



Philips Medical Systems

CPET Plus User's Manual

A manual describing how to use the C-PET Imaging System

DOC-USERMAN-C-PET, Rev C September 2002

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REVISION TABLE

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NOTES

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Chapter

UNDERSTANDING THE EQUIPMENT

The C-PET Positron Emission Tomography (PET) system is a Single PassTM whole body scanner designed to provide true volumetric imaging. C-PET is intended for use as a diagnostic imaging device. When used with appropriate radiopharmaceuticals, it produces images representative of the internal distribution of radioactivity in the head or the body.

The system allows the user to reconstruct high-resolution, three-dimensional, static, gated, dynamic images of biochemical and metabolic processes. It also enables you to display, process, and analyze these images according to your specific needs.

Positron Emission Tomography or PET is based on the fact that certain radionuclides decay by positron emission. The positron annihilation results in the emission of two 511 keV gamma-rays which are emitted in opposite directions. Coincidence detection of both gamma rays localizes the decay along a line.



Figure 1-1 Annihilation

By using 6 large position-sensitive detectors around the patient, data can be acquired simultaneously along any parallel lines and at any angles. By using reconstruction algorithms, the internal distribution of radioactivity can be determined.



Figure 1-2 Crystal Orientation

Count Rates

The total counts detected by the system is determined by the total number of events in coincidence. There are 3 possibilities when detecting events in coincidence.

The first, and most desirable, are called trues. This occurs when the 2 opposing photons hit the detectors within the set coincidence window at 16 nanoseconds.

- Events truly in coincidence window
- Desirable events



The second occurs when two separate, independent events hit the crystals within the coincidence window. These events are known as Randoms.

Separate events in coincidence window



The last occurs are for the photons to be compton scattered in the patient prior to the photon hitting the crystal. This is known as Scatter.



The C-PET system operates in 3D mode, meaning there are no septa or collimators on the system. This contributes having a higher sensitivity system than 2D mode and therefore executing better statistics. Additionally, less tracer is required per study thereby decreasing the patient's radiation exposure.



Figure 1-3 C-PET Operating in 3D Mode vs. 2D Mode

Note: The study may be contraindicated for pregnant women, because of the radiation exposure incurred as a result of a PET study. Before scanning, carefully compare the benefits of PET versus alternative procedures.

The scanner provides a 25 cm axial field of view for whole-organ coverage, as well as a 56 cm transverse scan field of view for body studies.

We have designed the C-PET system to give excellent image quality, a large axial field of view, easy operator interaction, as well as the reliability expected from Philips. Our modular hardware and software architecture allows upgrades to the system as the abilities of PET imagers continue to evolve.

System Components

The C-PET system includes the following system components:

- Gantry
- Patient Table
- Acquisition Hardware
- SRV and ACQ Workstations

Conventions Used in This Manual

The following conventions are used in this manual:

- Buttons on the Display Panel appear in uppercase letters.
- **Note** Optional information.
- **IMPORTANT** Necessary information that describes the use of Philips equipment or applications.
- Keys or combinations of keys are shown as symbols that represent actual keys. Examples of keyboard symbols include:

<Enter> Enter key

- Computer messages are represented using the Courier font.
- System software windows, menus, etc. are represented by an *italic* font.
- Keyboard entries are represented by a **boldface** font.

Chapter

SAFETY

The C-PET Single PassTM (whole body) imaging system should be operated by professionals trained in the use of the C-PET system only. Improper use of the C-PET imaging system may result in patient or operator injury, inaccurate patient images, or equipment damage.

To help reduce the likelihood of injury or equipment damage, it is important that you read this manual in its entirety and become thoroughly familiar with all operator controls and procedures before placing the equipment in use. Be sure to keep this manual handy at all times and review the procedures and safety precautions periodically. Contact Customer Support if you have any questions, or if you feel that additional training is necessary.

In the C-PET scanner, we have incorporated many safety features to protect the patient and user. However, as with all medical devices of this nature, safe use of the scanner relies on the knowledge and judgment of licensed medical professionals.

CAUTION: Do not use the system if a safety problem is known to exist. Remove the patient from the area and request assistance from your Service Representative.

This chapter contains information concerning potential hazards and general safety precautions.

Product Name and General Electrical Ratings

C-PET Imaging System.

Electrical rating: 200-240 VAC, 15A, 50/60 Hz.

1. Protection against electric shock: Class I (Sub-clauses 5.1, 5.2).

Note: The equipment must be connected to a protective earthing terminal.

2. Type B applied parts: Patient Table (imaging table).

Note: Patient table has been evaluated for "body contact" only.

3. Protection against harmful ingress of water (Sub-clause 5.3): Ordinary.

Note: The equipment is enclosed but has not been evaluated as providing protection against ingress of water.

4. Degree of safety in the presence of flammable anesthetics or oxygen (Sub-clause 5.5): Not suitable for use in the presence of flammable anesthetics mixture with air or with oxygen or nitrous oxide.

Note: The use and/or presence of oxygen tanks and other such devices (other than anesthetic mixtures as noted above) are acceptable.

- 5. Mode of operation (Sub-clause 5.6): Non-continuous. The following sub-systems are for non-continuous use:
 - ^D Patient Table Non-continuous use, 10% duty cycle
 - [□] Ring Non-continuous use, 20% duty cycle
 - ^D Gantry Continuous use

Note: PC and Power Towers have been evaluated for continuous use.

Safety, Electrical, and Electromagnetic Compatibility (EMC) Compliance

The C-PET imaging system has been designed to and tested to verify conformance to the following standards:

- IEC 60601-1, Medical Electrical Equipment, Part 1: General Requirements for Safety.
- EN 60601-1, Medical Electrical Equipment-Part 1: General Requirements for Safety
- EN 60601-1-1, Medical Electrical Equipment-Part 1: General Requirements for Safety, Collateral Standard: Safety Requirements for Medical Electrical Systems
- EN 60601-1-2, Medical Electrical Equipment-Part 1: General Requirements for Safety 2. Collateral Standard: Electromagnetic Compatibility - Requirements and Tests
- EN 60601-1-4, Medical Electrical Equipment-Part 1: General Requirements for Safety, Collateral Standard: Programmable Electrical Medical Systems
- EN 1441, Hazard Risk Analysis
- EN 1041, Terminology, Symbols and Information Provided with Medical Devices
 Information Supplied by the Manufacturer with Medical Devices
- UL 2601-1 Medical Electrical Equipment-Part 1: General Requirements for Safety
- CAN/CSA C22.2, No. 601.1 Medical Electrical Equipment-Part 1: General Requirements for Safety
- JIS T1001, General Requirements for Safety of Medical Electrical Equipment
- JIS T1002, General Rules for Safety Testing Procedures of Medical Electrical Equipment

Contact your Field Service Engineer (FSE) if it is suspected that the imaging system is experiencing EMC interference or that the system is interfering with other equipment.

Note: This equipment has been tested under this standard and no known compatibility problems exist with other electrical equipment. However, to minimize the possibility of electrical interference, it is suggested that you not use sensitive electronic equipment within a 3-meter radius of the equipment.

Safety Precautions



WARNING You must be familiar with how to operate the imaging system to ensure patient safety and prevent equipment damage. **DO NOT** acquire patient studies until you have read this safety information and have performed the practice exercises. Patient injury or equipment damage can occur from improperly using the imaging system.

While using the imaging system, observe the safety precautions described in the following sections at all times.

General Precautions

- Operate the system only in accordance with the procedures described in this manual.
- Ensure that a qualified operator is always present when a patient is on the imaging table.
- Vigilantly watch the patient to ensure that patient or table motion does not result in patient harm.
- Do not defeat any of the manufacturer's safety interlocks.
- Do not use the equipment if any intermittent problems occur with any mechanical control device (Landmark Switches, Emergency Stop switches, etc.).
- Do not use the equipment in the presence of flammable anesthetics or oxygen.
- Obey local and federal regulations regarding radiation, electrical, and mechanical safety.
- Operate the system only after it has been properly installed by the manufacturer.
- Call the manufacturer's Customer Service if there are any problems, questions, or equipment failures.
- Use the system only after complying fully with the Daily QC procedures.

Imaging Table Precautions

- Do not place patients who weigh more than 300 pounds on the imaging table.
- Before assisting patients onto or off of the imaging table and before acquiring studies, make sure that the table slide is locked in place.
- Always assist your patient onto or off of the imaging table to prevent patient injury.

Major Symbols - Requiring Operator Awareness

Throughout the manual there are three major symbols which denote various conditions requiring operator awareness. These symbols and their meanings are described below.

WARNING	The warning symbol next to the text indicates conditions or actions for which a specific hazard is known to exist. The hazard may cause severe personal injury or substantial property damage if instructions are ignored.
CAUTION	The caution symbol next to the text indicates conditions or actions for which a potential hazard may exist. The hazard may cause injury or property damage if instructions are ignored. Caution labels are always yellow.
RAYONNEMENT DANGER RADIATION	The radiation symbol next to the text indicates a condition where radiation may be present. Use caution.

Indications for Use

The C-PET Positron Emission Tomography (PET) Single PassTM (whole body) imaging system is a whole body scanner designed to provide volume imaging. C-PET is intended for use as a diagnostic imaging device. When used with appropriate radiopharmaceuticals, it produces images representative of the internal distribution of radioactivity in the head or body.

The system allows you to reconstruct high resolution, three dimensional static, gated, dynamic images of biochemical and metabolic processes. It also enables you to display, process, and analyze these images according to your specific needs.

Contraindications for Use

Because the radiation exposure incurred as a result of a PET study, the study may be contraindicated for pregnant women. Before scanning, carefully compare the benefits of PET versus alternative procedures.

Restrictions on Use



This equipment is intended for use by qualified personnel only. Federal Law restricts the sale, distribution and use of this device to, or on the order of, a physician

Emergencies

Emergency Buttons

With the C-PET system, there are two types of emergency buttons that the user should be familiar with:

Emergency Stop buttons halt all table motion and turn off the laser lights.

Emergency Off switch turns off all system components. Activating the emergency off switch aborts data acquisition.

Emergency Stop Buttons

There are two Emergency Stop buttons. These are located on the control panel on the front of the gantry, and near the ACQ Workstation.

If the Emergency Stop button is used to interrupt a failure condition, call your Service Representative. Do not reactivate the system until the failure condition is eliminated.

To reactivate the system following the emergency, simply turn the Emergency Stop button to its original position.

Emergency Off Switch

The Main switch, which is located at the rear of the gantry on the bottom control panel, stops everything. This is equivalent to pulling the plug on the entire system, and is obviously a more severe measure than hitting an Emergency Stop button.

Use this switch only in case of severe emergency - for instance fire, earthquake, flood, etc.

As soon as this switch is pressed, power shuts off immediately. If the Cs-137 source is out of the shield, it will not be retracted. The Radioactivity symbol (a circular device, a little larger than a silver dollar on the operator control panel on the gantry) stays on if the presence of Radioactive elements is detected, as it does whenever a pin source is out of the shield.

The acquisition stops as the Main switch is pressed.

Evacuating Patients in an Emergency

In the event of a patient emergency, follow these guidelines to ensure that the patient is evacuated safely and efficiently from the scan room:

1.Hit the Emergency Stop button. This disables all powered table motions. Move to side of the patient table and press foot pedal located at the end of the patient table. This disengages the cradle drive.

2.Pull the patient cradle all the way out of the gantry to its home position.

3. Remove any support and comfort accessories such as arm support straps, chin straps, etc.

4. Transfer the patient from the table to a wheelchair or gurney and evacuate the scan room.

5.Follow hospital emergency protocol.

Rebooting the system

Booting the system is completely different than logging off the system. The sequence of shutting down the workstations effects the system acutely, rather than in order which they are logged off or on.

To reboot the system, log off of all terminals. Once all terminals are at the login prompt, the acquisition and remote workstations are shut down by typing **shut** at the prompt. The next computer to be shutdown is the server. To reboot, first type **boot** at the prompt on the server and wait for the login prompt. The acquisition and/or the remote can be logged in any sequence as long as the server is booted first.

Hazards

In order to minimize the probability of injury, warn anyone who may enter the site about the potential dangers associated with the PET scanner system. Make sure everyone understands these hazards, as well as proper PET safety procedures.

Patient-Related Hazards

Severe injury may result should a patient fall from the table. To prevent injury due to falls:

- Provide assistance and support for those patients who may experience fainting or dizziness while transferring to or from the table, or during power motions.
- Keep the patient in full view at all times. Never leave a patient unattended while on the table.
- Use only those patient support devices or accessories specifically recommended for the system.

IMPORTANT Do not place patients who weigh more than 300 lbs on the table.

Diagnostic-Related Hazards

• Failure to follow proper procedures regarding patient information may result in misidentification of the patient.

To avoid misidentification:

Verify your patient's identification number and record it in the appropriate areas of your patient data files. The system prompts to enter a new patient ID at the start of each study.

 Errors in patient data and poor image quality may result in incorrect medical diagnosis.

To avoid incorrect medical diagnosis:

Observe and record the patient's orientation, position and anatomical landmarks prior to conducting a study.

Be sure that your patient has been properly immobilized prior to conducting a study.

Choose the appropriate acquisition and reconstruction parameters.

When performing quantitative image analysis using programs such as the Region-of-Interest (ROI) program, be sure to verify that the region is properly placed and labeled on the structure intended.

Mechanical Hazards



Equipment motion can cause severe injury and equipment damage. To avoid injury or equipment damage:

- Carefully observe all equipment motion as the user operates the controls. Uncontrolled or unmonitored movements can cause the table to collide with the patient or other equipment.
- Check for obstructions before moving the table.
- Make sure your patient's extremities and clothing are properly positioned so that they do not get pinched or trapped during equipment motion.

- Do not allow the patient to grab, hold or handle any nearby equipment. He or she could accidentally activate equipment control.
- Make sure patient-connected lines, tubes, or leads are long enough to allow for the maximum travel of the table. Also make sure attachments are positioned so that they do not get pinched or pulled when the equipment is moving.
- Do not lean any kind of materials against equipment. Patient or operator injury may result from tip-over of components.
- Stay alert to the condition of your equipment. Be familiar enough with the hardware to recognize equipment failures. Do not use the equipment if it fails or is damaged.
- Improper cleaning may result in equipment damage. Clean the equipment frequently, especially if corroding chemicals are present. Depending on the nature of the contamination, use a cloth moistened with warm water and mild soap. Do not use strong cleaners and solvents, as these may damage the equipment. If needed, isopropyl rubbing alcohol or diluted bleach may be used (1 part of bleach to 10 parts of water) for blood spills or stains.

Electrical Hazards



We have provided the system with equipment that protects the user and patient from electrical shock and mechanical hazards. Contact qualified service personnel for your servicing needs. Do not attempt to remove system covers or dissemble the unit; it does not contain user-serviceable components.

The computer workstations are powered by a multiple socket outlet strip that uses IEC connectors. This strip is rated for $120 \text{ V} \sim 10A 50/60 \text{ Hz}$. Connect only the C-PET workstation and peripherals to this strip. Do not connect any other equipment to this outlet strip, as overloading or performance degradation can occur.

Connect the computer equipment only to the outlet strip, not to a wall socket or any other power source. This compromises the grounding of the equipment, and can degrade the performance of the scanner.

Do not place the outlet strip on the floor. The outlet strip may be placed on a countertop or table, or installed in a wireway or duct.

Laser Radiation Hazards



Warning: Laser radiation from the patient alignment lights may cause eye injury. To avoid injury:

Do not stare into beam.

Instruct patients to close their eyes to avoid exposure while the laser alignment lights are on.

Do not leave the laser beam on after positioning the patient.

Note: The laser on/off switch is provided as an alternate for a beam attenuator.

Understanding PET Safety Precautions

Keep in mind that the potential for injury or equipment damage is always present. People who are unaware of these hazards may cause (or be the victim of) radiation exposure - particularly contractors and those from other departments, who may not be familiar with the precautions required around PET scanning equipment. Even those who work with the system every day must often be reminded.

Radiation Safety



Although radiation emission from the transmission source poses no threat to your patients, the effects are cumulative and may cause harm to anyone who operates the system on a regular basis. To avoid injury due to radiation exposure:

- Monitor the source exposure warning indicators, located on the gantry control panel. A radiation symbol indicates anytime the point source has been removed from its shield.
- Keep radiation sources within shielded enclosures whenever exposure is necessary.
- Maintain adequate distance from exposed sources.
- Keep exposure times to a minimum.
- If the point source does not retract into the shield, interrupt the study, remove the patient from the room, evacuate the area and call your Service Representative.
- Establish and follow radiation handling guidelines at your facility.
- Establish and implement procedures for leak testing sealed sources in accordance with the regulations for the country in which the device is used. Below are two examples of these requirements.

Wipe Testing

In US: US Nuclear Regulatory Commission, 10CFR, Part 35.59 requires wipe testing every six months.

In Canada: The General Nuclear Safety and Control, Section 18, Subsection 1, requires wipe testing every 12 months.

See the next section for the leak testing procedures.

Leak Testing the Cs-137 Source

The following procedure must be used to leak test the Cs-137 source replace every 6 months with at the frequency required by the regulatory Agency. A service representative must be present when performing the wipe test in order to assure that safety precautions are observed:

The Cs-137 source supplier performs an initial line source leak test. However, leak tests must be performed and documented by your Radiation Safety Officer (RSO) upon receipt of the source and at least once every six months (or as required by radioactive materials license states). The leak test analysis should be capable of detecting a minimum of 0.001 microCuries. Refer to the United States, Title 10, Code of Federal Regulations or the Barclays California Code of Regulations, Title 17, Section 30275 for more information on leak test regulations.

To conduct a line source leak test:

1. Open the back covers and remove the plastic cover from the patient aperture.

2.From the acquisition terminal, open a Service Menu and select Motion Control System Menu > Insert Source This inserts the source into source guide in the patient aperture.

3.At the Gantry, the source collimator can be seen inside the source guide.

4.Obtain a cotton-tipped swab and wipe the swab along the source collimator block lead as well as on the aluminum source guide.

5. Place the cotton-tipped swab into a well counter or equivalent device capable of detecting 0.001 $\mu \rm Ci.$

6. From the acquisition terminal, open a Service Menu window and select "Retract Source"

7.Type "0" to exit the menu.

8.Replace Gantry covers.

Results:

Sources are considered leak-free if they are measured to be less than 0.005 microCuries. When any leak test reveals the presence of 0.005 microCuries or more of removable contamination, the user shall immediately withdraw the source from use and shall cause it to be decontaminated and repaired or to be disposed of in accordance with applicable provisions set forth by the NRC or agreement state. Two copies of a report shall be filed within five days of the test, with the Department or other official agency specifically designated by the NRC or agreement state, describing the source involved, the test results, and corrective action taken.

Tests for contamination and leakage, decontamination, and repair of sealed sources shall be performed only by persons specifically authorized by the Department to do so in accordance with provisions of the NRC or agreement state.

Records of all leak tests shall be maintained as specified in United States, Title 10, Code of Federal Regulations, part 20, subpart L as incorporated by reference in section 30253. Authority cited: Sections 208 and 25811, Health and Safety Code. Reference: Sections 25801, 25802, 25815, 25875, 25876, Health and Safety Code.

Replacement Schedule for Radioactive Sources

The transmission source (Cs-137) has a half-life of 30 years and does not normally have to be replaced.

Labels

The following labels are attached to the C-PET Imaging System in accordance with 21 CFR 1040.10 and EN 60825. The purpose and location of each of these labels is described below.

EMERGENCY STOP TURN TO RESET MOTION ENABLE	EMERGENCY STOP LOCATION: Next to Emergency Stop button on Remote Hardkey.	
	INTERNATIONAL SYMBOL FOR EMERGENCY STOP LOCATION: Next to Emergency Stop buttons.	
Â	ATTENTION - (REFER TO EQUIPMENT DOCUMENTATION)	
Ο	POWER OFF Power off to part of system.	
	POWER ON Power on to part of system.	



LASER LIGHT DO NOT STARE INTO BEAM DIODE LASER 1.0 MILLIWATT MAXIMUM OUTPUT 630-670 nm WAVELENGTH CLASS II LASER PRODUCT	This label is the certification for laser products and is located near the gantry base. It describes the wavelength, maximum power and the class of operation of the laser output. Maintenance - No service adjustments or maintenance are necessary to keep the laser alignment lights in compliance with 21CFR 1040.10 and 1040.11.	
PHILIPS ADAC PHILADELPHIA PA. C-PET PATIENT TABLE SN: 120V~3A 50/60 Hz 10% DUTY CYCLE MAX. 300 LBS. MADE IN USA	ID LABEL LOCATION: Patient Table (lower Gantry end).	
PHILIPS ADAC PHILADELPHIA PA. MODEL: CPET 250 PLUS 200-240 V~15 A 50/60 Hz SN: MANUFACTURED:	This rating label is located on the rear of the Gantry base.	
COMPLIES WITH 21 CFR 1040.10 & 1040.11 CLASSIFIED OUTSOT OUTSOT CONFORMS TO UL STD 2801-1 CAN/CSA STD C22.2 NO.601.1 MADE IN USA	TYPE B EQUIPMENT LABEL The certification and rating labels indicates that this equipment is protected against electric shock by grounding and limited leakage current. The ACAC PET scanner is classified according to IEC-601-1 standard as Class 1, type B. This rating label is located on the gantry base.	

Quality Assurance

Keep your system calibrated and perform the periodic quality tests recommended (see Chapter 17 "Quality Control and Calibration"). Follow the calibration frequency indicated in this manual. The correctness of your patient's diagnosis depends on it.

Use sources traceable to National Institute of Standards & Testing (NIST) to calibrate the dose calibrator and well-counter.

Cleaning

Improper cleaning may result in equipment damage. Clean the equipment frequently, especially if corroding chemicals are present. Use a cloth moistened with warm water and mild soap, depending on the nature of the contamination. Do not use strong cleaners and solvents, as these may damage the finish. If needed, isopropyl rubbing alcohol or diluted bleach may be used(1 part of bleach to 10 parts of water) for blood spills or stains.

Water Ingress, Flammable Mixture and Operating Mode

The Gantry of the C-PET Scanner is intended for continuous operation. The Patient Table is intended for intermittent 10% operation. The Scanner is not anesthetic gas proof and is Ordinary Equipment without protection against ingress of water.

Factors Affecting Scan Quality

There are a number of extraneous factors that can impact the quality of scan results. This section describes the implication of:

- Patient history and status
- Seizure activity and EEG monitoring
- Patient-related hazards
- Patient positioning and movement
- Food and liquid intake
- Medications
- Attenuation
- Dose

Patient History and Status

To ensure a successful study, it is important to take an individualized approach to each new patient. Taking a brief clinical history prior to acquisition can alert the user to any number of concerns that might effect scan quality. Obtaining information about the patient's physical and emotional status allows the user to assess the feasibility of particular protocols for this patient, and the need for any special preparatory measures.

Patient-Related Hazards

Variations in a patient's physical and emotional status can make the task of positioning for an acquisition challenging. When handling a patient or performing a scan, it is important to be aware of the risk of accidents.

This section warns about the potential danger of serious injury to the user or patient should the user fail to use care during preparatory and scanning procedures.



Failure to use proper procedures when transferring a patient onto or off the table, or into and out of the gantry, may result in back strain or similar injury. Refer to your hospital procedures for placing patients on gurneys.

Severe injury may result should a patient fall from the table. To prevent injury due to falls:

- Provide assistance and support for those patients who may experience fainting or dizziness while transferring to or from the table, or during power motions.
- Keep the patient in full view at all times. Never leave a patient unattended while on the table.
- Use only those patient support devices or accessories specifically recommended for the system.
- Never exceed the rated patient load of the table.

Patient Positioning and Movement

Patient movement during acquisition can corrupt the results of any scan. One of the best ways to reduce this risk is to position the patients comfortably and securely to eliminate movement.

Note that patient positioning is especially crucial for measured attenuation corrections. It is essential that patients remain in exactly the same position for both the transmission scan as for the emission scan, to avoid corrupting the results.

Food and Liquid Intake

Certain studies can be hampered by food or fluid intake prior to a scan. Be certain to instruct patients undergoing these studies to hydrate immediately following a scan to reduce radiation exposure to the bladder.

Medications

Certain medications can affect the results of a scan by interfering with the action of various radiopharmaceuticals.

Attenuation

Be aware that metal attenuation from the head-holder's connecting support can distort the image quality. Take care to position patients properly to reduce the influence of this factor.

IVs

Since adequate count rate is crucial to good image quality, take particular care to avoid extravasation (the escape of fluid into the surrounding tissue) when the user is working with a protocol that demands IV infusion of a tracer. It may be possible to continue with the study even if a line does become partially extravasated, however, as long as the count rate from the scan area is still adequate.

Patient Dosing

The C-PET system operates in 3D mode allowing a much lower patient dose than used in systems that operate in 2D. Typically, patients receive between 2-6mCi FDG per study. This allows for a lower radiation burden to both the patients and staff. Dosing is based on weight and is adjusted for either a 60 or 90 minutes incubation time.

Optimal Imaging conditions for C-PET

The PET-scanner acquires all data in full 3D mode (no septa) which results in a very high sensitivity. Therefore the scanner requires less activity to be injected in a patient than a 2D-PET-scanner with septa. For whole body oncology studies, we recommend to follow the injected dose levels outlined in the table below. This ensures the optimal imaging conditions for the scanner and result in best image quality. Since the count rate of the scanner depends on the activity concentration in the patient it is important to inject depending on body weight. We provide injection values for uptake times of 60 min. and 90 min., the latter are recommended in literature for most oncologic applications. These dose values have been proved to lead to very good image quality at other C-PET sites. Shorter uptake times than listed below leads to higher activity concentrations in the patient and therefore to decreased image quality. Longer uptake times have a lesser impact, however, for to long uptake times (>2.5 h) the statistics in the images is reduced. For physical reasons there is no further increase of the injected dose needed for patients > 90 kg.

Patient Boo	Body Weight Recommended injection of FDG in mCi		Resulting activity concentration	
kg	lbs	60 min uptake	90 min uptake	mCi/kg at time of scam
40	88	1.8 - 2.2	2.2 - 2.7	0.035
45	99	2.0 - 2.5	2.4 - 3.0	0.035
50	110	2.2 - 2.8	2.7 - 3.3	0.035
55	121	2.5 - 3.0	3.0 - 3.6	0.035
60	132	2.7 - 3.3	3.3 - 4.0	0.035
65	143	2.9 - 3.6	3.5 - 4.3	0.035
70	154	3.1 - 3.8	3.8 - 4.6	0.035
75	165	3.4 - 4.1	4.1 - 5.0	0.035
80	176	3.6 -4.4	4.3 - 5.3	0.035
85	187	3.8 - 4.7	4.6 - 5.7	0.035
90	198	4.1 - 4.9	4.9 - 6.0	0.034
95	209	4.1 - 4.9	4.9 - 6.0	0.032
100	220	4.1 - 4.9	4.9 - 6.0	0.031
105	231	4.1 - 4.9	4.9 - 6.0	0.029
110	242	4.1 - 4.9	4.9 - 6.0	0.028
115	253	4.1 - 4.9	4.9 - 6.0	0.027
120	264	4.1 - 4.9	4.9 - 6.0	0.026
125	275	4.1 - 4.9	4.9 - 6.0	0.025
130	286	4.1 - 4.9	4.9 - 6.0	0.024
135	297	4.1 - 4.9	4.9 - 6.0	0.023

Optimal Operating Range

Schematic of countrate curves as function of activity concentration for C-PET.


GETTING STARTED

The Gantry

Detection Specifics

The C-PET uses 6 rectangular curved NaI(Tl) scintillation crystals, each of which is coupled to 48 photomultiplier tubes (PMTs). 42 of the PMTs are 2.5 inch diameter round tubes arranged in a close packed hexagonal pattern, and the remaining six are 1.5 inch PMTs positioned at the edges to fill out the rectangular crystal area. The detector separation is 90 cm.



Figure 3-1 Curved Crystal Technology (CCTTM)

The PMTs on each crystal are connected to four overlapping but otherwise independent trigger channels for event detection. For position determination, these four trigger channels define seven "zones" of PMTs which are read out after a coincidence is determined. The use of these overlapping trigger channels and zones is used to increase the count-rate capability of the system. In essence different sections of the crystal are connected to independent sets of electronics so that an event (which may not be in coincidence) in one part of the crystal does not interfere with the position determination in another part of the same crystal.

Number of Slices

Data is acquired with uniform 1 mm sampling in all 3 dimensions. The data set can be stored and reconstructed into 128 2 mm slices covering the entire 25 cm axial field-of-view (FOV) resulting in a 128x128x128 reconstructed volume.

Slice Separation

Both the slice thickness and the slice separation can be selected in software. The whole body default is a slice thickness of 16 mm and a slice separation of 8 mm.

The PET scanner allows finely spaced overlapping slices that allows the user to exceed the slice thickness over the slice separation. This feature is very important for accurate quantizations.

Field of View

The data volume on the C-PET system can be resliced after reconstruction to any arbitrary angle due to the large axial FOV and the collection of data in all three directions. Therefore, tilting and slewing of the gantry is not necessary. The wobbling effect of the detector motion is diminished by narrowing down the inherent data sampling to 0.5 mm.

Patient Aperture

The patient aperture and the useful transverse field-of-view are 56 cm in diameter.

Axial FOV

The axial FOV measured from the outer edges of the useful part of the crystals is 25 cm.



Figure 3-2 Axial FOV

Transverse FOV

The transverse field of view can be selected at the time of data collection. If a transverse FOV of 576 mm is selected, the mechanical opening (56 cm) defines the physical FOV. If a transverse FOV of 256 mm is selected, the operator must assure that the patient is contained within the reduced FOV.



Figure 3-3 Transverse FOV

Scatter Shielding

The detectors are shielded towards the front and back with a minimum of 2.5 cm of lead. This lead shielding extends 17 cm transversely in order to prevent direct and scattered radiation from outside the imaged volume from reaching the detectors. At the rear, the detectors have between 0.32 and 0.64 cm of lead shielding to prevent scattered radiation from the walls, floor and/or ceiling from reaching the detectors.

Arms in PET Studies

When performing PET studies, it is important to keep the patient's arms up because both photons must hit the detectors within 8 nanoseconds which is a very narrow timing window. By placing the arms at the patient's side, more attenuation is created between where the photon originated and where it hits the crystal. For every 4cm of distance added, the attenuation increases significantly.

The scanner is designed to perform cardiac studies with the patient inserted either feet first or head first. In the feet first position, the images are inverted to maintain proper image orientation. Feet first positioning has several advantages: 1) The distance between the edge of the FOV and the outside of the scanner is less than 1.5 inches 2) the technologist doesn't have to go to the back of the scanner to talk to the patient or have access to his arms for injections, 3) the technologist has access to the motion control panel while he/she is directly next to the patients head and chest, 4) the patient table has an accessory rail on each side of which arm boards can be mounted. The accessory rails can also be used to hold IV poles and other accessories.

Patient Orientation

The C-PET System supports the following acquisition patient positions:

- Head First standard image orientation
- Feet First images are inverted automatically to maintain proper image orientation
- Supine standard (face up) image orientation
- Prone patient is positioned face down, the image must be flipped to maintain proper image orientation (see *Flip Sinogram* in the *Advanced Parameters* window).

Distance (cm)	Attenuation	1/Attenuation	
0	1.000	1.0	
4	0.679	1.5	
8	0.461	2.2	
12	0.313	3.2	
16	0.213	4.7	
20	0.145	6.9	
24	0.098	10.2	
28	0.067	15.0	
32	0.045	22.1	
34	0.037	26.8	
36	0.031	32.5	
38	0.025	39.4	
40	0.021	47.8	
42	0.017	58.1	
46	0.012	85.5	
50	0.008	125.8	
54	0.005	185.3	

Laser Alignment Lights and Switch

As standard equipment the scanner is equipped with four lasers: a front and rear transverse, a sagittal and a coronal laser.

Laser alignment lights are provided to help position the patient within the imaging field of view. These lights indicate the axial field-of-view as well as the coronal and sagittal planes relative to the patient anatomy



WARNING: Advise patient not to look into laser beam(s).

They define the following planes:

- The X-Y (Transverse) front and rear planes, which extends across the patient, perpendicular to the patient's length.
- The **Y-Z** (Sagittal) plane, which extends along the length of the patient and divides the patient into left and right halves from the top.
- The X-Z (Coronal) plane, which extends along the length of the patient and divides the patient into upper and lower halves from the side.

Positioning Using Lasers

As an alternative to Scoutview, it is possible to use the lasers for positioning. To use the following chart:

- Position patient comfortably on the pallet.
- Turn the lasers on.
- Move the pallet in until the patient's starting position is in the FOV. Record this number.
- Push the Relative/Absolute button on the Gantry to REL and press the Landmarkbutton. This zeros the table.
- Continue moving the patient until the desired ending position is in the FOV.
- Look at the number on the control panel. This is the "change in table".
- Find the corresponding "change in table" value on the chart, rounding up to the next value.

Read across the chart for the *Scan Length*. Enter both the *Start Position* and *Scan Length* values in the acquisition setup window

C-PET Laser Positioning Using Chart						
Change in Table	# EM Positions	# TR Positions	Scan Length			
0	1	3	256			
112	2	4	368			
224	3	5	480			
336	4	6	592			
448	5	7	704			
560	6	8	816			
672	7	9	928			
784	8	10	1040			
896	9	11	1152			
1008	10	12	1264			
1120	11	13	1376			
1232	12	14	1488			
1344	13	15	1600			
1456	14	16	1712			

Emergency Stop Button

An Emergency Stop button is located on the right side of the Operator Control Panel, as well as at the Operator's Workstation. When you press either of these buttons all system motion stops. (See the section on Emergencies for further information.)

Source Exposure Warning

A source exposure warning indicator is located on the Operator Control Panel (in the form of a flipper). This indicator activates (flip on a radiation symbol) anytime the transmission source has been removed from its shield.

The indicator turns off after the source has been returned to its shield.

Note: This indicator remains in its last position in the event of a power shutdown.

Transmission Source

The transmission source is a sealed point source of Cs-137. It is a calibrated source that allows the system to measure positron annihilation events and to use that information to make fast accurate attenuation corrections to patient images.

The C-PET system uses a single Cs-137 point source, which is partially shielded at all times. The source is constructed of a long-lived isotope (30 years) and meets the appropriate regulations for sealed sources.

Note: Your site is responsible for complying with all local, state, and federal regulations applicable to dealing with sealed sources.

The source is stored in the gantry within a shielded container. The system withdraws the source from this container and loads it into the source drive when needed for acquisitions. The radiation indicator on the gantry turns-on to show the presence of the exposed source.

During acquisition of a transmission or a blank scan the source rotates around the patient aperture. After an acquisition the source is stored again within the shielded container. The radiation indicator turns-off when the source is returned to its shield. A switch is provided on the Operator Control Panel to insert and remove the point source.



Figure 3-4 Transmission Source

Electronic masking is used during transmission and blank scans to minimize the effects of random and scattered events.

Patient Table

The table in/out motion is electrically controlled from the front panel on the gantry. Front panel control always overrides any computer command; furthermore after manual override of a computer command the computer control is disabled until specifically enabled again by the operator. In/out motion control is possible from the gantry or from the operator workstation for studies such as whole body tumor surveys and is fully automatic; the presence of an operator is required during motion for safety reasons.

The vertical motion is controlled electrically from the front panel.

Table motion can be initiated from the gantry. The system allows movement of the table prior to acquisition or during scanning in order to cover large portions of the body.

In case it is necessary to remove the patient quickly or after a power failure the patient pallet can be moved manually after depressing the foot petal located at the end of the patient table. This disengages the motor drive and permits rapid manual motion of the cradle. To restore the patient table to remote, motorized control, the foot petal must be returned to the middle position and table locked.

Operator Control Panel

As illustrated in Figure 3-5, the Operator Control Panel is located on either side of the gantry port. It provides a combination of switches, pushbuttons and a visual display designed to assist the user during patient positioning and acquisition.

Table Position Pushbuttons

The pushbuttons that are located on the lower portion of the control panel are designed to control table up/down and table in/out motions.

Note: The table positioning buttons remains active throughout acquisition.

The table motion is automatically halted when travel limitations occur. By "interference conditions" we mean a situation in which the table is moving on a path that may cause the table or patient to collide with the gantry. If this happens, motion stops.

Landmark Switch

The landmark switch is activated by depressing the *LANDMARK* push button. Use this key to set a landmark.

The *CRADLE POSITION* indicates zero whenever this key is pressed, unless a scan is in progress.



Figure 3-5 Landmark Switch

Table Position and Display

The numeric reading located near the top of the Operator Control Panel provides a continuous report of the table position. If ± 10500 A is displayed, the table must be reinitialized.

To initialize the table, conduct Daily QC.

The reading indicates the longitudinal position of the table, according to either absolute position or patient relative position. A switch on the left side of the display switches between absolute and relative position.

Absolute position indicates the position of the table in relation to the gantry after system startup, once the pallet has been completely retracted. It reads 'AAAAA' when the table is fully retracted (at home position), and positive when the table is located in any other position.

Patient relative position is displayed whenever the landmark pushbutton is in the relative position, and you have established a landmark. It displays the location of the patient anatomy under the alignment light relative to the landmark location once a landmark is set.

Table Motion

For both horizontal and vertical motion the enable button must be pressed simultaneously with either the up/down or in/out button. The speed of the horizontal motion is 35 mm/sec. The vertical speed is 27 mm/sec.

Axial Precision/Accuracy

The pallet can be repositioned to within 1 mm of any previous position; the position readout is accurate to +/-0.5 mm.

Limits of Travel

The total vertical range is from 88 to 108 cm. For safety reasons vertical up motion is disabled unless the pallet is completely removed from the gantry, but vertical down motion is possible at all times. This makes it possible to start "in" motion with the pallet high and finish vertical positioning of the patient when the patient is inserted into the gantry without endangering the patient, as would be the case if vertical "up" motion would be possible at any time.

The range of horizontal pallet motion is 168 cm.

Head Support/Restraint

The headholder can be tilted over a wide range of angles. It is constructed of carbon fiber and can be used with Velcro straps to immobilize the patient's head.

Accessory Rails

The patient table is provided with an accessory rail on both sides. These can be used to mount armboards, IV poles or an ergometer. Specially designed mounting brackets to fit the accessory rails can be provided.

Whole Body Surveys

During a whole body scan, the technologist has to be present and press a button either on the gantry or near the operator workstation before the in/out motion actually starts. At the same time we have made sure that there is practically no case in which data are lost or a study must be aborted unnecessarily. For example, if the patient needs to be moved out of the scanner between frames because he/she became claustrophobic, or if the scan is aborted for any reason; the data that has already been collected is transferred to the disk.

Weight Limits and Pallet Flexing

The maximum patient weight is 300 lbs. Since no rear pallet support is provided, the pallet flexes as it is moved into the scanner with a patient on the pallet. The vertical deflection with a 200 lbs. person on the pallet is 4cm with the pallet fully extended. Vertical deflection within the gantry is a small fraction of the maximum deflection.

Acquisition Electronics

Pulse Shaping

The pulses from NaI(Tl) have a decay time of 240 nsec, which means that approximately 800 nsec would be needed until most of the pulse is integrated. The C-PET scanner uses pulse clipping to shorten the pulse to approximately 150 nsec, thereby allowing us to process a larger number of events without pulse pileup. This pulse clipping occurs on the preamplifier boards associated with each detector. The pulse clipping results in some loss of energy and position resolution, but due to the high light output of NaI(Tl), these losses are kept to a minimum.

Analog Coincidence Electronics

The physical boundaries between the detectors are largely ignored from the point of view of the electronics. The complete ring is first subdivided into 24 trigger channels, which overlap with each other unless they happen to fall on a crystal boundary. The total light output from each trigger channel is summed and represents the total energy of the gamma-ray hitting the area associated with each trigger channel. This signal goes to a constant fraction discriminator to obtain a logic signal. The discriminator also performs a lower level energy discrimination set to roughly 400 keV. The exact level of the energy discriminator is set to avoid dead spaces between the trigger channels and to avoid a large amount of double triggering. Double triggers between two adjacent channels indicates that the event took place between two trigger channels and these events are accepted. Double triggers between non-adjacent trigger channels are rejected.

The Trigger Channels

After coincidence between allowed trigger channels - determine which PMTs are read out and used for the position calculation. Groupings of PMTs used for position determination are called zones. We currently use a total of 42 zones (7 per crystal). These zones again define overlapping groups of PMTs. If only one trigger channel fires on each side, the zone centered over that trigger channel is read out. If two adjacent trigger channels fire, the zone between these two trigger channels is read out creating more zones than trigger channels.

Digital Event Localization

After a valid coincidence event has been detected, the signals from the PMTs - which are continuously digitized every 40 nsec - are integrated for 200 nsec. The PMT signals associated with the two zones identified during the coincidence are transferred to the position calculator. The position calculator first normalizes the PMT amplitudes by looking up a corrected amplitude from a calibration table, then it determines the PMT with the highest signal and calculates a local centroid using the PMTs in the direct vicinity of that peak PMT. In this way signals on PMTs which may receive light from some other event are excluded from the position calculation.

Distortion Removal and Digital Energy Discrimination

As in other single crystal position-sensitive detectors, the calculated positions do not correspond exactly to the point at which the scintillation occurred. To remove systematic errors we add position offsets to the calculated values. These position offsets are derived from previous calibration measurements.

Energy Discrimination

At this point in the event processing, the exact energy of the two events is known. A second energy discrimination is now performed by first correcting the energy signal for local spatial variation in amplitude and then applying upper and lower energy thresholds. This energy window is usually set with tighter energy limits, a lower energy level of 450 keV is typical. These energy thresholds are set in the acquisition program but are rarely changed.

Store Event

At this point of the event processing the detector coordinate pair is converted to polar coordinates (i.e. sinogram coordinates). For each event a single element in a fourdimensional matrix is incremented; the four coordinates are 1) the rotational angle in the transverse plane (phi), the radius in the transverse plane (r), the tilt angle with respect to the transverse plane (theta), and the axial location (z). The axial acceptance angle can be selected by the user; by selecting a very narrow axial acceptance angle, the scanner can be operated in the 2-D mode with a large resulting loss of sensitivity. This feature may be of interest if the user wishes to investigate the effects of the 3-D mode of operation.

In addition to the features described above, the electronics has numerous other features, which will be discussed in more detail in a latter section of this manual. Since the electronics makes extensive use of lookup tables, field programmable gate arrays (FPGAs) and programmable logic devices (PLDs), many other possible features can often be added easily by reprogramming these chips and without redesigning the hardware.

Dynamic Frame Mode

In the dynamic frame mode, the acquisition memory is subdivided into two frame buffers, so that the acquisition can switch from one buffer to the next without any appreciable deadtime depending on the upload mode of the Corrections and Rebinning Board (CRB).

After the acquisition of a frame of data, the contents of the buffer must be transferred from the acquisition memory to the SUN host computer and from there to disk. This requires 7 seconds per frame and the minimum acquisition time without encountering any deadtime is therefore approximately 10 seconds.

The following table shows the acquisition parameters and corresponding memory requirements (2 Gigabytes total available data space). Small sinograms (128*96) are stored as 128*128 matrices, 2 bytes each, seven tilt angles. Large sinograms (256*192) are stored as 256*256 matrices, 2 bytes each, seven tilt angles).

Sinogram Size	# of Slices	Frame Size	Max # of Frames
128*96	64	14.7 Mbytes	136
	128	29.4 Mbytes	68
256*192	64	58.7 Mbytes	34
	128	117.7 Mbytes	17

Deadtime

The detector deadtime is minimized through a number of techniques. First, the crystal is subdivided into four independent trigger channels. Secondly within each trigger channel only those photomultipliers within the direct vicinity of the event are utilized for position determination (which we refer to as local centroid). Thirdly, the pulses are clipped through delay line pulse shortening to less than 200 nsec.

The deadtime effects due to the light emission in the scintillation crystal effect every event, whether it is in coincidence or not, i.e. it is proportional to the detector singles rate. Furthermore, since at this stage it is not yet possible to buffer the data, the frontend deadtime follows the paralyzable deadtime model. Thus each trigger channel (of the total 24 trigger channels, about 18 are truly independent, since trigger channels overlap with each other) has a paralyzable deadtime of approximately 200 nsec.

The deadtime associated with the analog coincidence circuits is negligible, since the logic pulses at this stage are 4-5 nsec wide, i.e. small compared to the 200 nsec detector deadtime.

After a coincidence event has been detected, that is in a few percent of the singles, the pulses are digitized and integrated for 200 nsec, but due to other electronic switching times, the deadtime for integration is approximately 340 nsec. As soon as the coincident pulses are integrated they are stored in a FIFO buffer to reduce further deadtime losses.

The maximum countrate capability of the position calculator is 670,000 counts per second. Of these more than 50% are eliminated at high data rates because they are either outside the digital energy window, are outside the useful detector area, or are random coincidences.

Maximum Count Rates

The maximum single countrate is 1 million counts per second (cps) per detector or 6 million cps for the system. This rate is limited by pulse pile up in the detectors.

The maximum total coincidence rate in frame mode is 450,000 cps. This rate is further reduced by the count losses due to energy discrimination (450 - 585 keV) and elimination of counts falling outside the useful detector area to result in a maximum

number of 220,000 cps being acquired into the sinogram memory. The quoted rates apply to a uniform distribution of activity within a 20 cm diameter phantom, 20 cm long (the NEMA phantom).

Singles and Coincidence Countrates

The singles and coincidence rates are measured at the beginning and end of each frame and are recorded in the header of the scan files. In addition the singles and coincidence rates are determined every 5 seconds during the acquisition and are displayed.

Transmission Source

The transmission source contains 5 mCi of Cesium-137 (Cs-137). Compared to scanners utilizing septa, BGO and a Germanium-68 transmission source, the use of Cs-137 in singles mode for transmission measurements results in higher useful data rates and therefore shorter transmission imaging times. We achieve good quality transmission scans in 1 minute of acquisition time.

The transmission source is stored in a partially shielded container within the gantry. This transmission source can be inserted by remote control in approximately 10 seconds.

Particularly for whole body scanning it is important to perform extremely fast and accurate transmission scans with activity present in the patient.

To permit accurate transmission data collection in the presence of activity in the patient, it is necessary to subtract a certain fraction of the emission data from the transmission data. This however requires an accurate estimate of the relative deadtime losses in the emission and transmission scans. We have therefore implemented the capability to record a "mock" transmission scan shortly after the transmission scan, which records a set of sinogram data using the same scheme as is used for the transmission data, but with the source retracted. This "mock" transmission scan contains an accurate estimate of the emission data, which are also contained in the transmission data, and which are subsequently subtracted from the transmission data. This is referred to as the emission contamination scan.

The Cs-137 source has a primary emission at 662 keV and is used in the singles mode. A full discussion of this technique can not be given here. Briefly, since both the location of the source and the point of impact on the opposite crystal are known, the transmission can be measured. Since the energy is higher than the 511 keV radiation from the patient, activity from the patient can be differentiated from the transmitted radiation.

Physiologic Gating

The input provided for gating can be used to collect systolic/diastolic cardiac images or to control multi-frame cardiac data collection. This system is sold as an option on the C-PET system.

Computer Hardware

Acquisition Workstation (ACQ)

The daily quality control and all patient data acquisitions are controlled from the ACQ. This workstation features a color monitor, keyboard and mouse as well as an emergency stop control.

Server Workstation (SVR)

The operator's workstation is typically located next to the acquisition terminal and is used for image reconstruction, display and analysis of images and other patient data as well as archiving of all data.

The workstation features a high-resolution color monitor, keyboard and mouse. The workstation is a SUN Ultra computer, and a DAT tape drive, which comes with an optical read/write disk drive. DAT tape is standard.

Remote Workstation

Remote Workstations allow the user to conduct the same functions as the SVR Workstation, except for acquisition, calibration and archiving. This enables off-load reconstruction, analysis and filming functions - leaving the scanner free for acquisitions.

The Remote Workstation components are similar to those of the SVR Workstation.

Networking

The C-PET system allows networking with additional workstations for supplemental image display and analysis. The SVR Workstation communicates with other subsystems and image analysis consoles via an Ethernet connection.

Chapter **4 FILE MANAGEMENT**

File Management keeps track of every patient study performed on the system. It allows archiving patient studies onto Optical Disks (ODs) or optional CDRs*, see note below. File Management retains the information of the patient study and the particular OD to which the study was archived. It also permits many of the operations such as deleting, copying, moving of multiple files normally performed through the operating system.

It is recommended that a convention is made when entering data into the database (i.e. all caps). This aids in performing a query on the information.

If *File Management* is called from the Acquisition Terminal (ACQ), acquisitions can be setup and performed, but reconstructions and other functions are disabled. If *File Management* is called from the Reconstruction and Display Workstation (SVR), the acquisition function is disabled. This chapter describes only those functions that can be executed from the SVR Workstation. The use of *File Management* for acquisitions is described in the *Acquisition Chapter*.

Note: This software employs the following programs: cdrecord and mkisofs and device driver: scg. Copyright © 1995-2000 Jorg Schilling. This software is used as freeware to support the writing of patient files to a CD Writer device.

Archiving Study Files on the Hard Drive

The system compresses and saves study files that have not been used for more than 3 days. This is done automatically to save disk space. Compression is transparent to the user and occurs when required. The reduced file size is the only indication of compression, no file extension is added to the file name. Files uncompress automatically when required.

File compression does not interfere with any PetView program (e.g., wbd, reconstruction, viewing file headers). Refer to the *Compress and Uncompress File* chapter.

Egit System Files Database Acquisition Petrion Select Options	Helb
Device Account Study (ee/dd/vyyy) Last Name First Name Birth I (en/dd/	te _{VVI} Patient ID Consent
sand p13 s0 06/25/1998 Karp Joel 06/01/1 sand p12 s1 06/02/1998 Breast Carcines1 00/00/0 sand p12 s1 11/16/1997 BSNA Test First 00/00/0 sand p11 s0 11/16/1997 Test First 00/00/0 sand p13 s0 11/16/1997 Test First 00/00/0 sand p13 s0 11/16/1997 Test Carcines2 12/21/1 sand p13 s0 11/16/1997 Test Carcines2 10/01/1 sand p3 s0 11/16/1997 Terest Carcines2 00/00/0 sand p3 s0 11/16/1997 Terestistion Scan 00/00/0 sand p3 s0 11/16/1997 Eaca Carcines2 00/00/0 sand p3 s0 01/16/1997 Eaca Normal 00/00/00/00/0 s	9 654321 First C-PET images 5 12345 SNM Test acquisition 00 678 SNM Test acquisition 10 789 DEPTy 10 123452 vb bruest ca sue 00 123453 vb bruest ca 01 123454 Brain pontofiore 01 123455 vb bruest ca 01 123454 Brain pontofiore 01 123455 vb demo 01 123454 Brain pontofiore 01 123455 vb demo 01 123454 Brain pontofiore 01 123457 Bod mostor 01 123458 Liege vb demo 01 123454 moral cardia 01 123454 moral cardia 01 123454 no comment 01 123454 rolburg 01
Scheduled Acquisitions Device Status Patient Name Patient ID Comment	Filenane
sund NEW ACCOUNT Hauror, carl 213456 MB-lung sund NEW ACCOUNT Hiller, Chris 1984673 Brain-Seizur sund NEW ACCOUNT Schuster, Lisu 19846 no comment	naur ni 11 schu

Figure 4-1 File Management Window

Patient Data Entry Fields

File Management displays patient data that is usually entered through the acquisition program. The following fields are to be entered:

Device - This field shows the magnetic OD or CD-ROM on which the patient study resides. Since File Management keeps track of all studies performed on the scanner, it is easy to locate any study by looking at the disk identification.

Account Number - At the time of data acquisition, each patient is assigned a consecutive patient number starting with **p1**, **p2**, **p3** **p0** is reserved for quality control information.

Study - The first time a patient comes for a PET study he or she is assigned **s0** for the study. For subsequent scans the operator may choose to add data to the same study or start a new study number (s1, s2 ...). It is recommended to keep all scans performed on the same day in the same study (e.g. ammonia perfusion scan, FDG viability scan, transmission scan).

Acquisition Date - The date on which the study was acquired. The date can be shown either in the format mm/dd/yyyy or dd/mm/yyyy or in the format yyyy/mm/dd. The format can be selected at the time the scanner is installed.

Patient Name - The patient's first name and last name is listed separately to avoid confusion. If a patient name has been entered incorrectly, the entry in the database can be changed. Refer to *Edit Patient Information*, this chapter.

Birth Date - The date of birth should be entered at the time of acquisition and is displayed as additional patient identification information. The date can be shown either in the format mm/dd/yyyy or dd/mm/yyyy or in the format yyyy/mm/dd. The format can be selected at the time the scanner is installed.

Patient ID - The patient identification number can be either the patient's Social Security number (without hyphens) or the identification number used by the hospital. It is the primary and unique method for patient identification.

Comment - The comment is entered at the acquisition time but can be changed at any time. It is useful to be consistent in the choice of comment, since this field can be used for database searches later. For example, for every wholebody scan the comment starts with **wb** ..., then all wholebody scans can be displayed by searching **wb***.

Note: For detail information regarding the items about patient study, refer to the *Study Files* chapter.

File Management Menu Map

Located at the top of the File Management window are the drop-down menus which are listed and explained below:



System

- Archive Study
- Format New OD
- Mount OD
- Unmount OD/CD
- Show Disk Space

Archive Study

The Archive Function moves studies selected by the user to an Optical Disk (OD) provided the OD has 512 bytes/sector. First the OD must be formatted and mounted before the archive function can proceed, see following paragraphs. C-PET archives on the *STUDY* level (not file). Any number of studies can be archived simultaneously as long as they all fit on the destination OD. Typically, between 8-10 studies fit on one side of the OD. A warning is displayed if all studies do not fit. ALL files in a study must be archived and may not reside in two places. If a study does not fit on the destination OD, then either some files must be deleted from the study, or the study can be archived to another OD that has the available space.

When patient data are archived to a formatted OD, the files are physically moved off the hard drive and onto the OD. It is recommended to compress data prior to archiving. When data is restored to the hard drive, it is physically moved off the OD.

After files are moved to the destination, the device label field of each study is changed to reflect the new location provided the OD was formatted for database use. If database update fails, the studies are automatically unarchived so the system is left in a consistent state. When Archive completes successfully, the current database query in the *File Management* window is re-executed to display the new database information.

Archiving to CD-ROM

A CD-ROM may be used as an alternate archiving device to the OD. Files are moved onto the CR-ROM when archived, not copied. This allows *File Management* to track where the data is located. This is similar to a database-formatted OD listed in the *Device* column of *File Management*. After the data is compressed, select all the files to be archived and transfer them all at once as it is only possible to write to each CD-ROM one time. Transfer all the studies on the CD back to /sun0 if any restoring of data is desired. If any manipulation to the data is done, discard the CD and re-archive all the data to a new CD-ROM.

The CD-ROM is meant to be used as an archiving device. It is not possible to screen dump onto a CD-ROM at this time.

Note: A single file from a study cannot be archived via the File Management Window. When archiving back to sun0, the uncompress command may be selected for only study files needed for viewing.

Archive Study Procedure

- 1. From *File Management* double click the patient study
- 2. From *Study Files* select, *Select > Select All*
- 3. Select, *Options > Compress files*
- 4. Exit *Study Files* window
- 5. From *File Management* select, *System > Archive Study*
- 6. A popup menu is displayed, verify the archive destination

If only one OD is mounted and there are no additional 'home' partitions, the system asks to verify the OD as the destination.

If the destination is an OD, the OD must have a label that was defined by the system that indicates it is supported by the database.

Archive Procedure for Personal Use

Patient data can be copied for personal use but the files physically remain on the hard drive, see Format New OD, below.

- 1. From *File Management* double click the patient study
- 2. From *Study Files* select, *Select > Select All*
- 3. This step is optional (use to compress files) select, *Options > Compress files*
- 4. Select, *File* > *Copy files*
- 5. A popup menu is displayed, enter: **/OD** for the Destination Directory

Upon completion, *File Management* does not reflect where the files reside.

Format New OD

There are two options available in formatting an OD:

- For Personal Use
- For Database Use

For Personal Use

This operation formats and initializes a blank OD. Patient data can be copied for personal use but the files physically remain on the hard drive. The user may assign any label, the database does not know of its existence and will not track the files. It is the user's responsibility to properly label and track the OD. A personally labeled OD can be used only to copy files, archives or merges are not permitted. It is important that the user keep track of the labels on both sides of a personally formatted OD.

For Database Use

This operation formats and initializes a blank OD and assigns a label. The OD is intended for archived studies that are to be maintained by the database. The label is automatically assigned by the system and is of the form: **od#** where **#** is an integer that is automatically incremented with each new database OD that is initialized.

If the OD previously had a database-assigned label, and still has patient studies residing, the user is not permitted to reformat. If the previous label is database-assigned but has no patient directories on the OD, or if the previous label was user-assigned, the user is asked for verification to overwrite the OD. The user has the option to cancel the format operation at this point.

An OD may not be formatted on a Remote Workstation. The OD drive must be connected to the workstation running the *File Management*. If a remote format is attempted, an error message is displayed.

Format New OD Procedure

- 1. From *File Management* select, *System > Format New OD > For Personal Use* or *For Database Use*
- 2. A popup menu is displayed, enter:

Drive Used:

Enter the drive into which the OD is to be inserted. If only one OD drive is configured on the system, a 1 is automatically entered.

Default Label Assigned to OD:

Enter the new OD label. This label is retrieved from the database and cannot be changed in this window.





3. Click OK

The user is prompted to insert the OD with the appropriate side up into the drive, then formatting begins. The *Format* operation runs in the background, so other *File Management* functions can be performed while an OD is formatting. Formatting takes about 10 minutes. A message is displayed when the operation is complete.

Mount OD

In order to perform any operations on an OD, the OD must be mounted. To initiate the Mount OD process select the following:

From *File Management* select, *System* > *Mount* OD

When the Mount process completes, a message appears stating the ODs were mounted and where the directories reside.

Unmount OD/CD

To Unmount ODs or CDs, from *File Management*, select *System > Unmount OD/CD* from the drop-down menu. If one is mounted, the user is prompted to verify the unmount operation. If more than one is mounted, a list of mounted labels is displayed. Select the one to be unmounted, and click *OK*. The OD/CD(s) is unmounted and ejected.

If OD/CDs are mounted when Exiting *File Management*, the system prompts to unmount them. Clicking *OK* unmounts and ejects them before exiting. The OD/CDs remain mounted if *OK* is not selected. They are accessible when *File Management* is again executed.

Show Disk Space

This option displays the available space of all disks configured on the system and any mounted ODs. It also shows the names of the devices, the directory path names to the devices, the available space in Kbytes, and the percentage of space used so far on the devices.

This function allows the user to check available space on a device to which they plan to move files. It shows if deletes are necessary or using another device would be more appropriate with extra space.

From *File Management* drop-down menu select, *System* > *Show Disk Space*

Files

Study Files

This menu choice displays the Study Files window of the highlighted study. Displayed is information about the files that reside in the directory associated with the selected study or studies. This window can also be presented by double clicking the study or highlighting the study and pressing the **F1** function key.

From this window files can be copied, renamed, or deleted, and their headers, and general image or sinogram file information can be examined.

For details on functions see Chapter 5, Study Files.

Database

Execute Query

To search for a particular value for a particular field in the database, simply enter that value in the appropriate text field.

EXAMPLE: To search for all patients on OD3, type **OD3** in the text field under the *Device* column heading.

Execute Query Procedure

- 1. Enter data in a text field beneath a column name on the File Management window
- 2. Select *Database* > *Execute Query*
- 3. File Management displays only the studies with query data
- 4. To display the entire database again, select *Database > Clear Query*.

Searching on Keywords

There are three ways to specify a keyword in the text fields under the column names:

- Wildcard Characters
- Keyword Ranges
- Sorting Query Output

Wildcard Characters

Wildcard characters can be used in all fields but the *Account ID*, *Study ID*, *Acq Date*, and *DOB*. Wildcards are not allowed in the date fields because dates are stored as integers in the database. Use '*' to signify one or more characters in the wildcard search, and '?' to indicate any single character in a particular location in the string.

EXAMPLE 1: To search for all patients whose last name begins with a 'B', enter 'B*' in the text field under the *Patient Name* column heading.

EXAMPLE 2: To search for all studies that reside on OD1 to OD9, type **od?** in the text field under the *Device* column heading

Keyword Ranges

Ranges can be specified in the *Account ID, Study ID, Acq Date and DOB* fields because those are integer fields in the database. To enter a range of values, simply type the lower end of the range, a ' – ', and the higher end of the range.

EXAMPLE 1: To search for all patients whose acquisition dates are in the year 1992, enter 1/1/92-12/31/92 in the text field under the *Acq Date* column heading.

EXAMPLE 2: To retrieve just the first three studies of all patients in the database, enter **s0-s2** in the text field under the *Study* column.

Multiple keywords can be entered in both the same field and in separate fields. If multiple keywords are entered in the same field, separate them with commas. If several keywords are entered in the same field, their union is returned.

EXAMPLE: To search for all patients whose studies pertain to either the brain or the heart, type **brain**, **heart** in the text field under the *Comment* column heading.

If keywords are entered in several fields, their intersection is returned. Therefore, all conditions must hold for a database entry to match the criteria.

EXAMPLE: To search for all patients whose study organ is the brain AND whose study date is in March, 1991 type **brain** in the *Comment* field, and **3/1/91-3/31/91** in the *Acq Date* field.

All these methods can be combined, creating a somewhat complex query.

There are a few limitations to the queries. One limitation is that it is not possible to negate a value. For instance it is not possible to query all patients whose name is NOT 'Brown'. However, it is often possible to get around this by using wildcards or ranges in clever ways.

Sorting Query Output

To sort the results of a query by a particular field in ascending order (alphabetical or earliest date first), enter a '+' in the appropriate field. To sort in descending order (reverse alphabetical or last date first), enter a '-' in the appropriate field.

EXAMPLE 1: To return the query results in alphabetical order by name, enter '+' in the field under the *Patient Name* column heading.

EXAMPLE 2: To return query results in the order of last account first, type '-' in the field under the *Account* column heading.

Several sort criteria can be entered by prefixing each '+' or '-' with an integer indicating the priority for that particular field.

EXAMPLE: To sort the output first by name, and, in the case of duplicate last names, by Acq Date, type '1+' in the *Patient Name* field, and '2+' in the *Acq Date* field.

Ascending and descending orders can be mixed in a multiple sort criteria situation.

Sort criteria do not necessarily have to be entered for each query. If there is no userspecified sort order, the database returns the data sorted by Account number.

If keywords are entered along with sort criteria, the sort criteria MUST BE the first characters typed in the field.

EXAMPLE: To query all patients whose studies are on the brain, and were done in 1990, where the data are desired to be sorted by last name in reverse alphabetical order and then by earliest date first, type: **2+1/1/90-12/31/90** in the *Acq Date* field '**1-**' in the *Patient Name* field and **brain** in the *Comment* field

Clear Query

To display the entire database, select *Database > Clear Query*.

Edit Patient Information

The user can edit patient data in the database: *Patient ID, Last Name, First Name, Birth Date, Study Comment, and Technologist's name.* When the *Edit* option is chosen, a window pops up that displays the old database fields and blank text fields in which the user writes the new values desired. This window is also available via the **F4** function key.

If the patient's name is being changed, usually due to a typographical error, the entire name must be entered regardless of where the change is actually being made.

The *Study Comment* field can be any alphanumeric string that is no longer than thirty (30) characters.

Edit Patient Information Procedure

- 1. Select *Database > Edit Patient Information* from *File Management* The Edit Patient Information window below is displayed.
- 2. Enter new data and click *OK*
- 3. The current database query is rerun to display the new database values.

– Edit Patient Information 🛛 👘 🗖							
	Current Value	New Database Value					
Patient ID:	12345						
Last Name:	Miller						
First Name:	Joseph						
Birth Date: (mm/dd/yyyy)	01/10/1972						
Study Comment:	Whole body scan						
Technologist:	Jane	<u>^</u>					
	ОК	Cancel					

Figure 4-3 Edit Patient Information Window

PetView

Load PetView Image

Load an image into memory for use by other modules which interface to the directory that corresponds to the study that is selected in the File Management window. Only one study can be highlighted at a time. Once an image is loaded, it can be displayed and processed using the normal PetView interfaces from the *PetView Menu*.

To load and view an image in Wholebody Display, double click an image or sinogram in the *Study Files* window

This loads the image or sinogram with the default Load program settings and invokes the Wholebody Display program.

Note: Refer to *PetView Chapter* for more information.

Select

Choosing *Select All* results in all the items being highlighted. Choosing *Unselect All* deselects all the items in the window. The result of the *Unselect All* choice is to leave all the items unselected regardless of whether or not an item was selected before the *Unselect All* function was invoked.

To select several unselected patients, press *<Control>* and click patients to be selected.

Options

Site-specific File Management functions may be defined for your system, and are accessible from the *Options* menu. If no *Options* are visible, then there are no site-specific operations for your system.

The following are possible options:

- Directory Space
- DICOM Translation
- Transfer to Remote

Directory Space

Directory Space shows total amount of memory used in each subdirectory. Before clicking *Directory Space* select one or several patient studies to show disk space used.

DICOM Translation

DICOM Translate allows the user to import files from other devices such as a CT or MRI scanner. This option is only active if the DICOM option is installed.

Note: For detailed information, refer to the *Dicom Translation* chapter.

Transfer to Remote

The Off-Line Remote is a workstation that can view images independently; it does not require a continuous connection to the Server. The Server must still provide the images and the patient database, whether through a temporary connection (e.g., ISDN) or on ODs. Either way, this transfer is unidirectional.

The images and database are transferred using menu options presented in *File Management*. These options are always available on the Server and accessible on Off-Line Remote with a connection to the Server. Once a transfer has occurred, the Off-Line Remote is updated when the *File Management* is restarted.

Transfer to Remote (non-connected) Procedure

Off-Line Remotes can receive studies and the database on ODs.

- 1. Select one or more studies in *File Management*
- 2. From the drop-down menu select *Options > Send Study to Remote on OD* This also sends the current database
- 3. A text window appears displaying status messages. It indicates when the studies and database have been successfully written to the OD. This OD can then be inserted into the Off-Line Remote's OD drive.
- 4. Once the data is transferred, *File Management* must be re-started on the Off-Line Remote for the patient studies and database to be updated. Note, all *File Management* windows must be closed for the updates to occur.

Transfer to Remote (connected) Procedure

Off-Line Remotes connected to the Server can directly receive studies and the database.

- 1. Select one or more studies in *File Management*
- 2. From the drop-down menu select Options > Send Study to xXXX-olrX (where xXXX-olrX is the name of the Off-Line Remote) This sends the selected study or studies along with the database directly to the Off-Line Remote or

select *Options* > *Send Database to xXXX-olrX* This sends only the database

On the Off-Line Remote, there are corresponding entries: *Get Study from Server* and *Get Database from Server*

Once the data is transferred, *File Management* must be re-started on the Off-Line Remote for the patient studies and database to be updated. Note, all *File Management* windows must be closed for the updates to occur.

Chapter

STUDY FILES

The Study Files window is available in *File Management* under the drop-down menu *File > Study Files*. It can also be displayed by highlighting a study in *File Management* and pressing the **F1** function key, or by simply double clicking a study.

Study Files displays information files that reside in the directory associated with the selected study(s). This information includes the name of the *Device* where the file resides, *Account* and *Study* IDs associated with the file, *Patient Name* and *Patient_ID*, *File Name*, file *Type* (i.e. image, sinogram, region, count file), *Protocol* used if the file is an image or sinogram, and the *Size* of the file in Kbytes. Beneath this list are two boxes that display how many files are listed in this window and their total size in Kbytes. This is useful if the user wants to compare the total size of a set of files with the available space on a device before moving any files.

From this window files can be copied, renamed, or deleted, and their main headers, subheaders, and general image or sinogram file information can be examined.

To load and view an image in wholebody display, double click an *Image* or *Sinogram* in the *Study Files* window under the *PetView*. This loads the image or sinogram with the default settings in the whole display program.

Located at the top of the Study Files window are the drop-down menus which are listed and explained below.

-						Stu	dy Files			r 🗆
Quit	<u>S</u> ystem <u>F</u>	ile <u>I</u> n	formation	<u>P</u> etView	Se <u>l</u> ect	Options				<u>H</u> elp
Device	Account	Study	Patient Na	me		Patient_ID	File Name	Туре	Protocol	Size (KBytes)
sun0 sun0 sun0 sun0 sun0	р0 р0 р0 р0 р0	51 51 51 51 51		,, . , . , .			normal-brain Ka_melanoma Lung_with_liver_met AbdominalCa Cardiac	ing ing ing ing ing	brainft Body_with_atten Body_vecondpassjknb Body_with_atten Body_with_atten	2819 3263 2240 1838 1330
Total:	5	Files;	11490	Кb	ytes					



Study Files Menu Map

Located at the top of the Study Files window are the drop-down menus which are listed and explained below:



System

Refresh Files

Certain functions, such as Acquisition and Reconstruction alter the list of files. Selecting *Refresh Files* re-lists all files from the directories selected in *File Management*.

Show Disk Space

Displays available space of all disks configured on system and ODs that are mounted. It shows the name of the device, the directory path name to the device, the available space in Kbytes, and the percentage of space used so far on the device. No warning is given when the disk space is full to a certain extent, however, scan does not acquire.

File

- Copy File(s)
- Rename File
- Delete File(s)
- Add/Change Study Notes

Copy File(s)

Files that are listed in the *Study Files* window may be copied to another directory. This does not change any values in the database since the files continue to reside in the original location as well.

Multiple files can be copied to the same destination. The original filenames are preserved, so if the destination is a study subdirectory maintained by the database, the prefix, pxxx sxx, of the copied filenames does not match their new location. In that event, a message is displayed to use *Rename* to fix those prefixes when the copies are completed. If the file copied already exists in the destination directory, the user is prompted to overwrite. If the user denies an overwrite, that file is not copied, but the program continues copying the other selected files.

Before the copy begins, available space on the destination device is compared to the total space of all the files to be copied. If there is not enough space, the copy aborts.

There are some restrictions on what can be copied to where. If the destination directory is not maintained by the database, anything can be copied. If the destination directory is maintained by the database, image or sinogram files can only be copied to another study of the same patient account. Also, no more than 500 files can be selected for a single copy operation.

Copy Files Procedure

- 1. From *Study Files* highlight the files to be copied
- 2. Select, *File > Copy Files* from the drop-down menu
- 3. The user is prompted for the full path name of the destination directory.

If the user is not sure of the full pathname, select *System > Show Disk Space* This shows the full pathnames and mounted ODs. The destination directory must exist before the copy can proceed.

When all files are copied successfully, the study files are relisted to reflect any additions to the studies that are displayed in the *Study Files* window.

Rename File

Files that are listed in the *Study Files* window may be renamed within the same directory. This does not change any values in the database because the database does not keep track of actual filenames.

Rename File Procedure

- 1. From *Study Files* highlight the files to be renamed
- 2. Select, *File > Rename* from the drop-down menu
- 3. A window appears displaying the old name, and a text field for the new name.

The new name prefix is already in the text field because filenames must be prefixed to indicate the subdirectory so if the database has to be rebuilt for any reason the correct values can be restored from the filenames. This is why it is important to rename any files that have been copied to a database study directory.

The new filename must have no directory path. The rename function simply renames a file within the same directory. The new name must have the same three-character extension as the original file name. For example, if the original filename ends with a .img extension, the new filename must end with the same extension. Any overwrite possibility is checked. If the new filename already exists, the user is asked to approve or deny it. If denied, the rename operation aborts and the user may try another name.

'Rename'gives a	file a new name within the same directory
Renane Old Filenane	test2.ing
To New Filename	p1s0_
	0K Cancel

Figure 5-2 'Rename a file' Window

When operation completes, the study files are relisted to reflect the new filenames.

Delete Files

Files that are listed in the *Study Files* window may be deleted.

When the delete function is finished, the study files are relisted to reflect the new number of files. If all the files in a study are deleted, the subdirectory associated with that study is also removed, and the *Comment* field for that study is changed to *DELETED*. When the files are re-listed, that study is not able to open, so an error message is displayed. If new data is acquired for that particular patient, the *Acquisition* program may reuse a *Study ID* if it is indicated as being deleted.

Delete Files Procedure

- 1. From *Study Files* highlight the files to be deleted
- 2. Select, *File* > *Delete File*(*s*) from the drop-down menu
- 3. A verification window appears for each highlighted file for the user to OK or Cancel that particular delete. Use this function with caution, there is no recovery option. This function deletes patient data but not the database entries in the database.

Add/Change Study Notes

Text notes can be added or changed on a patient's study.

Add/Change Study Notes Procedure

- 1. From *Study Files* highlight the files to be modified with a study note
- 2. Select, *File > Add/Change Study Notes* from the drop-down menu

A window is displayed that allows the user to enter text to be added to the patient study. These study notes can be printed separately or with the patient's images.

- 3. Click *OK* to save the text in a file with the extension **.txt**
- 4. After typing and editing the text, This file can be viewed and edited by highlighting it and click *Add/Change Study Notes*

or

Select, *Options > View Text File* from the drop-down menu

Information Menus

- Img/Sino Information
- Mainheader Dump
- Subheader Dump

Image/Sinogram Information Display

- 1. Highlight one file type, *IMG* or *SCN* in the *Study Files*
- 2. Select *Information > Image/Sino Information* from the drop-down menu

The information displayed includes:

Matrix Filename

- Matrix File Type
- Matrix Dimension Dimension perfusion of image
- Diameter of FOV Field of View
- Slice Thickness
- Date Created
- Also lists: *Slice, Tilt, Frame, min, max* and *Total* [*Mcts*] for each slice in each frame in the data set.
- 3. Select *Quit* when done viewing

Mainheader Dump Display

- 1. Highlight one file type, *IMG* or *SCN* in the *Study Files*
- 2. Select *Information* > *Mainheader Dump* from the drop-down menu The information displayed includes:
 - Patient Information
 - Scanner Setup Parameters
 - Scanner Setup
 - Counting Statistics
 - Slice Thickness
 - File format
- 3. Select *Quit* when done viewing

When done viewing the information, pop down the window by selecting the *Quit* in the *Main Menu* of the *Main Header* window.

Subheader Dump Display

Since the information displayed pertains to a particular slice in an image or sinogram, the user must specify the *Frame*, *Tilt*, and *Slice* number of interest with the slider bars at the top of the window. When one of the sliders is adjusted, the information is displayed.

- 1. Highlight one file type, *IMG* or *SCN* in the *Study Files*
- 2. Select *Information > Subheader Dump* from the drop-down menu

The information displayed includes:

- Global Parameters
- Frame Parameters
- Slice Parameters
- Reconstruction Parameters
- 3. Select *Quit* when done viewing

Options

The possible *Options* in the *Study Files* window are shown below:

- Compress File
- Uncompress File
- View Text File
- Edit Mainheader
- Edit Subheader
- Extract
- Transfer to MAC
- Interfile Export
- Load Deadtime Factors
- Previous Version of Recon
- Current Reconstruction
- DICOM Send

Site-specific *File Management* Functions may be defined for your system, and are accessible from the *Options* menu in the main *File Management* window and/or in the *Study Files* window. If no *Options* menu is visible in either window, then there are no site-specific operations for your system.

All *Options* functions in the main *File Management* window must operate on directories, and *Options* functions in the *Study Files* window must operate on files.

Compress and Uncompress File

Study File options allow for files to be manually compressed and uncompressed. The compression option does not add a .z extension. This allows programs to function without having to first uncompress the data.

The system also has an automatic compression utility which is transparent to the user. It is designed to maximize disk space by automatically compressing patient data. By default, the utility compresses sinograms not used after 2 days and images after 3 days. Customer support can modify these defaults.

Uncompression occurs automatically when these files are used, so manual uncompression is not necessary. However, the uncompress option is still available.

View Text File

Files that contain text data, such as region-of-interest files (*.cnt) can be viewed with an editor program that is invoked by selecting a text file and clicking *View File*. The editor allows changes to this file; however, it is the user's responsibility to avoid changing the file in a way that it will be incompatible with other programs that may need to read this file, such as the *Region-of-Interest* (ROI) program.

Edit Mainheader/Subheader

- 1. From *File Management*, double click the patient file.
- 2. Select *Options > Edit Mainheader*
 - To change the *Patient Weight*, type: weight Enter patient's weight in grams.
 - To change the *Activity*, type: activity Enter activity in MBq (1 mBq = 37 mCi)
 - To change the *Assay Time*, type: meas_time Enter time in hh:mm
- 3. When edits are finished, type: **exit** This saves the changes. Note: typing **quit** does not save changes.

The mainheader and subheader of each file can be modified using the *Edit Mainheader* and *Edit Subheader* functions. This may be necessary to correct data that was incorrectly entered at the time of acquisition, or a field necessary for certain operations was left blank. For example, the SUV calculation requires the patient's weight, which is an optional entry in the acquisition program. Great care should be taken in modifying data in the headers, since numerous programs depend on the correct values in these fields.

Extract

This utility is a service tool used by the Field Service Engineer.

Transfer to MAC

This option is for future use.

Interfile Export

Files can be exported to another system in the Interfile format.

Load Deadtime Factors

The option to *Load Deadtime Factors* may be invoked, when the user wishes to use SUV values and did not follow the normal procedure (see *SUV Chapter* for details).

Previous Version of Reconstruction

Allows the user to access the reconstruction program from the previous UGM software release. This may be desired to compare a newly acquired image against an old image acquired with the previous UGM software release.

Concurrent Reconstruction

This option initiates the reconstruction portion of the concurrent acquisition/reconstruction process. This option is only used when reconstruction is stopped during a concurrent acquisition/reconstruction process.

Changing the protocol may be a reason for stopping reconstruction. When the desired protocol is selected, reconstruction must be restarted by selecting, *Option > Concurrent Reconstruction*.

DICOM Send

The *DICOM Send* options menu item allows the user to send images in DICOM format (see the *Dicom Translation Chapter* for details).

Help

Click the top level *Help* option in the *Menu Bar* of the current window pulls down a submenu. The submenu options usually correspond to the window's *Main Menu* options. For information about a specific function in that window, simply highlight the topic in the *Help* submenu and the *Help Text* is displayed. In some cases, selecting a topic in the *Help* menu cascades yet another submenu with more detailed options. Continue highlighting the topic of choice until the *Help Text* window is displayed with the information needed.

When finished reading the help text, collapse the *Help Text* window by pushing the *Quit Help* button in the *Help Text* window.
Chapter

PATIENT RECORDS DATABASE

Patient records database can be edited using the loaddb program which has a menudriven ASCII interface. Loaddb opens the database in shared access mode so other database applications may run concurrently if necessary, but it is recommended to run loaddb alone.

Database Access

- 1. Open an *Xterm Window* on the SVR Workstation with left mouse button on desktop.
- 2. At the prompt, type **loaddb**

The following menu appears:

MAIN MENU:

Patient-Related Functions:

- 1 Add Patient Record
- 2 Delete Patient Record
- 3 Display/Change Patient Record

Miscellaneous Functions:

- 4 Display/Change Last OD or ROM Label Assigned
- 5 Display Last Assigned Account ID
- 6 Clear Record Lock Bit
- 7 Test Date Conversion
- q Quit
- Enter Command Number:

Add Patient Record

Patient information should only be added if a patient record was lost that was initially added by *File Management*.

If a *Patient ID* already exists, the number of studies field is queried and a new study is assigned. The system prompts for the following study-related information.

- *Study Date (may be blank):*
- Device Label ('sun#', 'od#', or 'rom#'):
- *Study Comment (may be blank):*
- *Technologist (may be blank):*

If the *Patient ID* does not exist, a new patient record is created. For a new patient, the following information is requested:

When *Option - 1* is selected from the *loaddb Main Menu*, the system prompts for a new or existing *Patient ID (p#)*

- Patient ID or <Enter> for Main Menu): (unique patient identifier) value may be entered as p#, P#, or #
- Last Name (or <Enter> for Main Menu):
- First Name (may be blank):
- *Number of Studies:* <number of studies that is entered for patient>
- Account Date: <original account date of lost patient record>
- Patient Date of Birth (may be blank):
- Add Patient Record to Database (Y = yes, N = no)?
 - Y =loops according to the number of studies value for the study data
- Please Enter Data for Study 0:
- *Study Date (may be blank):*
- Device Label ('sun#', 'od#', or 'rom#'):
- *Study Comment (may be blank):*
- *Technologist (may be blank):*

The study information is redisplayed as it was entered, and prompts with the following question:

- Please Enter Action (Y = Enter in database; N = Edit Fields):
 - N system prompts again to enter the study field values Y - study is entered in database

Certain prompts for the Patient Record data allow the user to cancel the Add operation by simply pressing **<Enter**>.

The prompt indicates when a **<Enter>** cancels and a blank field is stored in the database. The number of studies are always compatible with the *Number of Studies* field in the patient record. The user can not cancel an addition to the database, the study must be added and can be deleted later.

Date fields must be entered in the form as mm/dd/yyyy, dd/mm/yyyy, or yyyy/mm/dd which can be confirmed by Customer Support. If the date is entered in the wrong format, the correct format is displayed and the system prompts to re-enter the date. Some fields (*Patient ID, Last Name, First Name, Study Comment, Technologist*) have a maximum length. If the entry exceeds the maximum length, the system prompts to re-enter the item.

Delete Patient Record

One patient record may be deleted at a time, this should be used when all studies associated with a patient record are removed. If all studies are deleted, the system prompts to delete the patient record.

IMPORTANT It is important the study directory be empty before removing the study. Or else those study files will be hidden and not listed in *File Management*.

- 1. From the *loaddb Main Menu* select, 2 - Delete Patient Record
- 2. The following is displayed, Enter Account ID to Delete (as p#, P#, or #) (or <Enter> for Main Menu):

At this point, all the patient information and associated studies are displayed to verify that it is the correct account to delete.

- 3. The system then prompts: *Enter Study ID* to delete (as s#, S#, or #) (or <Enter> to delete another account):
- 4. Study information is redisplayed, prompts to confirm study deletion are displayed. The deletion operation may be cancelled at the prompt of the Study ID (*a* <**Enter**> causes a prompt for another account ID to delete)

If the study to be deleted is not the latest study for the patient, the *Comment* field is changed to *DELETED*. If it is the latest study then it is removed, and the *Number of Studies* field is decremented.

5. **n** response is OK (i.e. it is OK for the *Number of Studies* field to be 0), however, the patient is not visible because *File Management* lists study records. If there are no study records the patient is ignored.

y deletes the patient record

Since the record no longer exists, loaddb reports that the account key is not found. This error message is normal - it means that the record could not be unlocked after it was deleted.

Display/Change Patient Record

This option lists all the patient and study information associated with the account ID.

- 1. From the *loadlb Main Menu* select, 3- Display/Change Patient Record
- 2. The following is displayed for edit:

Patient Information:

- 1 Account ID
- 2 Patient ID

- 3 Patient Name
- 4 Num Studies
- 5 Patient Date of Birth

Study Information:

- 6- Study ID
- 7- Study Date
- 8- Device Label
- 9- Comment
- 10- Tech Name

Enter field to edit (or <Enter> to view another account):

3. When a *Patient Information* option is selected, the old value is displayed, and the system prompts for the new value. Pressing <**Enter**> at the new field prompt without typing anything cancels that edit function.

or

When a *Study Information* option is selected, the system prompts for the *Study ID* to edit. The old *Study ID* is displayed and prompts for the new field value. A **<Enter>** at any of the new field prompts cancels the edit operation.

4. Whether an edit is cancelled or performed, the new patient information and associated studies are displayed with the edit menu. The option of editing another field is available, or press <**Enter**> to display another patient account.

Display/Change Last OD or ROM Label Assigned

This option displays data from the global information record which is the last assigned OD and ROM value. This is useful for verifying the OD label assigned when *Format New OD > Database Use* is selected in the File Management or to find out how many ROM disks have been created.

- 1. From the *loadlb Main Menu* select, 4 - Display/Change Last OD or ROM Label Assigned
- 2. The following is displayed for edit:

Global Information:

1 - OD Label

2 - ROM Label

Enter field to edit (or <Enter> for Main Menu):

3. When option *1* - *OD Label* is selected, The system prompts to enter to new OD label value

or

When option *2* - *ROM Label* is selected, The system prompts for the new ROM label

4. Pressing **<Enter>** at the prompt cancels the edit operation. Entering a new value causes the last OD or ROM label assigned to be updated in the database.

Display Last Assigned Account ID

Option 5 - *Display Last Assigned Account ID* is useful to verify database updates of *File Management* when a new patient is added. It displays the last *Account ID* in *p*# form.

Clear Record Lock Bit

The record lock bit is tested by other database applications, such as *File Management*, before changing a patient record. Occasionally a database update fails, and the record lock bit fails to be cleared. If the record lock bit is set, the database application assumes the record is in use, and displays an error message. If the record is not actually in use, then the record lock bit must be cleared.

This option is useful for clearing specific lock bits (the DBVISTA dbclrlb utility clears ALL lock bits that are set in the database). These bits may be set at the patient level or at the study level.

- 1. From the *loadlb Main Menu* select, 6 - Clear Record Lock Bit
- 2. The system prompts for: *Account ID (the p# value) Study ID (the s# value)*
- 3. If only the patient's lock bit is set, press <**Enter**> at the *Study ID* prompt The lock bit of the patient record is cleared

or

If a *Study ID* is entered, then the lock bit of the study record is cleared.

There is no verification of this operation, so make sure the record is not being accessed by any other program before clearing lock bits.

Test Date Conversion

Since date fields are stored as integers in the database, this option tests the conversion from a MM/DD/YYYY (preferred data format) to an integer. This option is useful for verifying values being stored in the database by the *File Management*.

1. From the *loadlb Main Menu* select, 7- Test Date Conversion 2. The system prompts for a date in MM/DD/YYYY format, and the integer stored in the database is displayed. This number should be:

(YYYY * 10000) + (MM * 100) + (DD)

Quit Loaddb

The option quit (**q**) under *Main Menu* must be selected to exit the loaddb program to ensure the database is properly closed.

Chapter **ACQUISITION**

Acquisition controls all routine data acquisitions including emission, dynamic, and transmission scans. It is normally invoked from *File Management*, where the patient name and parameters are entered and archived. When patient information is added, the database checks to see whether this patient had previously been examined.

Patient data can be entered for any number of patients before the patient arrives for their scan. It is possible to enter patient information in the morning for all patients scheduled that day, this saves time when the patient is on the table. The actual acquisitions can be performed during the day in any sequence. If a patient cancels an appointment, the information can be deleted.

Acquisition displays status such as counts collected, scan time remaining, etc.

Acquisition Menu Map



Acquisition Procedure

- 1. Left click desktop to open *File Management* on ACQ Workstation
- 2. If the patient has been scanned before and has a study in *File Management*, highlight that patient study

If the patient has not been scanned before proceed to next step

- 3. From *File Management* drop-down menus select, *Acquisition* > *Set Up Acquisition*
- 4. If no study was highlighted (step 1), then a *Patient ID* window is displayed. Enter the Patient ID and click OK. The database is searched for that ID.
- 5. The *Patient Information* window is displayed. Database information appears in the data fields if ID was located. Data fields are blank if ID was not found.

Filename: p?s0, enter: **pxxxs0** (use first 3 letters of last name)

- 6. *Study Comment:* enter type of study
- 7. Click *Acquire Now* or *Acquire Later*
- 8. Select *Protocol* > *SinglePass Emis/Trans* Select appropriate default and click *OK*
- 9. Click *Edit Protocol* to view the Acquisition parameters Then click *OK*
- 10. Click Start

Acquisition Setup

The *Patient Information* window is divided into two parts:

- Patient Information
- Study Information

Acquisition Setup				
Patient Information				
Patient ID: jacq/recon Re-enter Patient ID				
Last Name: I First Name: I				
Birth Date: 100/00/0000 Patient Weight: 10.00 kg (mm/dd/yyyy)				
Study Information				
Destination Disk New Study 🛏				
Directory: //sun0/patient/p202/s?				
Filename: p202s?_jiscn				
Study Date: (mm/dd/yyyy)				
Study Comment: jno comment				
Technologist: jnone				
Accession Number:				
Acquire Now Acquire Later Cancel				

Figure 7-1 Acquisition Setup Window

Patient Information

Patient ID - If the ID is in the database, the *Patient Information* fields are filled and are non-editable (except for *Patient Weight* which can be entered for each scan, it is stored in the sinogram's mainheader rather than in the database).

To edit fields select *Database > Edit Patient Information* from the *File Management* dropdown menu (or press the **F4** function key).

If a new *Patient ID* is entered, the fields become editable, and are entered and stored in the database when the acquisition program is invoked.

The following steps are performed while entering new patient information:

Last Name and First Name

Birth Date and **Patient Weight** in the format shown (this is optional). The format for birth date (**mm/dd/yyyy** or **dd/mm/yyyy** or **yyyy/mm/dd**) and the weight (**kg** or **lbs**.) can be system set by the Field Service Engineer.

Study Information

Old Study - *Destination Disk* cannot be changed, *Filename* prefix is set to the selected account and study ID, *Study Comment* and *Technologist* fields are displayed but cannot be edited. Select *Old Study* if several scans are being performed on the same patient on the same day.

New Study - A new study is created in the database and the scan files are stored in a new directory. The *Comment* and *Technologist* fields are editable, and a destination disk can be selected by pressing the *Destination Disk* button.

If no study is selected in the *File Management* when the *Acquisition Setup* window is invoked, the study type defaults to *New Study* whether or not the Patient ID already existed in the database.

Directory: Select sun0 for all patient studies (this is the default).

Filename: p?s0_(use first 3 letters of last name)

Study Date: is set by the system to current date

Study Comment and Technologist - fields are editable

Accession Number: Alphanumeric number up to 15 characters is assigned by the hospital. The *Accession Number* is entered during the acquisition setup when entering the patient information. The accession number is used by multiple users who send data via DICOM to a PACS as a means of identifying all images within a patient study. An error is returned if more than 15 characters are entered. The field can be left empty if the *Accession Number* is not known at the time of acquisition setup. If desired, it can be entered afterwards using the mainheader edit program (*mhedit*).

There are three buttons along the bottom of the Acquisition Setup window.

Acquire Now

Acquire Now button causes the database to update with the new patient account or new study. It invokes the Acquisition program with the information currently displayed in the *Acquisition Setup* window.

Acquire Later

Acquire Later button adds the *Acquisition Setup* information to the *Scheduled Acquisitions* scroll list at the bottom of the *File Management* window. Up to 20 patients can be displayed in that list. As the patients arrive for scans, the Acquisition program can be invoked.

If there are any Scheduled Acquisitions listed when *File Management* exits, they are redisplayed the next time the *File Management* is invoked, or the system is logged on.

Cancel

The *Cancel* button closes the *Acquisition Setup* window with no action.

Remove Scheduled Acquisition

A patient in the *Scheduled Acquisitions* list, at the bottom of *File Management*, can be removed without any changes to the database. This is necessary when an acquisition is scheduled and the patient cancels the appointment. When an acquisition is performed, the setup is automatically removed from the *Scheduled Acquisition* list.

- 1. Highlight the setup to be removed from the *Scheduled Acquisitions* list at the bottom of *File Management*
- 2. Select *Acquisition* > *Remove Scheduled Acquisition* from the drop-down menu. Only one scheduled acquisition can be removed in one operation.
- 3. The system prompts to verify the deletion.

Perform Acquisition

The Acquisition program can be invoked from the *File Management* window.

- 1. At the bottom of the *File Management* window, highlight an acquisition from the *Scheduled Acquisition* list.
- 2. Select *Acquisition > Perform Acquisition* from the drop-down menu

If more than one item is selected, the Acquisition interface is invoked with the first selection's setup information.

Also, double-clicking an item in the *Scheduled Acquisitions* list immediately invokes the Acquisition interface.

3. If there are scheduled acquisitions when the *File Management* exits, they are redisplayed the next time the *File Management* is invoked, so an Acquisition can be performed at a later date.

Acquisition Window

The Acquisition program can be invoked one of three ways:

Acquire Now - Invokes the acquisition interface with the information currently displayed in the setup window and does not add the setup to the *Scheduled Acquisitions* list in the *File Management* window.

Scheduled Acquisitions - Changes can be made to setup before selecting Acquire Now.

Perform Acquisition - Selected from the Acquisition drop-down menu after highlighting an item in the *Scheduled Acquisition* list in *File Management*, if no changes are required. Also double-clicking an item in the *Scheduled Acquisition* list invokes the Acquisition interface immediately.

- Acquisition 8.0.1				
<u>E</u> xit		<u>H</u> elp		
Sinogram Filena	me /sun0/patient/p0/s1/p0s1_			
	Patient Information	Acquisition Information		
Patient Name	kljlkjlj ======	Select Protocol		
Patient ID	a	Protocol		
Study Date (mm/dd/yyyy)	00/00/0000	Scan Type Edit Protocol		
Birth Date (mm/dd/yyyy)	0070070000 Weight 0.00 kg	Activity 0.00 MBq at Time (hh:mm)		
Account ID	p0	Start Position Read From Gantry		
Study ID	s1	Table Direction In		
Comment	Application Training Data	Scan Length Killing Scan Length Tr Frame		
Collection Statistics				
Singles	Rate Frame Time Rema	ining Estimated Total Time		
Coincidence	Rate Collection	Rate Collection Counts		
Status Message				
	Start	Pause Stop		

Figure 7-2 Acquisition Window

The acquisition window is divided into several sections which include:

- The Sinogram Filename
- Patient Information
- Acquisition Information
- Collection Statistics
- Control Buttons to *Start, Pause* and *Stop* the Acquisition

Sinogram Filename

The system assigns the first portion of the filename by using the account and study number such as plos0_. The user must complete the filename to uniquely identify the particular acquisition. Transmission and emission contamination acquisitions are given extensions, namely transmission files end with _tr.scn and emission contamination files end with _ec.scn. The extensions are added automatically depending upon the type of scan being performed.

When a patient study is initiated via *File Management*, certain parts of the filename and subdirectory cannot be edited.

Patient Information

Patient Information is entered in *File Management* and does not need to be modified in the acquisition interface. The only entry that can be modified is the patient's weight.

Patient Name - Supplied in File Management (up to 30 characters)

Patient ID - The most important and unique information is the *Patient ID* which is either the patient's Social Security number or the hospital's patient ID number.

Study Date - Current date is supplied automatically as the study was initiated. Customer Support can set the format of the date as a default; the selected format is either **mm/dd/yyyy** or **dd/mm/yyyy** or **yyyy/mm/dd**.

Birth Date - The birth date is normally supplied via *File Management*. Customer Support can set the format of the date as a default; the selected format is either **mm/dd/yyyy** or **dd/mm/yyyy**, or **yyyy/mm/dd**.

Patient Weight - The reconstruction program uses the patient weight to determine Standardized Uptake Values (SUVs). Customer Support can set the units to either pounds (lbs) or kilograms (kg). This field can also be configured to be "required".

Account ID, Study ID and Comments are entered in *File Management* for all patient studies and are included here for reference only.

Acquisition Information

Typically acquisitions are performed using a preset protocol in which case it is often sufficient to select the protocol and proceed. Sometimes it is necessary to change one or several of the acquisition parameters, this is done by selecting a protocol to edit. The edited protocol can then be used for the specific acquisition and can be saved for future use.

Acquisition parameters that are most likely going to be different for each acquisition, such as time and amount of activity injected. They are listed separately from the protocol parameters.

Select Protocol - Protocols are divided into different categories as follows:

- Emission Only
- Transmission Only
- Single-Pass Emission and Transmission
- Dynamic Studies
- Gated Cardiac (not available)

Note: See *Edit Protocol* later in this chapter

Protocol - After selecting a protocol, the protocol name is displayed in the protocol field. When a parameter is changed, the default file name is appended with an asterisk (*) to indicate that the original protocol parameters have been modified.

Scan Type - This field displays the type of protocol that has been selected i.e., emission only, transmission only, Single-Pass, or dynamic. By clicking *Edit Protocol* the selected protocol can be edited without losing any previous modifications to the protocol.

Activity / at Time (hh:mm) - The activity and the time of the activity measurement, entered in these fields, are stored in the file header. They are used by the reconstruction program to convert the absolute concentration in the images into Standardized Uptake Values (SUV) using the patient's weight. It is important that the time entered corresponds to the time the activity is measured and this time also corresponds to the internal clock of the computer. If the internal clock of the computer (obtained by looking at the clock in the upper left corner of the computer screen) does not agree with your local time, contact Customer Support.

Furthermore, if all measured activity has not been injected, the activity remaining in the syringe must be subtracted from the activity entered here (after compensating for the intervening decay).

Start Position - The start position must be selected to allow the scan to proceed in the selected direction for the full scan length without exceeding the total travel allowed by the table which is 168 cm. Initially the start position is read from the protocol. If it is desired to start at a specific location, it can be entered into this field. If it is desired to start at the current position (for example after visually positioning the patient to the correct position) the current position of the table can be obtained by clicking **Read from Gantry**, which inserts the present table position into this field.

Table Direction - Table direction may be selected to move either *In* or *Out*. This selection overrides any previous selection that has either been read from the protocol or selected in the protocol editor.

Scan Length - The default value shown is the value that has been read from the protocol or may have changed using the protocol editor. The scan length can be changed in this field, and the selected value overrides any previous selection that has either been read from the protocol or selected in the protocol editor.

The *Start Position, Table Direction,* and *Scan Length* fields are interrelated. If it happens that the acquisition screen is not allowing the user to enter in the *Scan Length*, edit the protocol and verify these parameters.

Collection Statistics

Initially the collection time remaining in the first frame and the estimated total acquisition time are displayed. After the start of the acquisition and when the acquisition is paused, the collection time remaining in the current frame, the time remaining in the study, the singles rate, the calculator rate, and the total counts collected are updated every 5 seconds.

Single Rate - The individual detector countrates are summed and the total singles countrate for all detectors is displayed as counts/sec.

Collection Time Remaining - At the beginning of each frame, the collection time is set to the value preselected in the protocol. Once the acquisition of the current frame of data collection has started, the time is decremented to show the collection time remaining for the current frame.

Estimated Total Time - This field shows the estimated total acquisition time for the entire study, i.e. for all frames in a whole body study, including the time to upload data, and move the transmission source in or out (if a transmission study is being performed).

Calculator Rate - The calculator rate (displayed as counts/sec) is either the coincidence rate in an emission study or the singles rate in a transmission study. In a transmission study, not all detectors are turned on at the same time. Therefore the calculator rate is not equal to the singles rate shown in the *Singles Rate* field.

Collection Rate - A large number of events that are found in coincidence are rejected because one or the other of the two events does not fulfill the energy requirements. The Collection Rate shows the rate at which data are actually added into the data storage memory.

Collection Counts - The total counts accumulated are displayed and updated every 5 seconds. The number displayed represents the counts accumulated for a particular frame, i.e. it is reset to zero at the beginning of each frame in a whole-body or dynamic acquisition.

Status Message - Gives information while the study is progressing that informs the user about the present activity such as upload of data, insertion of the transmission source, or the status of the patient table.

Start, Pause, and Stop Acquisition

Start, Pause and *Stop* indicate a desired action, not the status of the scanner. These controls are used to initiate and terminate the study.

Start

Initializes the scanner by transferring (downloading) the correct information to the scanner electronics. If *Pause* is not activated (clicked), the data collection starts immediately after the initialization, without requiring further user intervention. When *Pause* is activated, the user is prompted to *Resume* the acquisition and the scanner beeps until the *Pause* condition is removed so the acquisition can start.

If the table is not at the start position, the user may need to press the enable button. The user must press the enable button to move the table at each point in the scan. Automatic table motions are not permitted without the enable button.

Pause

When activated, a window is displayed to indicate that the *Pause* request is pending, since the scanner can be paused only at certain times. After the system has paused, a pop-up window will allow the user to *Resume* the acquisition and the scanner beeps until the *Pause* condition is removed. During certain operations, such as downloading data or performing a transmission study, the process cannot be paused.

Stop

If it is necessary to stop the data acquisition before the terminating condition has been reached (either preset count or time), click *Stop*. After clicking *Stop*, the user may stop and save the data or continue the acquisition. If the user wishes to discard the data, it is necessary to use *File Management* at a later time to delete the file.

Check Count Rate Prior to Scan on ACQ

- Click left desktop of the ACQ Workstation and select *File Management*
- From File Management select, User Menu > Measure Count Rates
- The current singles count rate is the left-most column total.

Select Protocol

1. Click *Select Protocol* from the Acquisition Window (Figure 7-2)

Different Protocol categories as displayed:

- Emission Only
- Transmission Only
- Single-Pass Emission and Transmission
- Dynamic Studies
- 2. Select a protocol, the associated Protocol window, shown below, is displayed

Protocol				
Protocols				
DefaultBody				
DefaultBrain				
DefaultNEMAresolution				
DefaultNEMAscatter				
DefaultNEMAsensitivity				
DefaultNEMAuniformity				
DefaultNormalization				
DefaultQC				
patient_last				
l				
Selection				
DefaultBody				
OK Edit Delete Cancel				

Figure 7-3 Protocol Window

3. Click *OK* to select a predefined protocol for the acquisition

or

Click *Edit* to add or edit an existing protocol

Clicking *Edit* displays the *Protocol Editor* window Figure 7-4 or *Dynamic Protocol Editor* window Figure 7-8, depending on the selection. All parameters can be edited.

- 4. Changes may be used for this particular acquisition or can be saved as a new protocol. The parameters that are available for editing depend on the category of the protocol.
- 5. The currently selected protocol name is displayed. This name can be changed before saving it as a new protocol.
- 6. User defined protocols may be deleted by first selecting a protocol and then clicking the *Delete* button. Default protocols cannot be deleted.
- 7. Clicking *Cancel* returns the user to the main window without selecting a protocol.

Protocol Editor

If only an emission study is to be performed by selecting *Emission Only* in the protocol drop-down menu, the transmission parameters are deactivated, and conversely, if only a transmission study is to be performed by selecting *Transmission Only* in the protocol drop-down menu, the emission parameters are deactivated.

The *Advanced Parameters* are normally not changed and may require different calibration files. They should only be changed after consulting Customer Support.

Protocol File DefaultBody				
FOV Diameter (mm) 576 🗖 Patient O	rientation Head First 📼			
Start Position (mm) 51 Table	Direction In 📼			
Total Scan Time 0:26:48 Scan Lei	ngth (mm) 🖾 🚺 🕞			
Concurrent Recon Off 🗖 Recor	n Protocol Body-RAMLA			
Advanced	Parameters			
Emission Parameters	Transmission Parameters			
Slice Thickness (mm)	Slice Thickness (mm)			
Sinogram Size 📃	Sinogram Size 📃 🗆			
Isotope F–18 📼	Singles Options Trans with EC 😑			
2nd Energy Window No 🗖	Rotations / Pos Constant 🗖 🔟			
Duration Type Time 📼	EC Rot / Pos Constant 🗖 2			
Time / Position Constant 📼 0:02:00	Trans Time 0:13:04 # of Pos 8			
Emiss Time 0:12:54 # of Pos 6				
Save Use	Reset Cancel			

Figure 7-4 Protocol Editor Window

FOV Diameter (mm) - The transverse Field-of-View (FOV) of the scanner can be selected:

576 mm for large organ imaging of which the central 560 mm represents activity within the useful field of view of the scanner.

256 mm for brain imaging has the advantage that the reconstructed image of the brain is twice as large. Care must be taken however to center the head in the central part of the 50 cm opening so the whole brain is contained within the FOV.

Start Position - The Start table position read from the protocol is displayed here. It can be changed by editing this field or during the actual acquisition time when the patient has been positioned on the table.

The minimum value for *Start Position* is 51 mm for emission, transmission and Single-Pass scans.

Total Scan Time - is computed from the selected scan length and the acquisition times per frame. It is displayed for informational purposes and cannot be edited.

Concurrent Recon - Concurrent Reconstruction is only available in SinglePass. When enabled, allows for image reconstruction during the acquisition process. This option may significantly decrease the amount of time it takes to reconstruct acquired images by starting the reconstruction process after each frame has been acquired. When an acquisition is started on the ACQ Workstation and this option is enabled, a *Reconstruction Status* window (Figure 7-6) is displayed on the SVR Workstation. The *Reconstruction Status* window provides feedback to the user regarding the reconstruction process.

When defining protocols, it is recommended to set the reconstruction protocols on the SVR Workstation before the acquisition protocols. The reconstruction protocol list is updated and the appropriate reconstruction protocol can be selected for concurrent reconstruction.

Note: When the *Start* button on acquisition is pressed, a reconstruction dialog box opens on the SVR Workstation. If this dialog box is closed, it stops the concurrent reconstruction.

Concurrent reconstruction is not supported with background subtraction as ROIs are required for the calculation. If background subtraction is desired, set concurrent reconstruction to reconstruct the uncorrected data, then manually reconstruct the corrected data with background subtraction after drawing ROIs.

As reconstruction occurs, the current slices update in the *Current Process* box. This reflects reconstruction being performed on processors and may appear out of sequence.



Figure 7-5 Concurrent Recon Option

	Reconstruction Status 7.2.4
iput Sinogram	/sun0/patient/p44/s0/p44s0_test.scn
Output Image	/sun0/patient/p44/s0/p44s0_test.img
	Patient Information
Patient Name	John Smith
Patient ID	123456789
Acq Date/Time	05/05/2000 16:00:08
Acq Protocol	DefaultBody-mjp.int
Recon Protocol	Reconstruction Information Body
	Reconstruction Status
Current Slice	Frame 0 of 1
Current Process	; Waiting for frame (31 secs).
lmages Available	
	Stop

Figure 7-6 Reconstruction Status Window

Patient Orientation - The user must indicate whether the patient is lying in the scanner head first or feet first to properly orient the reconstructed images, so the patient appears the same way in the images. This information is inserted into the file header and is used in the reconstruction program to properly orient the data.

Table Direction - When a table direction for scanning motion is selected (In or Out), the starting position and scan length are checked to ensure the desired scanning motion is within the overall travel restrictions of the table. If the selected parameters exceed the maximum table positions, a warning message is displayed or the start position is automatically adjusted.

Scan Length - The total scan length can only have a discrete number of values depending upon the number of positions. The minimum scan length is obviously equal to the axial field of view, i.e. 180 mm. Since the patient is moved by 84 mm between frames in a whole body scan, the scan length is incremented in steps of 84mm. The user may either drag the slider or click the triangle on either side of the slider bar to increment or decrement the scan length.

Emission Only or Single Pass

When selected in the protocol drop-down menu, the transmission parameters are deactivated

Sinogram Size - (not available)

Isotope - Used for the study, data is entered into the file header and is later used to perform decay correction.

2nd Energy Window - A second energy window can be selected to acquire data for later scatter correction.

Note: This option is included in the menu, but is not yet functional.

Duration Type - Acquisitions may be terminated either after a preset time or a preset number of events. Normally studies are performed for a preset time, particularly during whole body scans. The following field is displayed either *Time/Position* or *Counts/Position* depending upon the choice selected.

Time / Position - (Counts/Position) In a multi-frame acquisition the time per frame (or counts per frame) may either be selected to be constant or variable. If a constant acquisition time per frame has been selected, the acquisition time/frame is displayed and can be edited. The time can be entered as seconds or as minutes and seconds. For example, a 2 minute acquisition time can be entered either as **120** or as **2:00**

If a variable acquisition time/frame (or counts/frame) has been selected, the *Edit* field must be clicked to bring up the frame *Edit* window that allows different acquisition times (counts) to be entered for each frame. This is useful in body surveys, where a particular anatomical region has been identified as the region of interest, but the physician would nevertheless like to see a quick survey of other regions.

Emission Time # of Positions - The estimated total emission collection time and the total number of frames to be acquired are displayed, but may not be modified. Instead, these fields are calculated from the total scan length and the time/position and are displayed for reference only.

Transmission Only

When selecting *Transmission Only* in the protocol drop-down menu, the emission parameters are deactivated.

After the transmission source has been retracted, a separate short scan - the emission contamination (EC) scan- determines the amount of contamination from the 511 keV activity in the patient into the 662 keV energy window set around the emission from Cs-137, the transmission source. Obviously, if a separate transmission scan is being performed before the activity is injected, then an EC scan will not be necessary. The EC scan data are automatically saved using the same file name as the transmission scan, but with **_ec.scn** appended to the file name instead of **_tr.scn**.

The transmission data are collected by automatically inserting the transmission source, performing 1 or 2 rotations around the patient and retracting the transmission source. Typically the time per rotation is 40 seconds.

While it is necessary to subtract the emission contamination from the transmission scan in order to allow post-injection transmission scanning, the converse is not true, i.e. we must not subtract the transmission contamination from the emission scan, since the emission data are being collected while the transmission source is retracted.

Transmission Only or Single Pass

The following options for collecting transmission data are available:

- Transmission Only
- Transmission with Emission Contamination (EC)
- Emission Contamination (EC) Only

Rotation / **Position** - In a multi-frame acquisition the rotations per position may either be selected to be constant or variable. If a constant number of rotations per position have been selected, the number of rotations is displayed and can be edited.

If a variable number of rotations per position is selected, the *Edit* field must be selected to display the frame *Edit* window, which allows a different number of rotations per position to be entered.

EC Rotation / Position - During an EC Rotation the source does not rotate around the patient. Instead the emission contamination data are collected for a time that corresponds approximately to 12 seconds per rotation entered in this field. Typically the number of EC rotations is set to 1 for whole body scans and 2 for brain scans.

In a multi-frame acquisition the rotations per position can be constant or variable. When a constant number of rotations per position is selected, the number of rotations is displayed and can be edited.

If a variable number of rotations per position is selected, the *Edit* field must be selected to display the frame *Edit* window that allows a different number of rotations per position to be entered.

The following are legal parameters for the variable options in either the transmission or emission contamination fields:

- No rotations in the beginning of the scan and a set amount of rotations per position thereafter.
- Rotations in the beginning of the scan and no rotations at a set point thereafter.

It is not legal to have rotations in the beginning of the scan and end but set to 0 in the middle.

Transmission Time / # of Positions - The estimated total transmission collection time and the total number of positions to be acquired are displayed, but may not be modified. Instead, these fields are calculated from the total scan length and the rotations/position and are displayed for reference only.

Advanced Parameters

Parameters that are infrequently changed are set at the system level. Any changes may require a recalibration of the system. For example, changing the axial acceptance angle influences the axial normalization profile. Advanced parameters should be changed by a knowledgeable person who understands the system thoroughly. These parameters give the user flexibility, that may be desirable in special cases.

Emission and transmission scan parameters are similar, they are described together.

Advanced Static Editor

- 1. Select Advanced Parameters from the Protocol Editor window (Figure 7-4)
- 2. The Advanced Static Editor window is displayed (Figure 7-7)
- 3. Use extreme care when changing *Advanced Parameters*, changes should be performed by one who understands the system thoroughly.

Advanced Static Editor				
Clear Rebinner	Clear 🗖			
Variable Baseline	Yes 📼			
Upload Mode	Minimize Wait 🗖	_		
Emis	ssion Advanced Parameters	Transmission Advanced Parameters		
Slice Range (mm)	Image: start: 0 Image: start: 0	Slice Range (mm)		
1st Global Energy	Lower: 10 Upper: 200	Global Energy Zr Di Cover: 10 Upper: 200		
2nd Global Energy	Lower: 0 Upper: 0	Local Energy Lower: 90 Upper: 130		
1st Local Energy	Lower: 85	EC Global Energy Lower: 10 Upper: 200		
2nd Local Energy	Lower: O Upper: O	EC Local Energy Lower: 88 Upper: 128		
Rebin Type	4-D □ Tilt Angles: 7	Rebin Type 4–D Tilt Angles: 1		
Acceptance Angle	15.0	Acceptance Angle 16.0		
		Prescale 1.5 📼		
EC Prescale 1.5				
OK Reset Cancel				



Advanced Static Editor Parameters

Clear Rebinner - Under normal circumstances, the acquisition memory is set to zero before an acquisition. However, under special circumstances it may be desirable to add additional data to a data set that is known to reside in the acquisition memory. Therefore, the option is provided to not clear this memory. For example, if an acquisition has been stopped through an unusual event such as a computer crash and the data have not been transferred to disk, but subsequently it is decided that the data are worth saving after all, then it is possible to start a very short (1 second) acquisition without clearing the memory, that will then read the previously acquired data from the acquisition memory, thus saving a scan that would otherwise be lost.

Variable Baseline - may either be set to *Yes* or *No*. If variable baseline is turned on (set to *Yes*), baselines are collected at each bed position. For a dynamic study there is a third variable baseline option, *First Frame*, this option only collects the baselines before the first frame. The default is set to *No*.

Upload Mode - Uploading is the process of transferring the data from the acquisition memory to disk. There are three types of upload modes:

- Immediate upload mode means that as soon as the frame is collected it is transferred from the acquisition memory to disk. The acquisition pauses while the data is transferred.
- Minimize Wait upload mode means that the frames are collected such that the user does not have to wait to upload the data, except for the last frame. In the case of a Single-Pass acquisition, the data will be transferred to disk while the emission data is collected. Data can only be transferred from the acquisition memory during an emission frame. This is the preferred method.
- Delayed upload mode means that the frames are collected into the acquisition memory until there is no more space available. Once the acquisition memory is full, the acquisition is paused until all the data is transferred to disk. Once the data is transferred, the acquisition continues.

In normal operations it is recommended that Minimize Wait upload mode be used.

Delayed Events - This function is for *Emission Only, SinglesPass, and Dynamic* protocols that can enable online random subtraction. This is a hardware mode in which delayed events are subtracted from prompt events. Any resulting negative counts are set to zero once the sinogram us uploaded by the Acquisition.

Slice Range - This function is not yet implemented in this software version.

In cases where a small object is being imaged, that does not require the full axial field of view and where storing the extra slices presents a problem, the starting and ending slice can be set to a value other than 1 and 180 respectively. It is generally better to take data for all the slices and restrict the axial extent by only reconstructing and/or displaying those slices that contain useful information.

The slice range for transmission studies is normally 50 to 130. Slices outside this range contain only scattered events.

1st Global Energy / **Local Energy** - The energy windows have both a lower threshold and an upper threshold. These are usually set at installation time and should not be changed.

The scanner has both a lower level and an upper level discriminator, that is part of the timing (constant fraction timing) discriminator and is set in hardware to a lower level of approximately 400 keV. In software two more energy windows are set. The global energy window integrates all the light in a crystal *zone* and performs both upper and lower level energy discrimination on this total energy. Separately the light is integrated only in that small crystal area immediately surrounding the scintillation. This latter energy signal, the local energy, has a constant value subtracted from it; therefore the discriminator values are quite different between the global and the local energy windows. Both of these energy windows should only be changed after collecting and inspecting an energy spectrum. Consult a factory representative before changing any of the energy thresholds.

2nd Global Energy / Local Energy - This function is not yet implemented in this software version.

The hardware has provisions for a second energy window that could be used, for example, to collect scattered events in a lower window to be subtracted later. This feature has not been fully implemented and should therefore not be used at this time.

Rebin Type - The trajectories of the photons emitted from the patient are sorted into parallel projections (sinograms) using a method called 4-D rebinning. This rebinning method preserves more information than 2-D methods by recording the "tilt" angle of the photon. (This is the angle between the photon trajectory and the coronal axis of the patient). This additional information is used by a later processing step, called Fourier rebinning, to more accurately position the events in the axial direction.

The Tilt Angles function is not yet implemented in this software version. The user must specify the number of tilt angles, that is limited to 7 angles presently.

Acceptance Angle - This function is not yet implemented in this software version.

The axial acceptance angle influences the sensitivity and the spatial resolution as a function of radial distance. Since the axial sensitivity profile used in the system is a function of the acceptance angle, all protocols should use the same acceptance angle.

Prescale - The user is advised not to modify the prescale value for the singles transmission measurement.

EC Prescale - In order to subtract the Emission Contamination (EC) from the transmission data, a short data collection of the emission contamination is performed. Since the countrates for this measurement are lower than for the transmission scan, a lower prescale value can be selected for the EC measurement than for the transmission measurement. It is recommended that 2 rotations/position is used for all studies.

Dynamic Protocol Editor

When a dynamic study is performed, the corresponding transmission scan must be performed as a separate static study. Care must be taken that the transmission scan(s) overlap the full axial FOV covered by the dynamic emission data, that usually requires 3 transmission scans.

Many of the parameters for dynamic studies are identical to those for static emission scans and the use of the parameters are therefore not repeated here.

While static acquisitions can be terminated by either presetting a number of counts to be collected or a specific acquisition time, dynamic studies can only be performed by presetting acquisition times for a number of frames.

Multiple Frames Protocol Editor
Protocol File Default
FOV Diameter (mm) 576 🗖
Patient Orientation Head First 🗖
Start Position (mm) 77
Total Scan Time 0:04:26
Advanced Parameters
Slice Thickness (mm)
Sinogram Size Small 🗖
Isotope F-18 🗖
Time / Frame Constant 🗖 0:00:30
Frame Delay Constant 🗖 0:00:05
Total Frame Time 0:01:54 # of Frames 3
Save Use Reset Cancel

Figure 7-8 Dynamic Protocol Editor Window

Dynamic Protocol Parameters

Time per Frame - can be selected to be *Constant* or *Variable*. When a constant time is selected the number of frames to be acquired are selected via the *# of Frames* field described below. If a variable time per frame is selected, click *Edit* and a *Dynamic Frame Editor* window is displayed that allows both the time per frame and the delay between frames to be changed. Frames can also be added or deleted via the *Dynamic Frame Editor* by clicking >>*More or Less*<<.

Frame Delay - can be selected to be constant or variable. When a constant time is selected, delay time between frames can be edited directly. If a variable time per frame is selected, click *Edit* and the *Dynamic Frame Editor* window is displayed that allows both the time per frame and the delay between frames to be changed. Frames can also be added or deleted via the *Dynamic Frame Editor* by clicking >>*More or Less*<<.

Total Frame Time - field indicates the calculated total study time without taking into account the time to upload the data.

Number of Frames - to be acquired can be edited either by changing the entry in this field or via the *Dynamic Frame Editor*, when a variable time per frame or a variable frame delay is selected.

Advanced Dynamic Editor

- 1. Select Advanced Parameters from the Dynamic Protocol Editor window (Figure 7-8)
- 2. The Advanced Static Editor window is displayed (Figure 7-9)
- 3. Use extreme care when changing *Advanced Parameters*, changes should be performed by a one who understands the system thoroughly.

Advanced Dynamic_Editor					
Clear Rebinner	Clear	-			
Variable Baseline	None	-			
Upload Mode	Minimize Wait				
Slice Range	Start: ()	End: 180			
Global Energy 🖾	Lower: 70	Upper: 200			
Local Energy 🖾	Lower: 80	Upper: 130			
Rebin Type	4-D =	Tilt Anglass 2			
Accept Angle	,0000	· m. //mg(co. /			
ОК	Reset	Cancel			

Figure 7-9 Advanced Dynamic Editor Window

Advanced Dynamic Editor Parameters

Refer to Advanced Static Editor Parameters (page 7-18).

A dynamic study may have any number of frames, several of which may have the same acquisition time. Between frames, a waiting time (delay), may be inserted. Often the question arises, how short the acquisition time may be without causing unwanted dead time while data are being transferred from the acquisition memory to the storage disk.

Since no firm answer is possible due to a large number of variables, the following discussion serves to give the user some understanding of the interplay between parameters to allow a meaningful selection of acquisition parameters.

The total acquisition memory consists of either 256 or 512 Mbytes of RAM (random access memory) divided into two banks of memory (either 128 or 256 Mbytes per bank). To determine the size needed for a frame use the following:

256*256*(# of tilts)*2 bytes = slice size for large sinogram

128*128*(# of tilts)*2 bytes = slice size for small sinogram

In these equations (# of tilts) is 1, 2, 4, 8, or 16.

Normally 7 tilts are used, therefore the slice size for large sinograms is 1.05 Mbytes and the slice size for small sinograms is 262.1 Kbytes. A slice thickness of 2 mm gives 128 slices, therefore each large sinogram frame takes up 134.2 Mbytes and each small sinogram frame takes up 33.6 Mbytes.

For dynamic studies, it is desirable to use the 'small' sinogram mode in which the space occupied is reduced by a factor of 4. If it is necessary to store more frames in the acquisition memory, the slice thickness can be increased to 4 mm, thereby reducing the number of slices to 64.

The following table shows how many frames of each type (small or large sinogram with 7 tilts) fit in the total acquisition memory:

Sinogram	# of Slicos	Frame Size (MB)	# of Frames in	
Size	# OF SILCES		256 MB	512 MB
Small	64	16.7	15	30
Small	128	33.6	7	15
Large	64	67.1	3	6
Large	128	134.2	1	3

If the upload mode is set to Delayed in the advanced parameters window, the acquisition memory is filled until there is no more space available, then the frames are transferred to disk. For example, if the total acquisition memory is 256 Mbytes and small sinograms with 2mm slice thickness are collected, the first 7 frames can have an arbitrarily short acquisition time (minimum 1 second) without resulting in any dead time. In this upload mode (Delayed) when data are transferred from the acquisition memory to the computer RAM memory, the acquisition is paused until the entire acquisition memory is transferred. It must be kept in mind that the actual transfer time is dependent upon the size of the sinogram and the number of slices.

If the upload mode is set to Minimize Wait in the advanced parameters window, the frames are saved to alternating acquisition memory banks. In other words frame 1 is collected into bank 1, then frame 2 is collected into bank 2, then frame 3 is collected into bank 1, etc. While frame 2 is collected, frame 1 is uploaded, then while frame 3 is collected, frame 2 is uploaded, etc. If the frames have long enough acquisition time (greater than 1 minute for small sinograms and greater than 3 minutes for large sinograms), there should be no dead time and the acquisition does not need to pause.

Gated Cardiac

When a gated cardiac is performed, the corresponding transmission scan must be performed as a separate static study. Care must be taken that the transmission scan(s) overlap the full axial FOV covered by the gated cardiac emission data, that usually requires 2 or 3 transmission scans.

Many of the parameters for gated cardiac studies are identical to those for static emission scans and the use of the parameters are therefore not repeated here.

While static acquisitions can be terminated by either presetting a number of counts to be collected or a specific acquisition time, gated cardiac studies can only be performed by setting the total scan time.

Gated Cardiac studies can be set up either for 8 frames in which the cardiac cycle (R-R interval) is divided into 8 equal increments and data are collected during each increment. Alternately, a systolic and diastolic 2 frame acquisition can be performed where the data collection is turned off during some pause times. The user has control over the length of data collection for both - systolic and diastolic - frames independently, and can adjust the time between the 2 frames by adjusting the pause times.

Gated Cardiac Protocol Editor			
Protocol File Defa	ult8Frame		
FOV Diameter (mm)	576 📼		
Patient Orientation	Head First 🗖		
Start Position (mm)	77		
Total Scan Time	0:01:00		
Advand	ed Parameters		
Slice Thickness (mm)			
Sinogram Size	Small 🗖		
Isotope	F-18 📼		
Gated Acq Type	8 Frame 🗖 125		
Patient Pulse (BPM)	60		
R–R Interval (msec)	1000		
Save Use	Reset Cancel		

Figure 7-10 Gated Cardiac Protocol Editor Window

Gated Acquisition Type

The gated acquisition type can either be set to 8 Frame or Diastolic/Systolic.

If *8 Frame* is chosen, the R-R Interval (msec) is divided into 8 equal frames. At each heartbeat (R-wave) the data is collected into frame 1, after 125 msec (in this example with a pulse of 60 BPM) the data is collected into frame 2, after another 125 msec the data is collected into frame 3, and so on until the heart beats again at which point it starts again with frame 1. This is repeated until the total scan time has elapsed.

If *Diastolic/Systolic* is chosen, click *Edit* to display the *Cardiac Gate Editor* window.

🗖 🦳 Cardiac Gate Editor 🛛 🗖				
Frame %	Interval	Time (msec)		
Diastolic	3 <u>.</u> 0	<u>3</u> 00		
Pause	20	200		
Systolic	3.0	300		
Pause	20	200		
ОК		Cancel		

Figure 7-11 Cardiac Gate Editor Window

The % *Interval* column shows the percent of the R-R interval time data are collected for each frame. The values in the % *Interval* column for *Diastolic, Systolic,* and the first *Pause* may be edited. The last *Pause* takes up the remaining time. The *Time (msec)* column shows how many msec of data are collected into each frame; this column is for informational purposes only and cannot be edited.

In this example, at each heartbeat (R-wave) the data are collected into frame 1 (diastolic frame), after 300 msec the data collection is paused (no data is saved), after 200 msec the data are collected into frame 2 (systolic frame), and after 300 msec the data collection is again paused until the heart beats again at which point it starts again with frame 1. This is repeated until the total scan time has elapsed.

Patient Pulse

In this field enter the patient's pulse in BPM (heartbeats per minute).

R-R Interval

This field is calculated using the patient's pulse and may not be edited. The R-R interval is the cardiac cycle or the time between R-waves (electrocardiogram peaks

Save/ Use/Reset

After the acquisition parameters have been selected, the protocol can be saved for future use under a new name (*Save* option) or they can be used for this acquisition only (*Use* option). Alternately, by clicking *Cancel* any changes become void and the user is returned to the protocol selection window without editing.

Protocol Parameters (Recommended)

Acquisition Parameters	Whole Body	Cardiac	Brain
Scan Type	SinglePass Emis/Trans	SinglePass Emis/Trans	Emission Only
FOV Diameter (mm)	576	576	256
Start Position (mm)	(Patient Dependent)	Read from Gantry	Read from Gantry
Total Scan Time	(Calculated by program)	(Calculated by program)	(Calculated by program)
Concurrent Recon	Off/On	Off/On	
Patient Orientation	Head or Feet	Feet First	Head First
Table Direction	In/Out	Out	In
Scan Length (mm)	(Patient Dependent)	180	180
Recon Protocol	Body-RAMLA	Body-RAMLA	Brain-noattn
Emission Parameters			
Isotope	F-18	F-18	F-18
Duration Type	Time	Time	Time
Time/Position	Constant 2-4 minutes or variable depending on patient body size	Constant 10 minutes	Constant 20 minutes
Emiss Time # of Pos	(Calculated by program) (Calculated by program)	(Calculated by program) (Calculated by program)	(Calculated by program) (Calculated by program)
Transmission Parameters			
Singles Options	Trans with EC	Trans with EC	
Rotations/ Pos	Constant 2	Constant 2	
EC Rot/ Pos	Constant 2	Constant 2	
Trans Time # of Pos	(Calculated by program) (Calculated by program)	(Calculated by program) (Calculated by program)	

Chapter

RECONSTRUCTION

Acquisitioned data are organized into data frames where each frame corresponds to a separate acquisition in either a dynamic study or a step-and-shoot whole body scan. Each frame represents a volume of data in r, phi, theta, z space. For traditional reasons these are stored as two-dimensional projection matrices (r, phi) as separate slices (along the z-direction), and separate oblique tilts theta.

Each slice has a subheader and the entire file has a main header. As a confirmation, these headers display acquisition parameters and patient information. The main header contains information such as the date, patient ID, isotope used, patient orientation into the camera, etc. This information is copied to the image files during reconstruction. The headers may be viewed and edited to correct mistakes or for experimental purposes.

The user selects a protocol which presents pre-assigned options for editing. Other parameters which are typically not changed by the technologist are contained in *Advanced Parameters*. These parameters should only be changed by advanced users.

During reconstruction the following files may be generated:

- Emission Images
- Transmission Images
- Temp and Intermediate Sinogram scan files with corrections performed (i.e. just before reconstruction of images)

Sinogram and Image File Structure

The structure of the sinogram and image files are essentially the same. The main difference is the size of the arrays. A sinogram matrix of brain is typically 128 (radial) by 192 (phi azimuthal) pixels with 7 tilt angles theta, while image matrices are typically 128 by 128 pixels. The image matrices of wholebody is 144 by 144 pixels.

The matrices are identified by frame number, tilt number, and slice number, each frame having an equal number of tilts and slices. Each slice of each frame has an associated sub-header, which contains information specific to the slice or frame (e.g. total counts, count rates, start and stop times, patient table position, etc.).

Study Types

- Static Emission consists of one frame having one or more slices.
- **Dynamic Emission** has more than one frame, each frame corresponding to a different time period at the same table position.
- Whole Body has several frames, each frame corresponding to a different position of the patient table.

The reconstruction program identifies the type of study from information in the header and handles the types slightly different.

Input and Output Files

The patient's scan file is displayed when the reconstruction program is invoked from *File Management*. If the reconstruction program is invoked by another method, the user must enter the *Input Filename*. After a *Input Filename* has been specified, an *Output Filename* is generated automatically using the same file name but changing .scn extension to .img for the *Output Filename*. Only after the file name has been specified is it possible to select a protocol, since header information is compared in the protocol.

<u>E</u> xit	<u>H</u> elp
Input Sinogram	sun0/patient/p3/s0/p3s0_576FOV_test4.scn
Output Image	aun0/patient/p3/s0/p3s0_576FOV_test4.img
Patient Information	
Patient Name	Jane Doe
Patient ID	12345
Acq Date/Time	June 29, 98 at 14:25: 8
Acq Protocol	patient_last(*).ems
Reconstruction Information	
Recon Protocol	Edit
	Reconstruction Status
Current Slice	Frame
Current Process	
Print Status Output to Login Window	
Star	t Stop

Figure 8-1 Reconstruction Window

Reconstruction Protocol Menu Map



Starting/Stopping Reconstruction

After selecting and possibly editing the reconstruction protocol the main reconstruction window displays the selected protocol. An asterisk behind the protocol name (*), indicates that parameters are different from the parameters in the original protocol file. For example, whole body protocols allow all slices from 0 to 1700; since the actual scan contains some subset of all the possible slices, the protocol is automatically modified to reflect the smaller slice range and the (*) is appended to the protocol name.

To start the reconstruction, click START

After a brief initialization period, the slice and frame being currently reconstructed is displayed. Selecting a protocol containing transmission attenuation correction, means the transmission data are reconstructed first and the emission data subsequently, i.e. the slice counter cycles twice through all possible slices.

The reconstruction can be stopped at any time. After completing the reconstruction of the current slice, the system prompts to confirm the cancellation of the reconstruction process. Slices already reconstructed are not deleted.

When the reconstruction is complete a window is displayed. Detailed additional information about the reconstruction is stored in a temporary file.

The following files are generated with every acquisition:

<filename>.scn

This is the emission sinogram file

<filename>_ec.scn

This is the emission contamination sinogram file

<filename>_tr.scn

This is the transmission sinogram file

Additionally, 3 log files are created. All inputs into the acquisition workstation and all system activity is recorded in these files during the scan.

Transmission Reconstruction

The reconstruction program scans the sub-headers of the input transmission file to determine the patient table position for each frame. For each slice in each frame, the table-fixed slice number Zt is calculated. Slices which have the same value of Zt are summed into a sinogram of transmission data, and the corresponding slices from the blank scan are summed into a sinogram of blank scan data. The blank and transmission sinograms are divided by the respective acquisition times, and then by each other, which gives the sinogram of transmission probabilities for the slice Zt. These transmission probabilities are then smoothed along the Zt axis, using a Gaussian kernel. The full-width at half-maximum (FWHM) of the kernel is specified in the protocol file.
If transmission attenuation correction was specified by the protocol, the program reconstructs the transmission image before reconstructing the emission data, producing a matrix of attenuation coefficients for each slice in the output emission image. The attenuation coefficients are written to disk, to be read subsequently when the attenuation is applied. The program may also produce a transmission image from the logarithm of the attenuation coefficients.

- 1. On the SVR Workstation, click left on desktop to open *File Management*
- 2. Double click a patient file
- 3. Highlight study file with _tr (not _ec)
- 4. From the drop-down menu select *PetView* > *Reconstruct Sinogram*
- 5. Click Select Clinical Protocol
- 6. Highlight the appropriate protocol and click *OK*
- 7. Click Start
- 8. The Reconstruction dialog box appears

Emission Reconstruction

- 1. On the SVR Workstation, left click on desktop to open *File Management*
- 2. Double click a patient file
- 3. Highlight the *.scn* file (not one with *_tr* or *_ec*)
- 4. From the drop-down menus select *PetView* > *Reconstruct Sinogram*
- 5. Click Clinical Protocol
- 6. Highlight the appropriate protocol and click *OK*
- 7. Click Start

Note: It is recommended that both the attenuation corrected and non-attenuation corrected images be reconstructed.

Reconstruction Protocols

Reconstruction protocols are divided into clinical protocols and research protocols. This division is somewhat arbitrary; it is designed to help the technologist by presenting a short list of protocols, while giving the researcher maximum flexibility. The user specifies the type of reconstruction to be performed when choosing the protocol. This is done by selecting one of two options from the Reconstruction menu:

- Select Clinical Protocols
- Select Research Protocols

Upon selection, the *Protocol Selection* window is displayed. It contains a list of previously defined protocols for selection.

Select a predefined protocol and click *OK*. Alternately, the user may edit the protocol by clicking *Edit*.

-	Clinical Protocols	·
Protocol Files		
Body		
patient_last		
Calastian		
Selection		
patient_last		
ОК	Edit Delete	Cancel

Figure 8-2 Clinical Protocols Window

There are several steps in the emission study processing that can be edited in the protocol editor. Each falls into one of three categories: correction, rebinning, or reconstruction. The steps are performed in the following order:

- Perform Interpolation and Sampling
- Perform Efficiency Normalization. This corrects the data for non-uniformities in the detector efficiencies.
- Perform sampling normalization. (The sampling pattern comes from transforming detector coordinates to sinogram pixels).
- Perform decay correction
- Perform deadtime correction

- Perform background subtraction
- Perform ellipse attenuation correction or 3DAC Transmission
- Perform Fourier rebinning (based on reconstruction 2D algorithm)
- Sum adjacent slices, if slice adding is specified. Sum frames, if frame adding is specified. If reconstructing a whole-body study, add slices from different frames which have the same values of Zt
- Transmission attenuation correction (2DAC)
- Reconstruct (3D & 2D)
- Perform filtering

Note: Ellipse and Transmission Attenuation correction steps are mutually exclusive.

Edit Protocol

The previously selected protocol file name is displayed. When a parameter is changed, the default file name is appended with an asterisk (*) to indicate that the original protocol parameters have been modified. This protocol filename together with most reconstruction parameters is stored in the subheader of the reconstructed image. If the user generates a new protocol and name, the file name is changed at the time the protocol is saved.

- **CAUTION:** The parameters listed in this chapter are optimized and normally should not need to be changed. Changing default values may result in poor image quality. Changes should only be done by advanced users or by Customer Support.
- 1. On the SVR Workstation, left click on desktop to open *File Management*
- 2. Double click a patient file
- 3. Highlight the file, from the drop-down menu select *PetView* > *Reconstruct Sinogram*
- 4. Click *Clinical Protocol*
- 5. Select the appropriate protocol default
- 6. To verify or change the parameters, click *Edit* The Protocol Editor window is displayed
- 7. Displayed are the default values. Parameters can be changed and a new *Protocol File* name can be entered.
- 8. When changes are complete, click *Save* The new protocol is added to the protocol list

— Clir	nical Protocol Editor	
Protocol File Body-RAMLA*		
Slice Range Frame Range		
Begin: 881	Begin: 1	
End: 1805	End: 7	
Increment: 4	Increment: 1	
Slice Add Yes 💷	Edit Frame Add No 💷	
Normalization	Efficiency = Edit	
Backgrd Subtraction	None 🖃	
Attenuation Corr	Transmission - Edit	
Decay Correction	Yes 📼	
SUV Measurement	No	
Filter	3D Image Filtering - Edit	
Gap Compensation	Yes - Edit	
Emission Algorithm 3D RAMLA = Edit		
Advanced Parameters		
Save Use Reset Cancel		

Figure 8-3 Protocol Editor Window

Save - After editing the parameters, the new choices are saved as a new protocol by clicking Save, which prompts the user for a new protocol name.

Use - Alternately, if the new set of parameters has been selected only for this particular reconstruction, click Use. This appends an asterisk (*) behind the protocol name to indicate that the standard protocol has been modified.

Reset - Recalls the original protocol default settings, after one or several of the selections are modified and the user wishes to undo changes.

Cancel - Returns the user to the Protocol Selection window without taking any action.

Protocol Menu Options

Slice Range and Frame Range

Normally all frames (in a dynamic or whole body study) and all slices in each frame are reconstructed. The slices and frames to be reconstructed can be restricted using the windows and sliders provided.

Slice Numbers

Each slice in an image or sinogram file is labeled by a slice number. The slice number is either the number of millimeters between the origin of the z-axis and the center of the slice (in a sinogram) or the number of millimeters from the end of travel of the patient pallet (in an image).

For convenience, two different z-axes are defined. The first (Zc) is fixed with respect to the camera, the second (Zt) is fixed with respect to the patient table. For input sinogram files, the slice number refers to the Zc axis. For output image files, the slice number refers to the slice numbers are related as follows:

All scans:	Zt=Zc + T
Head-first:	Zp=Zt
Feet-first:	Zp=NBODY-Zt

where T is the patient table position for the frame and NBODY=2048mm. This scheme ensures that the image slice number (Zp) is always positive, and always increases in the direction of the patient's feet.

Slice Add

Since the slice thickness selected for acquisition is typically 2 or 4 mm, the number of counts collected in each slice are usually quite low. It is possible to add several slices to improve the statistical accuracy and thereby reduce the image noise, this procedure is axial smoothing. However, the slice thickness and the slice spacing can be adjusted separately. This leads to overlapping slices. For example, if the original scan file contains 2 mm slices and the slice thickness is selected to be 6 mm with a slice spacing of 2 mm in the reconstruction program, the following action is performed:

Input slices summed	Output slice number and lo	ocation
2 + 4 + 6	4	
4 + 6 + 8	6	
6 + 8 + 10	8	
8 + 10+ 12	10 etc.	

The output slices still have a spacing of 2 mm, but the same input data are used in several output slices. The use of somewhat thicker, overlapping slices is a powerful technique to improve the signal-to-noise ratio of small objects such as tumors by summing slices, while allowing the observer to visually select the slice which is best centered over the object to achieve the highest possible contrast.

Also in whole-body studies, slices near the end of the scanner are scaled down in intensity when summed with overlapping slices near the center of the scanner from different frames. These end slices are noisier and thus have less statistical significance than the central slices; this is due to decreased acceptance angle at the edge of the scanner. The scale factor for these slices is inversely proportional to the square of the acceptance angle for a given slice.

In order to clarify the action of the slice adding, the user may select the *Edit* > *Preview*

While it is possible to perform the slice addition as part of the reconstruction process, the user may alternatively select little or no slice addition in the reconstruction and perform the same function after the reconstruction as part of the image display. This has the advantage that the slice thickness and spacing can be changed in real time. More importantly, sagittal and coronal images can be viewed without the loss of resolution inherent in adding the transverse slices, but the same slice addition can then be performed on the sagittal and coronal views, each time in depth, i.e. at right angles to the plane of the image being viewed.

-		Slice Adding	'
	Thickness: 12	Spacing:	<u>1</u> 4
	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	1110 1114 1118 1122 1126 1130 1134 1138 1142 1146	
	1146 1150 1154 -> 1150 1154 1158 ->	1150 1154	T
	a		
	ОК	Preview	Cancel

Figure 8-4 Slice Adding Window

Frame Add

When *Frame Add* is enabled, in a dynamic reconstruction, the reconstruction program sums the data from 2 or more input frames into each output frame. If slice adding is enabled, 2 or more consecutive slices are summed into each output slice. In whole-body reconstruction, frame adding is not available, since the frames hold data from different parts of the body. The summed slice has an axial position

Zt=sum(w[i]*Zc[i])/sum(w[i])+ T,

where T is the table position and w[i] is a weight assigned to each slice (sum(w[i]) is an integer). The weight factor w[i] is basically a rectangular kernel, but is modified to make the values of Zt equally spaced. This is so slices with the same value of Zt, but from different frames, can be added together.

Normalization

Below are the choices listed for Normalization:

- Axial
- Efficiency
- Axial/Efficiency
- None

The normalization files are typically stored in a tables directory associated with image reconstruction. Clicking *Edit* displays the default normalization files in a pop-up window and allows changes. Except in unusual circumstances, both normalizations should be performed using the default normalization files.

Normalization Efficiency

Normalization Efficiency factors are kept in a sinogram file. The name of the sinogram file depends on the sinogram size (256 by 192 or 128 by 96), the diameter of the transaxial field of view, and the number of oblique tilts. The reconstruction program chooses the appropriate normalization file. The normalization files are generated by a separate program, using uniform cylinder data. The statistical accuracy of the normalization factors is improved using a procedure known as Casey averaging. This procedure takes advantage of the fact that the factors should be a product of detector efficiencies and known geometrical factors. The normalization is performed by multiplying the input data by the normalization sinogram for that slice.

Background Subtraction

The choices for Background Subtraction are:

- Non-Uniform
- Uniform
- None

Background subtraction looks at the level of the background outside the body and uses an assumed shape to estimate and subtract the background throughout the field of view. It requires an elliptical outline on the reconstructed image to define the extent of the body. The ellipses are automatically generated using transmission maps.

The background is assumed to have either a flat shape (uniform background) or the shape of a parabola in the radial direction (non-uniform background).

- Uniform background: BG = A(theta)
- Non-uniform background: $BG = A(theta)^*(1 a^*c^*(r-r0)2)$

Where c is a predetermined empirical constant which varies with the degree of tilt, a is a constant specified in the protocol file, and r0 is mid-way between the ellipse edges. The ellipse definition is used to define a locus in the sinogram which has a width w, a distance d from the edges of the ellipse (w and d are specified in the protocol file). The magnitude A(theta) is fitted independently at each angle, and then replaced by a running average over several angles (as specified in the protocol file). The resulting background function is then subtracted from the sinogram, channel by channel, with negative channels being set to zero.

Background due to random coincidences tends to be flat (uniform) in the sinogram, while background due to scattered radiation has a curved profile. By varying the constant a in the protocol file, the shape of the calculated background can be adjusted to approximately match the actual background in the data which comprises both randoms and scatter.

-	Non-Uniform
Region File	/sun0/patient/p0/s1/p0s1_demo_ec.reg
# Angles to Average	<u>.</u> 11
# Slices to Average	٢.
# Pixels to Fit	
# Edge Pixels	<u>10</u>
Fit Coefficient	
Auto-Region	Yes 📼
Ellipse Threshold	1000
Ellipse Edge	5
Ellipse Padding	<u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u></u>
Ellipse TH Count	<u>1</u>
	OK Cancel



Angles to Average - angles to include in fitting region for background subtraction

Slices to Average - slices to include in fitting region for background subtraction

Pixels to Fit - width (in radial channels) of the background filtering region

Edge Pixels - number of radial channels to skip between edge of ellipse and beginning of background fitting algorithm

Fit Coefficient - leading coefficient (curvature) of parabola used in the non-uniform background function

Auto Region - utilizes remapped transmission images to generate a region of interest file to be used by the background subtraction correction

Ellipse Threshold - tissue threshold used in auto-ellipse generation (e.g., 1000 for a small image and 300 for a large image

Ellipse Edge - number of pixels from the edge of the transmission image that limits the bounds of the generated ellipse

Ellipse Padding - number of pixels to back off from tissue boundaries for auto-ellipse generation

Ellipse TH Count - number of tissue pixels used to determine the region edge for autoellipse generation

Attenuation Correction

The choices for attenuation correction are:

- Ellipse
- Transmission
- Read
- Reproject
- None

Attenuation Correction Ellipse

Analytic attenuation correction uses an elliptical outline to define the body contour and uses the same ellipse file for background subtraction. It calculates the attenuation coefficients assuming that the attenuation is uniform inside the ellipses, and zero outside.

Generally, the value for water (0.095/cm) is used. For brain scans the calculated attenuation factors can be modified to account for the higher attenuation of the skull by multiplying them with an arbitrary factor also contained in the protocol file. This factor is typically 1.10.

To perform ellipse attenuation correction it is necessary first to reconstruct the image without attenuation correction, and then draw elliptical outlines around the body to define the body contour. In the second pass, reconstruction of the attenuation correction can be turned on. The system prompts for the region-of-interest (ROI) file if the default file does not exist. The default ROI filename is the same as the scan filename, but with the extension *.reg.* In the associated *Edit* window, it is also possible to add skull compensation for brain studies and to change the attenuation coefficient used in the calculation.

-	Ellipse Attenuation Correction
Region File	/sun0/patient/p0/s1/p0s1_demo.red
Skull Compensation	1.000
Attenuation Coeff	0.095
c	Cancel

Figure 8-6 Ellipse Attenuation Correction Window

Skull Compensation - Used only in ellipse attenuation to compensate for the higher density of the human skull, as compared to water (tissue). For brain studies, the typical factor is 1.10, but for wholebody studies this value should be 1.0. This value is used to scale each attenuation coefficient.

Attenuation Coefficient - Used only in ellipse attenuation correction as the attenuation of water (i.e. tissue). Default value is 0.095.

Attenuation Correction Transmission

Transmission attenuation coefficients are calculated and written to disk and applied to the sinogram when needed. The attenuation coefficients are forward-projected from the reconstructed transmission image. This image is always reconstructed but only saved by the user. There are post-reconstruction processing options available for the transmission image, they are remapping and segmentation. If either option is used, the attenuation coefficients are forward-projected from the post-processed image. Note that, like the transmission image, the segmented image is always created on disk, but unlike the transmission image, it is always saved so that the user may inspect the output. With the remapping option the user can either save or delete the resulting image. Since both the emission scan and the transmission scan are acquired in fully 3-D mode with real-time axial back projection, the attenuation correction can be performed on the projection data without introducing any approximation or errors.

After the axial smoothing, each set of attenuation coefficients is reconstructed using an iterative algorithm. The transmission image is scaled so that 100 counts/sq. mm corresponds to an attenuation coefficient of 0.095/cm (water). This image is then forward-projected into a sinogram of attenuation coefficients which are multiplied by a factor of 1000 and written to disk. There are two choices for processing the transmission images after reconstruction: segmentation and remapping. The purpose of both methods is to improve the uniformity and quantitative accuracy of the transmission images and attenuation coefficients.

Transmission			
Blank File	blnk256192576.scn		
Trans Sinogram	/sun0/patient/	p0/s1/p0s1_demo_t	r.scn
EC Correction	Yes	💷 Edit	
PT Sinogram	Save	💷 Edit	
Trans Image	Save	💷 Edit	
Trans Algorithm	Gaussian FBP	💷 Edit	
Post Processing	Remapping	🗆 Edit	
Radial Mask # Bins 5			
Axial Smoothing	al Smoothing		
Scatter Coefficient	Fixed	⊐ 1.15 0	
Attenuation Coeff 0.095			
Leak Sinogram	On	💷 Edit	
3DAC	On	- Edit	
	ж	Cancel	

Figure 8-7 Transmission Attenuation Window

Blank File and Trans Sinogram

When Transmission attenuation correction is selected, the system prompts for the file name of the blank scan and the transmission Sinogram scan, if the default files do not exist. The blank scan data are normally stored in a 'tables' directory associated with the reconstruction program. The default file name for the transmission scan is the same as the emission scan, but with a *_tr* appended to the filename.

Emission Contamination (EC) Correction

When EC Correction is toggled to *Yes*, an *Edit* button is displayed. Click *Edit* to display the EC Sinogram Edit window.

EC Sinogram		
EC Sinogram	/sun0/patient/p0/s1/p0s1_demo_ec.scn	
FWHM Rad Smooth		
FWHM Ang Smooth	<u>10.000</u>	
	Cancel	

Figure 8-8 EC Sinogram Edit Window

FWHM Rad Smooth - Used to smooth EC Sinograms in the radial direction. The value is the FWHM of the smoothing kernel (value is in mm). Default is 0 (i.e. no smoothing).

FWHM Ang Smooth - Used to smooth EC Sinograms in the angular direction. The value is the FWHM of the smoothing kernel (value is in channels). Default is 0 (i.e. no smoothing).

PT Sinogram

When Processed Transmission Sinogram is toggled to *Save*, an *Edit* button is displayed. Click *Edit* to display the filename and path, which is editable.

-	Processed Transmission Sinogram
Process Trans Sino	/sun0/patient/p0/s1/p0s1_demo_pt.scn
C	Cancel

Figure 8-9 Processed Transmission Window

Trans Image

When the Transmission Image is toggled to *Save*, an *Edit* button is displayed. Click *Edit* to display the filename and path, which is editable.

- Transmission Image		
Output Trans Image	/sun0/patient/p0/s1/p0s1_demo_tr.img	
C	Cancel	

Figure 8-10 Transmission Image Window

Trans Algorithms

Gaussian FBP Transmission Algorithm

The program calculates a ramp filter in frequency space, and multiplies it by a Gaussian window. The smoothness of the filter is determined by one of two parameters. The relevant parameter is the FWHM (mm) in coordinate space. Larger value leads to more smoothing. The sinogram is copied to a buffer, convolved with the filter (using standard Fourier transform techniques) and then back-projected. Both the filtering and the back-projection are affected by the orientation of the patient in the camera. The orientation is given in the main header of the input sinogram file.

Gaussian FBP Transmission Algorithm	
FWHM Rad Smooth	12.000
FWHM Ang Smooth	<u>i</u> 0.000
Filter FWHM	4.000
ок	Cancel

Figure 8-11 Gaussian FBP Transmission Algorithm Window

FWHM Rad Smooth - Used to smooth Transmission Sinograms in the radial direction. The value is the FWHM of the smoothing kernel (value is in mm). Default is 12.0.

FWHM Ang Smooth - Used to smooth Transmission Sinograms in the angular direction. The value is the FWHM of the smoothing kernel (value is in channels). Default is 0 (i.e. no smoothing).

Filter FWHM - Used to smooth Transmission Sinograms, a larger number leads to more smoothing.

Iterative Transmission Algorithm

The iterative routine is based on the Ordered Subsets - Maximum Estimated Likelihood method described in IEEE Trans. Med. Imag., MI-4:601-609, 1994. An estimated image is forward-projected and compared to the measured projection data (i.e. the sinogram). The estimated forward-projection is then corrected and back-projected into an image. This is done iteratively for each projection angle. The 192 projection angles are broken up into subsets, and the estimated image is updated after the projections have been adjusted for each subset. The algorithm takes the gaps into account when it updates the estimated image, resulting in a final image without gaps. There are 3 user-selected input parameters for this routine: number of iterations, number of subsets, and smoothing interval.

🖃 Iterative Tra	nsmission Algorithm
# of Iterations	¥.4
# of Subsets	<u></u>
Smooth Interval	1
Smooth Repetitions	2
ОК	Cancel

Figure 8-12 Iterative Transmission Window

of Iterations - The default value is 4. This is the number of complete iterations (forward and backward projections) that are made over every projection angle. Increasing this value (up to a point) leads to sharper images. However, after several iterations, high-frequency artifacts can appear and there is no improvement in image quality.

of Subsets - In PET scanners, the data are projected into 192 angles. In the iterative algorithm, these projections are grouped into ordered subsets. If the number of subsets is 8, then every 8th projection belongs to the same subset, e.g. 0, 8, 16, 24, ... 184, or 1, 9, 17, 25 ... 185. After every projection in the subset has been compared to the corresponding estimated projection for that angle, and the estimated projection has been corrected, the estimated image is updated. Then the process is repeated for the next subset. Increasing the number of subsets decreases the number of iterations necessary to obtain an acceptable image. If the number of iterations chosen is 2, choosing the number of subsets to be 8 results in a good image in a reasonable amount of time.

Smooth Interval - Smoothing can be applied to the reconstructed image in order to lessen the high frequency artifact. The smoothing interval controls how frequently the smoothing is applied. A smooth interval of 0 turns off the smoothing. A smooth interval of 1 smooths after every complete iteration. A value of 2 smooths every 2nd iteration, and so on. If the smooth interval is greater than the total number of iterations, no smoothing is performed.

Smooth Repetitions - This parameter controls the number of times smoothing is performed at each iteration. For example, if the smoothing interval were set to 2, and the smoothing repeat parameter were set to 3, the image would be smoothed 3 times at every 2nd iteration. If the smoothing repeat parameter is 0, no smoothing is performed.

Post Processing

The reconstructed transmission images undergo one of two types of further processing, both of which produce image sets which are more accurate reflections of the true tissue attenuation distribution.

Segmentation - uses an algorithm to determine which regions of the image are background, lung, soft tissue, and patient table. Background pixels are set to zero and pixels representing the other three are set to values (stored in the protocol file) corresponding to the known attenuation coefficients for each of the three regions. The result is a noiseless attenuation sinogram. If some modulation of the attenuation values is desired, e.g. to reflect the natural variation in lung density, the segmented image can be merged with a version of the measured transmission image. This version has been corrected such that the 'average' values of the lung tissue and soft tissue attenuation coefficients will be equal to the nominal values set in the protocol file. This merging of the segmented and measured transmission images is controlled through two input parameters which can be changed by the user. These are the lung uniformity parameter and soft tissue uniformity parameter. If these values are set to 1.0, then only the segmented image is used and no merging is performed. If the values are set to 0.0, then only the over-smoothed, mean-adjusted image is used. Intermediate values result in a mix between the two. Suggested values are .50 for lung, and 1.0 for soft tissue.

-	Segmentation	- 1
Lung Uniformity	. 500	
Tissue Uniformity	1.000	
Lung Coefficient	<u>.</u> 0.026	
Tissue Coefficient	<u>.</u> 0.095	
Table Coefficient	0.019	
FWHM Axial Smoothing	5.000	
Max Contour Change	0.100	
Tissue/Lung Ratio	1.800	
2D Gauss Smooth Index	ž	
Segmentation Image	/sun0/patient/p0/s1/p0s1_demo_sg.im	đ
ОК	Cancel	

Figure 8-13 Segmentation Post Processing Window

Lung Uniformity - Fractional contribution of original image to pixels in lung regions (a value of 1 represents a fixed value for all lung pixels.)

Tissue Uniformity - Fractional contribution of original image to pixels in tissue regions (a value of 1 represents a fixed value for all tissue pixels.)

Lung Coefficient - Attenuation value assigned to pixels determined to be in lung regions.

Tissue Coefficient - Attenuation value assigned to pixels determined to be in tissue regions.

 Table Coefficient - Attenuation value assigned to pixels determined to be in table region.

FWHM Axial Smoothing - Coefficient that determines the amount of axial smoothing (in mm.) applied to final attenuation map. Larger number provides more smoothing.

Max Contour Change - Value that controls fit of contour between background and tissue.

Tissue/Lung Ratio - Value that controls assignment of pixels into either lung or tissue regions.

2D Gauss Smooth Index - Value the controls amount of x-y smoothing applied to final images. Larger number provides more smoothing.

Segmentation Image - displays the filename and path, which is editable

Remapping - the attenuation coefficients in the image are modified based on parameters included in the protocol file. These parameters include a scale factor to account for scattered radiation and an upper and lower threshold. The thresholds define regions in the spectrum of attenuation coefficients which are treated differently in the post-processing. This is the current default on the PET system.

After the application of the scale factor, the average value of the attenuation coefficients in the region should be accurate if measured over a region which is large enough, however, statistical noise may cause local deviations from this value. Measured coefficients that fall above the upper threshold, which is generally set 10-20% below the average coefficient value for soft tissues (0.095 1/cm), are increased to the value of the soft tissue coefficient. This has the effect of eliminating most of the variations due to noise. Coefficients below the lower threshold which is generally set to about 50% of the attenuation coefficient of soft tissue, are left unchanged, allowing natural variations in lung tissue to remain. Attenuation coefficients between the two boundaries are scaled linearly to avoid sharp discontinuities.

- Remapping Post Processing 🛛 🖛		
Lung Uniformity	0.600	
Tissue Uniformity	0.800	
Save Remapped Image	No 🖃	
Remapped Image	/sun0/patient/p0/s1/p0s1_demo_rm.img	
ок	Cancel	

Figure 8-14 Remapping Post Processing Window

Lung Uniformity - Value that represents the fraction of the ideal tissue coefficient (which is generally 0.095 set from Transmission dialog) used a lower pixel value bound. Values below this are assumed to be lung.

Tissue Uniformity - Value that represents the fraction of the ideal tissue coefficient (which is generally 0.095 set from Transmission dialog) used a upper pixel value bound. Values above this are assumed to be tissue.

Save Remapping Image - Allows user to save the remapped image for latter inspection.

Remapping Image - Filename to be used if remapped image is to be saved.

Radial Mask # Bins

Controls the application of radial mask to the transmission sinogram in which all bins near the radial edges are set to 1.0 (no attenuation correction). This value determines the size of this mask. A value of 0 means that no radial mask is applied.

Axial Smoothing

Axial smoothing operation is performed after merging multiple single-frame input sinograms into a multi-frame whole body sinogram to reduce seam artifacts.

Scatter Coefficient

The reconstructed transmission image has pixels values less than would be expected from attenuation effect alone because the transmission singles are contaminated by scatter. There are two ways this scatter contamination can be corrected described below. Note that this correction is applied before post-processing (segmentation or remapping).

Automatic - For each image, a histogram is derived and correction factor is computed that will shift the location of the histogram peak (assumed to be tissue) to its desired value of 0.095.

Fixed - The supplied correction factor is applied to all slices.

Attenuation Coefficient

This value represents the assumed correct value for the tissue attenuation factor. It is used by remapping and automatic scatter correction.

Leak Sinogram

When leak sinogram is turned on, the emission contamination scan is corrected for source leak (which is unavoidably present) using a leak sinogram that is generated during system calibration. When Leak Sinogram is toggled to *On*, an *Edit* button is displayed. Click *Edit* to display the filename and path, which is editable.

Leak Sinogram		
Leak Sinogram File	leak256192576.scn	
0	DK Cancel	-

Figure 8-15 Lead Sinogram Window

3DAC

When *3DAC* is toggled to *On*, and *Edit* button is displayed. Click *Edit* to display the 3D Forward Projector window. When selected, the attenuation map image dataset is forward projected using a fully three-dimensional forward projection algorithm. If 3DAC is not selected, forward projection is done on a slice by slice basis.

= 3D Forward Projector		
Filter Type	Cosine 📼	
Filter Cutoff	Jo	
Axial Filter Type	Kaiser Bessel 🖃	
Axial Filter Cutoff	Į1	
Weights File Name	j/home/patient/recon_test/Paris/tables/w	
	Advanced Parameters	
	OK Cancel	

Figure 8-16 3D Forward Projector Window

Filter Type - The filter types are applied in the slice plane during forward-projection. The four possible filters, Rectangular, Cosine, Hanning, and Kaiser Bessel each have slightly different characteristics but essentially provide in-slice smoothing. Filter type "None" is also allowed.

Filter Cutoff - This value controls the degree of smoothing of the in-plane filter. A larger value provides more smoothing.

Axial Filter Type - The filter is applied axially during forward-projection. The four possible filters, Rectangular, Cosine, Hanning, and Kaiser Bessel each have slightly different characteristics but essentially provide slice-to-slice smoothing. Filter type "None" is also allowed.

Axial Filter Cutoff - This value controls the degree of smoothing of the axial filter. A larger value provides more smoothing.

Weights File Name - The weights file is used to speed 3DAC processing. This file name should not normally be changed.

Advanced Parameters for 3D Forward Projector

nterpolation Radius 2. 7 Kaiser Bessel Alpha 5. 8 Kaiser Bessel Order 2 =
Kaiser Bessel Alpha 6.8 Kaiser Bessel Order 2 =
Kaiser Bessel Order 2 =
nterpolation Type Bi-directional =

Figure 8-17 3DAC Forward (Advanced) Window

Interpolation Radius - Controls the inner operation of the 3D forward projection process (should not normally be changed).

Kaiser Bessel Alpha - Controls the inner operation of the 3D forward projection process (should not normally be changed).

Kaiser Bessel Order - Controls the inner operation of the 3D forward projection process (should not normally be changed).

Interpolation Type - Controls the inner operation of the 3D forward projection process (should not normally be changed).

Attenuation Correction Read

It may be desirable to perform some processing on the transmission data and the reconstruction program therefore has the provision to read in these processed transmission data as sinograms. For example, a separate segmentation program could be used to segment the transmission image and generate improved transmission sinograms. This option reads in a sinogram and uses it directly for attenuation correction during emission reconstruction. Currently this feature is used for research only and does not serve a useful purpose for routine applications.

Read Attenuation Correction		
Process Trans Sino	/sun0/patient/p0/s1/p0s1_demo_pt.scn	
OK		

Figure 8-18 Read for File Attenuation Window

Attenuation Correction Reproject

It may be desirable to perform some processing on the transmission data and the reconstruction program therefore has the provision to read in these processed transmission data as images. For example, a separate segmentation program could be used to segment the transmission image. This option reads an image dataset representing an attenuation map and performs forward projection to create the attenuation correction sinogram used by emission reconstruction. Currently this feature is used for research only and does not serve a useful purpose for routine applications.

F	Reprojection Attenuation Correction		
Input Trans Image	/sun0/patient/p0/s1/p0s1_demo_tr.img		
Output PT Sinogram	/sun0/patient/p0/s1/p0s1_demo_pt.scn		
OK Cancel			



Decay Correction

Decay factors for a frame are calculated from the half-life of the isotope used. Also, the duration of the frame and the time elapsed from the start of the first frame to the start of the frame in question. Half-lives of the most commonly used isotopes are stored in the program, and the isotope actually used is identified in the main header of the input sinogram file. The first frame, by definition, is corrected only for the mid-time, and subsequent frames are corrected both for their mid-times and for their delays. A decay factor is calculated for each frame, and is applied to the data before rebinning.

When *Decay Correction* is selected, the correct isotope must also be selected (in order to specify the half-life). Decay Correction is performed at the beginning of the scan.

SUV Measurement (Standardized Uptake Value)

When the amount of activity, patient weight, and the time of measurement is entered in the acquisition program, the reconstruction program calculates a conversion factor to convert counts/pixel into SUVs. This also requires a special calibration.

Filter

Emission data can be smoothed during the reconstruction process. This smoothing is controlled by the following Filter choices:

- Metz Pre-filter
- Wiener Pre-filter
- Wiener Post-filter
- 3D Image Filtering
- None

The Wiener filter is somewhat more complicated than the Metz filter but can address both image blurring as well as noise. Both filters operate the images on a slice-by-slice basis. 3D Image Filtering applies a filter to the entire dataset on a 3D basis.

Each filter has one or more parameters that control its operation. The default values have been optimized and would not normally need to be changed.

Note that if the 3D RAMLA emission algorithm is selected, neither the Wiener or the Metz filters can be used, even if selected. Only the 3D Filter affects the results.

Metz Filter

The Metz Filter is a simple low-pass filter. The single parameter controls the smoothing/ resolution trade off. The default value is optimized and should not normally need to be changed.

Metz Pre-filter		
Metz Cutoff	1.000	
ок	Cancel	

Figure 8-20 Metz Pre-filter Window

Wiener Filter

The Wiener filter is available as pre- and post- reconstruction filter. Both filters enhance the intermediate spatial frequencies and are generally preferred for brain image reconstruction. The filters use several parameters, which can be examined and/or changed using *Edit*.

The Wiener post reconstruction step is usable with RAMLA as well as all other image reconstruction algorithms. Wiener post-filter is required to obtain the best possible image quality on brain images reconstructed using RAMLA. The filter is provided as a general post-filter option applied to images processed by either FBP or OSEM as well as RAMLA. The Wiener post-filter works on 128 and 256 square matrix images, not 144 and 288 matrices. The Wiener post-filter is not intended to be used on whole-body studies. The default values are optimized and should not normally need to be changed.

- Wie	ner Pre-filter
Wiener Scaling	<u>i</u> 0.500
Scatter Fraction	<u>j</u> 0.500
Gaussian FWHM	<u> </u>
Rolloff FWHM	<u>i</u> 0.410
Scatter Tail	160.000
Cutoff Frequency	<u>i</u> 0.320
ОК	Cancel

Figure 8-21 Wiener Pre-filter/Post-filter Window

3D Image Filter

This capability effectively has four different filters with two combinations of two filter functions (Rotate Symmetric and x, y, z Separate and two Filter Types (Blob and Hanning). While more time-consuming, it can produce more accurate results. The default values are optimized and should not normally need to be changed.

- 3D Image Filter - 🗆	
Filter Function	Blob 🖵
Filter Type	Rot. Symmetric 🖃
Trans Convolution	10.3
Axial Convolution	9. Ž
Alpha Parameter	1
ОК	Cancel

Figure 8-22 3D Image Filter Window

Gap Compensation

The spaces between the detectors cause gaps, which are normally compensated for in the reconstruction algorithm. Therefore this function is usually turned on.

Emission Algorithm

Emission Algorithm controls the algorithm used to reconstruct the emission sinogram. There are two general classes of reconstruction algorithms available. In one category, the multi-tilt sinogram is rebinned to produce a sequence of single tilt sinograms, each representing a single slice. This occurs through a process know as Fourier Rebinning (FORE). The sinogram slices are then reconstructed a slice at a time. In the other class, the entire multi-tilt, multi-slice sinogram is reconstructed by a single 3D reconstruction algorithm with no intermediate rebinning step. In the first class falls the algorithms know as Filtered Backprojection (FBP), Iterative, and RAMLA. In the second class falls the algorithm know as 3D-RAMLA. Each of these algorithms has a set of associated parameters which controls its operation and can be accessed by selecting the *Edit* button located next to the algorithm selector. In general, reconstruction speed decreases in going from FBP to iterative to RAMLA to 3D RAMLA. However, image quality generally increases in this progression.

Fourier Rebinning

Fourier rebinning is a method of data compression used on 3D data sets that greatly reduces reconstruction time compared to many 3D algorithms, while providing excellent image quality. It was originally developed by Michele Defrise and is described in more detail in the journal <u>Inverse Problems</u>, November 1995. In this method, lines-of-response (LORs) in a 3D data set which had been stored in *oblique sinograms* according to their radial position, transverse angle, oblique angle, and

oblique axial position (r, angle, tilt, y') are resorted into *direct sinograms* based on radial position, transverse angle, and axial position (r, angle, z). Here *direct* refers to the direction perpendicular to the z-axis of the scanner, and *oblique* refers to any direction that is not. Fourier rebinning replaces an oblique LOR with a direct on while making a decision based on a proper of the data known as the *frequency-distance relation* which is described in more detail in the publication "International Workshop on Physics and Engineering of Computerized Multidimensional Imaging and Processing, Proceedings of the SPIE" 671, 8-18. The final result of the Fourier rebinning is a data set that has been reduced in size by a factor of 1/(number of tilts).

There is also a user option (available on the advanced parameters page) to choose the single-slice rebinning method instead of the Fourier rebinning method for either the entire data set or only certain components of it. This option is primarily for research, and it is not recommended for clinical studies.

Approximate Reconstruction Times

The time per frame on a dual processor Blade 1000 for a large sinogram with 3DAC background subtraction and RAMLA 3D (recommended parameters, i.e. 2 iterations) is 23 min/frame. Using the same parameters, see the following:

FBP	1 min/frame
2.5D RAMLA or OSEM	3 min/frame
1 RAMLA 3D iteration	5 min/frame

Filtered Backprojection

This reconstruction algorithm starts by calculating a ramp filter in frequency space and multiplying it by either a Gaussian, Hanning, or Butterworth filter. Each filter is controlled by one or two parameters that essentially controls the trade-off between image resolution and accuracy versus image smoothness. The sinogram is copied to a buffer, convolved with the filter (using standard Fourier transform techniques) and then back-projected. Both the filtering and the backprojection are affected by the orientation of the patient in the camera. The following screens show the parameters available for FBP with each of the three filter types.

Hanning FBP Algorithm

Hanning FBP Algorithm		
Hanning Smoothing	3.00	
OK	Connect	
OK	Cancel	

Figure 8-23 Hanning FBP Window

Hanning Smoothing - Controls the amount of smoothing performed during FBP. Larger numbers increase the smoothing.

Gaussian FBP Algorithm

🕞 Gaussia	n FBP Algorithm
Gaussian FWHM	8.000
ок	Cancel

Figure 8-24 Gaussian FBP Window

Gaussian FWHM - Controls the amount of smoothing performed during FBP. Larger numbers increase the smoothing.

Butterworth FBP Algorithm

- Butterworth FBP Algorithm	
Butterworth Cutoff	
Butterworth Dropoff	1.000
ОК	Cancel

Figure 8-25 Butterworth FBP Window

Butterworth Cutoff - Controls the amount of smoothing performed during FBP. Larger numbers increase the smoothing.

Butterworth Dropoff - Controls the amount of smoothing performed during FBP. Larger numbers increase the smoothing.

Iterative Algorithm Using Ordered-Subsets (OSEM)

The iterative routine is based on the Ordered Subsets - Maximum Estimated Likelihood method described in IEEE Trans. Med. Imag., MI-4:601-609, 1994. An estimated image is forward-projected and compared to the measured projection data (i.e. the sinogram). The estimated forward-projection is then corrected and back-projected into an image. This is done iteratively for each projection angle. The 192 projection angles are broken up into subsets, and the estimated image is updated after the projections have been adjusted for each subset. The algorithm takes the gaps into account when it updates the estimated image, resulting in a final image without gaps. There are 3 user-selected input parameters for this routine: number of iterations, number of subsets, and smoothing interval.

lterative Algorithm-filter		
# of Iterations	<u><u></u></u> <u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u><u></u></u>	
# of Subsets	<u>8</u>	
Smooth Interval	1	
Smooth Repetitions	1	
ОК	Cancel	

Figure 8-26 Iterative Window

of Iterations - The default value is 4. This is the number of complete iterations (forward and backward projections) that are made over every projection angle. Increasing this value (up to a point) leads to sharper images. However, after several iterations, high-frequency artifacts can appear and there is no improvement in image quality.

of Subsets - In PET scanners, the data are projected into 192 angles. In the iterative algorithm, these projections are grouped into ordered subsets. If the number of subsets is 8, then every 8th projection belongs to the same subset, e.g. 0, 8, 16, 24, ... 184, or 1, 9, 17, 25 ... 185. After every projection in the subset has been compared to the corresponding estimated projection for that angle, and the estimated projection has been corrected, the estimated image is updated. Then the process is repeated for the next subset. Increasing the number of subsets decreases the number of iterations necessary to obtain an acceptable image. If the number of iterations chosen is 2, choosing the number of subsets to be 8 results in a good image in a reasonable amount of time.

Smooth Interval - Smoothing can be applied to the reconstructed image in order to lessen the high frequency artifact. The smoothing interval controls how frequently the smoothing is applied. A smooth interval of 0 turns off the smoothing. A smooth interval of 1 smooths after every complete iteration. A value of 2 smooths every 2nd iteration, and so on. If the smooth interval is greater than the total number of iterations, no smoothing is performed.

Smooth Repeat - This parameter controls the number of times smoothing is performed at each iteration. For example, if the smoothing interval were set to 2, and the smoothing repeat parameter were set to 3, the image would be smoothed 3 times at every 2nd iteration. If the smoothing repeat parameter is 0, no smoothing is performed.

RAMLA Algorithm (Row-Action Maximum-Likelihood)

This algorithm is based on the same concepts that underlie the Ordered Subsets method described above. Like OSEM, this is an iterative reconstruction method that attempts to maximize the log of the likelihood that the reconstructed image matches the actual image. Also like OSEM, the gaps in the scanner are accounted for within the algorithm. RAMLA is explained in detail in the IEEE Trans. Med. Imag., MI-5:687-699, 1996, but the following should provide the user with an overview and a basic understanding of the input parameters.

RAMLA Algorithm		
# of Iterations	¥1	
Relaxation[1]		
Relaxation[2]		
Relaxation[3]		
Relaxation[4]		
Relaxation[5]		
Radius	ž. 500	
Bessel	ž	
Alpha		
BCC Relative Size	ž. 000	
ок	Cancel	

Figure 8-27 RAMLA Window

of Iterations - As in OSEM, this is the number of times each projection angle is used to update the image estimate. Unlike OSEM, RAMLA updates the image estimate at every projection, rather than collecting information from several projections before performing a single update. RAMLA can produce images of excellent quality with only one iteration, although up to four can be used on brain images. Reconstruction time increases linearly with this parameter.

Relaxation - This parameter controls how much of an effect each update is allowed to have on the image. The possible values range from 0.0 to 1.0 where a larger number leads to a larger effect from each update. Default values for this parameter range from .01 to .1. Large values can result in changes between updates that are too large, causing oscillation in the image rather than a smooth convergence to a good result. The relaxation parameter can be set independently for each iteration.

- Changing the Relaxation on parameter from 0.1 -> 0.12 -> 0.16 will increase the sharpness of the images.
- Changing the Relaxation parameter from 0.1 -> 0.08 -> 0.06 will increase the smoothness of the images.

An important feature of this implementation of RAMLA is the use of sphericallysymmetric basis functions. Rather than building the image volume out of an array of adjacent cubic voxels, the data are partitioned into overlapping spherical *blobs*. These *blobs* are called spherically-symmetric Kaiser-Bessel functions and their shape and size are determined by their *Advanced Parameters*.

Radius - This variable determines the size of the sphere. Typically a value of 3 Blobs is used for whole-body studies and 2 Blobs is used for brains. Increasing the size of the sphere does not necessarily lead to poorer resolution, but it will increase reconstruction time. If the size is made too large relative to the resolution of the scanner, ringing or overshoot artifacts can appear at object boundaries.

Bessel - This parameter is the order of the Kaiser-Bessel function. It determines continuity of the curve and its derivatives; it should always be set to 2.

Alpha - This parameter controls the shape of the Kaiser-Bessel function. The optimum values for this parameter has been determined for the blob radius and grid spacing and should not be changed.

BCC Relative Size - To speed up the reconstruction, blobs are placed on a bodycentered cubic grid with a spacing relative to the voxel spacing specified by this parameter. Because there are fewer blobs than voxels, the reconstruction time required is markedly reduced with no apparent loss of image quality, provided the blobs still overlap. The recommended value for the BCC grid is 2.0. This parameter should be changed without also changing the value for alpha.

3D RAMLA

I 3D RAMLA	
# of Iterations	<u>]</u> 2
Relaxation Param	<u>.</u> 0.005
System Attenuation	Yes = Edit
Advanced Parameters	
ОК	Cancel

Figure 8-28 3D RAMLA Window

of Iterations - As in OSEM, this is the number of times each projection angle is used to update the image estimate. Unlike OSEM, RAMLA updates the image estimate at every projection, rather than collecting information from several projections before performing a single update. RAMLA can produce images of excellent quality with only one iteration, although up to four can be used on brain images. Reconstruction time increases linearly with this parameter.

Relaxation Parameter - This parameter controls how much of an effect each update is allowed to have on the image. The possible values range from 0.0 to 1.0 where a larger number leads to a larger effect from each update. Default values for this parameter range from .01 to .1. Large values can result in changes between updates that are too large, causing oscillation in the image rather than a smooth convergence to a good result. The relaxation parameter can be set independently for each iteration.

- Changing the Relaxation on parameter from 0.1 -> 0.12 -> 0.16 will increase the sharpness of the images.
- Changing the Relaxation parameter from 0.1 -> 0.08 -> 0.06 will increase the smoothness of the images.

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System Attenuation - Several studies have demonstrated improved image quality when attenuation effects were included in the model of the system used by interative algorithms, including RAMLA (IEEE Trans. Nucl. Sci. 45: 1083-1089, 1998). The file containing the attenuation correction factors (*_pt.scn) generated by transmission or ellipse is used.

Blob Radius	<u>]</u> 2.5	
Blob Bessel Func	2 =	
Blob Alpha	8.63	
Blob BCC	2	
Pre-Knitting File	Do Not Save 😑	
Axial Weights File	//home/patient/recon_test/Paris/tables/i	
OK		

3D RAMLA Advanced Parameters

Figure 8-29 3D RAMLA (Advanced) Window

Blob Radius - This variable determines the size of the sphere. Typically a value of 3 Blobs is used for whole-body studies and 2 Blobs is used for brains. Increasing the size of the sphere does not necessarily lead to poorer resolution, but it will increase reconstruction time. If the size is made too large relative to the resolution of the scanner, ringing or overshoot artifacts can appear at object boundaries.

Blob Bessel - This parameter is the order of the Kaiser-Bessel function. It determines continuity of the curve and its derivatives; it should always be set to 2.

Blob Alpha - This parameter controls the shape of the Kaiser-Bessel function. The optimum values for this parameter has been determined for the blob radius and grid spacing and should not be changed.

Blob BCC - To speed up the reconstruction, blobs are placed on a body-centered cubic grid with a spacing relative to the voxel spacing specified by this parameter. Because there are fewer blobs than voxels, the reconstruction time required is markedly reduced with no apparent loss of image quality, provided the blobs still overlap. The recommended value for the BCC grid is 2.0. This parameter should be changed without also changing the value for alpha.

Pre-Knitting File - For wholebody studies, 3D RAMLA is performed on a frame-byframe basis. The resulting image frames are then combined by weighting overlapping slices to yield a single image frames. The individual image frames after 3D RAMLA reconstruction may be saved in this pre-knitting file.

Axial Weight File - This file contains the weights used to weight slices from overlapping frames.

Advanced Parameters

The *Advanced Parameters* window include parameters which are rarely changed by the user. They include the following:

- Perform sampling normalization
- Image size selection
- Convert body orientation from supine to prone
- Save the corrected sinogram
- Perform emission deadtime correction
- Perform interference correction
- Option to save sinogram before or after Fourier Rebinning
- Various parameters associated with Fourier Rebinning

- Advanced Parameters			
Sampling Normalization	Yes	💷 Edit	
Image Size	144x144	-	
Flip Sinogram	Supine	-	
Output Sinogram	Do Not Save	-	
Emiss Deadtime Corr	No	-	
Interference Correction	No	-	
FT Output Sinogram	Do Not Save	-	
K Width (integer)	<u>10</u>		
K Limit (integer)	<u>i</u> 0		
O Width (integer)	<u>i</u> 0		
O Limit (integer)	<u>i</u> 0		
Theta Limit (float)	9		
Single Slice Rebinning	No	-	
Rate Normalization	None 🖵		
Scatter Window	15		
ОК	Cancel		

Figure 8-30 Advanced Parameters Window

Sampling Normalization - This is now a fundamental part of reconstruction, the parameters should not be changed.

Image Size - Controls the size of the generated images (144 x 144 is the default).

Flip Sinogram - Select the acquisitioned patient position

- Supine patient was positioned face up during acquisition (standard image orientation)
- Prone patient was positioned face down during acquisition, reconstruction will flip the image and display it as a supine image which is the standard image orientation.

Output Sinogram - Determines whether to save a copy of the fully processed sinogram just before image reconstruction. This is the emission sinogram after all attenuation correction and filtering steps have be completed. The sinogram can be save either before or after Fourier rebinning. The option exists to specify the name of the save sinogram.

Emission Deadtime Correction - Determines whether to correct the emission sinogram for deadtime.

Dead-time factors are obtained by filling a uniform cylinder with F-18 and allowing it to decay. The observed sensitivity as a function of count rate determines the dead-time factors. These are calculated by a separate program, and written to an ASCII file. During acquisition, the singles count rate for each frame is obtained from the average of the beginning and ending count rates, which are in the sub-header. The correction factor at that count rate is interpolated from the table of dead-time factors using a cubic spline interpolation. A dead-time factor is thus obtained for each frame, is stored in the header, and is applied to the data before rebinning in the reconstruction program.

Interference Correction - Corrects emission sinogram for ripple effect interference pattern.

FT Output Sinogram - Determines whether to save a copy of the rebinned emission sinogram before measured attenuation correction and filtering has been performed. This option exists to specify the name of the saved sinogram.

K Width (integer) - Controls rebinning process (Not normally changed).

K Limit (integer) - Controls rebinning process (Not normally changed).

O Width (integer) - Controls rebinning process (Not normally changed).

O Limit (integer) - Controls rebinning process (Not normally changed).

Theta Limit (float) - Controls rebinning process (Not normally changed).

Single Slice Rebinning - Determines whether to do single slice rebinning instead of FORE rebinning. (Not normally changed).

Rate Normalization - This corrects the sinogram for activity decay that occurs during the acquisition. This can be performed either before or after rebinning (Not normally changed).

Scatter Window - The parameter determines the number of transmission slices used when calculating the scatter coefficient used in auto scatter correction. The scatter coefficient is calculated on a sliding basis.

Chapter **SCOUTVIEW**

This interface is used to facilitate positioning of an organ of interest in the scanner prior to taking an acquisition by displaying a projection image of Listmode data. The counts at each 4x4 mm pixel location are divided by the collection time at that location and displayed for every 1,000 events collected. After the patient table is moved to a new location, new data are added to the displayed image, giving a quick overview of the activity distribution in the patient. This allows identification of the axial extent to be scanned in detail using the acquisition program.

This overview describes the purpose of each of the functions in the main interface window. Please refer to the *Menu Commands* below for details about all the features.

The Scoutview interface main window consists of controls on the left half, and a display area on the right half where the projection image is displayed. The patient is positioned in the scanner using the table control buttons on the gantry display panel.

The most basic way of running Scoutview is to position the table to the approximate desired position and click *Start*. At that point, *Start* button becomes *Stop*, the hardware is initialized, and the Listmode data collection and display process begins.

The table can be moved any time during the Scoutview acquisition. The *Current FOV* bracket on the left side of the *Scoutview* display moves in response to the new table position, and Listmode data is acquired and displayed at the new location. Projected data from previous table locations remain until the *Clear* button is pressed. The data acquisition stops when the *Stop* button is pressed, but, again, the display is not cleared unless the *Clear* button is pressed. Pressing the *Stop* button closes the connection to the hardware, and resets the system to its original configuration.



Figure 9-1 scoutview Window

ScoutView Parameters

Start Position and Scan Length Sliders

The *Start Position* and *Scan Length* slider bars are generally used after the Scoutview process is over and the real acquisition is ready to begin. Changing the *Start Position* moves the tick marks on the right side of the projection image display and informs the user of the corresponding starting table position below the *Start Position* slider bar. This tells the user the starting position to enter in the Acquisition program, that depends on the direction of table motion that is used in the Acquisition. When the scan is in progress, the *Start* button becomes the *Stop* button. It is IMPERATIVE that activity be in the field of view when the *Stop* button is pressed.

The *Scan Length* slider bar controls the distance between the tick marks along the right side of the projection display. This distance is in increments of half the axial Field of View. This slider bar can be used to determine the scan length to enter in the Acquisition program.

It is important to note that these slider bars do NOT control the table motion - they are merely a means to correlate the actual table position with the part of the body the user wishes to scan.

Patient Orientation

The *Patient Orientation* toggle buttons control the location of the *Current FOV* bracket and the tick marks in the display area. The default orientation is Head First. If Feet First is toggled, the projection image is "flipped" so that the patient appears to be head first, but the position of the *Current FOV* bracket and the tick marks are moved to indicate the correct position.

Table Direction

The *Table Direction* toggle buttons are used to report the correct table position. The arrow along the right side of the display area points up if the table direction is *In*, and points down if the direction is *Out*. The table can be moved in either direction during the Scoutview process, but if the table direction is *Out* in the Acquisition, it should be so indicated in the Scoutview interface so that the table position reported under the *Start Position* slider is correct.

Transaxial Acceptance Angle

The *Transaxial Acceptance Angle* toggles are used to control the Scoutview data output. When Listmode data are collected, only those events that occur within the range of plus or minus the transaxial acceptance angle is displayed. The default is 10 degrees. The transaxial acceptance angle can be changed any time, but if it is changed while Listmode data are being collected the display clears itself because the normalization parameters depend on the acceptance angle.

Scoutview Buttons

The three buttons along the bottom of the left half of the interface control the Listmode data acquisition and display. The *Start* button initializes the hardware, and starts the acquisition and projection of Listmode data, and the button label becomes *Stop*. Pressing the *Stop* button stops the data collection process, and resets the hardware. The *Clear* button clears the display of the normalized countrate data. The display can be cleared at any time. The *Save* button is used to write out the projected data to an output image. Refer to *Save Image* under the *File Menu* section for details on this feature.

Beneath the display area the accepted and rejected true counts of the current projection image are reported for the user's information.

File Menu

File option in the top menu bar has two drop-down options:

- Save Image
- Exit Scoutview

Save Image

It is possible to write the currently displayed projected data to an output image file. When the *Save* button at the bottom of the Scoutview interface is pressed, the Listmode acquisition pauses, and the current normalized count rates being displayed are stored in an image file specified by the user.

The Save Image button in the File menu is used to specify the image name to which the projection data are to be saved. When the filename is entered in the window that pops up, Scoutview adds a .img suffix if it is missing. The program then checks if the file already exists. If it does, another window pops up asking if it is OK to append the new projection data to it. If the response is Yes, every time the user saves data, a new 9-slice frame is appended to the image file. If the response is No, the existing file is overwritten with the first frame of data, then each subsequent frame is appended.

If the user tries to save the projection image (by pressing the *Save* button while Listmode data are being collected), without entering a filename first, the program reminds the user to specify a filename by selecting the *Save Image* menu option.

Each time the *Save* button at the bottom of the Scoutview interface is pressed, a 9-slice frame is saved to the output image. Each slice is 128x128 pixels. Since each pixel in the projection image is 4x4 mm, the whole body array is no more than 512 pixels (or 2048 mm) high, so the array is divided into four sections of 128 rows each. The first four slices of the saved frame consist of the 4 sections of data. To help alleviate the problem of an organ spanning two slices, the data array is again divided into 5 128-row sections, but offset by 64 so that the fifth slice contains 64 rows of zero pixels, then the first 64 rows of the projection image, the sixth slice contains rows 64-192, etc. After the slices are written to disk, list data acquisition resumes.

Exit Scoutview

Selecting the *Exit Scoutview* option under *File* in the top menu bar exits the interface. If Listmode collection is still running, it is stopped, and the link to the hardware is closed, and the hardware settings are reset to the original configuration.

Options

Options in the top menu bar has two drop-down options:

- Change Bankpair
- Change Axial FOV

There are two constraints to the Scoutview data collection process that can be changed via the functions under the *Options* choice in the top menu bar of the interface - the bankpair to be activated, and the effective FOV to be displayed
Change Bankpair

Only one pair of opposite detectors can be activated when Scoutview is processing data, and the default bankpair is 2 (corresponding to detectors 1 and 4, which are the bottom and top detectors). To change the bankpair to 5 (detectors 2 and 5) or 8 (detectors 3 and 6) simply select the *Change Bankpair* option and toggle the desired bankpair in the menu that pops up. The bankpair must be changed before the *Start* button is pushed so the menu option is deactivated when Scoutview is processing.

Change Axial FOV

The axial factor file used in the axial normalization of the Listmode data has imprecise values at the end points, that leads to noisy data at the top and bottom of the field of view being displayed. To avoid this problem, events that occur in the first 8 mm and last 8 mm of the field of view are not processed and displayed. This range can be adjusted by moving the slider bar in the window that pops up when the **Change Axial FOV** menu option is selected. The slider bar moves in increments of 8 mm, so that at least 4 mm (or one row of pixels) is disregarded on both the top and bottom of the field of view. This effective FOV must be specified before the **Start** button is pushed. If Scoutview is processing, and noisy data are visible, the effective FOV can be changed after the **Stop** button is pressed.

Scoutview Procedure

- 1. On the ACQ Workstation, left click background and select *Scoutview*
- 2. Set table direction and patient orientation *head first-table out or feet first-table in* to match the acquisition protocol
- 3. Change the acceptance angle to **30** and Press *Start* to begin acquiring an image. The patient may be scouted in either direction, table in or table out.
- 4. Using the enable and table translate buttons on the Gantry, manually scout the patient through the Gantry for desired length of patient. Use a fluid table motion versus a start and stop motion.
- 5. Select *Stop* to end the image. Activity must be in the field of view when stop is selected.
- 6. Adjust brightness of the Scoutview image if necessary.
- 7. Use the *Start Position* and *Scan Length* slide bars to adjust the area needed for acquisition.
- 8. Record these values on the acquisition setup screen.

Scoutview and Variable Acquisition Parameter

Scoutview is especially helpful when varied acquisition times are desired. By examining the tick marks on the side of the *Listmode Projection*, it is possible to accurately know in which frames body structures reside simply by counting every other mark as 1 emission frame. Acquisition times may be varied based on this information.

Positioning Using Lasers

As an alternative to Scoutview, it is possible to use the lasers for positioning.

- 1. Position patient comfortably on the pallet.
- 2. Turn the lasers on.
- 3. Move the pallet in until the patient's starting position is in the FOV. Record this number.
- 4. Push the REL/ABS button on the Gantry to REL and press the Landmark button. This will zero the table.
- 5. Continue moving the patient until the desired ending position is in the FOV.
- 6. Look at the number on the control panel. This is the *change in table*
- 7. Find corresponding *change in table* value on the chart, rounding up to the next value.

Read across the chart for the *Scan Length*. Enter both the *Start Position* and *Scan Length* values in the acquisition setup window

Laser Positioning Using Chart				
Change in Table	# EM Positions # TR Positions		Scan Length	
0	1	3	256	
112	2	4	368	
224	3	5	480	
336	4	6	592	
448	5	7	704	
560	6	8	816	
672	7	9	928	
784	8	10	1040	
896	9	11	1152	
1008	10	12	1264	
1120	11	13	1376	
1232	12	14	1488	
1344	13	15	1600	

Chapter **10** COLOR SCALES

One or two color bars can be displayed (primary and secondary). They can be used simultaneously in two different windows to allow independent adjustments of threshold and contrast values. The scales are adjusted using cursors for the lower and upper limits. A numerical scale next to the color bar allows a quantitative value to be associated with a particular color or gray value. A variety of different color scales are available.





Configuring Color Scales

Up to 6 color scales can be made available for use. The colors can be chosen from a list available in the *Service Menu*.

- 1. Left click desktop and select, Service > Service Menu
- 2. From the *Service Menu* select, *Configure Color Scales* The following menu is displayed:

The first one selected will be the default primary scale. The second will be the default secondary scale.

- r. Reset default color scales
- u. Undo the most recent change
- 1. 10band_scale
- 2. CEqual_scale
- 3. GEM_scale
- 4. SUV1_scale
- 5. SUV2_scale
- 6. SUV3_scale
- 7. contour_scale
- 8. grey_scale
- 9. inverse_grey_scale
- 10. rainbow1_scale
- 11. rainbow2_scale
- 12. thermal_scale
- 0. Exit

Enter at most 6 color scales by number (the first number entered corresponds to the default primary scale; the second number entered corresponds to the default secondary scale). Alternatively, type \mathbf{r} to reset to the default color scales. An undo feature is available to back up to the previous setting via the \mathbf{u} key.

Once a new set of default color scales has been chosen, quit the Color Scales window (if necessary) via the *Quit* button. Then start a new *Color Scales* window by choosing *Color Scales* from the right mouse button.

Note: The configuration process must be done on each workstation individually.

Controlling Color Scales

The selected color scale can be inverted and the range from the minimum to the maximum value can be displayed using a linear, square, square-root or arbitrary power relationship.

The Square function greys twice as fast, giving it a power of 2.0. The Square root function greys half as fast, giving it a power of 0.5.

The minimum and maximum values can be changed by depressing the left mouse button on the value and dragging the cursor. Once the minimum and maximum values are selected, the range can be moved by depressing the right mouse button and dragging the cursor up or down the scale.

Use of the Color Scale:

From the Scale Menu, under Display, click the word *primary* to change the colorscale to the first color in the list of scales. Click *secondary* to enlarge the secondary color scales. To view both the primary and secondary scales, click *both*. The primary scale appears larger and on top of the secondary scale. *Invert* changes the physical relationship of the colorscales by placing the primary scale beneath the secondary colorscale.

The inverse mode will inverse any color.

To change any scale, click the *color*, then *option* then on the *colorscale*, either *primary* or *secondary*. If only one colorscale is chosen (not *both*) the color changes automatically.

SUV Scaling

When viewing an image with SUV Scaling, note that the pixel intensity ranges from 1 to 255, while the color scale range is 0 to 10. Because of this, any pixel intensity value equal to or greater then 10 is assigned to the upper limit color scale value (i.e. 10). Therefore, using the ROI application, it is possible to statistically evaluate a region with a min, max, mu, and Sd all above 10, while the entire region visually remains the color assigned to a value of 10 on the color scale.

See Standardized Uptake Value (SUV) Chapter.

Chapter **11** PETVIEW - IMAGE DISPLAY

The image display program can be set to various default options as selected by the user. At the time of installation the four display options are:

- Display Brain
- Display Cardiac
- Display Whole Body
- Display Sinogram

In each instance the same program is invoked, but with different preset parameters. These parameters are configured by Customer Support. Once the program has been invoked, the user can readily switch display modes to different presentations, such as transverse, sagittal, or coronal; and different zoom values, etc.

A powerful display feature is the ability to vary slice thicknesses, slice-to-slice spacing, and location of the displayed slices in real time, without requiring a new reconstruction from the raw data. Furthermore, the display adjusts the vertical image display size to accommodate the rectangular format of coronal or sagittal whole body displays to make optimal use of the available screen area.

Display Image

The display of whole body images presents special display conditions, which require a flexible display format. A whole body study may consist of several hundred transverse images, which can be displayed as transverse, sagittal, or coronal views. This permits the viewer to obtain an easy overview of a very large amount of data. It is also possible to display a transverse, sagittal, and coronal view simultaneously in order to establish the correlation and location of a structure in all three dimensions.

The program initially loads the last image from memory (the most recently loaded image), and displays coronal slices with a default zoom value of 1. Different default values can be installed by Customer Support. A new image may be selected by using the following procedure.

1. From *File Management* double click the desired Patient Study

The Study Files window is displayed listing the images currently loaded to memory

2. Double click the desired image

The new image is displayed. The image size in the coronal and sagittal views is

adjusted automatically to display all slices of the selected study. The information panel at the bottom of the window is updated to reflect the correct information.

Set Zoom and Projection Option

3. Click *Zoom* in the command bar, then select *Zoom* x 1.5

This enlarges the image size

4. Click *View* in the command bar and then *Three-Row TSC*

The display shows one row of transverse, one row of sagittal, and one row of coronal views to allow the viewer to see an overview of all the patient data at the same time

5. Use the slider bars on the right side of the display or use the cursor to move the crosshairs in the individual images to view different images. Zoom x 1.5 reduces the number of images which can be displayed simultaneously, but is useful for a detailed look at fine structures.

The available zoom ranges are: 0.5, .75, 1.0, 1.25, 1.5, and 2.0.

Select Slice, Thickness, and Increment

- 6. To change the slices displayed on the screen, click *Slice* either on the right side or the bottom of the display and click on one of the three choices, i.e. *Slice, Thickness* or *Increment (Frame* can only be used with dynamic studies). This changes the function of the scroll bar
- 7. Drag the slider to a new location with the mouse on the slider, or click in the triangular arrow on the right and left side of the slider bar.

The numerical value displayed is for information only, the value can not be change by overtyping. Note there is some lag between the time one of the arrows is clicked and the time the display has been completely refreshed. Rather than clicking several times on the arrows in quick succession, it is usually faster to move the slider bar to the new desired value. Clicking the mouse while the pointer is positioned in the area between an arrow button and the slider increments or decrements the setting by a larger amount then the arrows.

8. To achieve good typical parameters for a whole body scan in the coronal view, select a starting Slice of *170*, a Thickness of *16* and an Increment of *8*.

Since the transverse matrix size is 144 x 144, there are a total of 144 possible coronal views. Since the display can show approximately 24 slices simultaneously (depending upon the scan length), it is important to select slices spanning the whole body from anterior to posterior with a small enough slice-to-slice spacing to assure that small structures are not missed. An Increment of 8 reduces the total number of slices from 144 to 18. A starting slice of 170 eliminates the most anterior views, which are usually outside the body. In order to improve the statistical information in the images, i.e. make the images less noisy, images can be added by changing the thickness. If the thickness is made too large the contrast is reduced. Since the thickness can be changed easily, select different thicknesses and observe the effect on image noise and contrast.



Figure 11-1 Whole Body Scan Window

9. To make it more convenient to switch back and forth between Slice, Thickness, and Increment, use the F1,F2 and F3 function keys on the keyboard.

The slice, increment, and thickness settings are reflected in the bottom right hand corner of the display.

Thickness

It is important to remember that the whole body study is acquired in 4mm thick slices and the numbers represent millimeters. The numbers in the lower right hand of each frame reflect the setting for that frame. For instance, the whole body display program loads the images in the coronal cuts beginning at 170. The frame numbers read 170-182 and this frame is 16mm thick because slice 182 was acquired 4mm thick:

	170-	-182		
Slice	170 (#shown in display)	174	178	1 82 (#shown in display)
	171	175	179	183
	172	176	180	184
	173	177	181	185

Increment

Increment can best be stated as overlap. This parameter shows the millimeters of overlap between frames. The default is set at 8mm.

Slice	170	174	178	182	186	190	194	198	202	206
	171	175	179	183	187	191	195	199	203	207
	172	176	180	184	188	192	196	200	204	208
	173	177	181	185	189	193	197	201	205	209

Display Menu Commands



Figure 11-2 Display Image Window

File

- Select File 1
- View File 1 Headers
- Print
- Exit

Select File 1

1. From the *Display Image* window select *File > File 1*

The Select Image window is displayed listing the images currently loaded to memory

– Select Image 1	
Images	
Lung_with_liver_met.img	
AbdominalCa.img	
Ka_melanoma.img	
p0s1_demo4.img	
Load Method Sequ	ence 😐
Lower Threshold	0 %
Upper Threshold	101 %
Select Apply	Cancel

Figure 11-3 Select Image Window

- 2. Highlight the desired image in the *Select Image* window
- 3. Select the desired parameters which are listed and described below.

Load Method

- Sequence
- Slice
- File
- SUV Scale

The images or sinograms may be loaded by scaling them to the maximum value of the selected *Sequence* of images, the maximum value in each *Slice*, the maximum value of the whole data set *File*, or so the color scale values represent the *SUV Scale*. In which case the minimum and maximum are set to 0 and 10 respectively. To view the data as sagittal, coronal, or oblique images, the data should not be normalized to *Slice* to avoid artifacts. Loading data scaled to the image maximum allows the maximum detail to be seen in all the images. However, relative intensities between images are then meaningless.

Lower and Upper Threshold

In order to reduce the effect of 'hot spots' (such as the bladder) in an image, or to examine certain parts of the image in more detail, the minimum and maximum value can be adjusted by specifying a lower and upper threshold percent via the slider bars. The default values are set to 0 for the lower threshold and 100 for the upper threshold.

Setting the lower threshold value below 0 permits the user to examine negative values which can be obtained in the images if filtered back projection reconstruction is used. Setting the lower threshold value above 0 eliminates background; this feature is particularly important when CT images are used to register with the PET images.

Setting the upper threshold below 100 eliminates 'hot spots' such as the bladder and avoids loss of contrast in areas of low uptake, particularly in tumor studies. Setting the upper threshold above 100 avoids saturation in the color scale and makes it easier to visualize small intensity differences in the areas of highest uptake.

If SUV values are not desired, loading a whole body with an upper threshold of 30-50% and loading Brain scans at an upper threshold of 110-125% should be sufficient in most instances. When loading by the SUV scale, the program automatically defaults to 100% and it cannot be changed.

4. Click Apply when parameters are set.

The Display Image window appears.

View File 1 Headers

A large number of parameters are stored with the image files, which can be viewed by selecting *File* > *View File 1 Headers*

Parameters which are constant for all slices are typically stored in the *Mainheader*, while data which may change from slice to slice or from frame to frame are typically stored in the *Subheader*.

Exit

Terminates the application.

View

Images can be viewed in a number of different orientations which are listed below.

- Transverse
- Sagittal
- Coronal
- Projection
- Rotating/TSC
- Three-Row TSC

- Annotation
- Hide Patient Information
- File 1 Color Scale

Transverse/Sagittal/Coronal

Selecting *View* > *Transverse, Sagittal* or *Coronal* the whole screen is filled with images in the selected orientation. The vertical image size of the coronal and sagittal views are adjusted automatically to display all slices of the selected study. The size of the images can be adjusted as described below under *Zoom*.

Projection

Select *View* > *Projection* to view the data set from different angles using a depth weight which emphasizes prominent structures near the proximal surface. Using the scrollbar menu near the bottom of the window, different functions can be selected, namely *Angle, Depth Weight, Increment or Frame* (for dynamic studies). Typically a starting angle of 0 and an increment of 6 or 9 shows a sufficiently large number of angles simultaneously. This view is well suited for printing an image for the referring physician. For visual interpretation at the workstation the *Rotating/TSC* view is typically preferred.



Figure 11-4 Projection Window

Rotating/TSC

Selecting *View* > *Rotating/TSC* displays a window which combines a rotating depth weighted display with a single Transverse, Sagittal, and Coronal image. Each pixel in the rotating 2D view is the maximum value of a depth weighted projection through the data volume.

Depth weight shows fading as a function of distance. For example, the sternum and spine may be difficult to differentiate in the anterior and posterior views due to the appearance of superimposition. By manipulating this function, one structure may become more pronounced relative to the other. The *Start (Stop)* button displays the projection views for all pre-computed projection angles either in a clockwise or counterclockwise direction, which is controlled with the toggle button next to the *Start (Stop)* button. Often it is also useful to rotate the image manually by first Stopping the rotating display and then manually moving the *Angle* slider bar back-and-forth.

Note the first time the projection is rotated 180 degrees, the pixel values are calculated. Once the projections are calculated, the display rotates optimally.

The direction of the arrow corresponds to the direction the projection is viewed from. It is as if the arrow originates from the projection's *Point-of-View* and travels through the object being viewed in the image.

The starting angle, speed, and depth weight of the rotating display can be changed via the scrollbar menu beneath the rotating image. These features can also be selected via the **F5**, **F6**, and **F7** function keys, respectively. In addition, each image has a set of marker lines at the periphery. These indicate the location of the corresponding slices in the perpendicular direction. By clicking near the marker line and keeping the button depressed, the marker line can be moved and the corresponding perpendicular slice is displayed. For example, by clicking the horizontal marker line in either the coronal or sagittal view and dragging it vertically up, the transverse slice is moved towards the head.

By clicking near the intersection of the vertical and horizontal marker lines, both can be moved simultaneously as a cross hair. It is often convenient to scroll through the coronal images by clicking and holding the arrow next to the *Slice* slider bar.



Figure 11-5 Rotating/TSC window

Three-Row TSC

Selecting *View* > *Three-Row TSC* displays one row each of Transverse, Sagittal, and Coronal images. Each image has its own scrollbar, which allows the slice and thickness to be adjusted in the same manner as described above.

In addition, each image has a set of marker lines at the periphery. These indicate the location of the corresponding slices in the perpendicular direction. Clicking near the marker line and keeping the mouse button depressed, the marker line can be moved and the corresponding perpendicular slice is displayed. For example, by clicking the horizontal marker line in either the coronal or sagittal view and dragging it vertically up, the transverse slice is moved towards the head.

Clicking near the intersection of the vertical and horizontal marker lines, both can be moved simultaneously as a cross hair. For example, if one of the displayed images shows a tumor, the cross hair can be moved to its center and the two perpendicular views are displayed.



Figure 11-6 Three-Row TSC Images Display

Note the marker line has a perpendicular line at its end; the length of this line indicates the thickness of the corresponding perpendicular slice.

Annotation

Orientation annotations are displayed along the top, bottom, left and right of the first image in the whole body display window. The extent of these annotations are controlled by Selecting *View* > *Annotation* from the drop-down menu. Three choices are available:

- Full contains annotations such as ANT, POS, RIGHT, LEFT, HEAD and FOOT
- Abbreviated annotations are displayed as *A*, *P*, *R*, *L*, *H* and *F*
- Off option results in no orientation annotations displayed

In *Transverse, Rotating/TSC* and *Three-Row TSC*, cardiac annotation and data orientations are automatically used if the dataset was processed by the *Cardiac Oblique* program. The *Short Axis, Vertical Long Axis*, and *Horizontal Long Axis* annotations are used in place of *Transverse, Sagittal*, and *Coronal* annotation labels, according to the nomenclature agreed to by the American Heart Association, the American College of Cardiology, and the Society of Nuclear Medicine.

Info Utility

Info Utility is a tool for user annotation.

- 1. On the SVR Workstation desktop, left click and *Select Utility > Info Utility*
- 2. Add text. To make changes to the text
- 3. Click right in the *Info Utility* box and an additional menu appears allowing the following changes to be made:

Font: Helvetica, Courier, Times, or Fixed

Style: Medium or Bold

Size: Tiny, Small, Medium, Large X-Large or Huge

Borders: Show Shadow or Hide Frame

- Colors: Black on White, White on Black, Green on Black or White on Blue
- To change the name on the main window bar contact Customer Service

Note: If border hide frame is executed, press ALT & F-7 to move the box.

Hide Patient Information

At the bottom of the Whole Body Display window the following patient information is displayed: file name, the date of data acquisition, patient name, birth date, and the ID number of the patient. This information is retrieved from the header associated with the images. Select *View* > *Hide Patient Info* from the drop-down menu to remove the patient information from the display. The data can be presented to an audience while preserving patient confidentiality. Select *View* > *Hide Patient Info* a second time to redisplay patient information.

File 1 Color Scale

The Whole Body Display program allows the images to be displayed with either the Primary or Secondary color scale. This feature is useful for displaying a data set in the optimum color or gray scale with adjusted background subtraction and contrast. The default color scale is Primary. The Color Scale can be changed by toggling either the *Primary* or *Secondary* options in the *View* > *File 1 Color Scale* drop-down menu.

Zoom

Images can be viewed in a number of different sizes selecting on Zoom > xXX from the drop-down menu. Size constraints may be a factor when zooming TCS whole body images.

The possible options available for zoom are:

- Zoom x .5
- Zoom x .75
- Zoom x 1.0
- Zoom x 1.25
- Zoom x 1.5
- Zoom x 2.0
- Popup
- Spyglass
- Cine Loop

Zoom x .5, .75, 1.0, 1.25, 1.5, 2.0

Zoom x .5 - fifteen or sixteen images can be displayed in a horizontal row. For a normal whole body scan starting at the head and ending just below the bladder, three rows of images fit onto the display screen. This allows up to a total of 48 images to be viewed simultaneously.

Zoom x .75 - ten images are displayed in a horizontal row, and two or three rows of images fit onto the display screen for a normal whole body scan.

Zoom x 1 - eight images are displayed in a horizontal row, and two or three rows of images fit onto the display screen for a normal whole body scan.

Zoom x 1.25 - six images are displayed in a horizontal row, and two or three rows of images fit onto the display screen for a normal whole body scan.

Zoom x 1.5 - five images are displayed in a horizontal row, and two or three rows of images fit onto the display screen for a normal whole body scan.

Zoom x 2 - four images are displayed in a horizontal row. For a long whole body scan only a single row of images fit onto the screen. By reducing the number of slices which are loaded with the *Load* window, it is possible to reduce the vertical height of the displayed image so that two or three rows of four images fit onto the screen. Zoom x 2 is usually too big under normal viewing conditions if a single observer sits in front of a 20 inch display. Since the image is usually reduced when making a hard copy, zoom x 2 is a common format for making hard copies.

Popup

Individual images can be zoomed using *Zoom* > *Popup* option. Any image or set of images can be selected in any of the three sizes and arranged on the screen in arbitrary locations. This mode is particularly useful for comparing equivalent slices side-by-side and arranging images for slides.

The cursor changes to the shape of a hand. Move the cursor to a particular slice and click the mouse button. The selected slice is scaled as selected and can be moved and resized using the frame around the popped-up slice. Clicking anywhere in the popped-up image removes the popup window from the screen.

The entire *Popup* menu is disabled if *Spyglass* mode is active.

Spyglass

The **Spyglass** mode allows enlarging of a section of the image. This is particularly useful for cardiac imaging, where a large transverse field-of-view is usually selected, but the organ of interest occupies only a small fraction of the field diameter. The spyglass mode allows a magnifying window to be positioned anywhere on any of the slices. When the mouse button is pressed, all slices are magnified without changing the overall size of the displayed window. To return to normal slice sizing, the **Off** option from the **Spyglass** menu can be selected.

When Spyglass mode is active, the **Popup** and **Cine Loop** options from the **Zoom** menu are disabled. If the zoom factor is set to 2 or greater, only the **Spyglass x 2** factor is enabled. In zoom x 1 and x 1.5 modes, either **Spyglass x 2** or **Spyglass x 4** can be selected.

Cine Loop

If the image set which has been loaded is a multi-frame study, such as a gated cardiac study, then any selected image can be viewed in cine mode.

1. Select *Zoom > Cine Loop* and a magnification of 1, 2 or 4

The mouse pointer changes to a hand shape

2. Select a specific image and a cine window is displayed

In the cine mode the speed can be selected using a slider bar. The frame being displayed can also be controlled manually via the slider.

Tools

Dual Study/Registration

The Dual Study/Image Registration feature has extensive properties and is therefore described in a separate chapter. It is useful for side-by-side comparison of attenuation corrected and non-attenuation corrected images or alternately before-and-after treatment PET images.

Dual Study display and Image Registration with Fusion is an adjunct feature of the Whole Body Display interface. A second data set is displayed next to the first data set that can be rotated, translated, and fused with the first data set. If the second data set is a non-PET imaging modality such as MRI or CT, it must already have been translated from DICOM to PETVIEW-readable format using *DICOM Translate* and loaded via the *Load* program.

When the second set of images is displayed, its slice number is automatically aligned with the first data set. The image view, zoom factor, and slice number of the two data sets are correlated. The slice thicknesses, slice increment and color scales of the two data sets are decoupled.

Contrast Enhancement

The *Contrast Enhancement* mode is a powerful technique for visualizing 3-D structures in a coronal display. It is currently implemented for coronal images only.

Select *Tools* > *Contrast Enhancement* from the drop-down menu, a second tool bar appears which allows the contrast, slice thickness, and increment to be adjusted.

Note: The thickness and increment items in the scrollbar menu in the lower right corner are disabled since these controls are now in the contrast tool bar at the top of the window.

The default slice thickness in the contrast enhancement mode is set to 40 mm, which would normally result in low-contrast images. By selecting a high contrast, however, areas of increased radioisotope uptake are enhanced, thereby preserving the high contrast of thin slices, while at the same time allowing the visualization of structures such as blood vessels and intestines which frequently extend in the anterior/posterior direction.

If the contrast is set to zero and the slice thickness is reduced to a small value, the contrast enhancement feature is essentially turned off. By changing the contrast and slice thickness, different aspects of the data set can be enhanced.

DICOM Snapshot

If the DICOM option is installed in your system, a snapshot of the images can be sent as they appear in the *Wholebody Display* window to a DICOM recipient elsewhere on the network. The start of the snapshot is indicated by a beep; two beeps announce the completion of the snapshot (note: these 3 beeps may sound more like a single beep on certain systems). The snapshot is converted into a DICOM image and sent to the DICOM server specified in a configuration file. If there is more than one DICOM recipient, a dialog box presents choices. The user can select the destination and click *OK*, double click the destination, or press *Cancel* to abort the snapshot.

The type of DICOM image that is sent is Secondary Capture modality. This modality basically indicates that the image is a screenshot rather than a 3D volume of image data. Its further use is typically limited to viewing the screenshot, printing it as some later time, and archiving it. The orientation, slice numbering, and patient information seen in the window cannot be changed.

Other Display Parameters

In order to change the slices displayed on the screen, click on the pull down menu displayed either under or next to the images and click on one of the four choices, i.e. *Slice, Thickness, Increment*, or *Frame*. This changes the function of the scroll bar located next to or below the drop-down menu. The slider can be moved to a new location by dragging it to a new location, or by clicking in the triangular arrow on the right and left side of the slider bar. Clicking while the pointer is positioned in the area between an arrow button and the slider increments or decrements the setting by an amount larger than the arrows. The numerical value displayed is for information only, the value can not be changed by overtyping.

In order to make it convenient to switch back and forth between *Slice, Thickness, Increment*, and *Frame*, use the **F1**, **F2**, **F3**, and **F4** function keys on the keyboard instead of the drop-down menu. These "accelerator" keys are listed in the drop-down menu to the right of their respective commands.

Slice determines the first slice displayed in the window. The slice displayed consists of one or several of the reconstructed slices depending upon the *Thickness* parameter. The *Thickness* value determines how many of the reconstructed slices are added at the time the images are displayed. Note that slice adding is also possible during reconstruction. Adding slices during the display is independent of and in addition to any slice adding in the reconstruction program. Slice spacing is controlled by selecting *Increment*.

The following is a list of default options that can be customized on the C-PET system:

- Slice thickness
- Increment
- Default image display
- Starting slice number for the following views:
 - Transverse
 - Coronal
 - Sagittal
 - Three row TSC
 - Projection
 - Rotating projection

- Zoom
- Annotations on or off, full or abbreviated
- Cinemode display in milliseconds
- Depth weight
- Dual study image thickness
- Dual study magnification
- Contrast enhancement threshold

Printing

Currently, the following printers are supported:

- Codonics NP 1660
- Kodak 8100, 8300, 8500, 8700
- Helios 810
- Optima 850
- All HP Laser Compatable (postscript)
- All RP/IP Postscript Printers

DICOM Printers

- AGFA DRYVIEW series
- AGFA DRYSTAR 3000
- AGFA DRYSTAR LP400 (sterling)
- All printer that are DICOM 3 compliant

Print a Single Image

- 1. After the image is on the screen, right click the desktop and select, *printing* > *printer*
- 2. The cursor turns into a "+". Place the "+" in the window to be printed
- 3. Click the window, a double beep sounds
- 4. The image has been sent to the printer

Print Multiple Images

This can be accomplished 2 ways.

- 1. Open all images to be printed
- 2. Right click the desktop and select, *printing > printer*

- 3. The cursor turns into a "+". Place the "+" in the window to be printed
- 4. Click the window, a double beep sounds
- 5. This essentially performs a screendump to the printer.

or

- 1. Open an *Xterm window* and use it as a canvas
- 2. Place the images to be printed on top of the Xterm window leaving just enough space to click the "+" sign in the Xterm window, not the background or image windows
- 3. Click left and a double beep sounds
- 4. The images have been sent to the printer

Screendump to a Floppy Disk

Note: TIFF files do not work on this software version.

- 1. Left click desktop and select, *Select Utility > Mount Floppy*
- 2. Open the image
- 3. Left click desktop and select, *Screendump* > *TIFF file*
- 4. The File Selection Window is displayed. In the Output box, type: /floppy/floppy0/<filename>.tif



Figure 11-7 File Selection Window

- 5. The cursor turns into a "+"
- 6. Place the "+" in the window to be screendumped and click, a double beep sounds
- 7. Left click desktop and select, *Utilities > Unmount Floppy*

Load Image

This procedure loads images or sinograms and sequences of images from the disk into memory for later display and analysis. Images being loaded are normalized either to the maximum of each image or to the maximum of a sequence of images. It is important to realize that the images on disk are stored as 16 bit signed integers, after loading the data, they are stored in memory as 8 bit unsigned data. Negative values are eliminated. For quantitative analysis the Region-of-Interest (ROI) and Profile modules use the 16 bit data on disk.

To load images:

- 1. Highlight the patient in the *File Management* window
- 2. Select *Petview* > *Load Image* from the drop-down menu
- 3. The *Load* window is shown below.

-		Load 8.0		· [
Exit	Memory			Help
1 Law	0/nationt/n0	/a1		
^{7 sun}	of pactency po,	, s ц		
Abdon	ninalCa			
Cardi Ka me	lac			
Lung_	with_liver_m	et		
norma	l-brain l-brainOBL			
	Load	Directory	Expand Path	1
		_		
	Image 🗕	1	Sequence 🗖	
		-		
	Slices	Tilts	s Frame	s
0		0	0	
Bee	jín	Begin	Begin	_
0		0		
	<u> </u>	y a the		
Enc		End 0	End	
		ন ৰাইক	D aŭ	
In	rement	Incien	ient Incien	ent
4			86	
Low	ver Threshold	(%) Ur	oper Threshold	(%)

Figure 11-8 Load Window

Memory

Up to 15 images can be read into memory at the same time. By deleting all unnecessary image sets, system performance is optimized.

- 4. Click *Memory, List of Loaded* files is displayed as shown below. Listed are all loaded files which can be delete
- 5. To delete a file, highlight the name and click *Unload* or double click the name.

- Memory
Items
c046-p557s0_boc-br.img
p2052s0_clf3682_wbp1.img
p2052s0_c1f3682_nkp1.img
Selection
2052S0_CI13682_nkp1. mq
Unload Ouit

Figure 11-9 List of Loaded files

Load

Once all the loading parameters are set properly as described below, click *Load* to perform the Load function. Load Reads the data from disk to memory but does not automatically display the selected data set.

Directory

A particular directory can be selected in which the data are stored. All data from a particular patient are stored in the same directory and a patient's directory is selected automatically if the Load module is invoked from the *File Management* window. Clicking *Directory* updates the list of files being displayed; if any new files have been added since the *Load* window was invoked, they are displayed.

Expand Path

The full directory path of the selected image is displayed.

Image/Sinogram

By default, the load window is invoked in *Image* mode. This means that all files shown are reconstructed images. Toggle to *Sinogram*, the displayed files are sinogram data.

Scaling

The scaling selections are:

- Sequence
- Slice
- File
- SUV Scale

The images or sinograms may be loaded by scaling them to the maximum value of the selected *Sequence* of images, the maximum value in each *Slice*, the maximum value of the whole data set *File*, or the color scale values represent the *SUV Scale*, in which case the minimum and maximum are set to 0 and 10 respectively. If it is desirable to view the data as sagittal, coronal or oblique images, the data should not be normalized to *Slice* to avoid artifacts. Loading data scaled to the image maximum allows the maximum detail to be seen in all the images. However, relative intensities between images are then meaningless

Slices, Tilts, and Frames

After selecting a file, the range of the associated images or sinograms is displayed. The user either can load the whole sequence or select a particular starting and ending *Slice*, as well as a different increment. For dynamic studies the appropriate frames can be selected for loading.

The *Tilt* parameter applies only to sinograms and is not applicable to images. The sinogram data are acquired in such a way that axial tilt angles are preserved. When viewing sinogram data, a particular tilt angle can be selected for loading and viewing.

Since files often consist of tens of Mbytes, particularly in dynamic and whole body scan files, loading all slices, tilts, and frames can be very time consuming. Normally only a single tilt angle and frame is selected for loading to reduce the time to load the data.

Lower and Upper Threshold

In order to reduce the effect of 'hot spots' (such as the bladder) in an image, or to examine certain parts of the image in more detail, the minimum and maximum value can be adjusted by specifying a lower and upper threshold percent via the slider bars at the bottom of the *Load* window. The default values are set to 0 for the lower threshold and 100 for the upper threshold.

Setting the lower threshold value below 0 permits the user to examine negative values which can be obtained in the images if filtered back projection reconstruction is used. Setting the lower threshold value above 0 eliminates background; this feature is particularly important when CT images are used to register with the PET images.

Setting the upper threshold below 100 eliminates 'hot spots' such as the bladder and avoids loss of contrast in areas of low uptake, particularly in tumor studies. Setting the upper threshold above 100 avoids saturation in the color scale and makes it easier to visualize small intensity differences in the areas of highest uptake.

If SUV values are not desired, loading a whole body with an upper threshold of 30-50% and loading Brain scans at an upper threshold of 110-125% should be sufficient in most instances. When loading by the SUV scale, the program automatically defaults to 100% and it cannot be changed.

Reconstruct Sinogram

- 1. From *Study Files* window select *PetView* > *Reconstruct Sinogram* from the drop-down menu
- 2. The Reconstruction Interface is displayed with the Input Sinogram selected from the file list automatically appearing in the text field.
- 3. The output image file also is automatically defaulted by changing the **.scn** extension on the input file to **.img**

If this output file already exists, the Reconstruction Interface displays a warning. Only one file from the file list can be selected for reconstruction, and it must be type **SCN**.

If the Reconstruction Interface has a problem getting the input filename from the file manager, it is displayed but the *Input Sinogram* file field is blank.

12 DUAL STUDY / REGISTRATION

Dual Study display and Image Registration with Fusion is an adjunct feature of the Whole Body Display interface. A second data set is displayed next to the first data set that can be rotated, translated, and fused with the first data set. If the second data set is a non-PET imaging modality such as MRI or CT, it must already have been translated from DICOM to PETVIEW-readable format using *DICOM Translate* and loaded with the *Load* program.

When the second set of images is displayed, its slice number is automatically aligned with the first data set. The image view, zoom factor, slice number, and slice increment of the two data sets are correlated. The slice thickness and color scales of the two data sets are de-coupled.

It is useful for side-by-side comparison of attenuation corrected and non-attenuation corrected images, or image fusion before-and-after the treatment of PET images.

Dual Display

- 1. In *File Management*, double click a patient study
- 2. From the *Study Files* window highlight an image of interest
- 3. Select *PetView > Load Image* from the drop-down menu The Load dialog box is displayed.
- 4. From the *Load* menu, select the first image of interest, adjust the thresholds, click *Load*
- 5. From the Load menu, select second image of interest, adjust the thresholds, click Load
- 6. Right click on desktop and select *Display Whole Body* The last image loaded is displayed first.



Figure 12-1 Load Dialog Box

- 7. Select *Tools -> Dual Study/Registration* from the drop-down menu
- 8. The Select Image window is displayed, double click the second image to be displayed

– Select Image 1
Images
Lung with liver met.img
AbdominalCa.img
Ka_melanoma.img
p0s1_demo4.img
Load Method Sequence =
Lower Threshold 0 %
Upper Threshold 101 %
Select Apply Cancel

Figure 12-2 Select Image Window

- 9. Toggle the Slice button to match the *thickness* and *increments* of the images using the slide bar
- 10. If the image display is not symmetric, click the large bold arrows on the bottom of the image display. This adjusts the number of viewports on each side of the bold dividing line
- 11. To resized entire box, place the curser on the right or edge of the image box and left click. A small dialog box appears showing the dimensions of the box. For example, a dialog box stating 4 x 3 would imply there are 4 boxes across and 3 boxes down. It is easiest to view the dual display box in an even number of viewports across.
- 12. It may be useful to set the first loaded image to the primary colorscale and the second image to the secondary colorscale. This allows independent control of the relative intensities. To have both images the same color, match the color of the primary and secondary colorscales (the secondary colorscale is manually changed).



Figure 12-3 Dual Study Window

- 13. At the top right corner of the *Dual Study* window, toggle the *Fusion Off* button to *Fusion* ON
- 14. Translate to manually align the images (see *Aligning Images*, ahead in this chapter)
- 15. Select *View -> Three Row TSC* from the drop-down menu to align images simultaneously in all planes.

Dual Image Manipulation

In the Dual Study Screen, images can be viewed in a number of different orientations. Changing the View results in the same change for both data sets as described in the *PetView-Image Display* chapter.

- By selecting *View* > *Transverse*, *Sagittal*, or *Coronal* the whole screen fills with images in the selected orientation. The vertical image size of the coronal and sagittal views adjusts automatically to display all slices of the selected study. The displayed slices and their thickness can be adjusted as described below.
- By selecting View > Three-Row TSC, one row of transverse, sagittal, and coronal views is displayed for each of the 2 data sets. Each row has its own scrollbar which allows the slice, thickness, and increment to be adjusted. Adjusting the slice number causes the slice to change for both data sets. Adjusting the slice thickness affects only those slices in the data set and in the row selected.
- Tic marks in *TSC* mode are displayed to indicate the relative positions of the slices displayed in each view. The tic marks can be moved to change the current slice on the first (left hand) data set only. The corresponding slices of the second data set are changed automatically.
- It is possible to view a larger number of images from either data set by clicking the arrows below the dividing line between the two data sets. This is particularly useful when PET images are being fused with either CT or MRI images as described below.

To change the slices displayed on the screen, toggle the *Slice* button at the bottom of the screen and select, *Slice, Thickness, Increment,* or *Frame*. This changes the function of the scroll bar located on the bottom of the window for Transverse, Sagittal, or Coronal views, or located next to each view in Three-Row TSC mode, or located beneath each view in the Rotating/TSC mode. Either drag the slider to a new location, or click the triangular arrow on the slider bar. The numerical value displayed is for information only.

To make it more convenient to switch between Slice and Thickness, you may use the F1, F2, F3 and F4 function keys. These keys are listed in the drop-down menu. Slice determines the first slice displayed in the window. The slice displayed consists of one or several of the reconstructed slices depending on the Thickness parameter. The Thickness value determines how many of the reconstructed slices are added at the time the images are displayed. Adding slices during the display is independent of and in addition to any slice adding in the reconstruction program.

Changing the Slice number changes the first slice displayed for both data sets. Changing the Thickness affects the thickness of only one data set. The Image Registration thickness value can be specified as resource **wbdIrThick** in the Wbd resource file so that the thickness defaults to a different value. A slice thickness of 1 slice greatly increases the speed of the rotation and translation transformations. If no **wbdIrThick** thickness value is specified, it defaults to 1. To change the thickness of the registered image, contact Customer Support.

Zoom

Images can be viewed in a number of different sizes. Size constraints may be a factor when zooming TCS whole body images. Five zoom options are available.

Zoom x .5 - twelve images (six from each data set) can be displayed in a horizontal row. For a normal whole body scan starting at the head and ending just below the bladder, 4 rows of images fit onto the display screen. This allows a total of 24 images to be viewed simultaneously from each data set.

Zoom x .75 - ten images are displayed in a horizontal row, and three rows of images fit onto the display screen for a normal whole body scan.

Zoom x 1.0 - eight images are displayed in a horizontal row, and three rows of images fit onto the display screen for a normal whole body scan.

Zoom x 1.25 - two images are displayed in a horizontal row. For a long whole body scan only a single row of images will fit onto the screen. By reducing the number of slices which are loaded with the *Load* window, it is possible to reduce the vertical height of the displayed image so that two rows of four images fit onto the screen.

Zoom x 2.0 - usually too big under normal viewing conditions. Since the image is usually reduced when making a hard copy, zoom x 2 is a common format for making hard copies.

Changing the Zoom in the Image Registration window results in the same change in zoom factor for both data sets.

Color

The two data sets may be displayed with either the Primary or Secondary color scale. This feature is useful for displaying a data set in the optimal color or gray scale with adjusted background subtraction and contrast. It also helps differentiate the two data sets when Fusion is enabled. The default color scale for the second data set is *Secondary*.

The color scale can be changed by toggling either the *Primary* or *Secondary* in the *File* drop-down menu.

Image Fusion

Aligning Images

The data set for the right side display can be manipulated to align with the data set for the left side display. *Translate, Rotate* and *Magnify* of the second data set is selected from the *Dual Study* window.

1. From the upper left corner of the *Dual Study* window select either *Triangulate, Translate, Rotate,* or *Magnify* from the drop-down menu.

2. The rotation and translation parameters can be changed by moving the sliders, clicking the arrows, or typing the desired value in the text field adjacent to the scrollbars and pressing <Enter>. When the parameter is changed, the data set is redisplayed with the new transformation.

The rotation range in the transverse, sagittal, and coronal planes is 360 degrees. The translation parameters are reported in mm. The range of translation in the lateral (right-left) direction and anterior-posterior direction is 50 times the slice thickness in each plane from the starting slice that is displayed. The translation range in the axial (head-foot) direction is 1536 millimeters, which is the full extent of a whole body scan.

3. The translation value in the axial direction takes into account the axial offset needed to align the center slices of the two data sets being registered and fused. If the two data sets are of different axial extend, it may be desirable to expand the axial dimension of the displayed window.

Select the *Expand Off* drop-down menu and select a desired extension of the axial field of view. This allows the user to always view the full extent of both data sets, even when they are shifted axially relative to each other.

Magnify/Reduce

Data sets of other imaging modalities may have pixel sizes that differ from PET pixel sizes. The images displayed in the right side of the display window can be rescaled to match the pixel size of the data set in the left side.

- 1. From the upper left corner of the *Dual Study* window select *Magnify* from the dropdown menu.
- 2. A slider bar is displayed which can adjust the pixel size by a factor between 0.0 and 2.0. This change in pixel size magnifies or reduces the images while the outer dimensions of the image remain the same.
- 3. When the magnification is changed, all slices in the dataset are magnified at once, so that subsequent rotations do not distort the image. The magnification factor can be specified in the Wbd resource file as resource **wbdIrMag**, so the magnification is performed when the image is loaded into the display program. To set the magnification, contact Customer Support.

Image Fusion

Image Registration parameters can be checked by fusing the data sets from the left side of the display window and overlaying it onto the right side of the display window.

- 1. From the upper right corner of Dual Study window toggle *Fusion Off* to *Fusion ON*
- 2. This results in the interleaving of the two data sets in the right side of the display window (or on the bottom for Rotating/TSC mode).

- 3. If the color scales of the two data sets are different, both will be visible simultaneously. The contrast of either color scale can be adjusted from the color bar to optimize the fusion, or to dim one or the other data set while in Fusion mode.
- 4. Once the *Image Fusion* is toggled, the two data sets are fused until the toggle is turned off.

The image fusion is active in a large number of Views in order to facilitate the visual alignment of the two data sets.

File Manipulations

A large number of parameters are stored with the image files, which can be viewed by selecting either *File > View File 1 Headers* or *View File 2 Headers*. Parameters that are constant for all slices are typically stored in the mainheader, while data which may change from slice to slice or frame to frame are typically stored in the subheader.

Registration Parameters

When a data set has been rotated and translated to fuse with another data set, the transformation parameters can be saved on disk to be retrieved later so the registration session can be replicated.

- 1. To save parameters to a file select *File > Registration Parameters >Save Parameters*
- 2. A dialog box is displayed prompting for the parameter filename. The default name is the data set name with **IR** appended to it and a **.par** extension.
- 3. If the name is OK, press <Enter> with the cursor in text field, or click OK. If the file name already exists, the system prompts to overwrite. *Save* can be canceled at this point and another filename can be specified by reselecting the *Save Parameters* option.

The parameters that are saved include: the name of the data set, the angles of rotation in the transverse, sagittal, and coronal planes, the center of rotation coordinates, the translation offset in the Lateral, Anterior to Posterior, and Axial directions, the magnification factor, and the slice thickness for the transverse, sagittal, and coronal views. The registered images cannot be saved.

- 4. Once a file is created, the image registration parameters can be retrieved by selecting *File > Registration Parameters > Read Parameters* from the drop-down menu.
- 5. A dialog box is displayed prompting for the parameter filename to be read. The default name that appears is the name of the data set with **IR** appended to it and a **.par** extension.
- 6. If the filename is OK, press the <Enter> with cursor in the text field, or click OK. The parameters are retrieved and the data set is redisplayed in the right side of the display window with the new parameters.

13 REGION-OF-INTEREST (ROI)

The ROI module is the most powerful quantitative analysis tool available for PET images today. It allows the definition and manipulation of regions, which exist only in a single slice; volumes, which are defined as several regions in adjacent slices; groups, which consist of all the regions in one selected slice; and an atlas, which consists of all regions and volumes in all slices.



Figure 13-1 Region of Interest Display

These entities can be moved, rotated, resized, annotated, deleted, and saved to disk. The underlying images can then be analyzed quantitatively by calculating the area, determining the maximum and minimum pixel, integrating all the counts within all regions and performing additional statistical analysis on the data. The resulting data are saved on a disk file so they can be further manipulated to calculate such quantities as concentration, metabolic rate, blood flow, etc. In counting the areas and volumes, partial pixel sizes are utilized for circular and elliptical regions to increase the accuracy for small regions. All manipulations such as moving, rotating, resizing, and counting occur fast enough to make the system truly interactive and user friendly.

ROI Procedure

- 1. Double click a patient file in *File Management*
- 2. In the *Study Files* window, Highlight an image and select *PetView > Load Image*
- 3. From the Load dialog, highlight image, adjust thresholds (if necessary), and click Load
- 4. Right click desktop and select Region of Interest
- 5. The ROI Window is displayed. The Max and Min. counts for the ROI and SUV values (if loaded by SUVs) are displayed in the dialog box. The following values are also displayed below image.

Mu: average cts/pixel Sd: standard deviation

- 6. Select drawing region: Ellipse, Circle, Square, Irregular, or Mirror
- 7. The red ROI is active. Clicking right in any ROI will activate it.

edit_single_popup
♦ Move ♦ Rotate ♦ Resize
Type ğ X 59.0 A 7.5 Volm ĭ1 Y 72.5 B 7.5
Label No comment entered
Quit

Figure 13-2 Red ROI

Drawing Regions

Different region shapes can be selected and drawn onto the selected image slice. If the region is not the appropriate size or not in the appropriate location, it may be moved, rotated, and resized using the *Edit* function described in this chapter.

After a set of regions are drawn onto a slice, they can be mirrored about a line of symmetry such as the brain midline.
Enter the drawing mode by clicking one of the symbols along the right side of the ROI window as shown in Figure 13-1.

Ellipse

- 1. Click the ellipse symbol on the right side of the ROI window
- 2. Drag the cursor in the direction of the major axis of the ellipse, when the line drawn is the appropriate length, release the mouse and move the mouse pointer to the middle of the line just drawn
- 3. Drag the pointer at right angles to the first line until the ellipse is appropriate size

Circle

- 1. Click the circle symbol on the right side of the ROI window
- 2. Drag the cursor in any direction, when the line drawn is the appropriate length, release the mouse

Rectangle

- 1. Click the rectangle symbol on the right side of the ROI window
- 2. Drag the cursor in any direction, when the rectangle drawn is the appropriate size, release the mouse

Irregular ROI (Polygon)

- 1. Click the polygon symbol on the right side of the ROI window
- 2. Drag the cursor in any direction. Click the mouse to create lines at desired locations. A polygon of arbitrary shape may be drawn
- 3. When the last point is very near the beginning point of the polygon, the polygon is closed automatically. Alternately, the polygon may be closed by moving the mouse (not dragging it, i.e., without depressing button) outside the image area.
- 4. There are no provisions for editing a polygon by cutting or redrawing sections of the polygon

Mirroring

Use this procedure to mirror all regions drawn about an arbitrary line of symmetry.

- 1. Click the mirror symbol on the right side of the ROI window (fifth symbol in the row)
- 2. As indicated in the message area, draw a line of symmetry by dragging it in the desired direction
- 3. Click anywhere within the image area and all previously drawn regions are mirrored about the line of symmetry

Menu Commands

Image

The program initially loads the most recently loaded image with a default zoom value of 1. If this is not the desired image, a new image may be selected (provided other images have been loaded to memory using the *Load* program).

- 1. From the *ROI Display* (Figure 13-1) select *Image > Select* from the drop-down menu
- 2. A dialog listing the images currently loaded to memory is displayed. Highlight the desired image and click *OK*
- 3. The new image is displayed, and the information panel at the bottom of the window is updated to reflect the correct information for the selected image.

Count

- Single
- All slices
- Single, all slices
- All slices & frames
- Single, all slices & frames
- All regions, all frames
- Count above threshold
- Count no 0

Counting regions includes determining the area, the pixel minimum and maximum, total counts within the region, and some statistical parameters such as standard deviation. If individual regions are counted, the results are displayed on the screen in the message area of the ROI window.

To count an individual region do the following:

- 1. Select the region by clicking the right mouse button near the region The region outline changes from green to red
- 2. Select *Count* > *Single* from the drop-down menu
- 3. If all regions are counted (selecting *Count* > *All slices*) they are written to a disk file The file name is the same as the image file name with the extension .cnt and is placed in the same directory as the image data.
- 4. After a set of regions are defined, they can be applied to all frames of a dynamic study without loading, and/or displaying individual frames by selecting *Count* > *All slices* & *frames*
- 5. This can result in a very large amount of data. To reduce regions of no interest to the user, additional choices have been added to the *Count* menu. For example, it is possible to only record regions in which the counts are not zero.

Counting is normally performed on the original data which are stored as 16 bit signed integers on disk. Only if the 16 bit data are not available are the 8 bit unsigned integers in memory used (the display indicates that this is happening and the resulting count file has an appropriate comment). Since negative values are eliminated in the process of reading the image data from disk, different answers are obtained from 8 bit data in memory and from 16 bit data on disk.

SUV (Standardized Uptake Value)

If the patient's weight and the particular time injected were entered during the data acquisition, then the reconstruction program calculates the SUV scale factor.

Clicking the *SUV* button on the right hand side of the *ROI Display* window, the Count function described above displays the SUV instead of the total counts within the ROI.

Edit

- Single
- Volume
- Group
- Atlas

F	e	dit_single_po	opup
	¢ Move	💠 Rotate	💠 Resize
Γ	ype įg	× 59.0	A 7.5
V	'olm į́1	Y 72.5	B 7.5
L	abel 🕅	comment en	tered
	Delete		Quit

Figure 13-3 Edit Window

To edit a single region or volume follow this procedure

- 1. Right click in the region or volume to be edited
- 2. Select *Edit* > *Region* or *Volume*
- 3. An *Edit* window is displayed. Select *move, rotate* or *resize* the selected region.
- 4. There are additional functions available when editing a single region; namely, enter a comment or change the *Type* using a single letter. For example, the regions may be labeled **g** or **w** to denote whether the region is a gray matter or white matter region in the brain. This information is stored in the region file but not displayed on the image.
- 5. To edit a group or a whole atlas, Select *Edit* > *Group* or *Atlas*
- 6. An *Edit* window is displayed. Select to *move, rotate* or *resize* the group or atlas.

Single

Individual regions can be moved, rotated, and resized. Even if the region is resized to a very small size, it can be enlarged to its original shape.

Volume

By copying 1 region to 2 or more slices, volumes are formed. Since the regions in each slice can be edited, the volume can have a variety of shapes and extend through an arbitrary number of slices. Once a volume has been defined, it can be moved, rotated and resized as a unit, i.e. all regions in all slices move, rotate and resize simultaneously. Note however, that resizing changes the size in the transverse direction only, not in the axial direction.

Group

Multiple regions on 1 slice represent a group and can be edited simultaneously without changing regions in adjacent slices even if they have been defined as a volume. This feature is useful if the regions and volumes have been previously defined, have been superimposed on a new data set, but the patient was tilted in the new study, i.e. different slices are not aligned axially with respect to the original data set.

Atlas

Multiple regions on multiple slices, rotated and resized together as an atlas. This allows a previously defined region set to be superimposed on a new patient study, even if the image data were not aligned. The whole region set can be shifted axially in both directions. Thus, for example, a region set defined on an MRI scan can be superimposed on a PET scan even though the two image sets have a different scale and orientation.

🔷 Move	💠 Rotate	💠 Resize
<regions<< td=""><td>>Regions></td><td>Quit</td></regions<<>	>Regions>	Quit

Figure 13-4 Move, Rotate, and Resize Window

Display

A number of display options are provided as part of the ROI module to facilitate quantitative analysis.

The image can be zoomed by a factor of 2 to make it easier to draw and see small regions.

- Zoom/Unzoom
- View
- Label

- Distance
- No Regions
- Annotation Off
- Hide Patient Info

Zoom

- 1. Activate an ROI
- 2. Select *Display* > *Zoom*

This is useful when resizing a circular ROI. The smallest circular ROI the unzoomed image allowed is 2 pixels. By zooming the image and resizing the ROI, a size of 1 pixel can be obtained.

View

A large number (12) of transverse images can be shown in the background with regions superimposed. To draw regions on sagittal or coronal views, the oblique sectioning program can be used to generate an independent sagittal or coronal image set which can be imported to the ROI module for ROI analysis in the selected orientation. The same obviously applies to short axis views or any other oblique section. Since all regions are shown on the images in the background after *View* has been selected, it is easy to observe the effect of region, volume, or atlas manipulation on the whole data set.

- 1. Activate an ROI
- 2. Select *Display* > *View*

12 transverse slices are displayed on the screen to allow the user to view the regions drawn on several slices simultaneously. The slices which are displayed in this background mode can be changed.

All selected images are displayed.

3. Click *Region* to toggle to a specified starting, ending slice and distance between slices which are different from the initial values.

For example, sagittal slices are normally calculated and displayed every 2 mm. This fine spacing results in 64 slices which do not fit on the screen simultaneously. By selecting the appropriate range parameters, the most important images can be viewed on the screen simultaneously.

4. To **Page** through very quickly, click either *Previous Page* **or** *Next Page* More images can be displayed more rapidly than by using the *Region* function

Label

Labels can be added to identify displayed regions. Since these labels often obscure the underlying image, they can be hidden, but are still part of the region definition and are included in the region file on disk. They cannot be displayed in the ROI programs.

Distance

The distance between any two points in the image may be measured.

- 1. Select *Display* > *Distance*
- 2. Click the starting point of the distance to be measured and dragging the cursor to a second point. The distance (in units of pixels) is displayed in the ROI window
- 3. Multiply number of pixels displayed in the dialog box by 4 for whole body scans, or by 2 for brain scans. The result is the distance in mm.
- 4. The display can be cleared by moving the mouse outside the image area

Regions/No Regions

The regions can be drawn or removed from the image for easier visualization of image data.

Annotation Off

Annotation off causes annotation to be shown on each of the display windows. Clicking *Annotation* again hides display annotation in each active display window.

Hide Patient Info

Hide Patient Info causes patient's name and ID number to be eliminated from the display window. Clicking *Hide Patient Info* again displays patient's name and ID number.

Input/Output (I/O)

- Region File
- Auto Save
- To Screen
- To Printer

Defining a set of regions and volumes can be a time consuming task. A defined region set can be saved to disk and subsequently read from disk to superimpose the regions and volumes on the same or a different study. The region definitions can be written to disk by the following procedure.

- 1. From the ROI display, select *I/O* > *Region File*
- 2. A dialog is displayed which allows the user to specify the destination directory and the filename for both reading or writing the region file. The region file can have any name selected by the user; the default value is the same name as the image file with the extension **.reg**

3. Click *Auto Save* to save region definitions in the default directory using the default name without the user verifying or changing the destination. As a future enhancement, the region definitions can also be written to the screen or printer.

Сору

- Single
- Group

A region or all regions can be copied from the currently selected slice to another slice.

- Select *Copy > Single* or *Group* In either case, the slider bar or arrows may be used to indicate the target slice to which the region(s) are to be copied
- 2. When copying is complete, the display switches to the target slice. In addition, single slices may be copied to any other slice by typing the target slice number in the area below the displayed image. In this mode, the display continues to display the present slice rather than the target slice.

To Copy an ROI

- Draw an ROI(s)
- Select Copy > Single or Group
- Click right on the sliderbar and hold mouse button. Change to the desired slice to copy to and when release. When the mouse button is released, the ROI will be copied.

Note: The **COPY** command must be chosen before each copy. The ROI does not stay in memory.

To Print Counts to a File from an ROI

- Click left on *Count* > *All regions, all frames*
- Press Save when the dialog box appears. This saves a .cnt file in the patient's file.

To Read Back a Saved .reg file:

- Click left on *I/O* > *Read*
- Choose the .**reg** file on the popup window

14 CARDIAC OBLIQUE RESLICING

This application is designed to perform an oblique re-slicing of cardiac image data. The image data is reoriented in accordance with two angle specifications which correspond to the angle the long-axis of the left ventricle makes with the z and x axes (patient head-to-foot and left-to-right axes respectively). These angles are entered by drawing lines along the long axis of the left ventricle in transverse and sagittal display windows. Both angles may be easily modified by grabbing the arrowhead of the angle line, and using the mouse to rotate the line to the desired new angle.

The three oblique views (short axis, horizontal long axis, and vertical long axis) are displayed, and the boundaries of the cardiac data volume may be specified by drawing boundary boxes in each of the three views. These boundaries allow cinemode display of the oblique views, and are used to save or export the re-sliced image data. These boundaries may also be modified by grabbing the boundary lines and dragging them to the new desired position.



Figure 14-1 Cardiac Oblique Reslicing

Window Display

The scroll bars below each of the display windows may be used to change the current slice being displayed in the corresponding window.

Cinemode

The *CINE* button at the bottom of each oblique display, when enabled, starts a cinemode loop in the corresponding oblique display. The cinemode function simply displays sequential slices from the start to the end slice as indicated by the entered boundaries. Because the cinemode function uses the oblique boundaries, the *CINE* buttons are not active when the application is initially run, but becomes active when the oblique boundary boxes are entered.

When cinemode is activated for a display window, the *CINE* button changes to a Stop button, which may then be used to stop the cinemode for the corresponding display.

Transverse and Sagittal Views

These windows allow entry and modification of a rotation angle and rotation origin (point about which the rotation is performed) by using the cursor. A new angle may be entered at any time by positioning the cursor at the desired position of the start of the angle indicator line, and dragging it to the desired ending point of the line.

Oblique Views

These windows allow entry and modification of boundary boxes, used to indicate the start and end boundaries during cinemode operation or oblique save and export.

Cardiac Image

The program initially loads the last image from memory (most recently loaded image), and displays the middle transverse slice in the transverse display window. A new image may be selected (providing other images are loaded to memory).

- 1. In File Management, double click a patient study
- 2. From the *Study Files* window highlight an image of interest
- 3. Select *PetView > Load Image* from the drop-down menu The *Load* dialog box is displayed.
- 4. From the *Load* menu, select an image of interest and click *Load*



Figure 14-2 Load Dialog Box

- 5. Right click on desktop and select *Cardiac Oblique Section* The image is displayed.
- 6. Select *Tools -> Dual Study/Registration* from the drop-down menu
- 7. The Select Image window is displayed, double click the second image to be displayed.
- 8. Using arrows or slide bar, choose the best slice to process
- 9. Click and draw a line from Base to Apex on Transverse and Sagittal window displays
- 10. Adjust line in center of ventricle and angles if needed
- 11. Click and drag to draw a box around the *Short Axis, Vertical Long Axis,* and *Horizontal Long Axis.* Adjust boxes if necessary.
- 12. Select *File > Save File/Export to memory* from the drop-down menu The system adds **OLBC** to the filename
- 13. Select *File* > *Exit* from the drop-down menu

Display Image

- 14. Right click on desktop and select Display Cardiac
- 15. Select Zoom > Spyglass > 2X from the drop-down menu and set box over cardiac tissue
- 16. Line up the images using the slice slider bar or triangulate on the image.

Recommendation on Display

Short Axis:

- Thickness = 12
- Increment = 12

Vertical Long Axis/Horizontal Long Axis:

- Thickness = 8
- Increment = 8

Display Windows

- Transverse
- Sagittal
- Horizontal Long Axis
- Short Axis
- Vertical Long Axis

Transverse Cardiac Angle

To set the Transverse Cardiac Angle perform the following procedure.

- 1. Position the cursor on the center of the cardiac base (open end) in the *Transverse* display window
- 2. Drag the mouse through the cardiac apex (closed end), a line follows the cursor. The angle of this line with the vertical axis is displayed at the base of the line. The angle is measured counterclockwise from the vertical axis.
- 3. When the line is extended through the cardiac apex, release the mouse. The line is redrawn with an arrowhead at the apex and has a small cross indicating the center of the line.

The center of this line is used as the origin of rotation for the oblique sectioning process. It should be positioned in the center of the left ventricle to obtain best results.

4. To adjust the position of the center, position the cursor on the cross and click. The cross is replaced by a full-window cross-hair, and the center (x,y) coordinates are displayed in the window. The center may now be adjusted by dragging the cursor to the desired position. The angle indicator reverts to the normal display mode.

- 5. The angle of the line may be adjusted in a similar manner by clicking the arrowhead of the line and rotating the line to the desired angle.
- 6. Once the transverse angle is set, the *Sagittal Display* window is updated to show a sagittal view rotated about the patient's head-to-foot axis (z axis). If the *Sagittal* display is already active (meaning a transverse angle has previously been set), and a sagittal angle has been set, the oblique windows are also updated to reflect the new transverse angle of rotation.

Sagittal Cardiac Angle

Perform the same steps as above (*Transverse Cardiac Angle*), on the *Sagittal Display* window to set the sagittal rotation angle. As above, the angle line should start at the cardiac base (open end), and extend through the apex (closed end). When this angle is set, the oblique views are updated to reflect the selected rotation angles (transverse and sagittal).

Oblique View Cardiac Boundaries

Once the transverse and sagittal rotation angles are set, the boundaries of the cardiac image must be set in the oblique views to enable the cinemode buttons.

1. Click in an oblique window (*Short Axis, Horizontal Long Axis, or Vertical Long Axis*) and drag the cursor across the cardiac area to draw a box enclosing the area.

This operation also results in boxes appearing in the remaining oblique display windows.

- 2. The sides of the boxes may be adjusted by dragging the cursor. This procedure should be used on each box so the boxes enclose the cardiac area of the display window.
- 3. The boundaries are linked in a manner such that adjusting boundaries in one oblique view causes automatic adjustment in the other two oblique views. This linked behavior is summarized by the following:
 - short axis and horizontal long axis left and right
 - short axis and vertical long axis top and bottom boundaries are linked
 - horizontal long axis top and bottom boundaries are linked to the vertical long axis left and right boundaries.
- 4. When the boundary boxes are set, the CINE buttons may be used to step through the slices of the oblique views. The sequence in which the slices are displayed start at the solid boundary line and end at the dashed boundary line. The boundaries control the start and end slices in the following manner:

Horizontal Long Axis View

The starting and ending slices for the horizontal long axis cinemode are determined by the top and bottom boundaries of the short axis or vertical long axis boundary boxes.

Short Axis View

The starting and ending slices for the short axis cinemode area determined by either the top and bottom boundaries of the Horizontal Long Axis boundary box, or the left and right side boundaries of the Vertical Long Axis boundary box.

Vertical Long Axis View

The starting and ending slices for the vertical long axis cinemode are determined by the left and right boundaries of short axis or horizontal long axis boundary boxes.

Save Oblique Views

Once the oblique views are activated (by setting both transverse and sagittal rotation angles), the oblique image data may be saved to a file or exported to memory by using the appropriate menu options in the File menu. These operations save a sequence of short-axis oblique slices, which may be viewed by the Cardiac TSC mode of the PETView Display program.

Menu Commands

File

- Select Image
- Save Oblique to File
- Export Oblique to Memory
- Exit

Select Image

To load a new image from the images loaded into memory, perform the following procedure.

- 1. Select *File > Select Image* from the drop-down menu
- 2. An *Image Selection* dialog is displayed, listing the available images
- 3. Double click the desired file. The selected image is loaded into the application, using the same angle and boundary settings from the previous image.



Figure 14-3 Image Selection Dialog Box

Save to File/Export to Memory

To save the oblique re-sliced image data to a file on disk and export the oblique resliced image data to memory perform the following procedure.

- 1. Select *File > Save to File/Export to Memory* from the drop-down menu.
- 2. A dialog is displayed that allows the user to change the file name from the default and provides the option of canceling the save operation.
- 3. This command executes after both rotation angles and oblique boundaries are set.

Export to Memory

To export the oblique re-sliced image data to memory but not to disk, perform the following procedure.

- 1. Select *File > Export Oblique to Memory* from the drop-down menu.
- 2. A dialog is displayed, which allows the user to change the image name from the default value, and provides the option of canceling the export operation.
- 3. This command executes after both rotation angles and the oblique boundaries are set. If the data are saved to memory only and not to a file, the resliced data is lost when logged out.

Parameters

- Store to Memory
- Recall from Memory

- Save to File
- Recall from File

Store to Memory

Store the application parameters (transverse angle, sagittal angle, and oblique boundaries) to memory for later recall.

Recall from Memory

Recalls the application parameters previously stored to memory by the *Store to Memory* command.

Save to File

Saves the application parameters (transverse angle, sagittal angle, and oblique boundaries) to a text file. This text file may be used to provide a record of the parameter settings, and to restore the parameters by selecting *File* > *Load* command.

Load from File

Load the application parameters from a parameter file created by the *Save to File* command. This option also loads parameter files created by the general-purpose PETView Oblique program, and sets the transverse and sagittal angles to values equivalent to the three angles used by the Oblique program.

Options

- Annotation
- Hide Patient Information

Annotation

Selecting *Options > Annotation* causes annotations to be shown on each display window. Select *Options > Annotation* again hides the annotations.

Clicking the left mouse button while holding the **Ctrl** key, with the cursor in one of the active display windows results in toggling the annotation display in that window. This feature may be used to selectively show annotation, while the *Options* > *Annotation* menu changes the annotation setting for all of the active display windows.

Hide Patient Info

Selecting *Options > Hide Patient Info* hides the patient's name and ID number from the display window. Selecting *Options > Hide Patient Info* again displays the patient's name and ID number.

Chapter **15** CARDIAC POLAR PLOTS (BULLS EYE AND BULLET DISPLAY)

The *Bull's Eye* Display reorganizes short axis cardiac images - either one or a pair, such as rest and stress images, into polar plots, commonly called *Bull's Eye* displays. The resulting data can also be viewed as a rotating surface display, commonly called *Bullet* display (Figure 15-2). The surface displays can be rotated either separately or synchronously using the mouse pointer.

Cardiac Polar Plot Procedure

- 1. If not already loaded: From *File Management*, highlight a patient and select *PetView* > *Load Image* from the drop-down menu
- 2. Highlight the OBLC image(s) and click Load
- 3. Right click on desktop and select *Bull's-Eye* The *Bull's Eye* Display appears.
- 4. Select *Image* > *Select* from the drop-down menu The *Image Select* dialog box is displayed
- 5. Highlight the *OBLC.img* file and click *OK* The image is displayed

Radial Search

The polar plot shows a single intensity for each short axis slice. This intensity corresponds to the maximum pixel intensity along a radial profile. In order to control the radial profile search it is necessary to tell the program where to begin and end the search.

- 1. In the upper right hand image of the window, which shows the short axis views of File I, select a slice near the base of the heart.
- 2. Change the selected slice by moving the slider.
- 3. Position cursor in the center of the heart and drag to the right until the circle which appears is larger than cardiac wall of the left ventricle.

- 4. The program searches for a maximum along radial lines starting at the center of the circle and going as far as the radius shown. If the circle is not correct, it can be redrawn.
- 5. Step through all short axis slices to determine that the circle is centered on all short axis slices and the radius is always large enough to enclose the left ventricular wall.

The circle can be redrawn in any number of slices, the program interpolates the circle center and radius for any slices which do not have a circle drawn by the user.

Axial Search

The second image on the right side of the window shows the long axis view for File I. Properly indicate the desired axial search extent.

- 1. Position the cursor at the base of the left ventricle and click.
- 2. Position the cursor at the lower portion of the apex and click.
- 3. Position the cursor on the inside of the apical wall and click.
- 4. Horizontal lines indicate the selected ranges of the axial search. The program performs a radial search for all slices from the base to the inside of the apical wall and performs a full 3-D search at the apex.

All slices are displayed with the circular search region overlaid to allow visual inspection of the radial search volume. The corresponding polar plot image is shown in the left panel.

- 5. Radial search circles or axial search parameters can be edited by either redrawing the circular regions on the short axis views or by moving the horizontal lines on the long axis view.
- 6. Move the horizontal lines with the cursor on the line, drag the line to the new location.

Parameters for File II

If a second study was read in such as a stress study, the search regions are duplicated automatically. If the patient was not moved between the two studies, no editing has to be performed on the second study. This improves accuracy and allows a better comparison to be performed between the two studies. If, however, the patient moved between the two studies, the search parameters (axial search circles and axial search extend) can be adjusted as described above.



Figure 15-1 Bull's Eye Display

- Short Axis:
 - Right click in the mid ventricle and drag to right to size ROI close to but larger than the size of the ventricle.
 - ^D Move slide bar to check centering.
- Vertical Axis:
 - Right click at the base
 - Right click at the apex
 - ^D Right click inside the ventricle at the apex
- 7. Select *Plot* > *3D Plot* to display the 3D image
- 8. Click and hold to rotate image



Figure 15-2 Bullet Display

Menu Commands

Image

The program initially does not load an image. One or two short axis cardiac images may be selected (provided the images have been loaded to memory), by selecting the *Image* > *Select* drop-down menu. A dialog listing the images currently loaded to memory is displayed. Highlight the desired image(s) and click **OK**.

Plot

The 3-D or surface display is simply a redisplay of the polar image in a geometrically more accurate three-dimensional surface display. To generate the 3D plot, select *Plot* > *3D Plot* from the drop-down menu. The surface displays can be tilted or rotated by dragging the mouse horizontally or vertically over the surface display. Both surface displays can be rotated synchronously by dragging the cursor horizontally halfway between the two surface images.

Save

The Bull's Eye images can be saved to disk either in the patient's directory (default) or in any other directory, so the images can be further analyzed using other modules.

16 BRAIN PROGRAM AND OBLIQUE RESLICING

The oblique sectioning module allows a set of images to be generated at any arbitrary orientation through the data set. The direction of the new image set is indicated with cursor lines drawn on the transverse, sagittal, and coronal images. The set of oblique views can be saved to permit all of them to be viewed at a later time and to allow all other modules to manipulate the oblique sections.

Oblique Sectioning

An oblique section is generated by first drawing a cursor line along the desired direction on the sagittal, coronal, and/or transverse image. Since each direction (transverse, sagittal, coronal) consists of a complete set of images, it is desirable to first select the image in each direction which best shows the anatomical structure necessary for reslicing. This is normally the long axis of the heart, however any other image can be resliced as well. For reference an outline of a coordinate system is shown together with the oblique section indicated.

Oblique sections can be displayed in cine mode or singly by indicating a starting and ending slice and selecting an increment. If the major axis of the heart has been properly selected, the cardiac cavity will not appear to move sideways if the oblique sections are displayed in cine mode. This feature provides a convenient check on the accuracy of indicating the major axis.

Cardiac/Brain Mode

The oblique reslicing program is intended to work equally well for reslicing cardiac or brains studies. However, in the *Cardiac* mode the image volume is resliced at right angles to the line drawn in the sagittal plane to result in a short axis view when drawing a line along the major axis of the heart, while in the *Brain* mode the image volume is resliced parallel to the line drawn.

Exporting/Saving Oblique Sections

Since it is desirable to have all features of other modules such as the *Display, Region-Of-Interest,* and *Profile* modules available, the calculated oblique sections can be *Exported* to memory and/or Saved to disk for future use. If the oblique sections are only exported, other modules can be used to analyze the data during the current analysis session but new oblique sections must be calculated after the current analysis session has ended. Saving the data to disk avoids this problem, but requires additional disk space.

Brain Acquisition Parameters

Scan Type	Emission Only		
FOV Diameter (mm)	256		
Start Position (mm)	Read from Gantry		
Total Scan Time	(Calculated by program)		
Patient Orientation	Head First		
Table Direction	In		
Scan Length (mm)	180		
Emission Parameters			
Isotope	F-18		
Duration Type	Time		
Time/Position	Constant 20 minutes		
Emiss Time # of Pos	(Calculated by program) (Calculated by program)		

Brain using Ellipse Attenuation Correction

Reconstruct the *.scn* file using the default Brain protocol with attenuation correction set to *None*.

- 1. From the *Study Files* window highlight the newly reconstructed image
- 2. Select *PetView* > *Load Image*

(The image file should already be highlighted) In the *Load* window, set the slice increment to 16 mm. Click *Load*

- 3. Right click on desktop to select Region of Interest
- 4. An ellipse (not a circle) must be drawn around the brain for calculated attenuation correction
- 5. Use the gray color scale and click inverse (white background) and use square-root
- 6. Draw an ellipse and line up the ellipse with the activity in the skin
- 7. Click ellipse, Drag across the area of interest
- 8. Click in the middle of the line to pull to an ellipse
- 9. Draw an ellipse on every few slices (e.g., every third slice)
- 10. Draw an extra small ROI at the first empty slice located above the brain activity
- 11. Select *I/O* > *Region File* > *Save*
- 12. Select *Files > Study Files* (File Management)
- 13. Select the *.scn* file (not the *_tr.scn* or *_ec.scn* file).
- 14. Select *PetView* > *Reconstruct Sinogram*
- 15. Click Clinical Protocol
- 16. Select the appropriate protocol
- 17. Click *Start* to begin reconstruction

Brain Image Display

- 1. From *File Management* highlight a patient
- 2. Select *PetView* > *Load Image* from the drop-down menu
- From the Load dialog box highlight an image to load Change threshold if needed Brain scans may need to be loaded at ~ 110-125% upper threshold.
- 4. Click the *Load* button
- 5. Right click on desktop and select Display for Brain
- 6. Scroll bar options:
 - Brain:
 - ^{\Box} Thickness = 4 mm
 - □ Increment = 2 mm

Brain Image Reorientation

Use Oblique Section for Brain Reorientation. Use Cardiac Oblique for cardiac reorientation.

- 1. On the SVR Workstation, left click desktop to open File Management
- 2. Highlight a Patient and select *PetView > Load Image*
- 3. Right click the desktop and select *Oblique Section*
- 4. Adjust the slice viewed using the slider bar
- 5. Draw a line on transverse from *Posterior* > *Anterior* (bottom to top on the image) Note: Drawing this line the wrong way results in an upside-down image.
- 6. Skip the Coronal unless the patient's head is tilted to one side. If necessary, draw a vertical line on the coronal view from Superior to Inferior.
- 7. Draw a line on the *Sagittal* along the Cantho-metal line *Anterior* > *Posterior*
- 8. Set the *Start* to **0**
- 9. Set the *End* all the way to the right
- 10. Select *Cine* to see the slices
- 11. Set the start slice to 0 and the end to the right
- 12. Select *Save -> All* (will cine through again)
- 13. Select *Exit* > *Yes*
- 14. Select the OBL image and reload using the Load program



Figure 16-1 Brain Image Using Oblique Section

Menu Commands

Image

The program will initially load the most recently loaded image. A new image may be selected (provided other images have been loaded to memory), by executing the *Image* > *Select* from the drop-down menu. A dialog is displayed listing the images currently loaded to memory. Highlight the desired image and click *OK*.

Parameters

The reslicing parameters including angles and position of the resliced image may also be entered manually by clicking *Parameters* in the menu bar. The resliced image may be shifted or rotated in all three directions by moving the sliders in the window.

	325
Tran 🖪	
	312
	306
Sagi 🖪	
0 0	
X⊴□───≥⊻⊴□───	
M in M out Rotate	I/O Quit

Figure 16-2 Parameter Window

M in/M out

M in stores the selected reslicing parameters in temporary memory. *M out* reverts back to the last set of parameters which were stored in temporary memory when using the *M in* function. This allows a set of reslicing parameters to be stored temporarily while searching for a best set of parameters.

Rotate

Sometimes it is desirable to rotate an image by 90 or 180 degrees. This can be achieved by clicking *Rotate* in the *Parameter* window. Rotation is in the transverse plane only.

I/O

After an appropriate set of parameters are found, the parameters may be stored on disk by clicking *I/O* in the *Parameter* window. A window indicates the default directory and filename, which may be changed before storing the parameters on disk. The resulting file is an ASCII file which easily can be read or manipulated using a text edit program.

Options

- Annotation
- Hide Patient Information

Annotation

Selecting *Options* > *Annotation* causes annotations to be shown on each of the display windows. Clicking *Annotation* again hides annotations in each of the display windows.

Hide Patient Info

Selecting *Options > Hide Patient Info* hides the patient's name and ID number. Clicking *Hide Patient Info* again displays the patient's name and ID number in the window.

Chapter **17 DICOM TRANSLATION**

The DICOM Translation program is used to convert DICOM formatted image files to the PETVIEW format so the files can be loaded and displayed with PETVIEW software. The files listed in the *DICOM Translate Interface* window are received and deposited in the DICOM file directory. The list displays the *Patient Name, Patient ID, Acquisition Date, Modality* (CT or MRI, for example), *Image #,* and *Slice Location*; which are extracted from the DICOM file headers.

Each DICOM file represents a single slice of data. To create a multi-slice output image file, all the related files must be translated at the same time. The patient name and acquisition date information displayed with the DICOM filenames help select all slices that relate to the same DICOM data set.

One or more files can be selected from this list and converted to one multiple slice PETVIEW image file. All slices selected must belong to one single image. An error message appears if there is a conflict between the files. There is currently no capability of appending a new DICOM slice to an existing PETVIEW image file.

Images of different modalities can have uneven slice spacing and thicker slices than PET images. Once the *Translate* option is selected, a dialog box appears presenting the choice of keeping the default size of the slice or setting it to 2, 4, or 8 millimeter.

When the translation process starts, all selected files are checked to ensure they all pertain to the same patient. Each file is translated and inserted into the appropriate order in the output image file.

DICOM Translation Procedure

1. From *File Management*, highlight the patient study to be translated This is a patient done on C-PET

Note: A new patient or patient study can not be created during the translation process. This data is intended to be translated into an existing patient study. The user should know beforehand which patients have had data sent to C-PET. There is no easy way to find out which patients have data in the dicom-receive directory.

2. From the drop-down menu select *Options > DICOM Translation* This opens a DICOM Translation window.

<u>F</u> ile <u>S</u> li	ceSpacing	<u>P</u> ixelScaling	S <u>e</u> lect				<u>H</u> elp
Patient Name		Patient ID	Acq Date	Modal	Image #	Slice Loc	
CLARK^JANET		01421711	19991108	СТ	108	-509.50000000	
CLARK^JANET		01421711	19991108	СТ	109	-516.50000000	
CLARK^JANET		01421711	19991108	CT	110	-523.50000000	
CLARK^JANET		01421711	19991108	CT	111	-530.50000000	
CLARK^JANET		01421711	19991108	СТ	112	-537.50000000	
CLARK^JANET		01421711	19991108	СТ	113	-544.50000000	
CLARK^JANET		01421711	19991108	CT	114	-551.50000000	
CLARK^JANET		01421711	19991108	CT	115	-558.50000000	
CLARK^JANET		01421711	19991108	CT	116	-565.50000000	
CLARK^JANET		01421711	19991108	CI	117	-572.50000000	
CLARK^JANET		01421711	19991108	CT	118	-579.50000000	
CLARK^JANET		01421711	19991108	<u>ci</u>	119	-586.50000000	
CLARK^JANET		01421711	19991108	CI	120	-593.50000000	
CLARK^JANET		01421711	19991108	CI	121	-600.50000000	
CLARK^JANET		01421711	19991108	<u>ci</u>	122	-607.50000000	
CLARK^JANET		01421711	19991108	CI	123	-614.50000000	
SIMONS/LINDA	A	01464544	20000103	CI	1	-216.800003051	
SIMONSALINDA	A	01464544	20000103	CI	2	-221.800003051	
SIMUNS/LINDA	A	01464544	20000103	U	3	-226.800003051	
SIMUNS/LINDA	A .	01464544	20000103	CT CT	4	-231.800003051	
SIMUNS/LINDA	A .	01464544	20000103	U	5	-236.800003051	
SIMUNSALINDA -	ň	01464544	20000103	UI CT	b	-241.800003051	
SIMUNS/LINDA	ň	01464544	20000103	UI CT	6	-246.800003051	
SIMUNS/LINDA	A .	01464544	20000103	UI	8	-251.800003051	
STHONGALTNDA	n	01404544	20000103	CT CT	3	-236.733387733	
SIMUNSALINDA -	n	01464544	20000103	CT	10	-261.733387733 acc 200087703	
STHUNS/TTINDA	n 4	01464544	20000103	CT	12	-200./3336//33	
STRUMACTINDA -	n A	01404044	20000103	CT	12	-270 70007702	
STHUMS/LINDA	n 1	01404544	20000103	CT	10	-201 700007700	
STRUMS/LINDA	A	01404044	20000103	CT	15	_200 700007700	
STHUNS LINDA	п А	01404344	20000103	CT	16	-200.733367733	
STHUMSALTINDA	n	01404344	20000103	U.	10	-100007700	
Output File	/home/patier	nt/new.img					

Figure 17-1 DICOM Translate Interface Window

3. Enter the *Output File* field. Ensure the filename has an .img extension

If the program was invoked from *File Management*, the destination directory is already specified and cannot be changed, the file name must be entered. Otherwise the entire pathname of the output file must be specified. If no pathname is given, the output file is written to the */home/patient* directory.

- 4. Select the slices to be translated (hold **Control** key and click the desired selections)
- 5. From the drop-down menu, select *File* > *Translate* The *Protocol Conversion* window is displayed

🗕 Choose a protocol for conversion to imagio 🔹 🗖
Choices:
Native_Slice_Spacing
2_mm_per_Slice_144x144
2 mm per_Slice_144x144
4_mm_per_Slice_288x288
Selection
4_mm_per_Slice_144x144
0K Cancel

Figure 17-2 DICOM Translate Protocol Window

6. Highlight the Translation Protocol and click *OK* A busy dialog is displayed

- 7. Once the data has been translated, a dialog box displays the message, *The DICOM Image is Successfully Translated* Click *OK*
- 8. From the drop-down menu select *File* > *Exit* To close the *DICOM Translation* window
- 9. From *File Management*, the patient study initially selected should still be highlighted. From the drop-down menu select *Files* > *Study Files*
- 10. The translated image should be at the top of the window. Select and load the image in the usual manner.

Menu Commands

File

From the File drop-down menu the following options can be selected:

- Translate
- Delete
- Exit

Translate

Each DICOM file represents a single slice of data. To create a multi-slice output image file, all the related files must be translated at the same time. The patient name and acquisition date information displayed with the DICOM filenames help in the selection all slices that relate to the same DICOM data set.

When all DICOM files are selected, specify the output image file name in the text field at the bottom of the window. If the program was invoked from *File Management* the destination directory is already specified and cannot be changed. The file name must be entered. Otherwise the entire pathname of the output file must be specified. If no pathname is given, the output file is written to the */home/patient* directory.

When the translation process starts, all selected files are checked to ensure they all pertain to the same patient. Then, each file is translated and inserted into the appropriate order in the output image file.

Delete

The DICOM directory can be cleaned up by deleting all the selected files. This is accomplished by selecting the *Delete* option under the *File* top menu bar option. A file should be deleted only after it has been translated to an image file with the appropriate slice size or it is no longer needed. Otherwise, the file has to be re-sent.

When the *Delete* option is pressed, the system prompts to verify the deletion of each selected file. Any deletion operation can be canceled, and the program continues with the rest of the list.

Select

From the Select drop-down menu the following options are available:

- Select All
- Unselect All

All listed DICOM files can be selected by choosing the *Select All* option under the 'Select' main menu bar option. Likewise, all selected files can be deselected by choosing the *Unselect All* option from the *Select* drop-down menu.

Since each DICOM file represents a single slice of a total data set, it is necessary to make multiple selections of DICOM files for translation into a single multi-slice output image file. If all DICOM files from the same data set are contiguous in the list, they can all be selected by moving the mouse cursor to the first file pertaining to the patient of interest, pressing the left mouse button, and holding it down while moving the mouse cursor to the last file pertaining to the same patient. When the mouse button is released, all the selected files remain selected.

If all the required files are not listed contiguously, they can all be selected by pressing the **<CNTRL>** key on the keyboard while clicking each file with the left mouse button. Non-contiguous files can be deselected in this way as well.

Sending Snapshots

To send a snapshot of an image in DICOM format:

- 1. From the image display select *Tools > DICOM Snapshot* from the drop-down menu
- 2. When more than one DICOM destination exists in the configuration file, a list is displayed in a dialog box
- 3. Highlight the destination and click *OK*
- 4. The snapshot is sent immediately

Note: The snapshot is taken as soon as the menu option is selected; anything covering the display appears in the snapshot.

Sending Images

To send PETVIEW images in DICOM format:

- 1. Highlight one or more images from the *Study Files* window
- 2. Select *Options > DICOM Send* from the drop-down menu
- 3. When more than one DICOM destination exists in the configuration file, a list is displayed in a dialog box.
- 4. Highlight the destination and click *OK*
- 5. The images are sent when the destinations are chosen.

18 QUALITY CONTROL AND CALIBRATION

The system contains a number of components that are subject to change as a function of time. These include the photomultiplier tubes, power supplies and analog electronic components. To achieve and maintain proper operation, various data which are subject to change as a result of drift, are stored in tables that must be updated periodically. Most of these need to be updated only infrequently, a task which can be performed by a service representative, engineer or physicist.

In order to assure the scanner is working properly it is necessary to perform:

- AutoQC System initiated daily
- Daily QC User initiated, performed daily and is not time consuming
- Periodic QC User initiated, performed less frequently

AutoQC

The System starts AutoQC every morning at 6 am which is a full System Initialization and Baseline Collection.

System Initialization

The System Initialization downloads tables onto circuit boards, initializes boards, and runs diagnostics. If initialization fails, the program does not continue to the baseline collection. It takes approx. 5 minutes for this process to complete.

Baseline Collection

This process collects the baseline data (analog offsets of all photomultiplier channels). The values are then loaded into the 'calculator', which is part of the scanner processing electronics. This happens at the end of the baseline collection and at the beginning of each data collection.

If baseline values are outside the permitted range or if the baselines have changed drastically from the day before, an error message may appear. If a warning or failure occurs, the system may need a Preamp and Sumamp offset calibration by the Field Service Engineer.

When an error message appears, do one of the following:

- If the measured values are slightly outside the normal range, proceed with the scanner use, but call a service representative
- If the measured values are significantly outside the allowed range, do not use the scanner and call a service representative immediately

If no error message appears, the baseline collection has been performed successfully and a message to that effect appears.

DAILY QC

Daily QC checks should be performed at the start of each day prior to patient scanning. The Daily QC procedures are designed to quickly detect equipment malfunctions and assure the scanner is properly calibrated.

Daily QC Procedure

- 1. Login: patient
- 2. Password: 511kev
- 3. From the Acquisition Workstation, open *File Management* by left clicking desktop.
- 4. From the drop-down menu, select: *Acquisition* > *Daily Quality Control*
- 5. Place ²²Na point source in holder in center of FOV and press <ENTER> If the source is not centered, the program pauses and prompts to center source.
- 6. Once the source is centered, the system executes the following tests.
 - System Initialization (if not done prior by AutoQC)
 - Baseline Collection (if not done prior by AutoQC)
 - Energy Test and Analysis
 - PMT Gain Test
 - Emission QC
 - Transmission QC
- 7. After the system initialization, the system may prompt to move the patient table. If there is no prompt, but the system is beeping, press the enable button to move the table to the proper position for emission and transmission collections.
- 8. At the end of each step a PASS, NOTICE, WARNING, or FAILURE notice is displayed. The system keeps a daily QC log in the QC directory. The log file contains results for each of the QC steps and is named **qcResultsYYYYMMDD.log**

View Daily QC Log File

Daily QC Log Files are placed in the */home/patient/logfiles* directory on the Acquisition Workstation. Only the latest 10 log files are kept.

- 1. On the Acquisition Workstation, open *File Management*. Double click the *p0s0 Quality Control Acct*
- 2. The File Studies dialog box appears. Highlight the log file *qcResults<current date>*
- 3. From the drop-down menu select: *Options > View Text File* The QC Log file is displayed.

Energy Test and Analysis

This Daily QC step collects ListView data and calculates the global and local energy centroids and FWHM.

If the global and/or local energy centroids are not approximately 100, an error message appears. If the global and/or local FWHM are greater than 13, an error message appears.

If this test produces a warning or failure, it indicates that an energy correction may need to be run by the Field Service Engineer.

- Na-22, beta emitter, 2.602 yr. ½ life, 0.1 mCi
- Program counts events therefore it is not necessary to increase time of acquisition as source ages.
- Centroid should be at 100 +/- 4. A centroid value of 100 = 511KeV
- FWHM should be ≤ 13
- LE = Local Energy 7 PMTs surrounding a single scintillation event
- GE = Global Energy. All PMTs are not used, but all are displayed

PMT Gain Test

The PMT Gain Test measures the PMTs similar to a gain calibration. It does not pass or fail, it collects target deviations into the QC log file.

Emission Collection and Analysis

Daily QC does a short emission acquisition and analyzes the resulting sinogram. Before the acquisition can begin the table must be at 77, therefore if it beeps, press the enable button.

Each tilt of the sinogram is analyzed separately. The program sums all slices for each tilt and tries to fit a sine curve to the sinogram. The RMS deviation reported in the results file is a measure of how much the sinogram deviates from the closest sine curve.

If the Daily QC reports a warning or failure, the user may visually inspect the sinogram and look for missing or weak line segments. A properly collected sinogram is shown below. The missing data segments in this sinogram are due to the gaps between the 6 detectors. This effect is compensated for in the reconstruction algorithm.

View Emission Sinogram

The emission sinograms are kept in the QC directory /sun0/patient/p0/s0. The most recent emission sinograms are named **p0s0_emissQC.scn**

- 1. On the Server Workstation, open *File Management*. Double click the *p0s0 Quality Control Acct*
- 2. The Study Files dialog box is displayed. Highlight the scn file *p0s0_emissQC.scn*
- 3. From the drop-down menu select *Petview > Display Sinogram* The QC Emission Sinogram is displayed. Scroll to display the emission sinogram

Visually inspect the sinogram and look for missing or weak line segments. A properly collected sinogram is shown below.



Figure 18-1 Emission QC

If any deviation is noticed from the appearance shown here and the appearance of the sinogram of the scanner on a previous day, call your service representative. The Field Service Engineer (FSE) is able to inspect the sinogram using the modem and is advised about the proper action to take. A failure may indicate that a new distortion removal or gain calibration may need to be run.

Transmission Collection and Analysis

Daily QC step does a short transmission acquisition (2 rotations) and analyzes the resulting sinogram. Each slice of the sinogram is analyzed for uniformity and count rates. As a final test, the count rates are compared to the saved blank scan count rates, adjusted for scan time.

If the Daily QC reports a warning or failure, visually inspect the sinogram and look for non-uniformities or changes from the last transmission collection (picture below shows a good slice). Call Customer Support since a warning or failure may indicate a hardware problem.

View Transmission Sinogram

The transmission sinograms are kept in the QC directory /sun0/patient/p0/s0. The most recent transmission sinograms are named **p0s0_transQC_tr.scn**

- 1. On the Server Workstation, open *File Management*. Double click the *p0s0 Quality Control Acct*
- 2. The Study Files dialog box appears. Highlight the scn file *p0s0_transQC_tr.scn*
- 3. From the drop-down menus select *Petview* > *Display Sinogram* The QC Transmission Sinogram is displayed.



Figure 18-2 Transmission Collection

Visually inspect the sinogram and look for non-uniformities or changes from the last transmission collection (picture below shows a good slice). Call your service representative since a warning or failure may indicate a hardware problem.

Periodic Quality Control

At each institution or installation site a single individual should be designated to perform periodic quality control. This person should also be responsible that appropriate corrective action be taken. The test described below should be performed at least once every month to assure optimum scanner performance.

Uniformity

To check the uniformity, place a 30 cm uniform cylinder phantom containing no more than 2 mCi of FDG or F-18 activity and covering the whole axial field-of-view in the center of the scanner. Perform a data collection for 1 hour and reconstruct the data with ellipse attenuation correction. Inspect the data visually and compare the images to those obtained on previous occasions. If you notice any significant deviation in uniformity, call your service representative.

Acquire a Uniform Phantom

- 1. On the Acquisition Workstation, open *File Management*.
- 2. Highlight the *Quality Control Acct* (normally *p0s0*)
- 3. From the drop-down menu, select *Acquisition* > *Set Up Acquisition*
- 4. In the Filename field, enter: uniformity-yyymmdd
- 5. Click Acquire Now
- 6. From the *Acquisition* dialog box select *Select Protocol* > *Emission Only*
- 7. From the *Protocol* dialog box highlight *DefaultBody* and click *OK*
- 8. Click Edit Protocol
- 9. From the *Protocol* dialog box, change *Scan Length (mm)* to display **256** This can be done by dragging the slide bar to the far left
- 10. In the Time/Position field, enter: 1:00:00
- 11. Click Use
- 12. From the Acquisition dialog box click Read from Gantry
- 13. Click Start

Reconstruct Uniform Phantom without Attenuation Correction

- 14. On the Server Workstation, from File Management, double click Quality Control Acct
- 15. From the *Study Files* highlight the *.scn* file
- 16. From the drop-down menu, select *Petview* > *Reconstruct Sinogram*
- 17. Click Select Clinical Protocol
- 18. Select *Body-noattn* and click *OK*
- 19. Click *Start* A Busy Dialog box appears
- 20. The system beeps and displays a dialog box notifying Reconstruction is Finished. Click *OK*

Note: This outputs a non-attenuated image.
Generate Ellipse

- 21. From the *Study Files* highlight the *uniformity-yyyymmdd.img* file
- 22. From the drop-down menu, select *Petview* > *Load Image*
- 23. Select the *pOs0_uniformity-yyyymmdd.img* file and click *Load*
- 24. Right click desktop and select Region of Interest
- 25. The ROI image is displayed. To enlarge the image, from the drop-down menu, select *Display* > *Zoom*

		Region	of Inte	rest 8.0		· 🗆
Exit	Image	Count	Edit	Display	1/0	Сору
T RIGHT		ANT			EFT	 ◇○ ◇○ ◇ 公 ◇ SUV
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Nan Id: File Acq	ne: = = : p Date: 2	 Ds0_nom 7 Feb, 20	==== == = n02270	 11 .img		=

- 26. Using the Ellipse tool, draw an ellipse around the phantom
- 27. To edit the ellipse (Move, Rotate, or Resize), from the drop-down menu select *Edit > Single*

edit_single_p	opup
💠 Move 🛛 💠 Rotate	💠 Resize
Type jg X j62.5	A <u>¥</u> 48.3
Label No comment er	1tered
Delete	Quit

- 28. When the ellipse is around the phantom, copy the ellipse, select *Copy* > *Single* from the drop-down menu
- 29. Drag *Slice* bar to a beginning slice and release the mouse. The ellipse appears around the phantom, edit the ellipse
- 30. When the ellipse is around the phantom, copy the ellipse, select *Copy* > *Single* from the drop-down menu
- 31. Drag *Slice* bar to an ending slice and release the mouse. The ellipse appears around phantom, edit the ellipse
- 32. Select *I/O* > *Autosave* The files are saved for Quality Control procedures

Reconstruct using the Ellipse for Attenuation Correction

- 33. On the Server Workstation, from File Management, double click Quality Control Acct
- 34. From the *Study Files* highlight the *.scn* file
- 35. From the drop-down menu select, Petview -> Reconstruct Sinogram
- 36. Click Yes to overwrite the image
- 37. Click Select Clinical Protocol
- 38. Select Body-noattn and click Edit
- 39. Change the Attenuation Corr from None to Ellipse
- 40. Click Use, then click Start

After completing the reconstruction, visually inspect the phantom for non-uniformities.

Calibration Procedures

The scanner is calibrated at the factory and again at site installation. The system contains a number of components that are subject to change as a function of time. These include the photomultipliers, power supplies and analog electronic components. The quality control procedures described above are designed to detect these changes and serve as an indication that the system needs to be recalibrated.

Normalization Data

Collection of new normalization usually restores the systems performance to its original specifications. Since the components used in the scanner are carefully selected for maximum stability.

A FSE should perform collection of new normalization data. The procedure is described in detail in the Service Manual Calibration Section and is briefly summarized here. Place a 30 cm uniform cylinder phantom, part number NEMA-01, containing no more than 2 mCi of FDG activity and covering the whole axial field-of-view in the center of the scanner. Perform a data collection and data processing using the "normalization" procedure described in the Service Manual Calibration section.

After completion of data collection and processing, the new normalization data are loaded into the system. Perform a new check of uniformity as described above to verify the normalization data collection has restored the performance to the expected value.

Preamp and Sumamp Offset Calibration

This calibration adjusts the preamp and sumamp offsets to get the desired baselines and maximize the singles count rates.

The procedure is described in detail in the Service Manual Calibration Section and is only briefly summarized here.

Remove any activity in the scanner field of view. Open the *Calibration Menu* from the *Service Menu*. Select *Preamp and Sumamp Offset*. This calibration takes approximately 30 minutes to complete.

Energy Correction

This calibration generates an energy correction table to center the local and global energies on 100.

The procedure is described in detail in the Service Manual Calibration Section and is briefly summarized here.

Place the QC source holder on the ID cover with a 22Na source (DO NOT use the white Auto QC Elevation Block). Open the *Calibration Menu* from the Service Menu. Select *Energy Correction*. This calibration takes approximately 1/2 hour to complete.

19 STANDARDIZED UPTAKE VALUE (SUV)

SUV is the ratio of the concentration of activity in a structure to the average concentration in the entire body.

Obtaining SUVs requires that the scanner be calibrated to convert counts per pixel into mci/cc or millicuries per cc (performed periodically) and secondly, the SUV is calculated for a specific part of the image given the patient's weight and amount of activity injected.

Calibration

The calibration requires a 20-frame dynamic scan, which takes about 11 hours, which can be run overnight. The dynamic study is followed by a transmission scan. The entire 20 frame dynamic study is reconstructed using the transmission scan measured for attenuation correction. A calibration table is generated to calculate the attenuation correction. Finally, a validation scan is acquired. The acquisition for this mimics a wholebody scan to ensure proper calibration.

The SUV calibration process must be performed:

- Every 6 months
- Whenever system is recalibrated
- Calibration validation process shows a discrepancy in SUVs

The calibration table must be validated:

- Every two months
- When Preventive Maintenance is performed

Both the calibration and validation scans are the responsibility of the customer. The calibration should be performed as specific reconstruction methods and parameters which are used for patient reconstruction. It is recommended to perform "non-uniform" background subtraction for both SUV calibration and patient SUV reconstruction.

Calibration Procedures

The following two reconstruction protocols have been provided for the SUVs:

- Default_Suv_Cal used to reconstruct the entire calibration sinogram
- Default_Suv_Compute used to compute patient data SUVs.

Note: SUV procedures require the transmission source to be present to acquire a transmission scan. Ensure source is present before starting the acquisition of the phantom.

Prepare Phantom

A 20 cm diameter uniform cylinder phantom is required for the calibration. Use the phantom that is 30 cm long, and has an interior volume of 9293ml.

Note: Be as accurate as possible with the dose and time of assay. Use the SVR Workstation clock (military time format).

- 1. Attach phantom holder onto the table using the hex allen screws (3/16 inches)
- 2. Prepare Patient Table
 - Turn lasers on and fully retract the table pallet
 - Raise the Patient Table until pallet of the bed is above the level of side laser
 - Insert the bed until it is far enough through the Gantry that the phantom can easily be attached from the rear of the Gantry.
- 3. Fill the cylinder phantom with water and 2.0 mCi F-18 or FDG for the Emission Acquisition and the Transmission Scan. A small air bubble is helpful for leveling the phantom. Overtightened screws may cause leakage around the O-Ring.

Note: The SUV Validation Procedure (page 19-6) uses 0.5 - 0.75 mCi F-18 instead.

- 4. Attach phantom to the phantom holder on Patient Table. If the phantom is too tight, loosen the white screws until the phantom slides easily onto the holder.
- 5. Using the screw on the bottom of the phantom as a leveler, try to suspend the air bubble in the middle of the phantom.
- 6. Place the phantom in the FOV. Center it between the lasers so there is approximately 2.5cm of overhang at both sides of the phantom. To easily see the lasers, place a towel over the phantom while positioning.

Emission Acquisition

- 7. From the ACQ Workstation, left click desktop to open *File Management*
- 8. Highlight the *Service Only* account (*p0/s2*)
- 9. From the drop-down menu, select *Acquisition* > *Set up Acquisition*
- 10. Under Study Information, ensure *Old Study* is displayed.
- 11. In the Filename field, enter **suvcalyyyymmdd** as the sinogram file name (yyyymmdd = current year, month, day) The system adds the *.scn* extension
- 12. Click Acquire Now
- 13. In the *Acquisition Information* box, from the drop-down menu, select *Select Protocol > Dynamic*

- 14. From the Acquisition Protocol dialog box highlight: DefaultSuvCal576 (for 576 FOV) or DefaultSuvCal256 (for 256 FOV)
- 15. Click OK
- 16. In the Patient Information box, enter the weight of the phantom 9.293 kg or 20.50 lbs
- 17. In the *Acquisition Information* box, enter the activity measured and the time it was measured using the clock on the SVR Workstation (military time format).

Note: 1mCi = 37MBq

- 18. Click *Read From Gantry, The Start Position* entry should update to be the same as the readout on the Gantry.
- 19. Click Start
- 20. Acquisition time is approximately 11 hrs and acquires 20 frames.
- 21. Do not remove cylinder from scanner when the acquisition is finished.

Transmission Scan

- 22. Keep phantom cylinder in same position.
- 23. From *File Management*, highlight the SUV calibration account (*p0/s#*), use the same one that was used in the Emission Acquisition (previous procedure).
- 24. From the drop-down menu, select *Acquisition* > *Setup Acquisition*
- 25. In the Filename field, enter: **suvcalyyymmdd** (yyyymmdd = year, month, day) The .scn extension is automatically attached.

Note: Use <u>same date for the *Filename*</u> as the Emission Acquisition (previous procedure).

- 26. Click Acquire Now
- 27. From the drop-down menu, select *Select Protocol* > *Transmission Only*
- 28. Highlight selection, must have _tr.scn and _ec.scn extensions for transmission and emission contamination):
 DefaultSuvCal576 (for 576 FOV)
 or
 DefaultSuvCal256 (for 256 FOV)
- 29. Click OK
- 30. Click *Read From Gantry The Start Position* entry should update to be the same as the readout on the Gantry
- 31. Click *Start* The acquisition takes approximately 10 minutes.
- 32. Once complete, remove the phantom

Reconstruct Frame 11 of the SUV calibration sinogram

Each frame contains a complete image of the phantom acquired at different times. Frame 11 is the middle of the 20 frame SUV Calibration acquisition. This reconstruction is needed to obtain an image of the phantom.

- 1. On the SVR Workstation, from *File Management* select *Database* > *Execute Query* This updates *File Management*
- 2. Double click the SUV Calibration file, *p0/s*#
- 3. From the Study Files window highlight the **suvcalyyyymmdd.scn** file
- 4. From the drop-down menu select *PetView* > *Reconstruct Sinogram*
- For 576 FOV select *Clinical Protocol > Body_noattn* or For 256 FOV select *Clinical Protocol > Brain_noattn*
- 6. Click OK
- 7. Click *Edit*
- 8. On the top right of the *Edit Box*, change the beginning frame range to **11**
- 9. Change the ending frame range to 11 When both beginning and ending frame ranges are 11, only frame 11 is reconstructed.
- 10. Click Use
- 11. Click *Start* This runs for approximately 4 minutes.

Draw Region of Interest

This Region of Interest (ROI) is used in the Calgen program.

- 1. Left click desktop to open *File Management*
- 2. Double click SUV Calibration file, *p0/s#*
- 3. From the Study Files window highlight the **suvcalyyyymmdd.img** file
- 4. From the drop-down menu select *PetView* > *Load Image*
- 5. The *Load* window is displayed. The SUV file is automatically highlighted, click the *Load* button and then quit the *Load* window by selecting *Exit* from the drop-down menu.
- 6. Right click desktop and select Region of Interest
- 7. The ROI window is displayed. Click the Ellipse button (upper right corner).
- 8. Click the left edge of the image and drag the cursor, drawing a line, to the right edge of the image. Release the mouse button.

- 9. Click the center of the line and drag the cursor downward. This opens the ellipse.
- 10. From the drop-down menu, select *Edit* > *Single*
- 11. The edit_single_popup window is displayed, click *Resize*

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Label No comment entered	
Delete Quit	J

12. Resize the ellipse, click on the ellipse and drag the cursor up and down, left and right until the numbers in the A and B boxes are **25.0**

Note: Retyping numbers in the A and B boxes will not change the ellipse size.

- 13. Quit the edit_single_popup window
- 14. From the drop-down menu, select *Copy* > *Single*
- 15. Click and drag the Slices slider bar all the way to the left and then back off a few slices (approximately 4)

Note: THE ROI IS COPIED AS SOON AS THE MOUSE BUTTON IS RELEASED.

16. From the drop-down menu, select *I*/O > *Autosave*

Reconstruct Entire SUV Calibration Sinogram

Process takes approx. one hour. All 20 frames of data are reconstructed in this process.

- 1. Double click the *SUV Calibration* file (*p0/s#*) in *File Management*
- 2. Highlight the *suvcalyyyymmdd.scn* file
- 3. From the drop-down menu, select *PetView* > *Reconstruct Sinogram*
- 4. Click *yes* to overwrite existing image
- 5. Click *Clinical Protocol*
- 6. Highlight *Default_SUV_Cal*, then click *OK*
- 7. Click Start

Calibration Table

This program generates the calibration table and saves it to file.

- 1. Left click desktop and select *Xterm window*
- 2. Type: cd/sun0/patient/p0/s# <Return>
- 3. Type: 1s <Return>
- 4. Type: calgen <Return>
- 5. Enter the attenuation/decay corrected image file **suvcalyyyymmdd.img** <Return> (i.e.:p0/s#_suvcalyyyymmdd.img. There should only be one)
- 6. Verify the region file at the prompt, type: suvcalyyyymmdd.reg <Return>
- 7. For the percent of ellipse region area to use, type: 0.67 <Return>
- For the slices at each end of the axial FOV to be skipped, type: 4 <Return>
- 9. For the phantom volume in ml, type: **9293** <Return>
- 10. The program generates the calibration table and saves 576 FOV to: /home/ugm/recon/tables. The link is: dmax576_bg.cal >/home/ugm/recon/tables/suvcalyyyymmdd.cal or saves 256 FOV to: /home/ugm/recon/tables. The link is: dmax256_bg.cal >/home/ugm/recon/tables/suvcalyyyymmdd.cal

Validation

This process verifies the SUV calibration was properly completed and the scanner is ready for clinical SUV computation. Do not acquire this procedure until the 'calgen' Program is completed(page 19-10).

Validation Procedure

- 1. Using 0.5 0.75 mCi F-18 or FDG, prepare phantom (page 19-2).
- 2. Left click desktop to open *File Management*
- 3. Highlight the *Service Only* account (*p0/s2*)
- 4. From the drop-down menu, select *Acquisition* > *Set up Acquisition*
- 5. Under Study Information, ensure *Old Study* is displayed.
- 6. In the *Filename* field, enter: **suvvalidateyyyymdd** As the sinogram filename. The *.scn* is automatically added.
- 7. Click Acquire Now
- 8. In the *Acquisition Information* box, from the drop-down menu select, *Select Protocol > SinglePass Emis/Trans*
- 9. From the *Protocol* dialog box highlight *DefaultBody*
- 10. Click Edit
- 11. In the top panel, ensure the *Concurrent Recon*. is *On* and change the *Recon Protocol* to *body_ramla_suv*
- 12. Click OK
- At the bottom of the Editor box, click *Use* The following appears for Protocol: *DefaultBody(*)*
- 14. Enter the weight of the phantom 9.293 kg or 20.50 lbs
- 15. Enter the activity measured and the time it was measured. Use the clock on the SVR Workstation (military time format).

Note: 1mCi = 37MBq

- 16. Click *Read From Gantry The Start Position* entry should update to be the same as the readout on the Gantry
- 17. Click Start

Verify Procedure Using ROI Program

- 1. Load the image
 - Double click the *SUV Validation file* in *File Management*
 - Highlight the *suvvalidateyyyymmdd.img* file
 - From the drop-down menu select *Petview* > *Load Image*
 - Click the *Sequence* button and change it to *SUV Scale*
 - Click Load
- 2. Right click the desktop and select Region of Interest
- 3. *SUV* button should already be depressed (middle right of box) if the image was loaded using the SUV scale. If not, depress the *SUV* button.
- 4. Select the circle region, second on the list on the right side of the box.
- 5. Click and drag to create an ROI. (It is easiest to click on 11 o'clock and pull down diagonally to 5 o'clock). Keep ROI inside the boundaries of the image.
- 6. *mu* (which means average) should be 1.0 (.9 1.1). Since the phantom is mixed well, it only has average activity in it, hence an average of 1.0
- 7. If data is not correct, call Customer Support for troubleshooting the calibration process.

Computing SUVs

Once the SUV calibration table has been created, SUVs can be computed for patient data. When the patient study is acquired, on the main window of the Acquisition interface, enter:

- Activity measured
- Time the activity was measured
- Patient's weight (in kg)

An emission scan and a transmission scan must be acquired to be used for transmission attenuation correction.

The data should be reconstructed with the protocol body_ramla_suv

For the Color Scales to reflect the SUVs, the image must be loaded by *SUV Scale* in the Load interface. Displaying the image shows the SUVs pictorially, i.e. the color scale values directly reflect the SUV values in the patient images.

For quantitative analysis of the SUVs, the image can be loaded by *Sequence* or *SUV Scale*. After the image is loaded, invoke the ROI program. If the image was loaded by *Sequence*, press the *SUV button* that is below the icons along the right side of the *Region of Interest* display window. When counting the pixels in the regions (by doing a single count, the counts are displayed in the *ROI* interface), the SUVs are the values that are reported. If the image was loaded by *SUV Scale*, the *SUV* button in the *Region of Interest* window is pressed, and the counts are SUVs.

Loading Calibration Data into Studies Previously Acquired

This section deals with the situation in which the patient data were acquired when a calibration table was not present, or with the wrong calibration table. In this case, the SUV program needs to be run. Information from the most recent calibration table is loaded into a sinogram after an acquisition.

- 1. In *File Management* select the patient study
- 2. From the drop-down menu select *Files > Study Files*
- 3. In the *Study Files* window, select the proper patient scan (.scn file type)
- 4. From the drop-down menu select *Options > Load Deadtime Factors*

The program loads the information from the calibration files into the sinogram headers. The user may then proceed with the image reconstruction as described in the above section *Computing SUVs*.

The 'calgen' Program

The '**calgen**' program first computes the average singles rate for each frame by averaging the beginning and ending singles rates that are stored in the subheader. Calgen then calculates the activity concentration in nCi/ml at the midtime of each frame. The midtime of each frame is calculated with the following equation

$$midtime = \frac{1}{\lambda} \bullet ln \frac{(\lambda \bullet duration)}{(1 - e^{(-\lambda \bullet duration)}} + start_delay$$

where:

 $\lambda = (ln2)/(halflife)$ duration = 0.0 (in calgen)

halflife = 109.8 for F18

The activity at the midtime of each frame is computed as:

 $activity(mCi) = \langle assayed_activity \rangle \bullet e^{(-\lambda \bullet midtime)}$

The activity for each frame is therefore:

$$Concentration((nCi)/(ml)) = (activity \bullet 10^{\circ})/(volume)$$

Then calgen computes the counts per minute per voxel. The voxel size is pre-defined to be $2*2*2 \text{ mm} (vox_size = 8)$. The program calculates how many pixels per voxel by defining the pixel size as:

 $pixel_size = ((FOV)/(xdim)) \bullet ((FOV)/(ydim)) \bullet slice_thickness$

where:

FOV = 576 xdim = 144 ydim = 144 slice_thickness = 4

and dividing the voxel size by the pixel size.

$$vox_per_pix = \frac{vox_size}{pixel_size}$$

The counts per minute per voxel for each frame becomes:

cnts_min_vox = mean_counts/(duration • vox_per_pix)

where:

mean_counts = mean counts per pixel over an entire frame

duration = frame duration in minutes

The calibration factor for each frame is finally computed as:

cal_fact = concentration/cnts_min_vox^{(nCi/(ml)/cpm/voxel)}

The deadtime factor for each frame is calculated by dividing each calibration factor by the calibration factor for the last frame, which is assumed to have no deadtime.

An example for the output file for a typical calibration is shown below:

Rate Factor Table for p0s4_suvcal20020718.img - Voxel Size Used: 2x2x2 Activity: 2.08 mCi; Start Delay: 8.98 min; Phantom Volume: 9293 ml Ellipse %: 0.670; Slices Skipped: 4

FRM	Ave Singles	nCi/ml	duration (m)	cnts/pix	Cal Factor	DT Factor
1	9123420	223.685	15.000	9441.417	2.843	2.168
2	8137160	223.685	15.000	11090.166	2.420	1.846
3	7279620	223.685	15.000	12542.312	2.140	1.632
4	6528520	223.685	15.000	13781.213	1.948	1.485
5	5851660	223.685	15.000	14819.377	1.811	1.381
6	5243180	223.685	15.000	15700.172	1.710	1.304
7	4712360	223.685	15.000	16469.656	1.630	1.243
8	4245580	223.685	15.000	17114.615	1.568	1.196
9	3653260	223.685	30.000	35667.020	1.505	1.148
10	2975140	223.685	30.000	37206.551	1.443	1.100
11	2449800	223.685	30.000	38306.738	1.401	1.069
12	2003000	223.685	30.000	39040.746	1.375	1.049
13	1654920	223.685	30.000	39643.863	1.354	1.033
14	1363160	223.685	30.000	40067.379	1.340	1.022
15	1039760	223.685	60.000	80974.594	1.326	1.011
16	724100	223.685	60.000	81486.562	1.318	1.005
17	505680	223.685	60.000	81892.656	1.311	1.000
18	364400	223.685	60.000	82171.789	1.307	0.996
19	265600	223.685	60.000	82138.359	1.307	0.997
20	200220	223.685	60.000	81882.594	1.311	1.000

The above table is used during the SUV calculation, which is performed as part of the reconstruction (if the patient's weight, activity and time of activity measurement are entered during the acquisition, otherwise these fields must be added before reconstruction using the mainheader edit utility (see the options menu in the study window of the File Manager).

The SUV Calculation

$$SUV((\mu Ci)/(ml)/(mCi)/(kg)) = \frac{((Uptake)/1000)}{((activity)/(weight))}$$

where

$$Uptake(nCi / ml) = \frac{(cal_fact)}{(vox_per_pix^*duration)}$$

Since the values stored in an image are counts, each pixel is converted to an SUV by multiplying the pixel value by the new SUV scale factor, which is computed for each slice as

$$suvscl = \frac{(cal_fact / duration)}{1000 / (activity / weight)}$$

This SUV scale factor field is stored in the subheader of each slice of each frame of the image.

20 UNIX COMMAND SUMMARY

Listed below are the most commonly used Unix commands. To produce a more thorough explanation of each command, type:

man <command name>.

UNIX Command	Usage
bin	Alias for cd /home/ugm/scanner/bin
cat <filename></filename>	Display the contents of the specified file. The file specified by < filename > must be a text file. Equivalent to MS-DOS type command.
cd	Change to the home directory. The home directory for the patient login is /home/patient.
cd <directory name=""></directory>	Change to the specified directory. The path from the current directory must be given.
cd.	Change to the parent of the current directory, e.g. from /dir1/dir2/dir3 to /dir1/dir2.
cd /OD	Change to the root directory of the mounted optical disk. See odmount and odmount
chgrp <group> <filename></filename></group>	Change the group ownership of the specified file.
chmod <permissions> <filename></filename></permissions>	Change the permissions of the specified file
chown <owner> <filename></filename></owner>	Change the ownership of the specified file

UNIX Command	Usage
cp <filename1> <filename2></filename2></filename1>	Copies filename1 to filename2. cp -p preserves timestamp and ownership information in the new file.
df	Show total, used, and available disk space in kbytes on all mounted file systems.
du	Show disk space in kbytes occupied by files in current directory and, recursively, all subdirectories.
h	Alias for history. See below.
history	Print the command history. Aliased by ${f h}$ in the default patient shell.
<pre>ln -s <fname1> <fname2></fname2></fname1></pre>	Create a symbolic link, fname2, which points to fname1.
ls	List all files in the current directory.
ls <filename></filename>	List all files defined by <filename> in the current directory. Wildcard (* or?) can be used in <filename>.</filename></filename>
ls -l <filename></filename>	List files in the current directory, in filename alphabetical order, with all attributes such as permissions, ownership, and timestamp. <filename> is optional and may include wildcards.</filename>
ls -lrt <filename></filename>	List files in the current directory in reverse chronological order, newest files last. <filename> is optional and may include wildcards.</filename>
man < command name>	Display the Unix manual page for the specified command. Hit the spacebar to advance page by page.
man ugmapp	Display a summary of Philips/C-PET programs.
mkdir <directory name=""></directory>	Make a new directory called <directory name="">. Aliased to md under patient login.</directory>

UNIX Command	Usage
mv <fname1><fname2></fname2></fname1>	Move a file to a new location or rename a file.
odmount	Mount the optical disk in the drive at /OD.
odumount	Unmount the optical disk. Note that odumount fails if a process is accessing the optical disk.
<pre>pall2img <file.pall> <file.img></file.img></file.pall></pre>	Convert Profile-ready .pall file (PMT histogram file) to a Load-ready .img file. Each detector's worth of PMT histograms appears as a frame.
pwd	Echo the current directory name as the complete path.
rm <filename></filename>	Remove (delete) <filename>. When logged in as patient, rm is aliased by rm -i, which prompts the user before deleting each file. When logged in as root, rm simply deletes the file. Note that Unix provides no means of recovering deleted files.</filename>
rmdir < directory name>	Remove <directory name="">. The directory must be empty. Aliased by rd under patient login.</directory>
su <username></username>	Change user identity to <username>. User is prompted for the appropriate password. Type exit or ^d to return to previous status. Please heed Service Manual warnings regarding root privileges.</username>
tables	Alias for cd /home/ugm/scanner/tables.
textedit <filename></filename>	Opens textedit, a simple GUI text editor. Less powerful but much easier to use than classic Unix editors such as vi, emacs, and ex.
11	Repeat the previous command. Does not work when user is logged in as root.
! <string></string>	Repeat most recent command beginning with <string>.</string>

UNIX Command	Usage
<pre>!<command number=""/></pre>	Repeats the command specified by <command number=""/> . See history.

Notes

Appendix **A LISTVIEW ACQUISITION**

Listmode data are acquired one event at a time and can be buffered in the CRB or read directly via the VME backplane. The data can be stored as listmode events in several formats, can be rebinned into 1-D histograms or can be rebinned into 2-D histograms.

Transmission data can not be acquired in listmode, since the angle information is not included in the data stream.

Acquisition Menu:

- Left click desktop and select Service > Service menu
- Select *Listview/rawview* command interface
- At the *<user>* prompt type: listview

```
Enter your choice: 4

User program $Release: 7.3 $

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Enter a command or type 'h' for help.

user> llistview

Warning: unknown command.

Try again or enter 'q' to quit!

user> listview

Reading system configuration from /home/ugm/scanner/tables/sys.cfg.

Reading calibration configuration from calib.cfg

system has virtual PMTs.

List Mode Acquisition Choices

0 - Proceed to next menu

1 - Type of acquisition listview

2 - Take data from scanner

- Take data from file

4 - Number of events 100000

5 - Number of events 100000

6 - Acquisition duration 00:10:00 (in hh:mm:ss)

7 - Event triggering hardware

- Fake zone& (for MCB)

10 - Collection mode acon

- Fake zone& (for MCB)

11 - Print rejected list mode data off

12 - Print rejected list mode data off

13 - Energy correction tables file /home/ugm/scanner/tables/ecorr20001130.hex

15 - Distortion removal file /home/ugm/scanner/tables/distfact20001130.hex

16 - Distortion removal file /home/ugm/scanner/tables/distfact20001130.hex

17 - Save list mode events off

18 - Save gist mode events in file

21 - Save dist mode events in file

23 - List/gist/dist files will contain all events

24 - Generate 1D histogram on

25 - Generate 2D histogram on

26 - Ero histogram iarge (4x1 compressed)

27 - Type of 2-D histogram iarge (4x1 compressed)

28 - Zero histogram arrays on

29 - Save disting file iarge (4x1 compressed)

29 - Save disting file iarge (4x1 compressed)

20 - Save disting file iarge (4x1 compressed)

29 - Save disting file iarge (4x1 compressed)

20 - Zero histogram arrays on

20 - Save disting file iarge (4x1 compressed)

20 - Zero histogram arrays on

21 - Save disting file iarge (4x1 compressed)

20 - Zero histogram arrays on

21 - Save disting file iarge (4x1 compressed)

22 - Zero histogram arrays on

23 - Save disting file ia
```

A menu similar to the one above is displayed, depending upon the last listview acquisition used. Each item in the menu is described below:

1 - Type of Acquisition listview/gistview/VME listview

If **1** is selected, the following submenu will appear:

0 - listview

- 1 gistview
- 2 VME listview

<u>Listview</u> writes event-by-event data using a long data format which preserves the maximum amount of data.

<u>Gistview</u> is a shorter data format in order to preserve disk space by eliminating some data such as energy values.

<u>VME listview</u> writes data in the listview format, but takes the data, one event at a time from the input to the CRB while option 1, listview, accumulates one buffer of listview data in the memory of the CRB and then reads out the complete buffer.

2 - Take Data from

scanner/file

If **2** is selected, the answer will automatically switch between the two choices. If the data are taken from file, item **3** - Take data from file allows you to select a file name.

4 - Number of Events 1000000

If **4** is selected, you will be prompted for the total number of events which you want to collect.

5 - Number of Events per buffer 1000

If **5** is selected, you will be prompted for the number of events per buffer which you want to collect. After each buffer is collected the data are transferred to disk and you will see some CRT output. Making the buffer to big will reduce the screen output, but will not allow you to see the progress of the acquisition in real time. A buffer size between 1000 and 10000 is customary, usually a larger buffer size is selected for longer collections.

6 - Acquisition Duration 00: 00:00

If **6** is selected, you may enter a preset time for the data collection. If you enter 0, the acquisition will stop after a pre-selected number of counts (see 4 above). This option has not been tested recently.

7 - Event Triggering

hardware/hardware, fixed zone

If 7 is selected, the following submenu will appear

- 0 hardware
- 1 hardware, fixed zone

Normally data are triggered by the hardware. The option **hardware**, **fixed zones** has been added in order to allow testing of an acquisition mode used by dr4, the distortion removal program.

10 - Collection Mode

coincidence/singles

If **10** is selected, the answer will automatically switch between the 2 choices. Note that changing the collection mode from coincidence to singles will not change the high voltage to bring the 662 keV peak from Cs-137 to a value of 100.

11 - Print Listmode

data off/on

If **11** is selected, the answer will automatically switch between the 2 choices. If this option is **on**, all listmode data will be written to the screen.

12 - Print Rejected Listmode data off/on

If **12** is selected, the answer will automatically switch between the 2 choices. If this mode is **on**, only those events which have been rejected by the gating (to be described below) will be written to the screen. This feature is useful for debugging, particularly in those cases where most events are accepted.

13 - Energy Correction

off/software/hardware

If 13 is selected, the following submenu will appear

0 - off

- 1 software
- 2 hardware

The spatially varying energy correction can be applied either on the CRB or in software. If no energy correction is required, the file name (14) is blank. If either hardware or software energy correction is selected, the file name must be specified in option 14. Depending on the choice, the program will disable software energy correction, if hardware energy correction is selected and vice versa, i.e. the energy correction is never performed both in hardware and software simultaneously.

14 - Energy Correction Tables File

home/ugm/scanner/tables/eco rryyyymmdd.hex

All tables associated with data acquisition normally reside in the /home/ugm/scanner/tables directory. The energy correction file is usually named ecorr followed by the acquisition date of the correction data in the yyyymmdd format.

15 - Distortion Removal

off/software/hardware

if you select '15' the following submenu will appear

- 0 off
- 1 software
- 2 hardware

The distortion removal correction can be applied either on the CRB or in software. If no distortion removal correction is required, the file name (16) is blank. If either hardware or software distortion removal correction is selected, the file name must be specified in option 16. Depending on the choice, the program will disable software distortion removal, if hardware distortion removal is selected and vice versa, i.e. the distortion removal is never performed both in hardware and software simultaneously.

16 - Distortion Removal File

/home/ugm/scanner/tables/dis tfactyyyymmdd.hex

All tables associated with data acquisition normally reside in the /home/ugm/scanner/tables directory. The distortion removal file is usually named 'distfact' followed by the acquisition date of the correction data in the yyyymmdd format.

17 - Save Listmode Events on/off

If **17** is selected, the answer will automatically switch between the 2 choices. If you turn this option on, you must specify the file name in option **18**. The data format for list/gist and dist formats is explained under option 1 above.

18 - Save Listmode Event in File filename.list

Enter the desired directory and file name for the listmode data. If no directory is specified, the data will be stored in the **/home/patient** directory. The extension **.list** will be appended to the filename automatically.

19 - Save Gistmode Events on/off

If **19** is selected, the answer will automatically switch between the 2 choices. If you turn this option on, you must specify the file name in option **20**. The data format for list/gist and dist formats is explained under option 1 above.

20 - Save Gistmode Event in File filename.gist

Enter the desired directory and file name for the gistmode data. If no directory is specified, the data will be stored in the **/home/patient** directory. The extension **.list** will be appended to the filename automatically.

21 - Save Distmode Events on/off

If **21** is selected, the answer will automatically switch between the 2 choices. If you turn this option on, you must specify the file name in option **22**. The data format for list/gist and dist formats is explained under option 1 above.

22 - Save Distmode Event in File filename.list

Enter the desired directory and file name for the distmode data. If no directory is specified, the data will be stored in the **/home/patient** directory. The extension '.list' will be appended to the filename automatically. Dist mode is similar to gist mode and is only used by dr4, the distortion removal program. It is included here only to allow debugging of the program.

23 - List/Gist/Dist Files will contain all EventsList/gist/dist files will contain gated events

If **23** is selected, the answer will automatically switch between the 2 choices. The gating options are explained below.

24 - Generate 1D Histograms on/off

If **24** is selected, the answer will automatically switch between the 2 choices. The 1D histogram data are stored in the files specified in option 26 below. For a description of the files see option 26 below.

25 - Generate 2D Histograms on/off

If **25** is selected, the answer will automatically switch between the 2 choices. The 2D histogram data are stored in the file specified in option **26** below. For a description of the file see option 26 below.

26 - Histogram Filename Prefix <name>

The 1D and 2D files will be stored in the <code>/home/patient</code> directory using the selected file as a prefix.

The 1D histograms of all acquired events will be stored in ASCII files. The data will be sorted into histograms for x, y, local energy and global energy separately for each detector and also combined into a single file for all 6 detectors. These files can be displayed using the profile program.

The 2D histograms will be stored in a image file format and can be viewed using the **Load** and **Display Brain** programs.

Typical examples of these files are shown below.

27 - Type of 2D Histogram

small/large/binary

If '27' is selected, the following submenu will appear

- 0 small(4x4 compressed)1 large(4x1 compressed)
- 2 binary (uncompressed)

Both the large and small formats can be displayed using the 'Display Brain' program in different sizes. The binary format stores the data uncompressed in strict binary format which can be viewed using the **slicer** or **xloadimage** described in more detail below.

28 - Zero Histogram Arrays on/off

If **28** is selected, the answer will automatically switch between the 2 choices. Normally the histograms are zeroed out before acquiring data. Occasionally it is desirable to add data taken under 2 different conditions into the same histogram file, which can be achieved by turning the **Zero Histogram** option off.

29 - Saved Settings File

All the settings for the current acquisition can be saved in a file for future reference.

<name>

0 - Proceed to Next Menu

After all the options have been set to the desired values, enter **0** to proceed.

Gating

Listview events can be gated using a number of parameters in order to reduce the amount of data being stored in the listfile or being accumulated into the 1-D or 2-D histograms. The listmode data coming from the hardware are being examined event-by-event in order to test the various gating conditions. Note that both events must fulfill the requirements, but different energy windows zones can be enabled for detectors A and B.

The maximum range of the energy is 255. After energy correction, the photopeak should be located at channel 100. The maximum range of the X-coordinate is 1023 and the maximum range of the Z-coordinate is 255.

The gating menu allows the difference between the 2 x-coordinates and the 2 ycoordinates to be restricted. For example, if one wanted to investigate the effect of depth of interaction, it would be possible to select nearly parallel coincidences.

Finally, the gating allows various zones in each detector to be turned on or off.

The following gating menu is shown:

GATING OPTIO	NS SETUP			
Do you wish to	view current	gating options?	(y/n) (returr	n=y): y
*** GATING PARA	METERS ***			
Local energy: Global energy: X: Z: Delta X: Delta Z: Auxiliary: Timestamp:	on on on on on off off	A 25 250 A 25 250 A 0 1023 A 1 255 Max 1023 Max 255	B B B	25 250 25 250 0 1023 1 255
Bankpair: 1 2 3 4	on Enak 5 6 7 8 0 1	oled bankpairs: 9 Cones in A 2 3 4 5 6 7	0	zone: on Zones in B 1 2 3 4 5 6 7
Det 1: Det 2: Det 3: Det 4: Det 5: Det 6:	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$egin{array}{ccc} 0 & 0 \\ 8 & 0 \\ 16 & 0 \\ 24 & 0 \\ 32 & 0 \\ 40 & 0 \\ 48 & 0 \\ 56 & 0 \end{array}$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$
Do you wish to	change curre	ent gating options'	? (y/n) (retu	urn=y):

Most of these parameters are self-explanatory. The default settings can be changed using the submenu shown below and following the instructions.

Do you wish to change gating options? (y/n) (return=y): Reset gating options to DEFAULT settings? (y/n) (return=y): Gating Modify Selections: 1 Local Energy 2 Global Energy 3 X Axis 4 Z Axis 5 Zone A 6 Zone B 7 Bankpairs 8 Delta X Delta Z 9 10 Auxiliary 11 Time-Stamp

12 View Selected Options

Enter Selection(0 to exit):

After the gating options are selected, the data acquisition begins, giving a screen output once per buffer to indicate the progress of the acquisition as shown below.

689996 events processed of 1000000 total; 4 rejected.
699996 events processed of 1000000 total; 4 rejected.
709996 events processed of 1000000 total: 4 rejected.
719996 events processed of 1000000 total: 4 rejected.
729996 events processed of 1000000 total: 4 rejected
739996 events processed of 1000000 total: 4 rejected
749996 events processed of 1000000 total: A rejected
750006 events processed of 1000000 total, 4 rejected.
769006 events processed of 1000000 total, 4 rejected
109996 events processed of 1000000 total; 4 rejected.
11 streport invalid zones: 2602. zoneA = 63; Valid range 1s 1 to 47.
(19995 events processed of 1000000 total; 5 rejected.
789995 events processed of 1000000 total; 5 rejected.
799995 events processed of 1000000 total; 5 rejected.
809995 events processed of 1000000 total; 5 rejected.
819995 events processed of 1000000 total; 5 rejected.
829995 events processed of 1000000 total; 5 rejected.
839995 events processed of 1000000 total; 5 rejected.
849995 events processed of 1000000 total: 5 rejected.
859995 events processed of 1000000 total: 5 rejected.
listReportInvalidZones: 2601, zoneA = 63: valid range is 1 to 47.
869994 events processed of 1000000 total: 6 rejected
879994 events processed of 1000000 total: 6 rejected
889994 events processed of 1000000 total: 6 rejected
899994 events processed of 1000000 total, 6 rejected.
POPOA events processed of 1000000 total, 6 rejected
Just and the second sec
listReport invalidzones: 6111. zoneA = 63; Valid range is 1 to 47.
919993 events processed of 1000000 total; / rejected.
929993 events processed of 1000000 total; / rejected.
939993 events processed of 1000000 total; 7 rejected.
949993 events processed of 1000000 total; 7 rejected.
959993 events processed of 1000000 total; 7 rejected.
969993 events processed of 1000000 total; 7 rejected.
979993 events processed of 1000000 total; 7 rejected.
listReportInvalidZones: 5958. zoneA = 63; valid range is 1 to 47.
989992 events processed of 1000000 total: 8 rejected.
999992 events processed of 1000000 total: 8 rejected.
Waiting for events from hardware
arony for evenes from hardware
avhCloarMawBank() Evit measure -361
Ciderent Membalk() ball, miseus – Joi
(100000 symbol provide the state of the
ibbobbb events processed of ibbobbb total; 6 rejected.
LIST_CMD - HAVE READ ALL 1000000 CNT_EVENTS, NOM_EVENTS 10000000; 8 REJECTED

Writing 1D Histogram files
Writing LFOV 2D Histogram file test.scn.
Freeing factor and ecor tables
lser>

Output Examples

The following shows a list of all the files generated when saving list mode, 1-D and 2-D histograms. The 1-D histogram files for global energy (ge), local energy (le), x-coordinate and z-coordinate are saved separately for each detector and also in a combined file in ascii format.

-rw-rw-r	1	patient	1854	Nov	12	08:53	test.ge1
-rw-rw-r	1	patient	1852	Nov	12	08:53	test.ge2
-rw-rw-r	1	patient	1851	Nov	12	08:53	test.ge3
-rw-rw-r	1	patient	1858	Nov	12	08:53	test.ge4
-rw-rw-r	1	patient	1843	Nov	12	08:53	test.ge5
-rw-rw-r	1	patient	1855	Nov	12	08:53	test.ge6
-rw-rw-r	1	patient	6120	Nov	12	08:53	test.geall
-rw-rw-r	1	patient	1820	Nov	12	08:53	test.le1
-rw-rw-r	1	patient	1822	Nov	12	08:53	test.le2
-rw-rw-r	1	patient	1821	Nov	12	08:53	test.le3
-rw-rw-r	1	patient	1823	Nov	12	08:53	test.le4
-rw-rw-r	1	patient	1809	Nov	12	08:53	test.le5
-rw-rw-r	1	patient	1821	Nov	12	08:53	test.le6
-rw-rw-r	1	patient	5923	Nov	12	08:53	test.leall
-rw-rw-r	1	patient	12001388	Nov	12	08:53	test.list
-rw-rw-r	1	patient	790528	Nov	12	08:53	test.scn
-rw-rw-r	1	patient	8111	Nov	12	08:53	test.x1
-rw-rw-r	1	patient	8112	Nov	12	08:53	test.x2
-rw-rw-r	1	patient	8112	Nov	12	08:53	test.x3
-rw-rw-r	1	patient	8112	Nov	12	08:53	test.x4
-rw-rw-r	1	patient	8112	Nov	12	08:53	test.x5
-rw-rw-r	1	patient	8112	Nov	12	08:53	test.x6
-rw-rw-r	1	patient	28203	Nov	12	08:53	test.xall
-rw-rw-r	1	patient	2280	Nov	12	08:53	test.z1
-rw-rw-r	1	patient	2270	Nov	12	08:53	test.z2
-rw-rw-r	1	patient	2279	Nov	12	08:53	test.z3
-rw-rw-r	1	patient	2276	Nov	12	08:53	test.z4
-rw-rw-r	1	patient	2263	Nov	12	08:53	test.z5
-rw-rw-r	1	patient	2277	Nov	12	08:53	test.z6
-rw-rw-r	1	patient	8657	Nov	12	08:53	test.zall
:057-acg:42>		22 2 23 4 2 5 5 5 5 6 5 6 5 6 5 6 5 6 5 6 5 6 5 6					

The following shows a sample output from the program 'listprint', which lists the various fields from the list mode to the screen. The first event stored per buffer is the time stamp, after that the printout shows the following data:

column

- 1 (#) event number,
- 2 (auA) auxiliary data for detector A
- 3 (d,zA) detector, zone for event A
- 4 (xA) x coordinate for detector A
- 5 (zA) z coordinate for detector A
- 6 (elA) local energy for detector A
- 7 (egA) global energy for detector A
- 8 (auB) auxiliary data for detector B
- 9 (d,zB) detector, zone for event B

10 (xB)x coordinate for detector B11 (zB)z coordinate for detector B12 (elB)local energy for detector B13 (egB)global energy for detector B14 (dX)15 (dZ)16 (ts)

								0				_	_	_		
- c057-acc	q:51> lis	stprin	t tes	t.lis	t mc	re	xterm									· .
LISTPR:	INT, Vers	sion 7	.3 													
# aı	uA d,zA	xA	zA	elA	eqA	auB	d,zB	хB	zВ	elB	eqB	dX (dZ t	s bp	1	
0 (0000000f 3f 1,6*	(time 816	stamp 36) 93	94	7f	4,6*	789	222	96	97			. 2		
2* 3 3* 3 4* 3	31 1,6* 3f 2,6* 3f 2.4*	908 831 476	166 126 56	102 102 102	95 102 100	7f 7f	4,/* 5,6* 5,3*	902 823 469	62 129 192	95 96 80	99 96 78			• 5		
5* 3 6* 3	3f 1,7* 3f 2,4*	988 589	200 110	99 104	100 104	7f 7f	4,7* 5,5*	966 594	37 113	99 61	97 62	÷		. 2		
7* 3 8* 3 9+ 3	3f 1,1* 3f 3,7*	93 889 460	116 228	102 99	101	7f 7f 7f	4,1* 6,7*	98 915 456	123 2	105	102 102	8. 0	9 11	. 2		
10* 3 11* 3	3f 1,2* 3f 1,1*	258 37	250 214	123 101	122 101	7f 7f	3,6*	805 37	$141 \\ 44$	94 106	93 104	÷		· 1		
12* 3 13* 3	Bf 1,7* Bf 4,1*	929 45	132 115	98 94	102 100	7f 7f	4,7*	897 604	107 197	105 88	106 87	2		. 200		
14* 3	31 4,5* 3f 2,2* 3f 2,1*	522 280 137	203 124 104	58 101 101	54 99 104	71 7f 7f	6,1* 5,2* 5 1*	65 262 145	99 124 140	93 95 94	95 96 96	÷	•			
17* 3 18* 3	3f 3,1* 3f 2,1*	40 117	188	101 78	100 85	7f 7f	6,1* 5,1*	42 112	59 182	102 100	100 99			. 8 . 9		
19* 3 20* 3	3f 2,6* 3f 2,2*	797 251	240 97	99 75	103	7f 7f	5,6*	792 260	5 149	98 110	107 114	6				
22* 3	Bf 2,2*	309 435	160 167 91	90 100 101	104 103	71 7f 7f	5,2* 4,3*	300 429	- 39 - 73 - 138	101	102	÷				
24* 3 25* 3	3f 3,6* 3f 1,2*	861 235	41 67	119 98	117 99	7f 7f	6,7* 4,2*	934 231	$\frac{167}{177}$	87 91	91 93	2	8	. 8		
26* 3	Bf 1,7* Bf 1,7*	977 886	178 60	102 110	129 129	7f 7f 7f	4,7*	954 846	79 182 72	107	121 125			. 2		
29* 3	3f 2,6* 3f 1.2*	793 227	164	97 101	97 100	7f 7f	5,7*	810 208	75 123	64 104	100 77 101					
31* 3 32* 3	Bf 1,2* Bf 1,4*	318 583	96 17	116 101	112 94	7f 7f	4,2* 4,5*	309 585	149 233	100 100	101 97	ій. С		. z		
33* 334* 3	3f 1,2* 3f 3,4* 3f 2,2*	333 473 179	18 29 66	106 102 121	105 101 143	71 71 71	4,3* 6,4* 5 2*	323 468 210	228 216 162	101 107 99	101 107 98	÷	·	. 8		
36* 3 37* 3	3f 3,2* 3f 3,5*	305 796	154 131	104 72	105	7f 7f	6,2* 6,6*	296 814	97 119	99 101	97 97		÷	. 8		
38* 3 39* 3	3f 3,1* 3f 2,2*	68 169	131 60	103 102	102 102	7f 7f	6,1*	53 162	113 175	99 94	97 99		•	. 8		
40* 3 41* 3 42* 3	Bf 1,5* Bf 2.2*	955 565 258	53 160 134	96 101 103	97 99 103	7f 7f 7f	3,7* 4,4* 5.2*	988 568 242	193 82 108	105 100 99	102 101 98			. 2		
43* 44*	3f 1,7* 3f 3,3*	827 342	73 88	88 95	96 96	7f 7f	4,6* 6,2*	811 335	185 159	99 99	101 100		1	. 2 . 8		
45* 3 46* 3	3f 2,6* 3f 1,6*	687 793	119 183	109 95	$\begin{array}{c} 108 \\ 100 \end{array}$	7f 7f	5,6* 4,6*	693 779	129 58	106 97	105 98	•	•	. 2		

17 (bp) bankpair

The 1-D histograms can be viewed using the **Profile** program (see User Manual for instructions). Below is shown the spectrum for list.leall, i.e. the local energy spectra for all 6 detectors.



The local energy spectra for all 6 detectors

Below is shown the 2-D histogram for a point source centered in the scanner, which shows a uniform irradiation for all 6 detectors. The data is loaded using the **Load** program as a sinogram; each detector 2-D histogram is shown as a separate **slice**



Each detector 2-D histogram is shown as a separate "slice"

Listview and Gistview Data Formats

This section describes the two formats used to save and transmit Listmode events on C-PET scanners. The most common format is listmode format, and this is described first. The other format, distmode format, is used by the spatial distortion removal program dr4. This second format is more compact, but contains only position information.

Definitions

detA	The lower numbered detector (the A detector) of a coincidence event.
detB	The higher numbered detector (the B detector) of a coincidence event.
zPosA	The Z position of the half of the event hitting the A detector. This is typically an 8-bit number.
xPosA	The X position of the half of the event hitting the A detector. This is typically a 10-bit number.
zoneA	The zone of the half of the event hitting the A detector. This is typically a 6-bit number. The top 3 bits contain the detector number, in a 0-based number scheme. The bottom 3 bits indicate coarsely the position (i.e. X coordinate) on that detector. (This coarse X positioning information normally has already been figured into xPosA.)
auxA	Extra information about the A half of the event.
eLocalA	Local energy of the detector A event.
eGlobalA	Global energy of the detector A event.
zPosB	Like zPosA.
xPosB	Like xPosA.
zoneB	Like zoneA.
auxB	Like auxA.
eLocalB	Like eLocalA.
eGlobalB	Like eGlobalA.

Listmode Event Format

An event in listmode format consists of 3 words, each word 32 bits long. The first word contains information about the half of the coincidence hitting the A detector. The second word contains information about the half of the coincidence hitting the B detector. The third word contains information the energy of the events hitting the A and B detectors.

For word 0:

Bits 0 .. 7 contain zPosA

Bits 8 ..17 contain xPosA Bits 18 ..23 contain zoneA Bits 24 ..31 contain auxA

For word 1:

Bits 0..7 contain zPosB

Bits 8..17 contain xPosB

Bits 18 .. 23 contain zoneB

Bits 24 ...31 contain auxB

For word 2:

Bits 0..7 contain eLocalA

Bits 8..15 contain eGlobalA

Bits 16 .. 23 contain eLocalB

Bits 24 .. 31 contain eGlobalB

Listmode Capacity

In list mode the detector coordinates, detector zones, energies of the two events and auxiliary data are stored in 12 bytes per event. This mode gives the greatest flexibility in analyzing the data after the fact but requires the most disk space. List mode data can be stored either on the fixed disk or on removable optical disks. Assuming 2 Gbytes are available on the fixed disk, 166 million events can be stored. It must be emphasized that list mode is intended for research applications and is not useful for routine use due to the large disk space requirements and long processing times.

Listmode File Format

A listmode file contains an 80-byte header, followed by some number of listmode events.

The first 4 bytes of the header contain an integer, the buffer size used to acquire the events. This is also the maximum distance between "timestamps" in this file. (See below for information regarding timestamps).

The second 4 bytes in the file contain the 32-bit magic number 0x4C697374, which is the ASCII string "List". This may be used as a check, to verify that your I/O routines have actually been presented with a listmode data file.

The third 4 bytes of the header contain the file format version number. You should expect this to be either version 2 or version 3. Version 2 lacks timestamps, version 3 has timestamps embedded in the data.

The next byte, the 13th byte in the header, indicates what kind of events are in this file. If this byte is 0, it is coincidence data. If this byte is 1, then it is singles data. If the data are singles data, then two single events are packed into a listmode coincidence datum. The A fields correspond to one single event, and the B fields correspond to another. The two halves are unrelated.

The remainder of the 80 bytes of the total header is currently unused.

Timestamps are added to the stream of listmode events by some programs, to mark boundaries of acquisition buffers and to supply additional information about each buffer of events. A timestamp is the same size as a listmode event, and timestamps are embedded in the stream of listmode events. They form a linked list of sorts in the data, one timestamp giving the offset of the next one (or considered a different way, each timestamp telling how many events following it). Normal listmode acquisition programs insert timestamps that mark acquisition buffer boundaries, but these timestamps carry no additional information. These timestamps are typically ignored in subsequent processing. Timestamps can be recognized, and safely simply discarded, by noting that they have 0 for all their energy fields.

Distmode Event Format

The distmode format may be appropriate when energy gating has already been done, and energy information is no longer important, and when there is no extra information in the auxA or auxB field of listmode events. Because the distmode format discard the energy and aux fields, it takes half the size of the listmode format, and so may be helpful when extremely large numbers of events must be saved on disk or transmitted.

An event in distmode format consists of six bytes of information.

Byte 0 contains zPosA.

Byte 1 contains the low 8 bits of xPosA.

Byte 2, bits 0 .. 1 contain the high 2 bits of xPosA.

Byte 2, bits 2 .. 7 contain zoneA.

- Byte 3 contains zPosB.
- Byte 4 contains the low 8 bits of xPosB.

Byte 5, bits 0 .. 1 contain the high 2 bits of xPosB.

Byte 5, bits 2 .. 7 contain zoneB.

Distmode File Format

A distmode file consists of a header of 20 bytes, followed by zero or more events in distmode format. The header is divided into five 4-byte words.

The first word of the header contains the magic number 0x44697374, which is the ASCII string "Dist". This may be used as a check, to verify that your I/O routines have actually been presented with a distmode data file.

The second word of the header contains the file format version number. You should expect this to be 2.

The third word of the header contains the acquisition buffer size. This information may be useless, because distmode format does not have embedded timestamps.

The fourth word of the header contains the number of events in the file.

The fifth word of the header contains the duration of the acquisition, in seconds.

The header is followed by the distmode events.

Gistmode Event Format

The gistmode event format is very similar to the distmode format. The information conveyed is the same; its location is different. The gistmode format is a slightly earlier variant of distmode format. Pairs of coincidence events are packed into 12 bytes, in a slightly scrambled interleaved fashion. Here is how to decode each 12 bytes:		
Byte 0	contains event 0 zPosB	
Byte 1, bits 01 contains event 0 high 2 bits of xPosA		
Byte 1, high 27 contain event 0 zoneA		
Byte 2	contains event 0 low 8 bits of xPosA	
Byte 3	contains event 0 zPosA	
Byte 4	contains event 1 low 8 bits of xPosA	
Byte 5	contains event 1 zPosA	
Byte 6	, bits 01 contain event 0 high 2 bits of xPosB	
Byte 6, bits 27 contain event 0 zoneB		
Byte 7	contains event 0 low 8 bits of xPosB	
Byte 8	, bits 01 contain event 1 high 2 bits of xPosB	
Byte 8, bits 2 contain event 1 zoneB		
Byte 9	contains event 1 low 8 bits of xPosB	
Byte 10) contains event 1 zPosB	
Byte 11, bits 01 contain event 1 high 2 bits of xPosA		

Byte 11, bits 2..7 contain event 1 zoneA

If you look closely, you will realize that this is the same as distmode, but with some unfortunate byte-swapping superimposed.

Gistmode File Format

The format of a gistmode file is very much like a distmode file. A 20-byte header is followed by 0 or more pairs of listmode events. The events that follow the header in the file are slightly different, as described above. The header is the same, except for two fields.

The first difference is in the first 4-byte field, the magic number. The magic number is 0x47697374, which is the ASCII string "Gist".

The second difference is in the second 4-byte field, the file format version number. This should be 1.

Appendix B GLOSSARY

2 1/2**D DATA:** A 3D sinogram formed by applying some corrections to 4D data and then merging data from multiple tilts using Fourier Rebinning; the slices of the resulting 3D data are then reconstructed independently using 2D algorithms.

3D DATA: A single-frame, single-tilt sinogram (R, Phi, Slice); the format of single-tilt input data or the result of FORE applied to multi-tilt data during 2½D reconstruction.

4D DATA: A single-frame, multi-tilt sinogram (R, Phi, Slice, Tilt); the format of multi-tilt input data used by 3D reconstruction or by 2½D reconstruction prior to FORE.

4DAC: Attenuation correction performed on 4D data.

ABS: Absolute

ABSOLUTE POSITION: The position of the table in relation to the gantry after system startup, once the cradle has been moved all the way out.

AC: (Attenuation Correction) The purpose of attenuation correction is to correct for absorption of some particles by the object being scanned. There are two methods supported by reconstruction.

ACCELERATOR KEYS: Keyboard combinations that you may use in lieu of using the mouse to invoke functions.

ACQ: Acquisition Workstation

ACQUISITION: The act of collecting image data.

ACTIVITY LEVEL: In PET, the amount of radioactivity recorded at any point in time from a given radio tracer.

AFOV (Axial Field of View): The useful axial dimension of the scintillation crystals.

ALIGNMENT LIGHTS: These lights are used to help position the patient within the field of view (FOV). Two planes within the detector are defined by the laser alignment lights.

ANNIHILATION EVENTS: The collision of a positron with an electron, which emits 2 gamma rays with an energy of 511 keV.

ANNOTATION: Generally, system-supplied text which accompanies an image when it is displayed onscreen, describing when and how the image was acquired, of whom, and with what parameters. Also, user-supplied text.

APEX: In the heart, the top-most slice.

API: Application Program Interface

APPLICATION SOFTWARE: System-supplied software that runs primary system features such as Display, Region-of-Interest analysis.

AWS: Acronym for the C-PET system's image Analysis Workstation, which allows you to perform all the same functions as the Operator's Workstation, with the exception of acquisition, calibration and archiving.

BASE: In the heart, the bottom-most slice.

BLANK SCAN: A scan which verifies that all the detectors are functioning by directly measuring system sensitivity for each coincidence line, without attenuation or decay correction.

BLOB: Spherically symmetrical volume element

BUTTONS: Graphical features that allow you to invoke specific functions.

CAR: (Concurrent Acquisition and Reconstruction)

CCA: Circuit Card Assembly

CFD: Constant Fraction Discriminator

CINE: An image display mode used for viewing a series of images at a prescribed number of images per second. This gives the effect of motion and allows you to see how images taken at the same location change over time.

CLICK: To press and release a mouse button without moving the cursor.

CLICK AND DRAG: To press and hold the mouse button while moving the cursor across the screen.

cm: centimeter
COINCIDENCE EVENT: The annihilation of a positron and an electron results in the generation of tow gamma rays traveling in opposite directions. If these two gamma rays each strike detector crystals at nearly the same time (within nanoseconds), the are said to be in coincidence. A coincidence event is characterized by the location of the interaction of the two events in the crystals.

COINCIDENCE LINES: Lines drawn between the point of interaction of the two gamma rays found in coincidence.

COLORMAP: A vertical color spectrum accompanying displayed images, which indicates the color shades used to represent pixel intensities.

CONCURRENT RECONSTRUCTION: Concurrent reconstruction allows images to be reconstructed as soon as possible. This involves starting a reconstruction at the time the acquisition is started. The reconstruction coordinator monitors the incoming data, once enough raw data is available in the sinogram, the reconstruction program is invoked. This process repeats as the raw data becomes available until the last image is reconstructed.

CORONAL PLANE: A horizontal plane along the longitudinal axis of the body, dividing it into anterior (front) and posterior (back) portions.

CORONAL VIEW: This view displays multiple rows and columns of coronal views with a specified starting slice, thickness, and increment.

CRB: Correction Rebinning Board

CURSOR: A maneuverable on-screen feature used to invoke specific functions.

CURVE: A graphical representation of numerical data.

DD: Day

DEFAULTS: A pre-defined filed or selection that the system automatically offers for your use.

DELETE: The act of erasing data from the disk to make room for additional data.

DETECTOR: The system component that detects the gamma radiation emitted during annihilation.

DICOM: (Digital Imaging and Communications in Medicine) Used to convert DICOM formatted image files to the PETVIEW format so files can be loaded and displayed with PETVIEW software.

DIG: Digitizer

DOUBLE-CLICK: To press and release the mouse button twice in rapid succession.

DYNAMIC IMAGES: Generally, images collected over time to see changes over time at specific slice locations.

DYNAMIC IMAGING: A scan mode that lets you view images in a single FOV over a period of time. Usually used in conjunction with region drawing (ROIs), these studies are used primarily for viewing tracer kinetics and observing uptake over time.

EC: (Emission Contamination) emissions other then from the transmission source

ECG: Electrocardiogram

ECORR: Energy Correction

ELECTRON: A negatively charged particle found in all atoms.

EMERGENCY OFF: A switch that turns off all system components.

EMERGENCY STOP: A button that halts all table and gantry motion.

Emitcollect: An emission collection that measures the distribution of activity in the field of view. During an emission collection, all event processing (triggering, energy determination, position calculation, and rebinning) is performed in hardware.

E-Stop: Emergency Stop

F-18: Fluorine 18

FBP: (Filtered Back Projection) an analytical image reconstruction algorithm

FDG: Fluoro-2-deoxy-glucose

FLUORINE-18: The radioisotope used in 90% of current clinical PET procedures. It is most commonly tagged to deoxy-glucose.

FOURIER REBINNING: A method of data reduction that converts the oblique trajectory of a photon pair from oblique sinogram coordinates (x',y',phi,theta) to a trajectory contained in one perpendicular slice, as in our current sinogram coordinates (z, r, phi).

FOV: Acquisition transverse field of view.

FRAME: A frame consist of up to 127 slices that can be generated during an acquisition. The term frame is really a shortened form of time frame. All coincidence events that occur during an operator-specified time frame are stored in a single set of slices.

FWHM: Full Width Half Maximum

GAMMA RAYS: Electromagnetic radiation emitted by radioactive substances.

GANTRY: The gantry contains the detectors, the alignment lights and the operator controls for the table.

GAP COMPENSATION: A method by which missing data from sinograms, due to the gaps between the detectors, are estimated. There are two methods currently used: the Constrained Fourier Method and the Iterative Method.

GATED IMAGES (or Cardiac Gated Images): Images acquired with gating leads to monitor the patient's heartbeat, with acquisition triggered by the R-wave of the EEG.

GATING: A scan mode that lets you reduce the blurring effects of motion by collecting data within a patient's cardiac cycle - essentially, freeze-framing the anatomy of interest. The cardiac cycle is divided into a number of collection points or frames.

GB: Gigabyte

GDR: (GSO Distortion Removal) A spatial calibration that converts measured event positions to real, physical positions on the face of the detector.

GE: Global Energy

GRAPH (or plot): A diagram used to display numerical data.

GSO: (Gadolinium Orthosilicate) Each module is populated with an array of 638 Gadolinium Orthosilicate (GSO) crystals, totalling 17,864 crystals.

HALF LIFE: The length of time required for a given radioisotope to lose half of its original radioactivity through the process of decay.

HARD COPY: A paper print, transparency, or film.

HIDE/SHOW ANNOTATION: A function that allows you to temporarily remove image-specific and userentered annotation from an image.

HISTOGRAM: A bar plot that shows you the relative number of pixels in each of a series of intensity value ranges.

HV: High Voltage

ICON: A small, graphical representation of an on-screen feature or window.

IMAGE: A cross-sectional representation of anatomy or physiologic function, reconstructed from data acquired during a scan.

IMAGE ANALYSIS: Denotes a family of functions that allow you to extract additional information about the image.

IMAGE MATH: An image analysis function that allows you to perform a variety of mathematical computations on images to obtain derived images.

INTERFERENCE CONDITION: A situation in which the operator is moving the table on a path that may cause either the patient or table to collide with the Gantry.

I/O: Input/Output

kCPS: kilo Counts Per Second

keV: kilo electron Volt

KNITTING: Combining multiple single-frame reconstructed images to form a single full-body image.

LANDMARK: Part of a patient's anatomy used as an anatomic reference for locating transverse slices.

LAYOUT: The format in which windows are displayed on-screen.

LE: Local Energy

LOG OFF: A procedure resulting in the termination of current user activities, including all related applications.

LOG ON: A procedure that enables the user to access the system's application software and primary system features.

LOR: Line of Response

LSD: Least Significant Bit

MBq: Mega-Becquerel

mCi: mili-Curie

Mcps: Million counts per second

MCS: Motion Control System

MCT: Master Controller and Timing

ml: milliliter

MM: Month

mm: millimeter

Na²²: Sodium 22

MOUSE: A hand-operated device used to move the cursor across the screen and to invoke specific functions.

NETWORKING: Transferring data between workstations.

NORMALIZATION SCAN: A scan which measures system sensitivity for each coincidence line, to correct the data in emission scans.

ns: Nanosecond

OBLIQUE SINOGRAM FORMAT: [slice][phi][ray] - Normal UGM sinogram format

OD: Optical Disk

OSEM: (Ordered Subset Expectation Maximization) an iterative statistical image reconstruction algorithm

PAC: Preamp CFD

PATIENT RELATIVE POSITION: The location of the patient anatomy under the alignment lights relative to the landmark location.

PDU (or Power Distribution Unit): Equipment that supplies electrical power to the entire PET system.

PET: Positron Emission Tomography

PIN SOURCES: Sealed linear containers of Ge-68, used to make attenuation correction.

PIXEL: Abbreviation for "picture element". The smallest unit displayed on the computer screen.

PLD: Programmable Logic Device

PM: Preventive Maintenance

PMT: Photo-Multiplier Tubes

POLAR DISPLAY: An automated, computerized technique that lets you view a volume of image data in a single image display. Used most often with myocardial images. Also called polar mapping.

POSITRON: The anti-particle of an electron, having the same mass and opposite charge. Positrons are the product of the decay of certain isotopes.

POSITRON EMISSION: The release of positrons from a radioactive isotope.

PPP: (Point-to-Point Protocol) For communications between two computers.

PPU: Positron Processing Unit

PROCEDURE: A set of scans performed for a common purpose on a single patient.

PROJECTION SINOGRAM FORMAT: [phi][slice][ray] - Original UPENN sinogram format

PROJECTION VIEW: This view presents projection data at consecutive angles in multiples rows and columns.

PROTOCOL: A procedure file which allows you to execute predefined steps automatically.

QC: Quality Control

RAMLA: (Row Action Maximum Likelihood Algorithm) an image reconstruction algorithm

RAW DATA: Acquisition data before reconstruction, which may contain information of trouble-shooting value for the service representative.

REBOOT: A method of system start-up that allows you to reset system operating software and results in a series of diagnostic system tests.

RECONSTRUCTION: The process of creating a displayable image from raw acquisition data.

REFORMATTING: The process of taking image data from a set of transverse scans and reconfiguring them to produce images on any plane within that image set.

ROI (Region of Interest): A user-defined region of the displayed image to be quantitatively analyzed. Also, the system-supplied tools used to define an ROI.

ROTATING/TSC VIEW: This view displays a transverse, sagittal, and coronal images coupled with a 3D rotating projection of the data.

R&R: Removal and Replacement

RU: Relay Unit

SAGITTAL PLANE: A plane dividing the right side of the body from the left.

SAGITTAL VIEW: This view displays multiple rows and columns of sagittal views with a specified starting slice, thickness, and increment.

SELECT: To activate, usually by clicking with the mouse button.

SHUT DOWN: Refers to logging off, or powering down the system.

SINGLE PASS: A type of acquisition that combines emission and transmission.

SINGLE SLICE REBINNING: Method of data reduction that converts the detector coordinates of a photon pair, i.e., the positions at which they hit the detector, to sinogram coordinates.

SLICE ADDING: Axial smoothing operation performed after merging multiple single-frame input sinograms into a multi-frame whole body sinogram to reduce seam artifacts.

STANDARD DEVIATION: A statistical measurement that provides a measure of variability.

SUV (Standardized Uptake Value): The ratio of the concentration of activity in a structure to the average concentration in the entire body.

SVR: Reconstruction Workstation

SYSTEM DISK: The system component on which image, scan files and other patient data are stored until archiving. Also contains all system and applications software.

TABLE: The person or object being scanned is placed on the table and is positioned inside the bore of the gantry. Controls for positioning the table are located on the gantry.

TILT: The tilt or oblique angle is defined as the angle between the line-of-response and the X-Y plane of the scanner. This assumes a right-handed Cartesian coordinate system with the positive Z-axis pointing out of the front of the scanner along its cylindrical axis, and the positive Y-axis pointing straight up. The tilt angle of a line-of-response pointing in the X-Y plane is defined to be 0 degrees. Tilts that would project onto to positive Z-axis are defined as having a positive tilt. Each positive tilt has a negative partner with the same absolute oblique angle. The only exception is the zero-degree tilt, which has no partner.

TIME ACTIVITY CURVE: A curve that you might use to track multiple images acquired at a single location to show how the level of activity within a given area of interest changed over time.

TOGGLE: A term used to describe a function you select once to turn on, and again to turn off.

TRANSVERSE VIEW: This view displays multiple rows and columns of transverse views with a specified starting slice, thickness, and increment.

TRIGGER: In cardiac gating, a signal sent by the cardiac monitor to activate data acquisition.

VAC: Volts Alternating Current

WBD: (Whole Body Display)

WINDOW: A graphical box-shaped tool used to display features (such as images or graphics) on-screen.

XTERM: A window that provides the more experienced user with access to the UNIX operating environment.

YYYY: Year

ZOOM: An image presentation function that allows you to magnify a displayed image within its window.

Appendix **SYMBOLS**

No.	Symbol	Description
1	~	Alternating current
2	3 ~	Three-phase alternating current
3	(l)	Protective earth (ground)
4	<u>+</u>	Earth (ground)
5	N	Connection point for neutral conductor on permantently installed equipment
6	Ŷ	Equipotentiality
7	<u>!</u>	Attention, consult accompanying documents
8	0	OFF (power: disconnection from the mains)
9		ON (power: connection to mains)
10	Ċ	"Off" (only for a part of equipment)
11	ullet	"On" (only for a part of equipment)
12	Ť	Type B Equipment

Notes

Appendix **D SAMPLES OF PATIENT PREPARATION**

University of Pennsylvania PET Center Protocol

Whole Body/Oncology

1. NPO four hours prior to study.

Note: An earlier non-sugar breakfast is allowed.

- 2. Glucose level should be less than 140 mg/dl (is preferred).
- 3. If the glucose level is greater than 140 mg/dl the physician has to decide whether to continue the procedure.
- 4. The patient is encouraged to drink water after injection.
- 5. No patient sedation is required.
- 6. Usually no catheterization for abdominal disease is required.
- 7. The patient should empty the bladder prior to the study.
- 8. Patient relaxation is important, but can be schedule dependent.
- 9. Injection dose:
 - 0. 068 mCix kg =FDG dose

Note: The above mentioned amount is the minimum dose given to a patient and the maximum dose should not exceed 6.5mCi).

10. The standard wait time post injection is 60 minutes

Neurology

1. NPO four hours prior to study.

Note: An Earlier non-sugar breakfast is allowed.

2. Measure Glucose level.

If the glucose level is greater than 180mg/dl, then the physician determines whether to proceed with the procedure.

3. The patient is encouraged to drink water after injection.

- 4. No patient sedation is required.
- 5. Pediatric patients are often given oral sedation post injection.
- 6. Patient relaxation is very important.

After injection, patient rests for 30- 50 minutes in a quiet location

7. Injection dose:

0. 068 mCix kg =FDG dose

Note: The above mentioned amount is the minimum dose given to a patient and the maximum dose should not exceed 6.5mCi)

8. The standard wait time post injection is 30- 50 minutes.

Cardiology for Non Diabetic Patients

1. NPO 12 hours prior to study.

Note: No intake of fats or caffeine is advisable, 24 hours prior to the study (exception: water). Smoking is also prohibited - 24 hours prior to the study.

2. The preferred glucose level is less than 150 mg/dl.

Note: Contact the Cardiologist prior to injection or oral administration of Glucola if the glucose level is above 150 mg/dl.

- 3. Drink Glucola one hour prior to FDG injection.
 - Blood Glucose level < 100 mg/ dl = 1/ 2 bottle Glucola
 - Blood Glucose level 100 -150 mg/ dl = 1/ 4 bottle Glucola
- 4. Monitor the glucose level every 30 min.
 - Identify point when Glucose level peaks (just begins to decline)
 - Inject FDG just after Glucose peak
- 5. Patient relaxation:
 - Resting before injection approximately 30 min for NH₃ -perfusion
 (0. 053 mCi x kg = NH₃ dose, drawn into a total of 10cc, infused over 30 sec)
 - Resting 20- 30 min after injection prior to the scan
 - Scan starts 20-30min post injection FDG
- 6. Patient should not be forced to drink water.
- 7. No patient should be sedated
- 8. Injection dose:

0.045 mCi x kg = FDG dose

- 9. The wait time post injection is 20- 30 min for FDG circulation
- 10. Singles count rate should be below 5 million

Cardiology for Diabetic Patients

1. NPO four hours except water prior to study.

Note: An Earlier light carbo breakfast is allowed with no intake of diabetic medication.

2. The preferred glucose level is less than 150 mg/dl.

Note: Contact the Cardiologist prior to injection or oral administration of Glucola if the glucose level is above 150 mg/dl.

- 3. Drink Glucola one hour prior to FDG injection.
 - Blood Glucose level < 100 mg/dl = 1/ 2 bottle Glucola
 - Blood Glucose level 100 -150 mg/dl = 1/ 4 bottle Glucola
- 4. Monitor the glucose level every 30 min.
 - Identify peak Glucose level (just before Glucose level falls)
 - Inject FDG just after peak
- 5. Patient relaxation:
 - Resting before injection approximately 30 min for NH 3 -perfusion
 (0. 053mCix kg= NH 3 dose, drawn into a total of 10cc, infused over 30 sec)
 - Resting 20- 30 min after injection prior to the scan
 - Scan starts 20- 30min post injection FDG
- 6. Patient should not be forced to drink water.
- 7. No patient should be sedated.
- 8. Injection dose:

0.045 mCi x kg = FDG dose

- 9. The wait time post injection is 20- 30 min for FDG circulation
- 10. Singles count rate should be below 5 million

Protocol from Cedars-Sinai PET Department

Whole Body/Oncology

1. NPO six hours prior to study.

Note: An earlier non- sugar breakfast is allowed.

- 2. No measurement of the Glucose level is required.
- 3. Patient hydration:

Drink water liberally after injection (excluding head and neck studies).

4. Patient sedation:

This decision is provided by the referring physician.

- 5. Unless ordered by a referring physician, usually catheterization is not applicable for abdominal disease. Patient empties bladder prior to the study.
- 6. Patient relaxation is important.

Patient sits quietly in waiting room for 90 minutes after FDG injection. (No talking, chewing, etc., for head and neck studies)

7. Injection dose

0.068 mCix kg =FDG dose

Note: The above mentioned amount is the minimum dose given to a patient and the maximum dose should not exceed 6.5mCi).

8. The standard wait time post injection is 90 minutes.

Neurology

1. NPO six hours prior to study:

Note: An earlier non- sugar breakfast is allowed.

- 2. No measurement of the Glucose level is required.
- 3. Patient sedation:

This decision is provided by the referring physician.

4. Patient relaxation is important.

The patient should rest in a quiet room with IV in place for 15 to 30 minutes post injection.

5. Injection dose:

0. 068 mCix kg =FDG dose

Note: The above mentioned amount is the minimum dose given to a patient and the maximum dose should not exceed 6.5mCi).

6. The standard wait time post injection is 45 minutes.

Cardiology

1. NPO six hours prior to study.

Note: An earlier non- sugar breakfast is allowed.

- 2. Supplies: 1Amp D50, Regular Insulin, IV Dextrose, Glucola.
- 3. Procedure:
 - Start IV with 0. 9% NaCl
 - Run the baseline AccuCheck:
 - ^o If 60-100: Give 50mg Glucola
 - ^o If 101-120: Give 25mg Glucola
 - ^o If 121-130: Give 15mg Glucola
 - ^D If >130: Give nothing and proceed with FDG injection for scan
 - Re- run AccuCheck every 10 min intervals for 30 min until the glucose stops rising.

If after the 30min:

- <130: Repeat procedure step 2
- ^a 130-160: Inject 2 units of Insulin IV
- >160: Inject 4 units of Insulin IV
- When the Glucose level starts to drop, inject FDG.
- Re- run AccuCheck 30min post FDG injection if insulin was given.
- Re- run AccuCheck 30min post Scan if Insulin was given
- 4. Precaution:
 - If the final AccuCheck is 50- 70 and patient is asymptomatic, provide crackers and juice (no orange juice in renal patient) and encourage eating a full meal as soon as possible. Repeat AccuCheck before discharging.
 - If AccuCheck <50 or if< 70 and patient becomes symptomatic, follow the hospital policy and procedure for the treatment of hypoglycemia.
- 5. Injection dose:

0.068 mCi x kg = FDG dose

Note: The above mentioned amount is the minimum dose given to a patient and the maximum dose should not exceed 6.5mCi)

6. The standard wait time post injection is 40 to 60 minutes.

Cardiac Rest MIBI/FDG- PET Scan

- 1. Dose/Material:
 - 99mTc-Sestamibi, 25mCi, IV
 - Glucola, 50 g, PO
 - F- 18 FDG, 6 mCi, IV
- 2. Camera equipment
 - ADAC Vertex w/Vantage for Rest MIBI Spect
 - C- PET for FDG- PET Scan
- 3. Patient preparation
 - NPO 4 hours prior to REST MIBI study
- 4. General Procedure
 - Inject 99mTc-Sestamibi at rest
 - Wait 1 hour
 - Acquire Rest MIBI Spect study
 - Gated Rest MIBI- supine w/Vantage
 - Non- gated Rest MIBI-prone
 - Have patient to drink Glucola
 - Wait 45-60 min
 - Inject F-18 FDG at rest (follow the patient preparation procedure)
 - Wait 30 min
 - Acquire FDG-PET scan

Metabolic Imaging of Boca PET Center Protocol

Diabetic Patients, WholeBody/Oncology

- 1. NPO six hours prior to study.
- 2. No smoking 24 hours prior to the study.
- 3. Diabetic patients are scheduled first in the morning.
- 4. All patients will continue their required medications.
- 5. Patients instructed to measure their Glucose level immediately in the morning and bring their glucometer for consistency in reading.
 - Glucose level less than 140 mg/dl is preferred.
 - If the glucose level is greater than 140 mg/dl, then insulin or glucotrol is administrated and the glucose level is monitored to the desired level.
- 6. Patient is encouraged to liberal hydration starting 24 hours prior to the PET scan.
 - Patient is encouraged to drink 4-12 oz cups of water after injection.
- 7. Patient is asked to void frequently through the waiting time.
- 8. No patient sedation is required. If sedation is desired, patient is responsible for obtaining their own prescription
- 9. No catheterization is required
- 10. Patient relaxation is important. "HOT" waiting and restroom available.
- 11. Injection dose
 - 0.06 mCi x kg = FDG dose

Note: The above mentioned amount is the minimum dose given to a patient and the maximum dose should not exceed 7mCi)

12. The wait time post injection is standard 60 min to 90 min.

Neurology

1. NPO six hours prior to study.

Note: An earlier non- sugar breakfast is allowed.

- 2. No smoking is recommended 24 hours prior to the study.
- 3. Diabetic patients are scheduled first in the morning.
- 4. All patients continue their required medications.

- 5. Patient is instructed to measure their Glucose level immediately in the morning and bring their glucometer for consistency in reading.
 - Glucose level less than 140 mg/dl is preferred
- 6. Patient is encouraged to hydrate starting 24 hours prior to the PET scan.
- 7. No patient sedation is required. If sedation desired, patient is responsible for obtaining their own prescription.
- 8. No catheterization is required.
- 9. Patient relaxation is important. "HOT" waiting and restrooms are available.
 - Patient lies down and relaxes (minimal light & sound) for 15 min.
- 10. Injection dose:

0.06 mCi x kg = FDG dose

Note: The above mentioned amount is the minimum dose given to a patient and the maximum dose should not exceed 7mCi or else there is an hour waiting period).

11. The wait time post injection is 15 min prior to external stimulation.

Our Lady of the Lake Protocol

Whole Body/Oncology

1. NPO four hours prior to study.

Note: An earlier non- sugar breakfast is allowed.

- 2. No exercise is recommended 2 day's prior to the study to avoid muscle uptake.
- 3. Patients instructed to measure their Glucose level immediately in the morning and bring their glucometer for consistency in reading.
 - Glucose level less than 140 mg/dl is preferred.
 - If the glucose level is greater than 140 mg/dl, the physician has to decide whether to continue the procedure.
- 4. The patient is encouraged to drink water after injection...
- 5. No patient sedation is required.
- 6. Catheterization at the discretion of the physician occurs usually for suspected pelvic disease.
 - Patient empties their bladder prior to the study
- 7. Patient relaxation is important, but is schedule dependent.

- 8. Injection dose
 - 0. 068 mCix kg =FDG dose

Note: The above mentioned amount is the minimum dose given to a patient and the maximum dose should not exceed .5mCi or else there will be an hour waiting period.)

9. Wait time post injection is standard 60 minutes.

Neurology

- 1. NPO four hours prior to study: earlier non- sugar breakfast allowed
- 2. Measure Glucose level
 - If the glucose level is greater than 180mg/dl, the physician determines whether to proceed with the procedure.
- 3. Patient is encouraged to drink water after injection.
- 4. No patient sedation is required.
- 5. Pediatric patients are often given oral sedation post injection.
- 6. Patient relaxation is important. After injection, patient rests for 30-50 minutes in a quiet location in a dimly lighted room and is asked not to talk.
- 7. Injection dose:
 - 0. 068 mCix kg =FDG dose

Note: The above mentioned amount is the minimum dose given to a patient and the maximum dose should not exceed .5mCi or else there will be an hour waiting period.)

Cardiology for Non-Diabetic Patients

Goal: Attain and maintain elevated serum glucose levels (130- 200 mg%) with oral glucose and elevate levels of insulin via IV administration of regular insulin.

- 1. <u>Accuchek # 1</u>:
 - If the glucose level is less than 120 mg%, give 25-50gms.
 - If the glucose level is between 120mg% and 150 mg%, give 25gms.
 - If the glucose level is more than 150mg%, call M.D. for insulin
 - Measure after 30 min the glucose level
- 2. <u>Accuchek #2</u>:
 - If the glucose level is between 130mg% and 160 mg%, give 3-5u and if the glucose level is between 161mg% and 200 mg%, give 5-8u and proceed for the FDG injection.

- If the glucose level is less than 130 mg%, give 25-50 grams and if the glucose level is more than 200mg%, give 5-8u. Proceed for the FDG injection only if the glucose level normalize, otherwise do "Accuchek #3:."
- 3. <u>Accuchek #3</u>:
 - If the glucose level is between 130mg% and 160 mg%, give 2-4u and if the glucose level is between 161mg% and 200 mg%, give 3-6u and proceed for the FDG injection.
 - If the glucose level is less than 130 mg%, give 25-50 grams and if the glucose level is more than 200mg%, give 5-8u. Proceed for the FDG injection.
- 4. <u>Accuchek #4</u>:
 - If the user did not reach the "Accuchek #2:." numbers, repeat "Accuchek #3:."

Cardiology Diabetic Patients

Goal: Attain and maintain elevated serum glucose levels (130- 200 mg%) with oral glucose and elevate levels of insulin via IV administration of regular insulin.

- 1. Accuchek # 1:
 - If the glucose level is less than 120 mg% or the intake of glucose has been more than one hour post meal, give 25-50gms.
 - If the glucose level is between 120mg% and NPO is less than one hour post meal, then no oral glucose is necessary.
 - If the glucose level is more than 200 mg%, give 5-8u
 - If the glucose level is between 120mg% and 200mg%, then no oral glucose is necessary.
 - Measure after 30 min the glucose level
- 2. Accuchek #2:
 - If the glucose level is between 120mg% and 160 mg%, give 3-5u and if the glucose level is between 161mg% and 200 mg%, give 5-8u and proceed for the FDG injection.
 - If the glucose level is less than 120 mg%, give 25-50 grams and if the glucose level is more than 200mg%, give 5-8u. Proceed for the FDG injection only if the glucose level normalize, otherwise do "Accuchek #3:."
- 3. Accuchek # 3:
 - If the glucose level is between 120mg% and 160 mg%, give 2-4u and if the glucose level is between 161mg% and 200 mg%, give 3-6u and proceed for the FDG injection.
 - If the glucose level is less than 120 mg%, give 25-50 grams and if the glucose level is more than 200mg%, give 5-8u. Proceed for the FDG injection.
- 4. <u>Accuchek #4</u>:
 - If the user did not reach the "Accuchek #2:." numbers, repeat "Accuchek #3:."