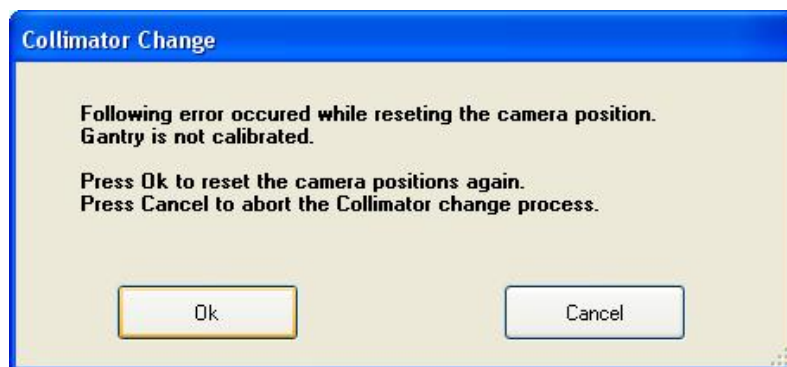
When an on going process is interrupted by hitting a “stop” button, these type of messages will show up asking for confirmation.

Processing Error:



This type of check point message will show up is the gantry sensors for bed position, camera position or gantry position does match a setting. The ROR mistake is the most common case for the program request a very precise value. When shown with this message, double check the setting value and hit “set” again till it stops showing.

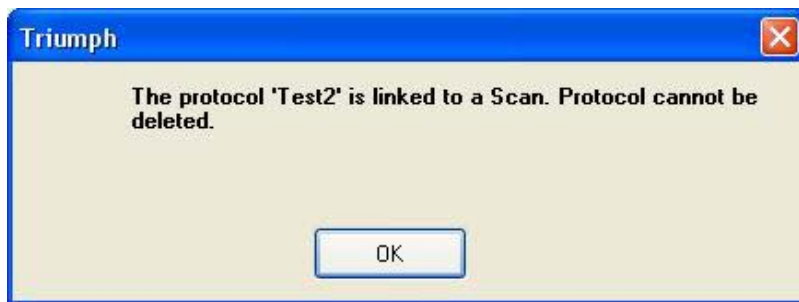
Gantry performance Error





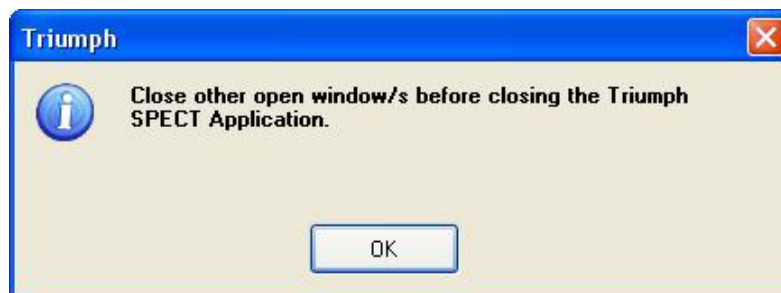
When a gantry calibration is out of date, which will happen after 1 month or anytime with the machine powered down, any action that requires a gantry position sensor will produce such messages. Click OK and proceed with a gantry calibration should solve the problem


Data Management Error



Just like the clinical system, studies, protocols and patients are tightly controlled. Once set up in the database and a scan has been performed, it will not be removable.

Final Exit



This is the final check up point for exiting Triumph_SPECT™. Before hitting the “Exit” button , all windows have to be closed.

Note: These are only partial of the messages implemented in the program. Other message boxes will show up when induced with errors or checkpoints. Follow the instructions the boxes and you should be able to carry out a scan smoothly.

FLEX™ SPECT Software and SPECT Reconstruction


To launch the FLEX™ SPECT program for reconstruction of SPECT data acquired with pinhole collimators, double-click on the “*FLEX™ SPECT*” () icon located on the desktop. The start-up screen shown in Figure 2.4.1 will appear:



Figure 2.4.1 The start-up screen for FLEX™ SPECT .

Under “*Select mode*”, there are three options available in the drop-down menu: *Single Reconstruction*, *Batch Processing*, and *ColorSPECT*. Each of these options will be described in detail in their corresponding section of this chapter.

Single Reconstruction

Single Reconstruction is the simplest reconstruction option in FLEX™ SPECT.

Once *Single Reconstruction* has been selected, the screen shown in Figure 2.4.2 will appear:

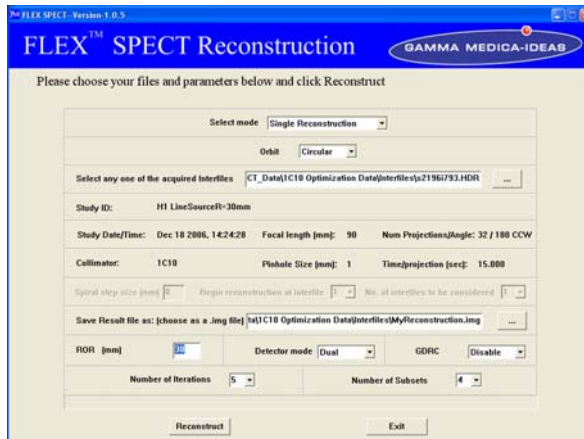


Figure 2.4.2 Single Reconstruction mode.

- First, select an Interfile to be reconstructed. Interfiles are a standard nuclear medicine file format for image data that consist of two separate files for each data set: one is a header file (.hdr) containing information about the data set, and the other is the image data (.img) in a binary data format. Interfiles can be either acquired tomography data or reconstructed data, and are usually exported from Triumph_SPECT™ data export function into C:\Interfile folder. Under “Select any one of the acquired Interfiles”, click the *browse* button () to open a browse dialog window. Locate and select the Interfile header file to be reconstructed. Once the Interfile has been selected, information about the study will automatically be displayed on the screen.
- The desired name of the resulting reconstruction file must be entered under “Save Result file as: (choose as a .img file)”. Click the browse button in this field, and a dialog box will appear. Here, select a file path and name for the reconstruction file.
- The Radius of Rotation (ROR) of the study must be entered under “ROR (mm)”. This information is normally available in the “Study ID” name and needs to be filled out in units of millimeters (mm).

When these last two fields have been filled out, the reconstruction is ready to be started. Click on the *Reconstruct* () button to start the reconstruction. A progress bar will appear at the bottom of the screen and will track the state of the reconstruction. When the reconstruction is complete, a message showing the location of the saved resulting file will be display.

Four optional controls can be modified in the Single Reconstruction mode if so desired:

- The Detector mode is normally set to the default value of the user’s

system (“*Single*” for one gamma camera and “*Dual*” for two gamma cameras). However, there are situations in which the user might need to change the detector mode (e.g. if one gamma camera is currently unavailable then a single head reconstruction may be necessary).

- GDRC is an option to enhance the physics of the reconstruction and is discussed in more detail later in this chapter.
- The Number of Iterations and Number of Subsets fields relate to the nature of the iterative reconstruction algorithm used in FLEX™ SPECT. FLEX™ SPECT uses an Ordered Subset Expectation Maximization (OSEM) iterative reconstruction algorithm for its pinhole reconstructions.
 - “*Number of Iterations*” controls the number of full iterations (“full” in this sense means the complete set of projections are used) used before the OSEM is stopped. This number can be as small as 1 and as large as the user desires, though the time of reconstruction is proportional to the number of iterations, and so large values (i.e. greater than 10) are not recommended.
 - “*Number of Subsets*” controls the number of projection subsets used as updates in the reconstruction for each iteration of forward-projection/back-projection. The Number of Subsets therefore must divide evenly into the number of projections for the given study. As the number of projections is a multiple of 16 (e.g., 32, 64, and 128) the possible values of the Number of Subsets are 2, 4, 8, and 16. GM-I currently recommends for a general-purpose reconstruction, 5 iterations of 4 subsets (as shown in Figure 2.4.2).

FLEX™ SPECT can be closed by clicking the “*Exit*” button in the lower right-hand corner of the screen, or by clicking on the red X in the upper right-hand corner. A warning will appear to ensure that the user does not accidentally exit the program.

GDRC: SuperSPECT

FLEX™ SPECT is capable of modeling the physics of the pinhole and the pixilated detector, and can thus dramatically improve the spatial resolution and noise characteristics of the reconstructed images. Figure 2.4.3 shows a cross-section of a pinhole collimator with the four key parameters that define

the pinhole geometry. FLEX™ SPECT automatically accounts for these parameters, based on the name of the collimator (*For more information, please reference Chapter 1 of this manual*) detected in the Interfile being reconstructed.

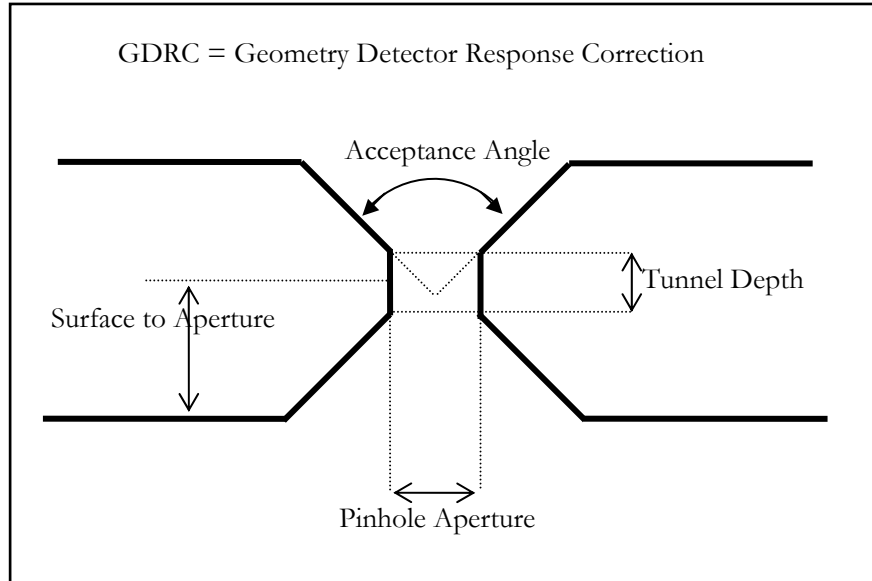


Figure 2.4.3 Cross-section of a pinhole collimator.

FLEX™ SPECT uses a *Geometric Detector Correction Response* (GDRC) in modeling the collimator and detector. This means a geometric approximation to the pinhole point-spread-function (PSF) is convolved with a Gaussian representation of the detector intrinsic spatial resolution (as defined by the pixel-pitch of the detector) in order to approximate the combined collimator-detector PSF. This geometric approximation proves to be quite accurate and greatly shortens the reconstruction time compared to using an empirical model of the PSF.

The four parameters (as shown in Figure 2.4.3) that characterize the collimator are the pinhole aperture, the tunnel depth, the surface-to-aperture distance and, the full acceptance angle. The pixilated detector is characterized by its intrinsic pixel-pitch. Please note that at present, pinhole penetration and detector depth of interaction are not directly taken into account by *SuperSPECT*.

GDRC can be enabled (or disabled) in FLEX™ SPECT by selecting “GDRC” in the drop-down menu. GDRC is currently supported for single-pinhole reconstructions of both circular and spiral orbits. GDRC-enabled is somewhat slower than GDRC-disabled due to the increased computational requirements of modeling the collimator-detector PSF. GDRC-enabled is


recommended in cases in which the user wants to achieve maximum spatial resolution, and is not overly-concerned with reconstruction times. Reconstructions with GDRC-enabled take typically three times as long as GDRC-disabled reconstructions with the same number of iterations.

Spiral SPECT Reconstruction

Once a *SpiralSPECT* tomographic dataset has been acquired, select the *Single Reconstruction* mode, and select “*Spiral*” under the “*Orbit*” drop-down menu. Three new fields will become active (as shown in Figure 2.4.7); in most cases, only one of these fields needs to be filled out.

Enter the value of “*Spiral step size (mm)*” that was used in the acquisition (i.e., the same number Δz that was used in the *gantry.ini* file to acquire the tomo dataset) along with the sign (+/-) to ensure proper translation direction. The “*Begin reconstruction at Interfile*” and “*No. of interfiles to be considered*” fields may be modified for the uses listed below, but in most cases, their default values should be adequate.

- “*Begin reconstruction at Interfile*” is an optional field that allows the user to discard any number of the first orbits (e.g. if this field is set to 2, the first orbit will be discarded in the reconstruction). The default value of this field is 1 (i.e. to start with the first orbit available).
- “*No. of interfiles to be considered*” is an optional field that allows the user to limit the spiral reconstruction to a smaller subset of the total number of orbits acquired (e.g. if the number of orbits in a spiral acquisition is $N_{\text{orbits}} = 4$, and this field is set to 3, the last orbit will be discarded in the reconstruction). The default value of this field is “*All*” (i.e. to consider all available orbits in the reconstruction).

Fill out the remaining fields, as described under the “*Single Reconstruction*” section of this chapter. Spiral reconstructions work in both single and dual detector mode, and with and without GDRC enabled. Only one of the tomo dataset Interfiles needs be selected; the others will automatically be located as long as they reside in the same directory as the selected Interfile. Click on  to start the reconstruction.

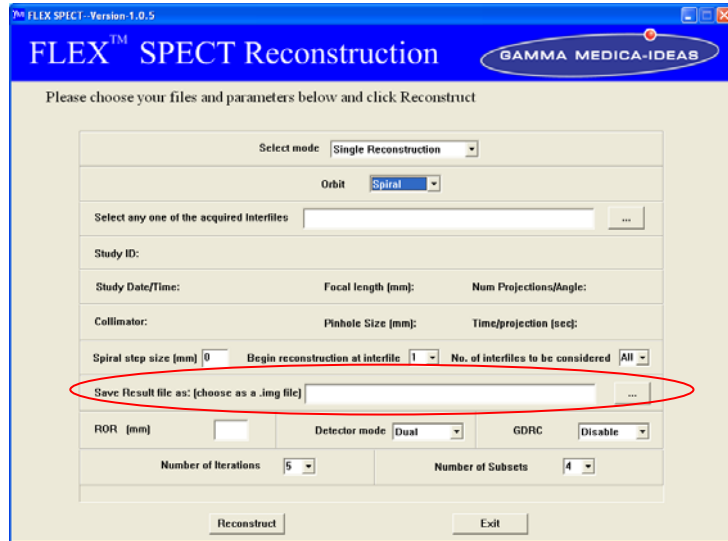


Figure 2.4.7 Single reconstruction of a spiral orbit.

Spiral data can be reconstructed into a rectangular size or zero-padded into a cube. Rectangular reconstructions require less disk space, but may not be viewable by all images viewing software. In the parameter file *spect.ini*, “*spiral_cube*” can be set to 0 (rectangular) or 1 (cube). *For more information on parameter files, please reference the appendix of this section.*

Batch Processing

Batch processing is a convenient tool for processing a large number of reconstructions of all types (circular, spiral, multi-pinhole, single-pinhole, etc.). Each reconstruction is filled out individually and the batch job is started at the user’s convenience. Batch processing is particularly convenient for starting long jobs intended to run overnight. It is also an integral part of *ColorSPECT* processing (see the *ColorSPECT* section of this chapter for more information). The *Batch Processing* screen (shown in Figure 2.4.8) can be opened by selecting the “*Batch Processing*” option in the “*Select mode*” drop-down menu. *An alternate method is to create a batch file. For more information, please reference the “Batch Files” section in the appendix.*

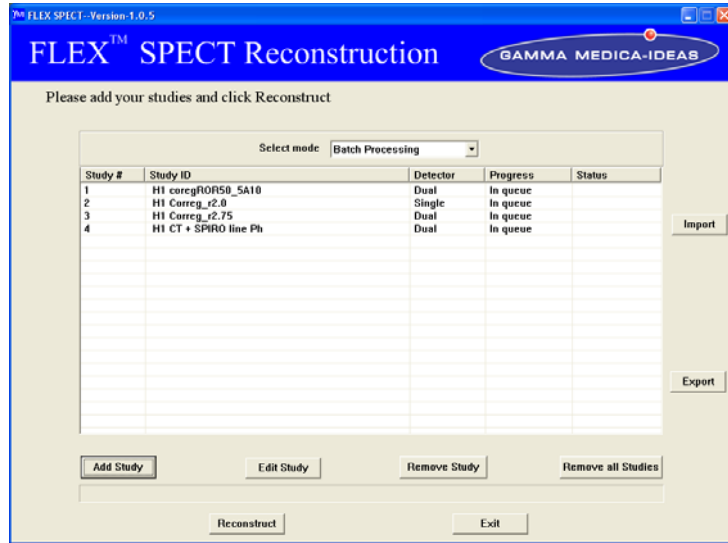


Figure 2.4.8 The Batch Processing screen.

By pressing the “Add Study” button, the user can enter as many studies as desired using an interface screen that is nearly the same as that for the *Single Reconstruction* mode. The key difference is that the Interfile to be reconstructed has been selected, the user presses the “OK” button and the new reconstruction will be added to the batch list, as shown in Figure 2.4.8. Displayed in the *Batch Processing* screen are the *Study #* (a sequential number identifying the particular batch job), the *Study ID*, the *Detector* mode, a *Progress* and a *Status* column.

The *Progress* column specifies the current state of the batch job. Possible values for this column are given in the table below. The *Status* column specifies the final state of the batch job. Its possible values also given in the table below:

Progress/Status	Description
In queue	Study added and ready to be reconstructed
In progress	Study currently being reconstructed
Done	Study finished reconstruction
No errors	Reconstruction finished with no errors
Failure	Reconstruction failed

Possible values of the Progress/Status column in the Batch Processing screen.

When all the studies have been added to the *Batch Processing* screen, the reconstruction can be started by clicking on the “*Reconstruct*” button. When the batch process is running, a progress bar appears at the bottom of the screen, and the progress of individual studies can be tracked in the *Progress* column.

When all of the batch reconstructions are complete, an additional button labeled “*View Report*” will appear to the right. Upon clicking this button, a report of warnings and/or errors will be displayed. If no warnings and/or errors exist for a given study, the report will simply read “*No Errors*”. If any errors and/or warnings are generated, please refer to the “*Troubleshooting*” section in the appendix. Clicking on the “*Hide Report*” button in the right-hand column will return to the list of batch jobs.

ColorSPECT

Note: ColorSPECT™ is no longer needed for multiple isotope processing for it has already been implemented in Triumph_SPECT™ during the acquisition in the post-acquisition process invisible to user.

The ColorSPECT™ session is remained for UCT re-generation and spectra processing. In the near future, both will also be implemented in the Triumph_SPECT™ and the colorSPECT function will be removed from the FLEX_SPECT™ package.

The *ColorSPECT* feature in FLEX™ SPECT allows the user to process list-mode data. List-mode data is a data format in which every radiation event detected by the gamma camera(s) is recorded as raw data (in most cases to be processed at a later time). The raw data is usually in binary format and can be processed to recover the estimated position and energy deposited in the gamma camera of each event. List-mode data are to be compared with frame-mode data, which include standard tomography datasets. Frame-mode data are list-mode data that have already been processed (e.g.

events outside the desired energy window have been discarded and events inside the energy window have been counted and binned into their corresponding estimated physical detector pixel). The *ColorSPECT* feature thus allows the user to re-process acquired data using any desired energy

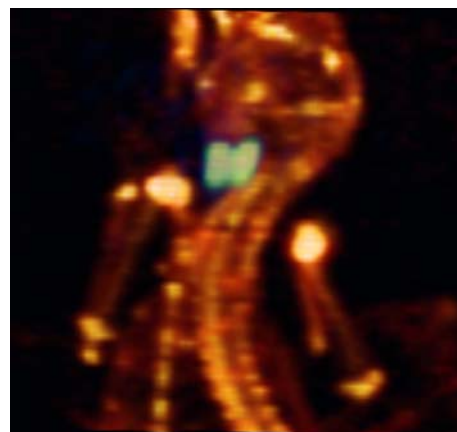


Figure 2.4.8 Image of a nude mouse with I-123 (159.0 keV) in the thyroid and Tc-99m (140.5 keV) labeled MDP in the bones.

windowing after the data has been acquired and at the user's convenience. This type of post-processing is not possible with frame-mode data.

The primary use of *ColorSPECT* for the typical user is to apply different and/or multiple energy windows to the same acquired data set (see Figure 2.4.8 for an example), and thus the term “*ColorSPECT*” to describe this feature, which allows the user to create “color-like” SPECT reconstructions along the lines of standard television palettes that use three primary colors (red, green, and blue) to create any color combination.

The use of *ColorSPECT* requires that FLEX™ SPECT be installed on the SPECT or CT acquisition host computers in order to have access to the pertinent gamma camera calibration files. *ColorSPECT* may be disabled on computers that do not have access to these files (*for more information on installation, please reference the appendix*).

If *ColorSPECT* is enabled, the user can access it by selecting the “*ColorSPECT*” option in the “*Select mode*” drop-down menu. There are two protocols currently supported in *ColorSPECT* – static and tomo – which can be toggled between using the “*Protocol*” drop-down menu. The *static* protocol is used to process individual list-mode datasets. The *tomo* protocol is used to process tomographic projection data that consist of many views of the object being imaged over various angles. The two types of protocols are processed in a similar manner in *ColorSPECT*, but this manual will treat them as different for the purposes of describing how to process them.

To enable list-mode acquisition, the user must open the file *D:\LumaGEM\acqcnf.ini* and set the parameter “*bLMFile*” to be 1 (as shown in Figure 2.4.9). To disable list-mode acquisition, the same parameter must be set to 0. **Please disable list-mode acquisition when finished acquiring list-mode data**, as list-mode data can generate many gigabytes of data and may fill the user's hard drive very quickly if left enabled.

Static Protocol

To process a dataset using the *static* protocol, select the list-mode file to be processed by clicking on the *browse* (⋯) button of the “*Choose Color SPECT File*” field. A dialog box will appear in which the user can search for the desired list-mode data. List-mode data needs to be extracted out of *C:\gamma\savelistmode* directory. All the .bin files are named with Triumph_SPECT special code and user will need to remember the data and time of the acquisition to pull out the correct file.

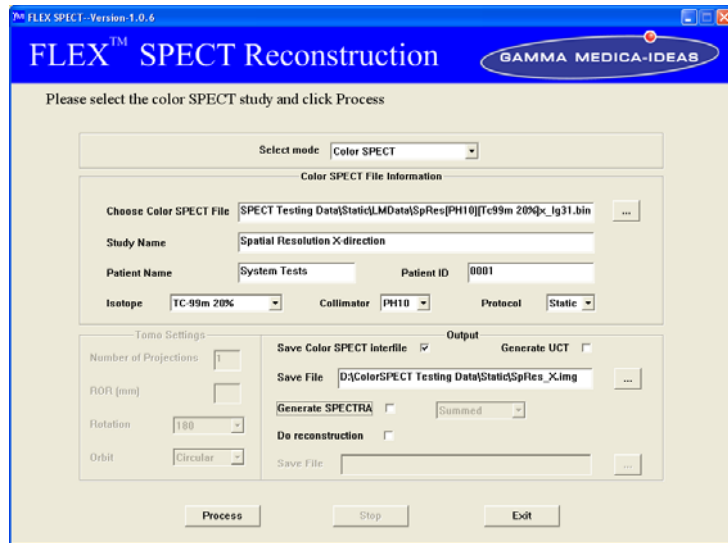


Figure 2.4.10 The ColorSPECT static protocol.

Static list-mode files have the same name as the Study ID that was supplied by the user when the data was acquired. Once the list-mode data have been selected, a new *Study Name*, *Patient Name* and *Patient ID* must be entered in order to populate the new static Interfile that is to be generated. It is a good practice to give a descriptive name for the *Study Name*, and to use the same *Patient Name* and *Patient ID* that was used in acquiring the data.

Next, from the “*Collimator*” drop-down menu, select the collimator that was used to acquire the data. It is important to choose the correct collimator, as an incorrect choice will severely distort the resulting data.

From the “*Isotope*” drop-down menu, choose the desired isotope and energy window. There is no inherent constraint in the choice of isotope and energy window.

To obtain the best possible images, each projection should be uniformity corrected. In order to perform the uniformity correction, the Uniformity Correction Table (UCT) must exist for the selected isotope and energy window; however, this UCT can be acquired after acquisition if necessary.

ColorSPECT has the ability to generate UCTs with any energy window if the necessary list-mode flood data has been acquired with the needed collimator and isotope. Generating UCTs from list-mode data is discussed further later in this chapter. If the required UCT is not available, a warning message will appear, and the user can choose to continue processing the static data without a UCT (not recommended) or abort the static processing and acquire the necessary UCT (which can always be acquired and applied post acquisition).

Finally, select a name for the generated Interfile by clicking on the *browse* button in the “*Save File*” field, which opens a dialog box in which the user can navigate to the desired directory and select a file or type a new name. Reconstructions are not supported under the static protocol, and, in general, the “*Generate UCT*” checkbox should be un-marked unless a UCT is to be created. A spectra-file of the static list-mode data can be generated by marking the “*Generate Spectra*” checkbox (*for more information, please reference the “Generate Spectra” section of this chapter*).

Once all of the fields have been entered, press the “*Process*” button to begin processing. The status bar at the top of the screen displays any pertinent information about the process, and will alert the user when processing is complete.

Upon exiting FLEX™ SPECT from *ColorSPECT*, a window will open, prompting the user to save the *ColorSPECT* configuration file, which saves the last *ColorSPECT* settings used by the user to the *LMPro.ini* file. *For more information on parameter files, please reference the appendix of this chapter.*

Tomo Protocol

ColorSPECT's *tomo* protocol is very similar to the static protocol described in the previous section, but a few additional fields need be filled out. As in the static protocol, first select the list-mode file to be processed by clicking on the *browse* (...) button of the “*Choose Color SPECT File*” field. A dialog box will appear in which the user can search for the desired list-mode data. The *tomo* list mode files are in the same “*Savelistmode*” directory and should be selected in the similar way as for the static files, except that only one projection file need to be selected, the program will identify the rest.

Figure 2.4.12 the *ColorSPECT* *tomo* protocol

Figure 2.4.12 shows a dialog box opened to the *D:\LumaGEM\LMData* folder and displaying the two types of list-mode data. The first two files listed are examples of static list-mode data, for which the Study ID has been used as the base-name for the list-mode data stored as *.bin files. The highlighted file, *Tomo_13_29_49_000.bin*, is an example of tomo list-mode data, in which each individual projection is stored with the base-name *Tomo_13_29_49* with the projection number (counting from zero) appended onto this base-name. For example, *Tomo_13_29_49_000.bin* and *Tomo_13_29_49_001.bin* are the first two projections of the *Tomo_13_29_49* acquisition. The number in the tomo base name refers to the start-time of the first projection in an hours_minutes_seconds format (based on a 24 hour clock). If 32 projections were acquired over a 180° gantry rotation, then 32 tomo list-mode files would be generated. Each tomo file contains list-mode data from one or two gamma cameras. The user only needs to select one of the tomo list-mode files (it does not matter which projection is selected), and the remaining files will be automatically detected.

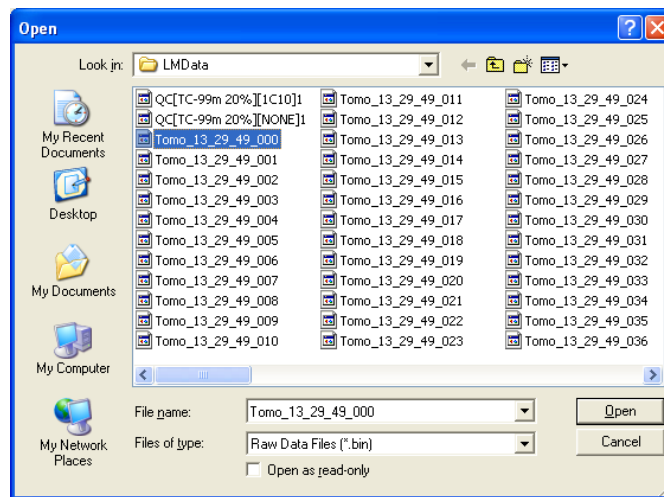


Figure 2.4.12 Dialog box showing static and tomo list-mode data in the *D:\LumaGEM\LMData* folder.

Once the list-mode data has been selected, a new *Study Name*, *Patient Name* and *Patient ID* must be entered in order to populate the new static Interfile that is to be generated. It is a good practice to give a descriptive name for the *Study Name*, and to use the same *Patient Name* and *Patient ID* that was used in acquiring the data.

Next, from the “*Collimator*” drop-down menu, select the collimator that was used to acquire the data. It is important to choose the correct collimator, as an incorrect choice will severely distort the resulting data.

From the “*Isotope*” drop-down menu, choose the desired isotope and energy window. There is no inherent constraint in the choice of isotope and energy window.

To obtain the best possible images, each projection should be uniformity corrected. In order to perform the uniformity correction, the Uniformity Correction Table (UCT) must exist for the selected

isotope and energy window; however, this UCT can be acquired after acquisition if necessary.

ColorSPECT has the ability to generate UCTs with any energy window if the necessary list-mode flood data has been acquired with the needed collimator and isotope. Generating UCTs from list-mode data is discussed further later in this chapter. If the required UCT is not available, a warning message will appear, and the user can choose to continue processing the static data without a UCT (not recommended) or abort the static processing and acquire the necessary UCT (which can always be acquired and applied post tomo acquisition).

Once the “*Choose Color SPECT File*” field has been entered, the “*Number of Projections*” under the *Tomo Settings* will automatically update, reflecting the number of list-mode projection files found. Next, enter the Radius of Rotation (in millimeters) in the “*ROR (mm)*” field, and select the gantry rotation angle from the “*Rotation*” drop-down menu (either 180° or 360°). *ColorSPECT* currently does not support spiral orbits.

Finally, select a name for the generated tomo Interfile by clicking on the browse button in the “*Save File*” field, which opens a dialog box in which the user can navigate to the desired directory and select a file or type a new name. A spectra-file of the tomo list-mode data can be generated by marking the “*Generate Spectra*” checkbox (*for more information, please reference the “Generate Spectra” section of this chapter*).

Once all of the fields have been filled out, presses the “*Process*” button to begin processing. The status bar at the top of the screen displays any pertinent information about the process, and will alert the user when processing is complete.

If the “*Do reconstruction*” checkbox is marked, and the “*Save File*” field below the checkbox has been filled out, the tomo Interfile and necessary information are passed to the *Batch Processing* screen. After the *ColorSPECT* processing is complete, the user can start reconstruction by selecting “*Batch processing*” from the “*Select mode*” drop-down menu.

Alternately, multiple *ColorSPECT* jobs (either the same tomography data set with different isotope/energy windows or any number of different tomography data sets) can be processed, each with a reconstruction request (if the “*Do reconstruction*” checkbox is marked) passed to the *Batch Processing* screen. When all *ColorSPECT* processing jobs are complete, the user can switch to the *Batch Processing* screen to start all the reconstructions in one batch job.

Generate UCT

ColorSPECT has the ability to generate Uniformity Correction Tables (UCT's) with any energy window if the necessary list-mode flood data has been acquired with the required collimator and isotope. UCTs are used to normalize the tomography data – that is, to correct for any pixel-to-pixel variation in gamma camera sensitivity and to account for the collimator sensitivity response across the FOV. *For instructions on how to acquire UCTs and QCs (Quality Control images), please reference Chapter 3 of this section.* Flood acquisitions with a given collimator and isotope can be acquired with list-mode enabled, and with such list-mode data, any number of UCT's for this collimator/isotope pair can be generated with any energy window. *For instructions on how to create arbitrary isotope/energy windows, please reference the ColorSPECT section of the appendix in this chapter.* These UCTs can be generated and applied to list-mode data AFTER the original data has been acquired.

To generate a UCT in *ColorSPECT*, process the UCT list-mode data as normal static list-mode data, making sure that the “*Generate UCT*” checkbox is marked. Once the “*Process*” button has been pressed, the UCT will automatically be generated in the proper directory (usually *D:\LumaGEM\Calibrations*). If a UCT with the same collimator-isotope-energy-window already exists, a warning will be displayed, asking whether the user wishes to overwrite the original UCT (not recommended). In addition, a warning may occur if dead-pixels (i.e. pixels with zero counts) or low-statistics-pixels (i.e. pixels with counts < 50) are present in the UCT list-mode data. If any such dead- or low-statistics-pixels occur in the generated UCT, GM-I recommends trying to acquire the UCT again with a larger number of counts.

Generate Spectra

ColorSPECT can generate spectra file(s) from both static and tomo list-mode data. This can be useful when trying to determine which isotopes/energy windows can be distinguished by the gamma camera(s) in question (see Figure 2.4.13). To generate spectra file(s), check the “*Generate SPECTRA*”

checkbox in the *ColorSPECT* screen. The adjacent drop-down menu will

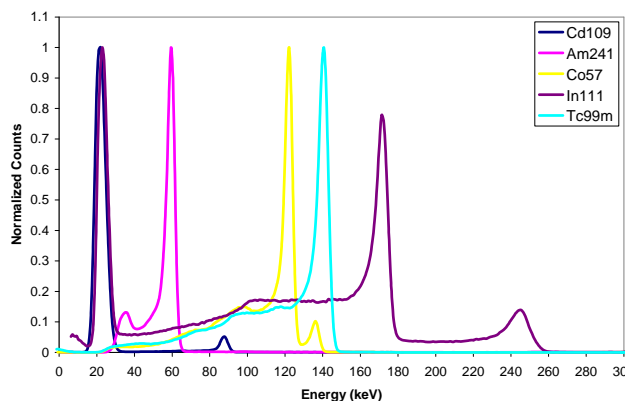


Figure 2.4.13 Example energy spectra acquired from various isotopes (In-111, Tc-99m, Co-57, Am-241, and Cd-109) using a CZT gamma camera.

become active and two options are available: Summed and Individual spectra. The *summed* option generates a spectrum per gamma camera, in which the resulting spectra are the sum of all the individual pixel spectra. The *individual* spectra option generates a file containing the spectra for each pixel in the gamma camera(s) separately, and stored in a 2-D array of pixel versus energy bin. The spectra files generated are text files (with extension *.spe*) that can be read with any text editor or spreadsheet. The energy bins are 1 keV in size, and the low/high value of the energy axis can be controlled in the *LMPro.ini* file using the two parameters *EnergyWinLow* and *EnergyWinHigh* (*please reference the section on parameter files in the appendix of this chapter*).

Cardiac Gated SPECT

Cardiac Gated acquisition and processing will be made available once the reconstruction in FLEX_SPECT™ is completed.



Appendix

This chapter covers further information on the FLEX™ SPECT software: installation, parameter files, batch files, troubleshooting, customer service, and finally a general warranty.

Installation Guide

FLEX™ SPECT is a stand-alone package that can be installed on multiple computers to facilitate ease of use and speed of reconstructions. The program has the following system requirements:

- XP or NT operating system
- 1 GHz CPU or faster
- 1 Gbyte or more of RAM
- 15” monitor or larger (resolution 1024x768 or larger)
- 1 Gbyte or more of free disk space

The program may run at a reduced performance on systems that fail to meet these minimum requirements. To install FLEX™ SPECT, follow these steps:

- Copy the folder FLEX™ SPECT from the supplied installation CD to the *C:\Program Files* directory.
- Open the folder *C:\Program Files\FLEX SPECT* and make a shortcut to the executable *FLEX SPECT.exe* on the desktop for easy access.
- Open the file *C:\Program Files\FLEX SPECT\spect.ini* with a text editor such as Microsoft™ Notepad. In the “GeocalPath” parameter, enter the local *\LumaGEM\Pinhole* path (typically, this will be *D:\LumaGEM\Pinhole*, as shown in Figure 2.6.1). To enable/disable

```

File Edit Format View Help
pixmap=1
AttenCorr=0
printinfo=1
DataFrom=-1
GeomEffc_single=0
GeomEffc_synap=3
nbIterations=5
nbSubsets=4
SaveIntv=1
interpFlag=1
collMatchFlag=0
GeocalPath=D:\LumaGEM\Pinhole
OrbitMode_single=0
OrbitMode_synap=B
OrbitMode_spiral=0
OrbitMode_synap_spiral=B
phanxyz_synap=60
phanxyz_single=80
maxextrapolation[mm]=5
default_detector=2
default_gdrc=0
spiral_cube=0
Color_SPECT=1
Priority=-1
verbose=0
Ln 12, C

```

Figure 2.6.1 The spect.ini file.

ColorSPECT, set the “*Color_SPECT*” parameter to 1 (enable) or 0 (disable). Typically, if the list-mode data resides on the installation computer, *ColorSPECT* should be enabled; if not, *ColorSPECT* should be disabled.

- If *ColorSPECT* is enabled, open the file *C:\Program Files\FLEX SPECT\LMPro.ini* with a text editor. In the “*LumaGEM_Path*” parameter, enter the installation computer’s set-up (typically, this will be *D:\LumaGEM*), as shown in Figure 2.6.2).

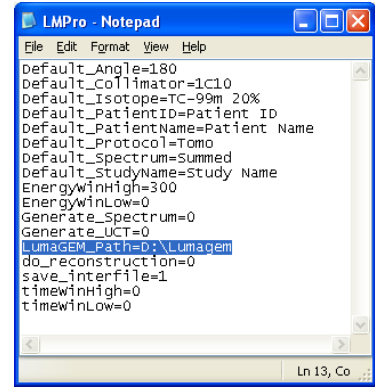


Figure 2.6.2 The LMPro.ini file.

- Double-click on the *FLEX™ SPECT* icon on the desktop. The *FLEX™ SPECT* start-up screen should appear, as in Figure 2.4.1. If the start screen appears, the program is working properly. If an error message is displayed, please reference the troubleshooting section of this chapter.

Parameter Files I (spect.ini & LMPro.ini)

FLEX™ SPECT accesses two parameter initialization (*.ini*) files that set up paths, reconstruction options, and default values. Both files reside in the installation directory (typically, this is *C:\Program Files\FLEX SPECT*) and have the filenames “*spect.ini*” and “*LMPro.ini*”. Please note that the parameter names in these files are case-sensitive (i.e. “*GeocalPath*” in *spect.ini* is not the same as “*geocalpath*”).

spect.ini

The *spect.ini* parameter file is the main parameter file and controls the reconstruction options and default values. Short descriptions of the parameters and their possible values are given in the table below:

Parameter	Valid Choices	Default Value	Notes
pixmag	1	1	Interpolation in reconstruction
GeomEffic_single	float	0.0	Pinhole sensitivity cosine power term for single-pinhole collimators

GeomEffic_synap	float	3.0	Pinhole sensitivity cosine power term for multi-pinhole collimators
AttenCorr	0	0	Attenuation correction, currently not used
printinfo	1	1	Print debug info during reconstruction
DataFrom	-1	-1	Debug parameter in reconstruction
nbIterations	integer	5	Number of OSEM iterations
SaveIntv	integer	1	Number of save iterations (only works if verbose turned on)
nbSubsets	1,2,4,8,16	4	Number of OSEM subsets
interpFlag	0,1	1	GeoCal interpolation scheme
collMatchFlag	0,1	0	Collimator match flag (0 = requires exact collimator match, 1 = requires only 1 st two collimator characters match)
OrbitMode_single	A,B,C,...,J	G	GeoCal orbit model for single-pinhole collimators with circular orbit
OrbitMode_synap	A,B,C,...,J	B	GeoCal orbit model for multi-pinhole collimators with circular orbit
OrbitMode_spiral	A,B,C,...,J	D	GeoCal orbit model for single-pinhole collimators with spiral orbit
OrbitMode_synap_spiral	A,B,C,...,J	B	GeoCal orbit model for multi-pinhole collimators with spiral orbit
phanxyz_synap	integer	80	Reconstructed matrix size for single-pinhole collimators
phanxyz_single	integer	60	Reconstructed matrix size for multi-pinhole collimators
GeocalPath	valid path	D:\LumaGEM\Pinhole\	Path to GeoCal files
verbose	0,1	0	Verbose 0=disable, 1=enable (verbose enabled generates *.par and *.dat files)
maxextrapolation[mm]	float	5	Maximum extrapolation without a warning in mm
default_detector	1,2	2	Number of gamma cameras
default_gdrc	0,1	0	Default GDRC enable/disable
spiral_cube	0,1	0	Spiral reconstruction cube/rectangle
Color_SPECT	0,1	1	ColorSPECT enable/disable
Priority	-2,-1,0	-1	CPU priority flag, higher number means process gets higher priority

LMPro.ini

The *LMPro.ini* parameter file controls the operation of *ColorSPECT*. Short descriptions of the parameters and their possible values are given in the table below:

Parameter	Valid Choices	Default Value	Notes
Default_Angle	180,360	180	The gantry rotation angle
Default_Collimator	char	5B10	Collimator name
Default_Isotope	char	TC-99m 20%	Isotope and energy window
Default_PatientID	char	Patient ID	Patient ID

Default_PatientName	char	Patient Name	Patient Name
Default_Protocol	Static, Tomo	Tomo	Protocol (Static or Tomo)
Default_Spectrum	Summed, Individual	Summed	Type of spectrum file to generate (summed over all pixels or individual pixel spectra)
Default_StudyName	char	Study Name	Study Name
EnergyWinHigh	integer	300	Maximum energy in spectra (keV)
EnergyWinLow	integer	0	Minimum energy in spectra (keV)
Generate_Spectrum	0,1	0	Generate spectra flag (0=false, 1=true)
Generate_UCT	0,1	0	Generate UCT flag (0=false, 1=true)
LumaGEM_Path	valid path	D:\LumaGEM	LumaGEM base path
do_reconstruction	0,1	0	Do reconstruction flag (0=false, 1=true)
save_interfile	0,1	1	Save Projection Interfile (0=false, 1=true)
timeWinHigh	integer	0	Highest time stamp to consider (ms; 0=consider all)
timeWinLow	integer	0	Lowest time stamp to consider (ms; 0=consider all)

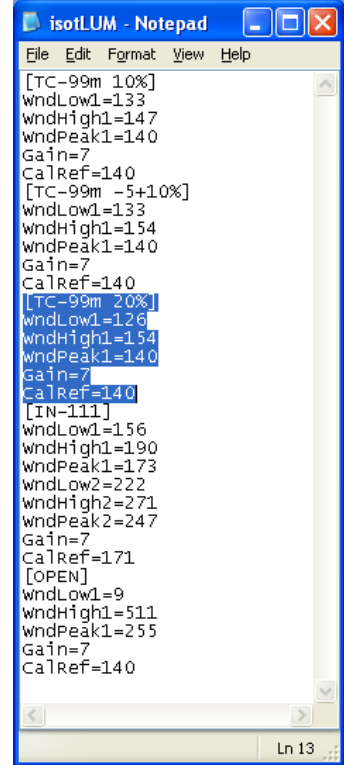
Parameter Files II (ColorSPECT Files)

The files shown in the table below are necessary for the proper operation of *ColorSPECT*:

Camera File Name	Default Full Path	Description
acqcnf.ini	D:\LumaGEM\acqcnf.ini	Acquisition configuration file
isotLUM.dir	D:\LumaGEM\Acquisition\isotLUM.dir	List of available isotope/energy windows
collimators.dir	D:\LumaGEM\Acquisition\collimators.dir	List of available collimators
CalReference.ini	D:\LumaGEM\Acquisition\CalReference.ini	Calibration reference file
LUT_*.bin	D:\LumaGEM\Calibrations\LUT_*.bin	Look-Up-Table (LUT)
EPT_*.bin	D:\LumaGEM\Calibrations\EPT_*.bin	Energy-Peak-Table (EPT)
[U_COLL. *][*]	D:\LumaGEM\Calibrations[U_COLL. *][*]	Uniformity correction table (UCT)

Most of these files should not be modified after installation of the gantry by GM-I personnel, but one file might need to be modified if the user needs to specify new isotope and/or energy windows; this file is the *isotLUM.dir* file, and is located in the *D:\LumaGEM\Acquisition* directory. The *isotLUM.dir* file may be opened and edited with any text editor and contains entries partitioned into blocks of rows that belong to specific isotope/energy-window combinations (see Figure 2.6.3).

Each new isotope/energy-window block begins with a name designation contained in brackets (e.g. *[TC-99m 20%]*, as highlighted in Figure 2.6.3). Following this bracketed-name can be any number of energy windows defined by three parameters – *winLow1*, *winHigh1*, and *winPeak1* – all specified in units of keV (e.g. a second energy window can be added to the same isotope/energy-window name by adding the fields *winLow2*, *winHigh2*, and *winPeak2*). The parameters *Gain* and *CalRef* should remain the same as for isotopes of similar peak energy.



```

isotLUM - Notepad
File Edit Format View Help
[TC-99m 10%]
wndLow1=133
wndHigh1=147
wndPeak1=140
Gain=7
CalRef=140
[TC-99m -5+10%]
wndLow1=133
wndHigh1=154
wndPeak1=140
Gain=7
CalRef=140
[TC-99m 20%]
wndLow1=126
wndHigh1=154
wndPeak1=140
Gain=7
CalRef=140
[IN-111]
wndLow1=156
wndHigh1=190
wndPeak1=173
wndLow2=222
wndHigh2=271
wndPeak2=247
Gain=7
CalRef=171
[OPEN]
wndLow1=9
wndHigh1=511
wndPeak1=255
Gain=7
CalRef=140
Ln 13

```

Figure 2.6.3 The *isotLUM.dir* file.

For help modifying this file, please contact customer support at Gamma Medica-Ideas, (877) 426-2633.

Batch Files

An alternate method to fill out a batch job is to create a batch file in a text editor (such as Microsoft™ Notepad) that contains the necessary information for each study. Batch filenames need to end with the extension “.batch” and the files must include the first two lines highlighted in Figure 2.6.4 to be recognized as legitimate batch files.



Figure 2.6.4 Example batch-file illustrating three studies.

The easiest way to generate a template batch file is to enter a number of studies of the desired type into the batch screen and then export a batch file. Batch files can be imported and exported by using the “*Import/Export*” buttons in the *Batch Processing* screen. When either button is pressed, a dialog box will open, asking the user either to name a batch file (*Export*) or to select an existing batch file (*Import*). Once a batch file has been exported, the user can open the file with any text editor and edit the salient parameters of interest. Each study must begin with and end with the study number. Spiral studies contain an additional three parameters not included in circular studies. See the table below for a list of valid parameters and their possible valid arguments with a description:

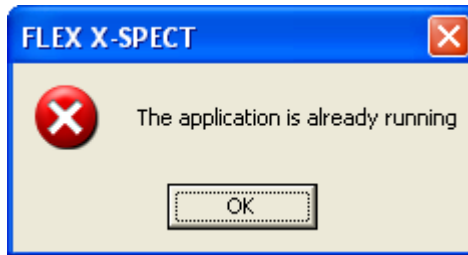
Batch Parameter Name	Valid Choices	Description
Study	integer	Study Number
InputFile	valid file	Interfile (*.hdr)
ResultFile	valid file	Interfile (*.img)
ROR[mm]	float	Radius of Rotation in mm
DetectorMode	1 or 2	Number of gamma cameras
GeomResp	0 or 1	0 = GDRC disabled, 1 = GDRC enabled
Niterations	integer	Number of OSEM iterations
Nsubsets	2,4,8, or 16	Number of OSEM subsets

Spiral	0 or 1	0 = circular orbit, 1 = spiral orbit
Numberofimages	integer or All	Number of spiral orbits, N_{orbits}
Startimage	integer	First spiral orbit to use in reconstruction
Stepsize	float	Spiral step size in mm
Endstudy	integer	Study Number

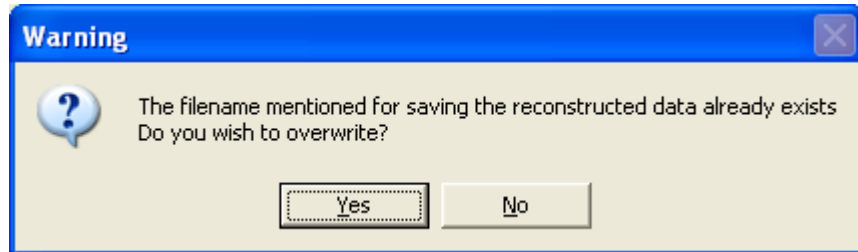
Please note that the parameter names are case-sensitive (i.e. “EndStudy” is not the same as “endstudy”).

Troubleshooting

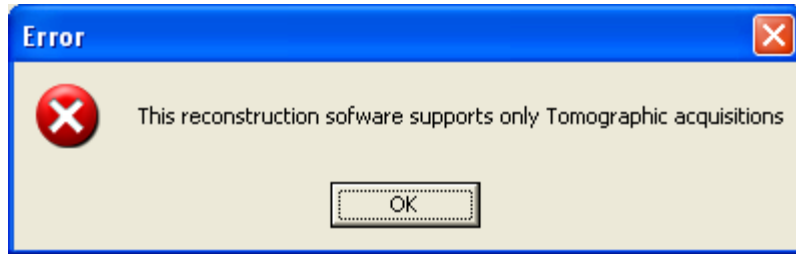
This section covers the most commonly encountered warning and error messages generated by FLEX™ SPECT. Please consult these for further information on each error/warning message. If the warning and/or error cannot be resolved, please contact customer support at Gamma Medica-Ideas, (877) 426-2633.



The error above is displayed when the user tries to start FLEX™ SPECT multiple times. Only one FLEX™ SPECT application may run at any time on a given computer.



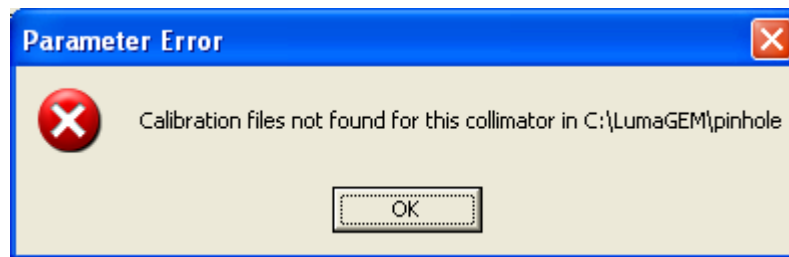
This warning above is displayed if the user tries to create a result file that already exists. The user may overwrite the file (*Yes*) or abort the action and rename the result file (*No*).



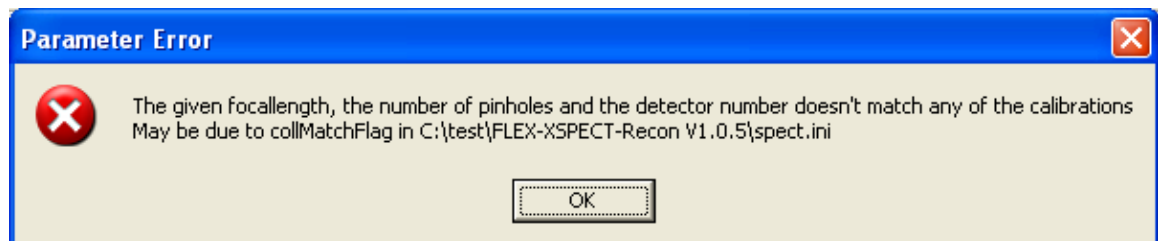
The error above is displayed when a non-tomographic (e.g. static or dynamic) Interfile is selected for the reconstruction. Only tomographic Interfiles may be reconstructed.



The error above is displayed when an Interfile acquired in a CW direction is chosen for reconstruction, as only CCW orbits are allowed. Please contact GM-I customer support if this error occurs.



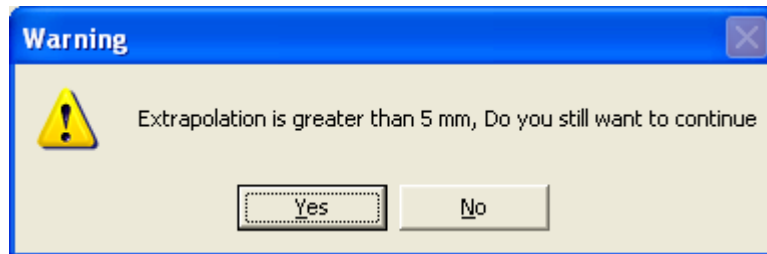
The error above is displayed when the GeoCal files are not found in the designated calibration path. Check the *spect.ini* file to ensure that the parameter GeocalPath is set to a valid path that contains GeoCal files.



The error above is displayed when GeoCal files are found, but files for this particular collimator are not found (e.g. PH05 is found, but not the exact collimator match PH10). The “*collMatchFlag*” in the *spect.ini* file may be the source of the problem. Alternatively, there may not be any GeoCal files for this particular collimator. Please contact GM-I customer support if this error occurs.



The error above is displayed when the “*interpflag* = 0” in the *spect.ini* file and the GeoCal file(s) at the particular ROR are not found. The user can either acquire and process GeoCal data at the desired ROR, or set the “*interpflag* = 1” to interpolate/extrapolate between GeoCal points.

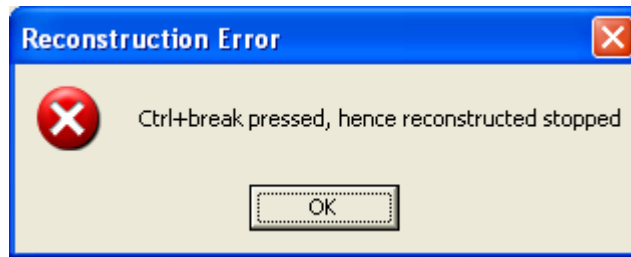


The warning above is displayed when the GeoCal extrapolation is greater than the value that specified in the *spect.ini* file by the parameter “*maxextrapolation[mm]*”. This message is simply a warning and can be ignored in most cases, though large extrapolations can result in poor reconstructions.

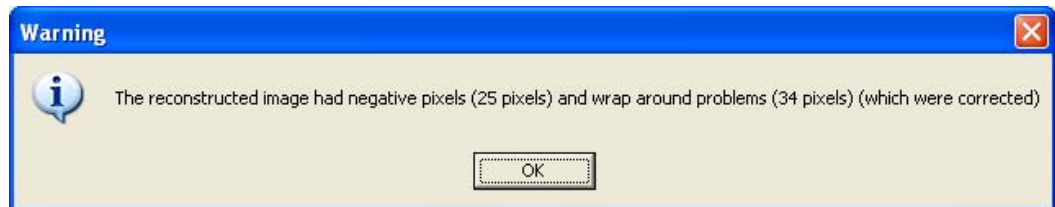


The error above is displayed when an internal error in the reconstruction

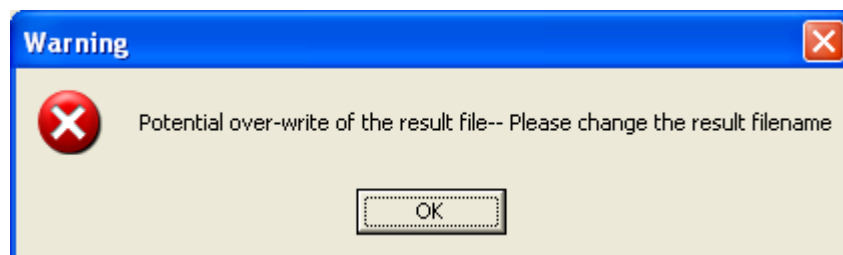
occurs (unrelated to the GeoCal file(s) or anything on the system). Please contact GM-I customer support if this error occurs.



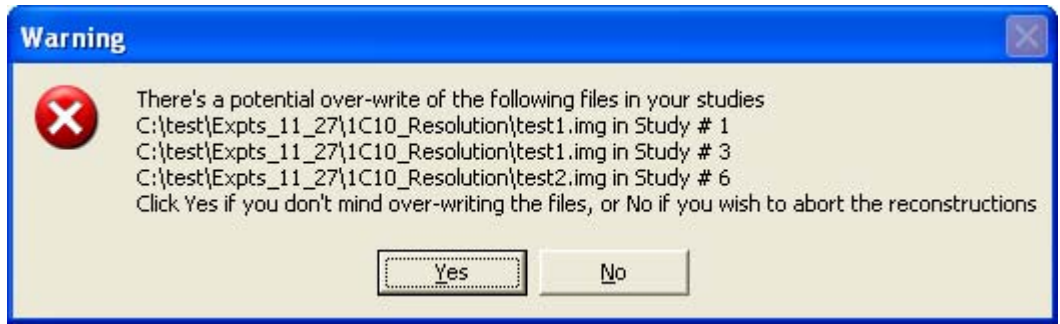
The error above is displayed when the reconstruction is stopped by pressing ctrl+break (the reconstruction stops only after the completion of the current iteration).



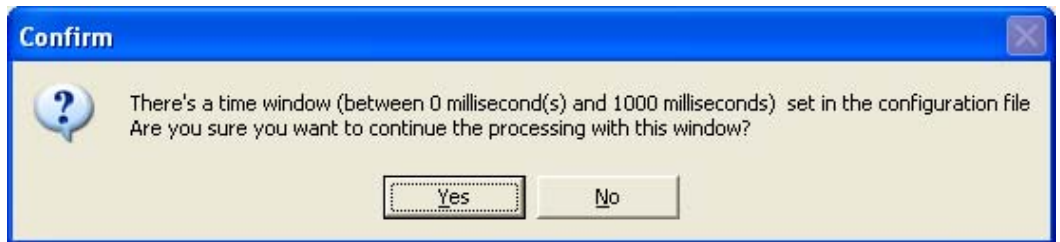
The warning above is displayed if the reconstructed image had negative pixels and/or 16-bit wrap around problems during float to integer scaling. This message is simply a warning and can be ignored in most cases.



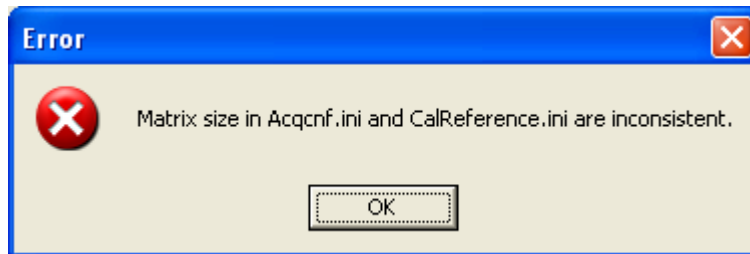
The warning above is displayed when the result file added in one of the studies has already been used in one of the previous studies (e.g. if the user used "test.img" as the result file for study 1 and attempted to also use the name "test.img" for the result file for study 2). Make sure all result file names are unique in batch processing mode.



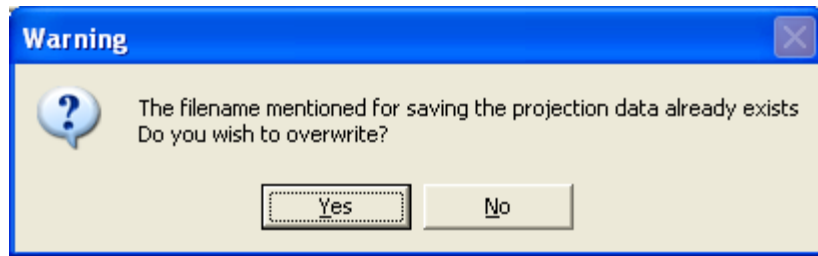
The warning above will be displayed after the user clicks “Reconstruct” from the Batch Processing screen if there is a chance of overwriting some files that already exist. Press “Yes” to overwrite the files, or “No” to abort the batch job and change the result filenames.



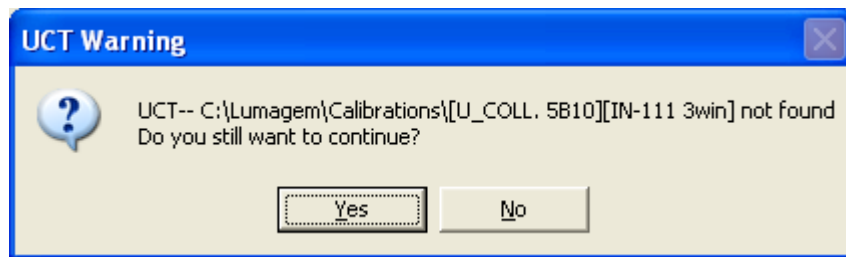
The confirmation message above is displayed when there is a time window set in the LMPro.ini file. The time window may be disabled by setting both of the LMPro.ini parameters “timeWinHigh” and “timeWinHigh” to 0.



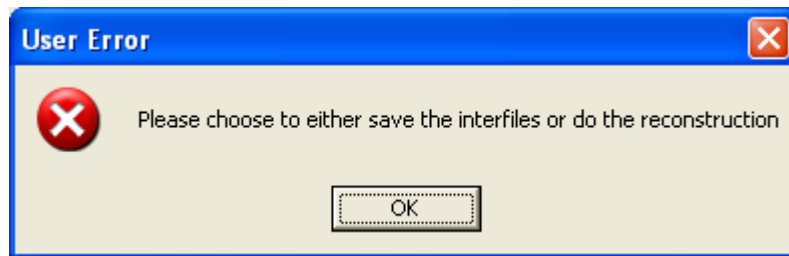
The error above is displayed when the matrix sizes are inconsistent between the two files. Please contact GM-I customer support if this error occurs.



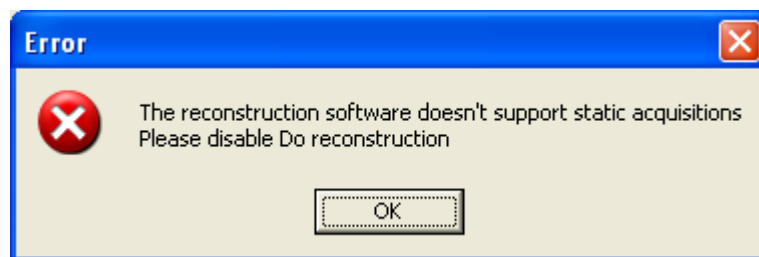
The warning above is displayed when the filename to be generated already exists.



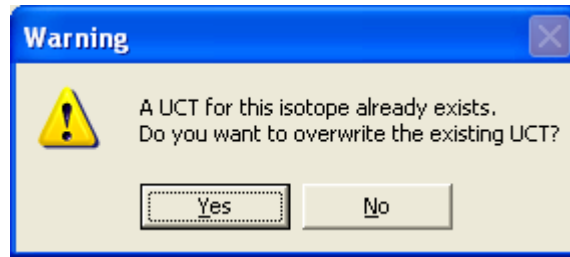
The warning above is displayed when the UCT is not found for the particular collimator-isotope-energy-window combination.



The error above is displayed when a ColorSPECT process has been started but neither a projection Interfile nor reconstruction has been selected.



The error above is displayed when the user tries to perform a reconstruction with static protocol.



The warning above is displayed when the user is creating a UCT in *ColorSPECT*, and a previous UCT with the same collimator-isotope-energy-window already exists. It is not recommended to overwrite pre-existing UCTs without first backing them up.

Customer Support

If technical assistance or support is needed, please contact the Gamma Medica Technical Service Department by phone at (818) 709-2468, or through GM-I's web site at www.gammamedica.com.

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