

**Alzheimer's Disease Neuroimaging Initiative
PET Technical Procedures Manual**

**Version 9.5
January 23, 2006**

Table of Contents

General Information	3
Contact Information	3
Site Qualification	4
Phantom Scan	4
Anticipation of Imaging System Upgrades.....	4
Continued Quality Monitoring During Execution Phase	5
Dedicated PET Scanner:	5
PET/CT Scanner:	5
Ancillary Equipment:.....	5
PET Pre-Scan Procedures / General Information	7
Participants Pre-screening	7
Subject Preparation	7
Participant Positioning.....	7
Ambient Conditions.....	8
Image File Identification.....	8
Documentation / PET Scan Information Form Example	9
PET Imaging Protocol	10
Appendix A – Examples of Scanner Specific Protocols	12
Siemens PET Systems (HR+, ECAT EXACT, and ACCEL using V7.2.2 software).....	12
Siemens PET Systems (Biograph).....	15
Siemens PET Systems (Biograph HiRez).....	17
GE Systems - General Information.....	19
GE Advance.....	19
GE Discovery LS.....	23
GE Discovery ST.....	25
Phillips Allegro/Gemini (Additional information to be added later)	27
Appendix B – Data Transfer	30
Preparing to Upload Reconstructed Images to LONI	30
Siemens HR/HR+/EXACT/ACCEL	30
Siemens Biograph	31
GE Advance and Discovery LS.....	34
GE Discovery ST	35
Philips Allegro.....	38
Philips Gemini.....	39
Uploading Reconstructed Images to LONI*.....	42
Image Data Archive Overview	42
System Requirements.....	42
User Registration.....	42
IDA Log In.....	45
Image Archive Overview	46
Archive Instructions For Original Files.....	47
Query And Download Instructions.....	52
Appendix C - Quantitative PET Imaging Protocol	55
Pre-Visit Preparation Specific to Quantitation:	55
Procedure.....	55
Appendix D Scanner – Well Counter Cross-Calibration Procedure	59
¹⁸ F Method.....	59
⁶⁸ Ge Method	60

General Information

The purpose of this manual is to further explain the PET imaging component of the ADNI protocol. Standard procedures are needed to ensure consistency of data collection in this longitudinal study.

This manual contains information for study-site clinical staff involved with the care of study participants during the imaging procedure and those involved with the processing and transfer of PET imaging data.

During the course of the study 50% of the subject populations will receive FDG-PET scans in addition to 1.5T MR scans at the following time points:

MCI Group (n=200) at 0, 6, 12, 18, 24, 36 months

AD Group (n=100) at 1, 6, 12, 24 months

Control Group (n=100) at 0, 6, 12, 24, 36 months

Sites participating in the PET protocol may perform a qualitative or quantitative study. The qualitative study involves a procedure to use dynamic scanning to derive an arterial input function from the imaged carotid artery, in conjunction with several venous blood samples. This is a more technically demanding protocol that also requires a well counter and calibration of the well counter/PET scanner efficiency. Sites who have volunteered to do the quantitative studies will be contacted as the study begins. All other sites will perform a qualitative study that is a standard static acquisition.

Contact Information

If you have any questions or concerns regarding the PET imaging study please contact

adnipet@adni.ucsd.edu

If you have any questions or concerns regarding individual participants please contact the study coordinator at your referral site.

If you have question regarding the scan uploading to the LONI website please contact

adni@loni.ucla.edu

Site Qualification

Prior to any patients being scanned at a particular site, that site must first meet the site qualification guidelines. The guidelines include the following steps:

Phantom Scan

- i. Each site must scan a Hoffman 3-D brain phantom on 2 separate days using the specified ADNI protocol for each scanner that will be used in the ADNI PET imaging trial.
- ii. Sites may use their standard procedure for scatter reduction (i.e. with or without an external shield such as the “Neuroshield) as long as the phantom studies and subsequent subject studies are performed under identical conditions.
- iii. After the phantom has been scanned, the site will send the image data to LONI and the ADNI QC team from the University of Michigan will review the images to determine if the correct parameters have been used and assure there are no other underlying problems seen during the scan.
- iv. If you are interested in participating in the *quantitative* portion of this study, you may be asked to perform a test protocol to ensure your system is capable of performing the rapid dynamic framing sequence. This procedure is also detailed in the phantom imaging section included at the end of this manual
- v. An email will be sent to your site notifying you of the results.

Once your institution has received IRB approval, radiation safety subcommittee approval, AND your site has passed the phantom QC imaging your site is ready to scan ADNI subjects.

IMPORTANT: It is imperative that the human subjects be scanned using a protocol identical to that used for the phantom scans. It is strongly recommended that the sites create a new imaging protocol specifically for use with the ADNI project.

Anticipation of Imaging System Upgrades

It would be ideal if no hardware or software upgrades of the PET imaging system occurred during the duration of the study. In the event of such an upgrade, we ask that you inform the ADNI PET team *prior* to the anticipated upgrade. Depending on the nature of the upgrade the site may be asked to repeat the phantom scans prior to scanning any additional subjects.

Continued Quality Monitoring During Execution Phase

To ensure scanner/ancillary equipment stability and quality throughout the project, each site is required to perform ongoing quality control procedures.

Dedicated PET Scanner:

- PET scanner should have an up to date calibration and normalization on the date of each imaging session.
- A daily QC/blank scan (empty port transmission) scan should be done at the beginning of the day the scanning is to be completed. This scan should be visually inspected for abnormalities. If there is a possibility that the abnormality could impact the quality of the PET scan the study should be rescheduled.

PET/CT Scanner:

- PET scanner should have an up to date calibration and normalization on the date of the imaging session.
- A daily QC check should be done at the beginning of the day the scanning is to be completed. This scan should be visually inspected for abnormalities. If there is a possibility that the abnormality could impact the quality of the PET scan the study should be rescheduled.
- Daily CT should be performed as recommended by the specific vendor, but typically should include a "checkup/calibration" procedure and a water phantom scan. The checkup/calibration procedure guarantees optimum image quality by warming up the x-ray tube and should be performed at startup and within 1 hour prior to any scan. The water phantom provides quality measurements of 3 parameters. The parameters are the CRT value of water calculated in Hounsfield units (HU), the pixel noise of images calculated as a standard deviation, and the tube voltages measured directly on the x-ray tubes. These three measurements should be determined for all available kVp values.

Ancillary Equipment:

- Quality control of blood glucose meter should be performed according to the manufacturer's or institution's procedure to ensure proper functioning.

- Quality control of dose calibrator should be performed throughout the course of the study. This typically will include daily constancy, quarterly linearity and annual accuracy.
- Well Counter (quantitative studies only). This typically includes a daily optimization of high voltage, constancy and chi-square test.
- Pipette (quantitative studies only). Routine calibrations to ensure accuracy of dispensed volume.

PET Pre-Scan Procedures / General Information

Participants Pre-screening

All participants should have been screened by the study coordinator for the following contraindications

- Inability to cooperate/claustrophobia (sedation is not offered for this protocol)
- Inability to lie on the scanner bed for 45 minutes (non-quantitative study) or 75 minutes (quantitative study)
- Inability to achieve venous access sufficient for tracer administration (and venous blood sampling for quantitative protocols).

Subject Preparation

Subjects to be imaged in the morning are asked to omit all food and fluids (except water) from midnight the night before the scan until after the imaging is completed. Subjects scanned later in the day are asked to omit food and fluids (except water) for at least 4 hours prior to the imaging session.

Participant Positioning

Proper patient positioning is a key aspect of the successful completion of the PET exam. It is important to take the time necessary to ensure not only that the patient is properly positioned but can comfortably maintain that position throughout the duration of the scanning session.

- Have the patient remove any bulky items from their pockets such as billfolds, keys, etc. In addition, they should remove eyeglasses, earrings, hair clips/combs if present. If possible they should try and remove hearing aids also.
- Position the patient so that their head/neck are relaxed. It may be necessary to add additional pads beneath the neck to provide sufficient support. Use the lasers to ensure there is little or no rotation in either plane. The head should be approximately positioned parallel to the imaginary line between the external canthus of the eye and the external auditory meatus.
- Use support devices under the back and/or legs to help decrease the strain on these regions. This also will assist in the stabilization of motion in the lower body. If you are performing a quantitative study, it is helpful to have a small bedside table so the patient can rest the arm that will be used for tracer administration and venous blood draws.

- Once the patient has been positioned foam pads can be placed along side the head for additional support. Velcro straps and/or tape should also be used to secure the head position. Vacuum bean bags can also be used in this process.
- If using a dedicated PET system it is helpful to perform a short emission or transmission scan to determine optimal axial position.
- The patients should be offered a “panic button” or be reassured that someone is watching or able to hear them at all times.

Ambient Conditions

Standardization of the environment during the 20-30 minutes following tracer administration is essential.

- During the uptake phase, subjects should be asked to remain still and keep awake with eyes open looking straight ahead (not into lights).
- Lights should be dimmed to a level similar to twilight. The subjects’ position (e.g., sitting or lying), their visual environment, and the room’s ambient light should be the same throughout the longitudinal study.
- The patient should be monitored periodically to be certain of compliance and to ensure that the eyes do not close and the patient remains awake.

IMPORTANT: The subjects’ position during the uptake period, their visual environment, and the room’s ambient light conditions should be the same across all scans of the longitudinal study. It is important to standardize these conditions as the PET scans are performed over a 2-3 year period.

Image File Identification

It is **VERY** important that each site follow standard file identification so that all scans can be easily identified. The file ID will be assigned by the Clinical Study Coordinator at the clinical site prior to the PET visit. The naming convention is SSS_C_#### where SSS is the three digit site ID, C is either S (subject) or P (phantom), and #### is the unique four digit number assigned by the site. For example, 129_S_0012 is the 12th subject enrolled in ADNI across all sites, from Banner Good Samaritan.

Documentation

Be sure to complete the metadata sheet *as the study is being acquired*. The PET scan information form must be provided by the study coordinator prior to the scan. The form is similar, but not identical, to the image below as it was modified after the initial publication of this manual

ADNI - Execution Phase

PET Scan Information

Participant:
Participant ID

Visit: *Baseline Visit*

Was the scan conducted?

- Yes
 No

Reason why the scan was not conducted:

- Illness
 Participant unavailable
 Participant unwilling
 Administrative problems
 Withdrawn consent
 Other (specify)

If Other, specify:

Scan Date

<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>
Month	Day	Year					

Technologist Initials

Scanner Type:

- GE
 Siemens/CTI
 Phillips

Time of today's Scanner QC

Time of blood glucose measurement

Blood Glucose (prior to FDG injection)

 dL/mL

Time of FDG dose assay

FDG dose assay

 mCi

Time of FDG injection

Any variations from protocol during FDG uptake?

- Yes
 No

If Yes, describe:

Predefined acquisition protocol ID

Number of Frames

Frame Duration

 sec

PET Imaging Protocol

IMPORTANT: Sites qualified to perform the quantitative PET imaging should use the protocol detailed in Appendix C.

- Upon arrival to the imaging center, compliance to the dietary requirements should be confirmed. If they have not complied with the preparation instructions then the following procedures should apply:
 - If < 2 hours have elapsed since food/drink, wait until 2 hours have elapsed from last ingestion.
 - Once >2 hour have elapsed since last ingestion, measure the blood glucose levels. If the blood glucose level is <180 mg/dL (9.9 mmol/L) then proceed with the scan. If not, the subject will need to wait an additional amount of time until the blood glucose levels meet the above criteria or reschedule.
- Have the patient use the restroom and empty their bladder.
- Allow them to lie comfortably in a bed or reclining chair in a room in which the ambient noise is minimal and the degree of lighting can be controlled and minimized as previously described. Supply them with blankets/pillows as needed to maximize their comfort.
- Obtain intravenous access using either a small butterfly needle or angiocath. Obtain baseline blood glucose level if not already performed.
- Draw 5 ± 0.5 mCi (185 MBq) of [¹⁸F]-FDG and assay with a dose calibrator. **Record the assay time to the nearest minute.**
- Inject the [¹⁸F]-FDG. Rinse the syringe and flush the line with at least 10 cc of normal saline. **Record the injection time to the nearest minute.** The IV line can be discontinued at this time.
- Re-assay the dose syringe. If the residual activity is 0.1 mCi or greater, record the amount and correct the amount of the injected dose for the residual activity.
- Allow the subject to rest comfortably in the room for 20 minutes for the incorporation of [¹⁸F]-FDG into the brain. During the incorporation period, the patient's eyes should be open and the ears should remain un-occluded.
- At the end of the 20 minute incorporation period, have the patient use the restroom and empty their bladder.

IMPORTANT: This should be timed such that the patient will be on the scanner at 30 minutes after injection, ready for acquisition to begin.

- Position and secure the subject in the scanner using methods previously described.
- Acquire a *dynamic*, 3D scan consisting of six-5 minute frames.

IMPORTANT: Biograph PET/CT users should acquire a single 30 minute frame since dynamic scanning capability is not currently available.

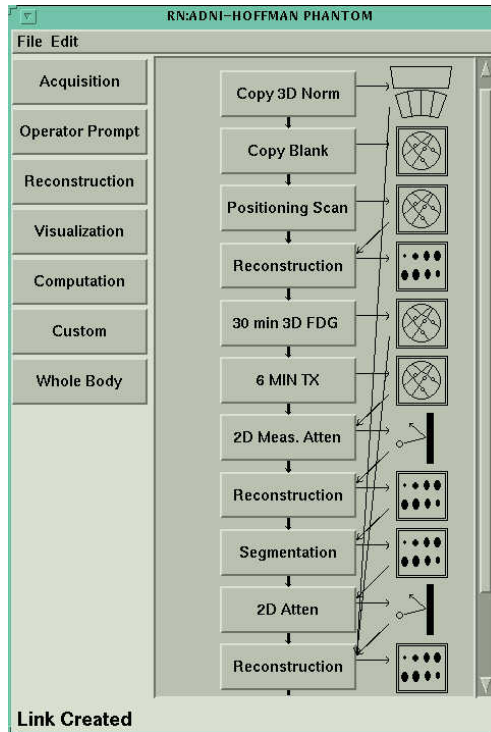
- All images will need to be corrected using measured attenuation.
 - PET Only Scanners
 - Acquire an attenuation correction scan using rod sources for 5-6 minutes after the acquisition of the emission scan.
 - Segmentation and re-projection routines will be applied for attenuation correction.
 - PET/CT Scanners
 - Standard CT acquisition parameters
- Upon completion the subject can be removed from the scanner and encouraged to void. The subject should also be instructed to drink plenty of fluids and void frequently throughout the day to help reduce radiation exposure.
- Reconstruct images using parameters specific to the system used for scanning. (See Appendix A in this document).
- Upon completion of the reconstruction, review all the images to assess for artifacts and motion.
- Archive **ALL** raw and processed study data including copies of the normalization and blank scans. It is necessary to archive and store raw and processed data at the imaging site for the duration of the ADNI project (approximately 5 years).
- Transfer image data to the Laboratory of Neuroimaging (LONI) at UCLA using the procedure detailed in Appendix B.

IMPORTANT: Data uploads to LONI should be performed as soon as the images have been acquired & reconstructed as it will be important to promptly QC the data to identify if the scan needs to be repeated.

Appendix A – Examples of Scanner Specific Protocols

Siemens PET Systems (HR+, ECAT EXACT, and ACCEL using V7.2.2 software)

1. Example acquisition protocol on an HR+ system running ECAT version 7.2.2 software.



2. Reconstruction parameters for the dynamic emission scan

The screenshot shows the "Protocol Operation Editor" window. On the left, there are several configuration options: "Display: Frame Definition", "Plane Definition: 3D", "Scan Description: 30 min 3D FDG", "Logger Sampling Interval: 0", "Axial FOV (cm): 15.52", "Emission/Transmission Type: Emission", and checkboxes for "Septa Retracted", "Bed Motion Out", "Blank Scan", and "Online Reconstruction". On the right, there is a table with columns: "Frames", "Time (sec)", "Bed Offset", "Delay", and "KCounts". The table has 15 rows, with the first row containing the values 1, 6, 300, 0, 0, 0. At the bottom, there are "OK" and "Cancel" buttons.

Frames	Time (sec)	Bed Offset	Delay	KCounts	
1	6	300	0	0	0
2					
3					
4					
5					
6					
7					
8					
9					
10					
11					
12					
13					
14					
15					

3. Acquisition parameters for the transmission scan.

The screenshot shows the 'Protocol Operation Editor' dialog box. On the left, there are several configuration options: 'Display' is set to 'Frame Definition', 'Plane Definition' is '2D', 'Scan Description' is '6 min TX', 'Logger Sampling Interval' is '0', 'Axial FOV (cm)' is '15.52', and 'Emission/Transmission Type' is 'Transmission'. Below these are four unchecked checkboxes: 'Septa Retracted', 'Bed Motion Out', 'Blank Scan', and 'Online Reconstruction'. On the right, there is a table with columns 'Frames', 'Time (sec)', 'Bed Offset', 'Delay', and 'KCounts'. The first row contains the values '1', '360', '0', '0', and '0'. The rest of the rows are empty. At the bottom are 'OK' and 'Cancel' buttons.

	Frames	Time (sec)	Bed Offset	Delay	KCounts
1	1	360	0	0	0
2					
3					
4					
5					
6					
7					
8					
9					
10					
11					
12					
13					
14					
15					

4. Reconstruction parameters for the transmission scan.

The screenshot shows the 'Protocol Operation Editor' dialog box with reconstruction parameters. 'Method' is 'Backprojection', 'Image Size' is '128', 'Zoom' is '1.00', 'Brain Mode' is 'On', 'Offset (cm)' X and Y are '0.0', 'Filter' is 'Gaussian', and 'Kernel FWHM (mm)' is '9.0'. 'Axial Filtering' and 'Scatter Correction' are both 'On'. 'Matrix' is '*****'. Under 'Inputs', '2D Meas. Atten - Attenuation Correction' is selected. A callout box points to the 'Brain Mode' dropdown with the text 'NOTE: Brain Mode should be turned "ON"'. 'OK' and 'Cancel' buttons are at the bottom.

5. Acquisition parameters for the dynamic emission scan.

The screenshot shows the 'Protocol Operation Editor' dialog box with the following parameters and callout notes:

- Method:** Iterative
- Image Size:** 128
- Iterations:** 4 **Subsets:** 16
- Zoom:** 2.00 **Brain Mode:** On
- Offset (cm):** X 0.0 Y 0.0
- Filter:** All Pass (Ramp)
- Kernel FWHM (mm):** 5.0
- Axial Filtering:** Off
- Scatter Correction:** On
- Matrix:** *****

Inputs:

- Get Sinogram - Sinogram
- Get Normalization - Normalization
- Get Attenuation - Attenuation Correction

Callout Notes:

- NOTE: A zoom of 2.5 is preferred.** (Points to the Zoom field)
- NOTE: Siemens ACCEL and Exact-47 scanners use 6 iteration instead of 4.** (Points to the Iterations field)
- NOTE: The kernel FWHM (mm) field is ignored when the All Pass (Ramp) filter is selected.** (Points to the Filter and Kernel FWHM fields)

Buttons: OK, Cancel

Siemens PET Systems (Biograph – Note only a portion of the computer screen is represented in the screen shots)

Examination
PET Exam
OnlinePETR...
Viewing
Filming
3D

Count Rate vs Time

Trues (cts/sec): -12 Randoms: 1156 Singles: 978376 LM Events: 0
 Trues Acquired (cts) 2.0057912e+008
 Acquiring Bed 0 of 0 Time Remaining in Current Bed 0 sec
 Est. Time Remaining in Study 0 sec

NOTE: Obtain True & Randoms rate from these fields at the start of the scan. Phantom scan only

NOTE: 5 mCi FDG should be used.

NOTE: Acquire a single bed position for an 30 minute period.

Radiopharmaceutical Information

Radioisotope: F-18 Pharmaceutical: FDG

Injected Dose: 10 mCi

Injection Time: 13:27:42 Monday, August 08, 2005

Scan Duration: 3 Beds at 30 min per Bed

Table Position:

Begin	Current	End	Height
1000	269.0	1500	155.0

Caudocranial

Routine **Recon** **Advanced**

PET Scan Information **Recon Configuration** Recon Parameters

Description

Output Image Type

With Attenuation Correction No Attenuation Correction Both

Reconstruction Method

FBP

Iterative

DIFT

Image Size

Filter Axial Filtering

Filter FWHM (2.0-20.0 mm)

Zoom (1.0-3.0) Pixel Size (mm)

Scatter Correction

CT Segmentation

PET Scan Information Recon Configuration **Recon Parameters**

Offsets

X (-20.0 - 20.0 cm)

Y (-20.0 - 20.0 cm)

Z (0.0 - 0.0 cm)

3D Sinogram Rebin Method

FORE

SSRB

Segment 0

Iterative Reconstruction

Iterations

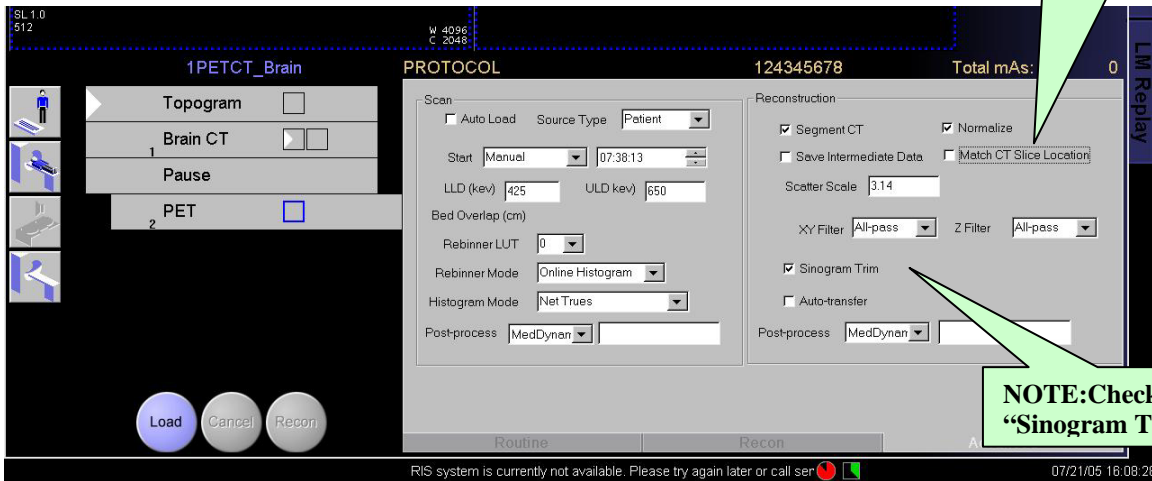
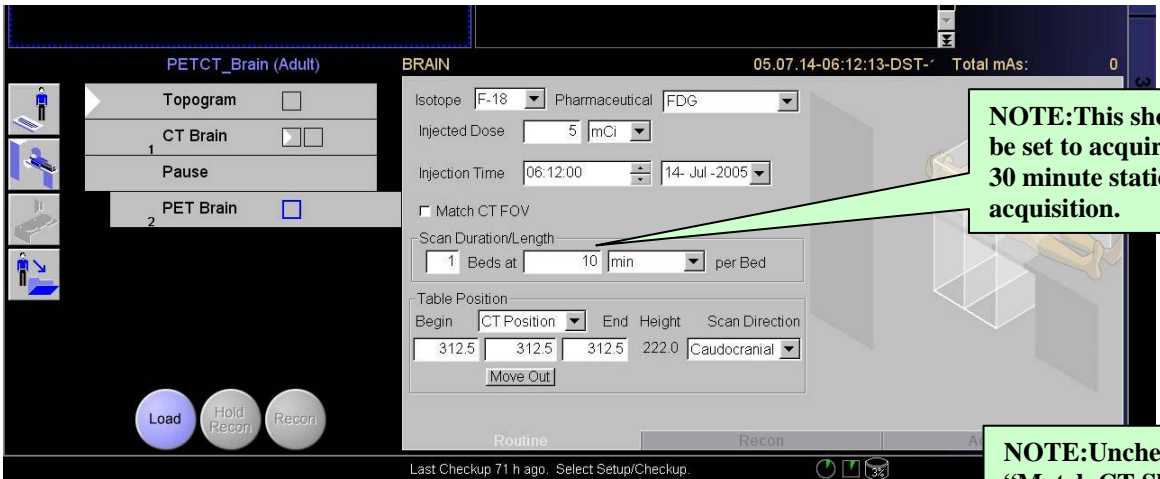
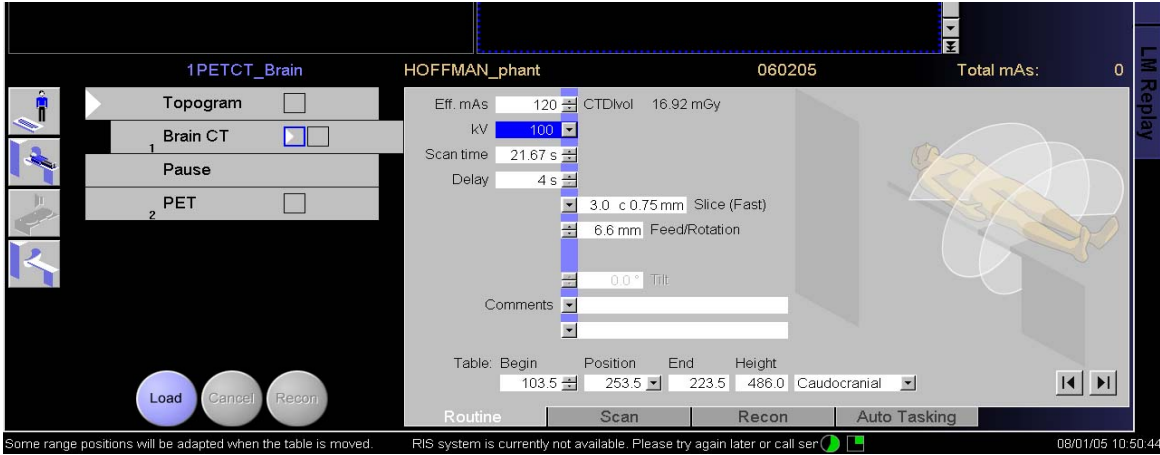
Subsets

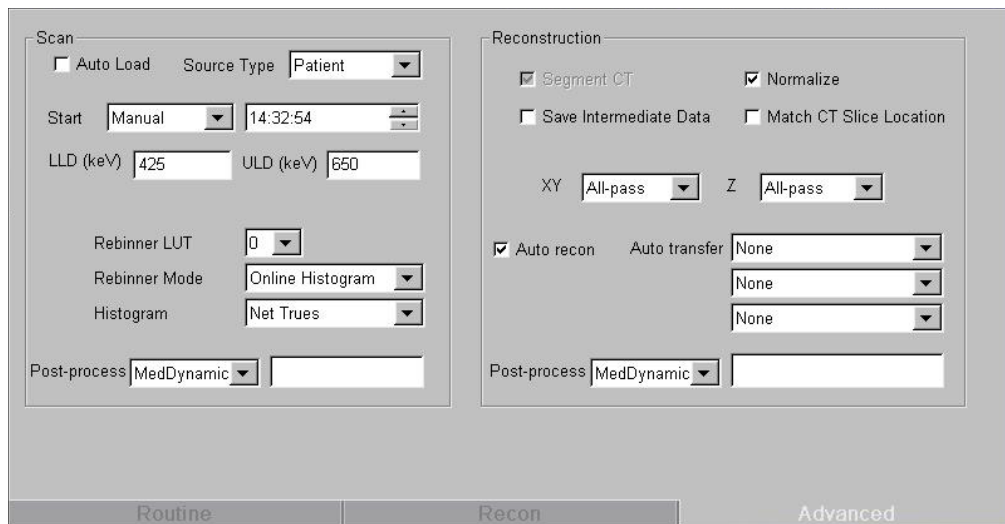
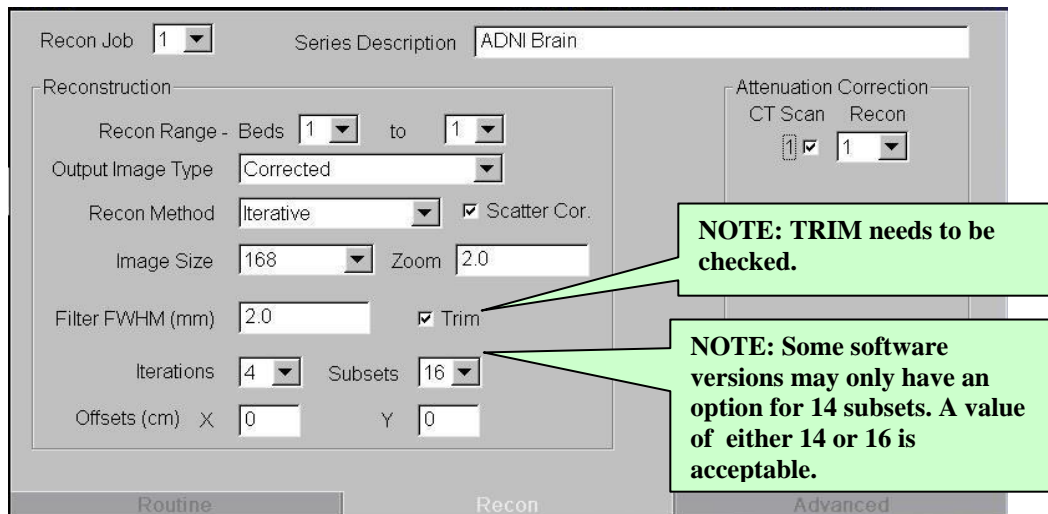
Sinogram Trim Factor (1.0-3.0)

NOTE: For early LSO BioGraphs (ACCEL-type), use 6 iterations; for early BGO BioGraphs (HR+ type) use 4 iterations.

NOTE: Be sure to set the Sinogram Trim Factor to 2.0

Siemens PET Systems (Biograph HiRez – Note that only the lower half of the computer screen is represented in the first screen shots)





GE Systems - General Information

The procedure for a GE CT/PET scanner (either DLS or DST) will consist of the following steps:

1. Start a new exam with GE protocol named “PET-CT Brain 3D” (or “PET-CT Brain 3D – 3.75 mm” on DST).
2. Perform the CT scout scan using the default technique (Accounts for variation in certain attributes of the CT technique among 4-, 8- and 16-slice CT’s in the various PET-CT scanners.).
3. Perform the CT scan for AC using the default technique.
4. Go to “Pet Exam.” When the acquisition window appears, select New Exam and prescribe the 6-frame dynamic as described above (see screen shots below).
5. Select the PET Recon screen and prescribe the reconstruction as described above.
6. Close PET acquisition, then return to the CT interface and end the exam.
7. Note that this procedure can be incorporated into a User protocol, which would be helpful if a site were planning to run this procedure many times.

GE Advance

1. Transmission Scan Range Rx window:

Static Scan Range Rx

◆ Prescribe Start ◆ Read Start Group #: # AFOVs in Group:

Table Location of First Slice: ◆ Towards Head
Table Location of Last Slice: ◆ Towards Feet

Duration of each AFOV:

■ Auto Table Move

Group Number	Number of AFOVs in Group	First Slice	Last Slice	AFOV Duration	Correction AFOV Duration	Overlap
1	1	0.0	144.5	00:06:00	--:--:--	0

Add Update Delete

OK Apply Cancel

2. Transmission Acquisition Rx window:

Acquisition Options ▾ New Procedure New Scan Load Defaults

Patient ID: ADNI0001 Scan Type: Transmission
 Patient Name: ADNI Demo Scan Mode: Static
 Procedure Description: --- Defaults Name: ---

Patient Position Total Scan Time: 00:06:00 Prescribe Scan Range

Set Landmark OM

Supine

Group Number

1500 1000 500 0K -500 -1000 -1500

Table Location (mm)

Scan Information

Realtime Subtraction ▾

Standard ▾ Word ▾

Scan Description: ADNI Transmission Stop on kCounts

3. Emission Scan Range Rx window:

Dynamic Scan Range Rx

◆ Prescribe Start ◆ Read Start

Group #: 1 # Frames in Group: 6

Pre-Frame Delay: 00:00:00

Duration of Each Frame: 00:05:00

Table Location of First Slice: 0.0 ◆ Towards Head
 ◆ Towards Feet

Table Location of Last Slice: 144.5

Pre-Scan Delay: 00:00:00

Group Number	Number of Frames in Group	Pre-Frame Delay	Frame Duration
1	6	00:00:00	00:05:00

Add Update Delete

OK Apply Cancel

4. Emission Acquisition Rx window:

The screenshot displays the 'Acquisition' window with the following sections:

- Acquisition Header:** Options, New Procedure, New Scan, Load Defaults.
- Patient Information:** Patient ID: ADNI0001, Patient Name: ADNI Demo, Procedure Description: ---.
- Scan Parameters:** Scan Type: Emission, Scan Mode: Dynamic, Defaults Name: ---.
- Patient Position:** Includes a 'Set Landmark' button and a 'VX' label. A diagram shows a patient in a 'Supine' position on a table.
- Scan Range:** Features a 'Prescribe Scan Range' button, a 'Group Number' dropdown set to '1', a 'Time (minutes)' scale from 0 to 60, and a 'Table Location (mm)' scale from 1500 to -1500 with a 'VX' marker.
- Scan Information:** Includes 'Realtime Subtraction', '3D (Brain/Body)', 'Word', 'Save Rates Data', 'Start on kcps', and 'Counts' options. The 'Scan Description' field contains 'ADNI Static Brain (6x5)'. A green arrow points from this section to the note below.
- Tracer Information:** Nuclide: 18F, Additional Tracer Info, and Tracer: FDG -- fluorodeoxyglucose.

NOTE: Some older systems have a "3D Brain" option. Use ONLY the "3D Brain/Body" option.

GE Discovery LS

1. Emission Scan Range Rx window:

Dynamic Scan Range Rx

Prescribe Start Read Start Group #: # Frames in Group:

Pre-Frame Delay:

Duration of Each Frame:

Table Location of First Slice: Towards Head
 Towards Feet

Table Location of Last Slice:

Pre-Scan Delay:

Group Number	Number of Frames in Group	Pre-Frame Delay	Frame Duration
1	6	00:00:00	00:05:00

2. Emission Acquisition Rx window:

Acquisition Options ▼ New Procedure New Scan Load Defaults

Patient ID: ADNI0001 Scan Type: Emission
 Patient Name: ADNI Demo Scan Mode: Dynamic
 Procedure Description: --- Defaults Name: ---

Patient Position

VX

Supine

Scan Range

Group Number: 1

Time (minutes)

Table Location (mm)

Scan Information

Realtime Subtraction

3D (Brain/Body) Word Save Rates Data

Scan Description: ADNI Static Brain (6x5) Start on keps

Stop on kCounts

Tracer Information

Nuclide:

Tracer:

3. Emission Reconstruction window:

Extended Recon Options ▾ Next Recon Load Defaults

Patient ID: ADNI0001 Scan Type: Emission
 Patient Name: ADNI Demo Scan Mode: Dynamic
 Scan Description: ADNI Static Brain (6x5) Defaults Name: --- Total Slices: 210

Output: Image ▾ Matrix Size: 128 x 128 ▾

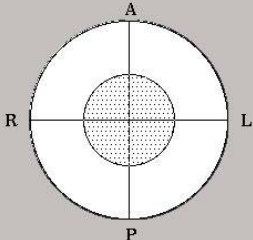
3D Recon Method: Reprojection ▾

Transaxial Filter: Ramp ▾ 4.0
 Cutoff (mm) ▾

Axial Filter: Ramp ▾ 8.5
 Cutoff (mm) ▾

Image Set Description: ADNI Static Brain (6x5)

Display Field of View (cm)



Diameter: 25.6 ▾
 Center L: 0.00 ▾
 Center P: 0.00 ▾

Attenuation

Type: Measured ▾

Transmission Scan: 10:20:24 CTAC client ▾

T + E Subtraction: None ▾

Smooth: None ▾ Smooth (mm) 8 ▾

Axial Smooth: No ▾ Blank: None ▾

Randoms: None ▾

Corrections

Well Counter File: Default ▾ 3DHi-FORE-WC 8/6 200Ment dpl

Well Counter: Sensitivity & Activity ▾

Randoms: Realtime Subtraction ▾

Normalization: Default ▾ 3DHi Norm 9/17 200Ments dph

Geometric: Yes ▾ Deadtime: Yes ▾

Decay: Yes ▾ Scatter: Yes ▾ Model

Queue Status

Number	Patient ID	Patient Name	Type	Mode	Description	Slices

Submit to Bottom Submit to Top Delete All in Queue

GE Discovery ST

1. Emission Scan Range Rx window:

Dynamic Scan Range Rx

Prescribe Start Read Start

Group #: 1 # Frames in Group: 6

Pre-Frame Delay: 00:00:00

Duration of Each Frame: 00:05:00

Table Location of First Slice: 0.0 Towards Head

Table Location of Last Slice: 150.4 Towards Feet

Pre-Scan Delay: 00:00:00

Group Number	Number of Frames in Group	Pre-Frame Delay	Frame Duration
1	6	00:00:00	00:05:00

Add Update Delete

OK Apply Cancel

2. Emission Acquisition Rx window:

PET Acquisition Options New Procedure New Scan Load Defaults

Patient ID: ADNI Demo Scan Type: Emission

Patient Name: ADNI Hoffman Phantom Scan Mode: Dynamic

Procedure Description: --- Defaults Name: 3D_Brain

Patient Position

Set Landmark vx

Supine

Scan Range

Prescribe Scan Range

Group Number

Time (minutes)

Table Location (mm)

Scan Information

Realtime Subtraction

3D Word

Save Rates Data

Start on kcps increase

Stop on kCounts

Tracer Information

Nuclide: 18F Additional Tracer Info

Tracer: FDG - fluorodeoxyglucose

3. Emission Reconstruction window :

Extended Recon **Options** Next Recon Load Defaults

Patient ID: ADNI Demo Scan Type: Emission
 Patient Name: ADNI Hoffman Phantom Scan Mode: Dynamic
 Scan Description: 3D Brain Defaults Name: — Total Slices: 282

Output: Matrix Size:

3D Recon Meth:

Transaxial Filter: Cutoff (mm)

Axial Filter: Cutoff (mm)

Image Set Description:

Display Field of View (cm)

Diameter:
 Center L:
 Center P:

Attenuation **Corrections**

Type: Well Counter File: 3D WCC 05 April 2005

Transmission Scan:

Well Counter:

Smooth: Smooth: (mm)

Randoms:

Axial Smooth:

Normalization: PET 3D NORM

Geometric: Deadtime:

Decay: Scatter:

Queue Status

Number	Patient ID	Patient Name	Type	Mode	Description	Slices

Philips Allegro/Gemini (Additional information to be added later)

Please contact adnipet@adni.ucsd.edu prior to conducting a scan on a Philips Allegro/Gemini scanner.

IMPORTANT: All reconstructions on Philips PET systems should use a lambda value of 0.016.

ALLEGRO/GEMINI 256 FOV BLANK CALIBRATION PROCEDURE

256 FOV transmission scans work in 8.1 and 8.1.2. Transmission attenuation correction is possible for Brain scans in 256 FOV.

It does not require a software or hardware upgrade. The work was completed in 8.1 but insufficient time and resources to verify/validate the changes. For these reasons, 256 FOV transmission scans were excluded from the 8.1 feature set in the documentation. Requirements to perform 256 FOV transmission scans:

- A) Acquire Blank Calibration
- B) Generate Brain_CsAC Recon Protocol
- C) *Generate Single Pass Emis/Tran Brain_CsAC Acquisition Protocol***

A) Acquire 256 FOV Blank Calibration

- 1 - On the acquisition workstation, execute a query for the p0s2. Highlight p0s2 and select Acquisition Setup Acquisition.
- 2 - Ensure "Old Study" is selected. Enter blank filename as follows: blnk12896256-YYYYMMDD <current date>
- 3 - Acquire Now
- 4 - Enter weight (0.01), Activity (0.01), time (OK to enter computer time as this value is not used for decay correction).
- 5 - Select Protocol Transmission Only DefaultBlank576 Edit
- 6 - FOV 256
- 7 - Save Output Protocol DefaultBlank256 OK
- 8 - Use Start.

This acquisition takes approx. 20 minutes to acquire a blank transmission sinogram <p0s2_blnk12896256-YYYYMMDD_tr.scn> and EC sinogram <p0s2_blnk12896256-YYYYMMDD_ec.scn>.

- 9 - Interpolate each sinogram file on the PET Server (Processor) using Xterm Unix commands.

On PET Server, left mouse click in the blue background, select Xterm from the drag down menu. In the Xterm, enter the following:

```
cd /sun0/patient/p0/s2 <Return>
```

```
pwd (confirm you are in the correct directory)
```

Interpolate the Blank sinogram into two separate Blank files

```
sino_interp -fov 256 -minslc 49 -nslice 42 -slcthk 2 p0s2_blnk12896256-YYYYMMDD_tr.scn blnk12896256-YYYYMMDD_int_tr.scn
```

Interpolate the Leak sinogram (EC) into two separate Leak files

```
sino_interp -fov 256 -minslc 49 -nslice 42 -slcthk 2 p0s2_blnk12896256-YYYYMMDD_ec.scn
```

```
blnk12896256-YYYYMMDD_int_ec.scn
```

10 - Move interpolated Blank and Leak sinograms to /home/ugm/recon/tables

```
mv -p blnk12896256-YYYYMMDD_int_tr.scn /home/ugm/recon/tables/blnk12896256-YYYYMMDD_int_tr.scn
```

```
mv -p blnk12896256-YYYYMMDD_int_ec.scn /home/ugm/recon/tables/leak12896256-YYYYMMDD_int.scn
```

Change directory: cd /home/ugm/recon/tables

Remove <rm> old 256 blank links if they already exist in this directory.

(Note there is an extra "2" on the second file name for GEMINI16 & 1B & Allegro GS.)

```
rm blnk12896256.scn
```

```
rm blnk128962562.scn
```

```
rm leak12896256.scn
```

```
rm leak128962562.scn
```

Link the files in /home/ugm/recon/tables

```
ln -s blnk12896256-YYYYMMDD_int_tr.scn blnk12896256.scn
```

```
ln -s blnk12896256-YYYYMMDD_int_tr.scn blnk128962562.scn (Note there is an extra "2" on the filename)
```

```
ln -s leak12896256-YYYYMMDD_int.scn leak12896256.scn
```

```
ln -s leak12896256-YYYYMMDD_int.scn leak128962562.scn (Note there is an extra "2" on the filename)
```

B) Create Brain Cs-AC Recon protocol

Note Create Recon Protocol before Acquisition protocol so the concurrent recon will be available.

1 - Select a sinogram file from the p0s1 (Applications Training) account.

2 - Highlight an emission sinogram ☺ PETVIEW ☺ Reconstruct Sinogram ☺ Overwrite image file☺ No.

3 - Edit the name of the output Image file and then left mouse click on Select Clinical Protocol.

Note if you fail to edit the name of the output image file then you will be unable to select a Clinical Protocol

4 - Select Brain-ramla3d_elac Protocol ☺ Edit

5 - Change Attenuation Correction ☺ Ellipse to Transmission ☺ Edit ☺

EC Subtraction ☺ Measured

Output Transmission Image ☺ Save

Post Processing ☺ Segmentation ☺ O

6 - Change Background Subtraction ☺ Non-Uniform ☺Edit ☺ Region Type ☺ Body Contour ☺ OK

7 - Make sure that 3DAC is "ON"

8 - Save ☺ Change Output Protocol name to Brain-ramla3d-ac ☺ Save

9 - Then Cancel.

Now 256 FOV sinograms can be reconstructed with Cs Attenuation correction.

Note that Estimated Emission Contamination Correction is not supported for 256 FOV. The protocol used to acquire the 256 FOV brain transmission scan needs to collect the EC at the time of the transmission collection (i.e., edit the protocol).

C) Generate Brain-AC Acquisition protocol using Cs-Ac

- 1 - Highlight account p0, s1 in File Manager ☺ Acquisition ☺ Setup Acquisition
- 2 - Enter Patient weight at .001 ☺ Confirm Old Study is selected ☺
- 3 - Create a bogus Sinogram Filename ie: braintest
- 4 - Acquire now ☺ Select Protocol ☺ Single Pass Emiss / Trans ☺ Edit
- 5 - FOV ☺ 256
- 6 - Orientation ☺ Head First ☺ S Supine
- 7 - Scan Length ☺ 180mm
- 8 - Concurrent Recon ☺ On ☺ Concurrent Recon Protocol ☺ Brain-ramla3d-ac
- 9 - Time per position ☺ Constant ☺ 20mins
- 10 - Singles Options ☺ Trans with EC
- 11 - Save ☺ Output protocol ☺ DefaultBrain

Philips Allegro scanner

Reconstruction Diameter: 256.000000 mm

Field of View Shape : 16 : CYLINDRICAL RING

Field of View Dimension(s): 864\180

Pixel Spacing: 2.000000\2.000000 (in-plane\axial)

All corrections: DECY\RADL\ATTN\SCAT\LAN\NORM

Attenuation Correction Method: Attenuation Cor=ELLIPSE,Emission Contamination
Cor=MEASURED

Reconstruction Method : RAMLA_3D

Appendix B – Data Transfer

A. Preparing to Upload Reconstructed Images to LONI

After images have been reconstructed, the image files must be uploaded to LONI. Before they can be uploaded, you need to know where the image files are, and be able to access them. The procedure for doing this may be different for each site, but some guidelines are given below, according to the type of scanner. In general, for sites that have DICOM files (GE scanners, Philips scanners and Siemens Biograph scanners), the DICOM files must be exported from the patient database, and put into a single folder, in a known location on a local workstation. For sites that have ECAT file formats (Siemens HR, HR+, EXACT, and ACCEL scanners), you must find the location and filename of the appropriate image files.

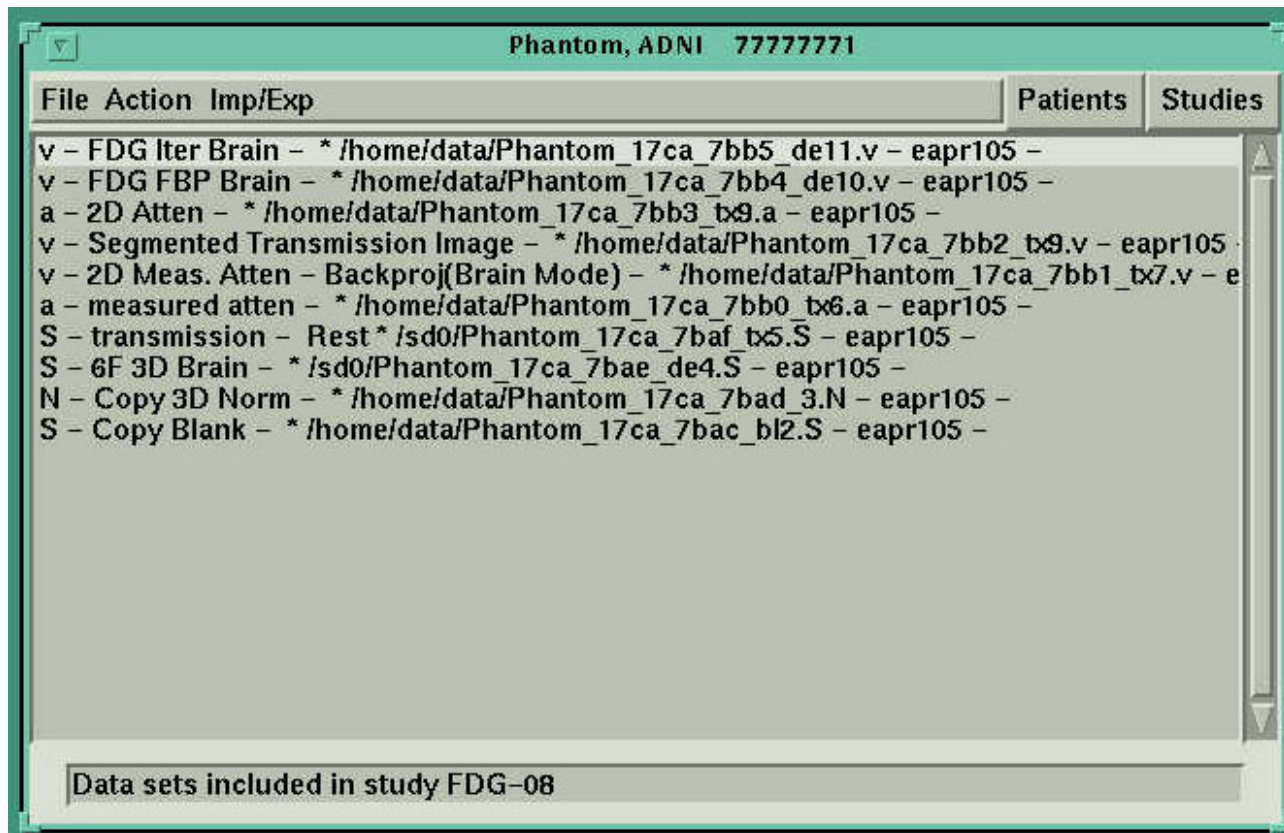
Siemens HR/HR+/EXACT/ACCEL

To locate the image files using the ECAT software, first open the Database Utilities and highlight the patient whose files you are uploading. Click on the *Studies* button to see the patient's studies, as seen in this example:

File	Action	Imp/Exp	Patients	Data
FDG-08		03/16/05 10:50:57		
FDG-08		03/14/05 14:00:11		
FDG-07		03/14/05 13:34:58		

Studies performed for ADNI Phantom

Next, highlight the correct study (FDG-08 on 3/14/05 in the previous image), and then select the **Data** button to see all of the files belonging to the study. An example of the list of study files is shown here:



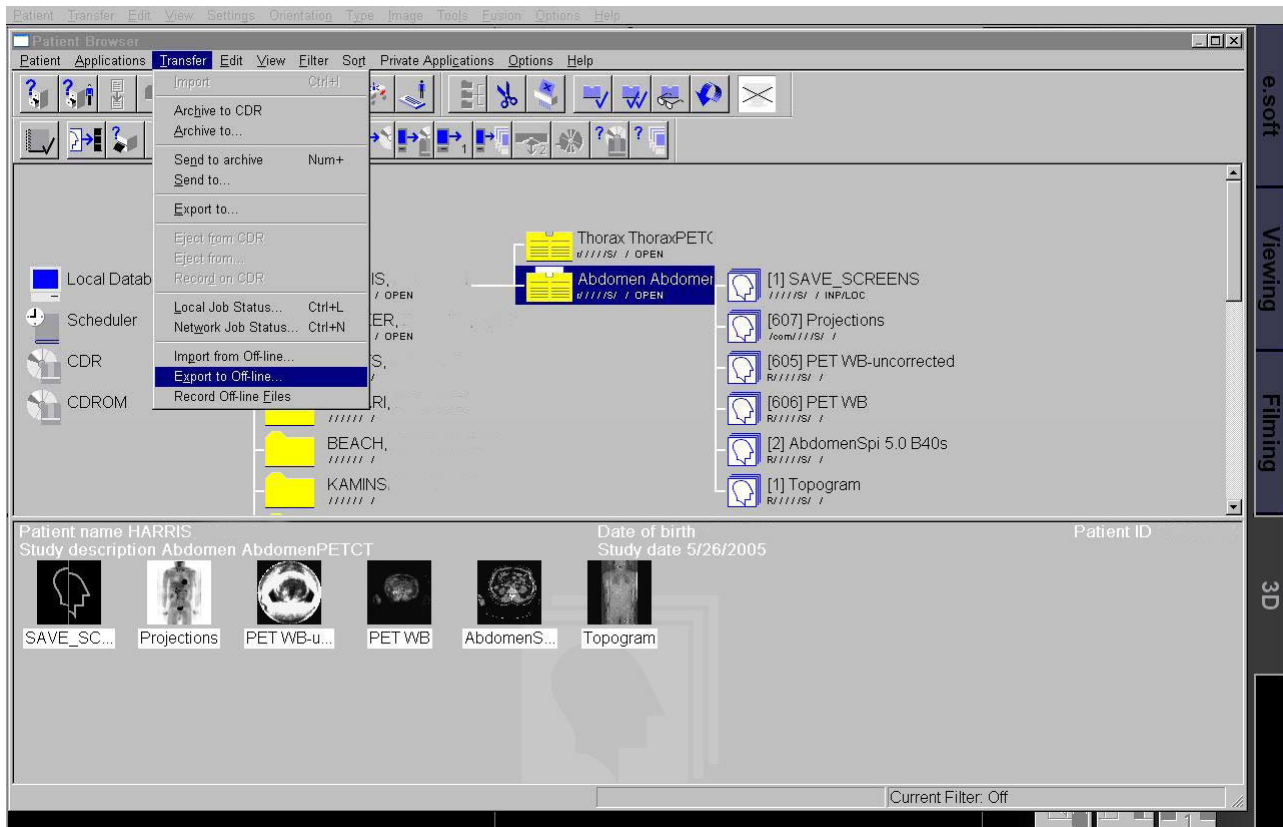
Note that in this window you can see the location of the file and the complete filename. In the above window, the highlighted file is located in the directory `/home/data/`, and the complete filename is `Phantom_17ca_7bb5_de11.v`.

Depending on the way your site is configured, you may wish to move the image files to another location or another computer before uploading the images to LONI, especially if you plan to upload the images at the same time as another acquisition is taking place.

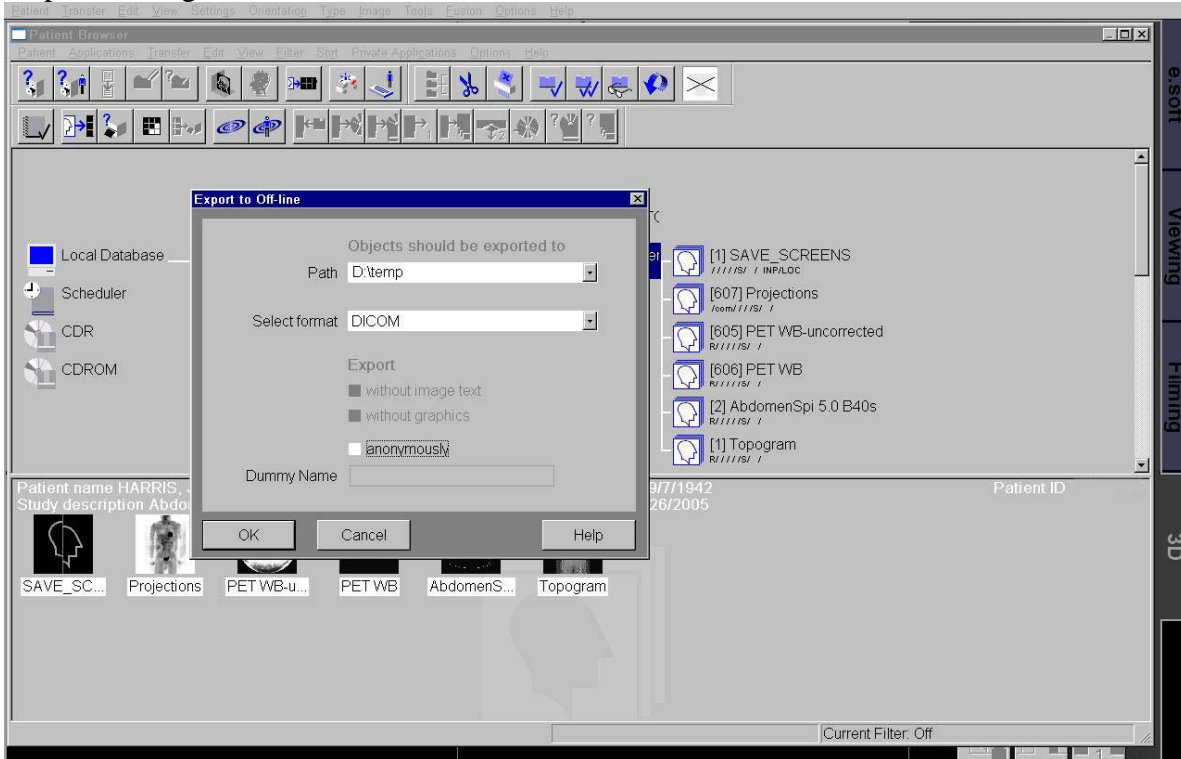
Siemens Biograph

If you are using a Siemens Biograph scanner, you need to export the patient's images from the database before they can be uploaded to LONI. If you have a second workstation separate from the acquisition workstation, it is preferable to send the images there before doing the upload so as not to interfere with acquisition system.

Before exporting the images, create an empty folder to put them in. Then, from the *Patient Browser* utility, select the patient and the study you are planning to upload. From the *Transfer* menu, select the *Export to offline...* option as shown below:



After you choose this option, a dialog will appear allowing you to select the folder in which to put the exported images, as shown here:



In the *Path* field, select the empty folder you just created. In the *Select format* field, make sure **DICOM** is selected. It is not necessary to select the *anonymously* check box because the images will be de-identified as part of the upload procedure. Then select the **OK** button. The individual DICOM files will be exported from the database and placed into the selected folder. Note that there is a separate DICOM file for each image plane.

GE Advance and Discovery LS

For GE Advance and Discovery LS systems, the following is an excerpt from the [PET Advance Operator Manual 2280383 Rev 4](#), which explains how to export the DICOM files:

9-2-3.2 Export a DICOM Part 10 File

Refer to section 9-2.1 for additional Network Operations panel information.

- 1.) Refer to [Figure 9-4](#). Select the local host name as the *Source* station.
- 2.) Select the local host name DICOM file as the *Destination* station.
- 3.) Type the pathname into the *Dest. Path* data field.
- 4.) Select/highlight the files you plan to export.
- 5.) Select **EXPORT** to start the file transfer.
 - Monitor the *Export Progress* area of the panel for status messages.

Figure 9-4: Network Operations - Export DICOM Part 10 File

The screenshot shows the 'Network Operations' panel with the following details:

- Source:** hawkmoth
- Destination:** hawkmoth DICOM File
- Type of Data:** Patient
- Dest. Path:** /operator
- Include Data:** Image
- Sort by:** Patient Name

Date	Patient Name	ID	Mod Investigator	Image Sets Procedure
18-Jul-2000		BLANK SCAN	PT	2 Blank Scan
17-Jul-2000		NOVELLIZATION	PT	2 Novelization
17-Jul-2000		BLANK SCAN	PT	2 Blank Scan
17-Jul-2000		BLANK SCAN	PT	2 Blank Scan
17-Jul-1999	3D-Normal Brain	0608	PT A2053	3 Slice 3-D 60
15-Jul-2000	ADP import test data	0772704	PT	12 TX
06-Jul-2000	DEAN.HOTB	012	PT	1

Buttons: Select, Reset, Make list

Export Progress: 0% (0/0) MB

Buttons: Export, Stop

GE Discovery ST

For GE Discovery ST systems, the following is an excerpt from the Xeleris Functional Imaging Processing & Review System Operator Manual 2364204 Rev 3, which explains how to export the DICOM files. When exporting, be sure to choose *Export to DICOM Part 10 format* as the Type of Export Operation in the *Export Configuration Panel*.

Exporting

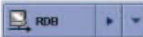
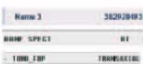


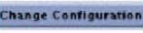
Description – Multiple studies can be selected for exporting, but each study is exported separately to a different file.

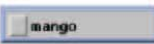





Purpose – Converting system database data to DICOM Part 10 and Interfile 3.3 files.





Note

System database curve data can not be exported to Interfile 3.3 file.

Exporting to remote stations is available only for remote stations with DICOM/Interfile **Store** facilities.

Data Management Screen	
[Source Repository]	 Connect to the source repository from where you want to export data (Xeleris, eNTEGRA V2.0 and higher, Genie P&R).
Data to be exported	 Select the data to be exported (study/studies, series or dataset(s)).
[Import/Export]	 Selects the Import/Export application residing in the Housekeeping category. Click [Start] to open the import/export panel.
Export/Import Panel	
Export tab	 Open the Export tab. If the information under the Current Configuration Details does not match the required export configuration, proceed to [Change Configuration]. Otherwise, proceed to Select Data to be Exported .
Export Panel	
[Change Configuration]	 Opens the export configuration panel.

Export Configuration Panel	
Station to Export to	 <p>Click on the station to export to (the remote stations were configured by the service engineer during system installation).</p>
Type of Export Operation	 <p>Click on the type of export operation to be performed:</p> <ul style="list-style-type: none"> • Export to Interfile format • Export to DICOM Part 10 format
Station to Export to	 <p>Click on the station to export to (the remote stations were configured by the service engineer during system installation).</p>
Destination Path	 <p>If the path of the destination directory to which you want to export the file appears in the Path Window, click on it.</p> <p>Otherwise, type in the new Directory Path, click [Add Path], then click on the new path which appears in the Path Window.</p> <p>Note: If the selected station is the local station and the typed in path is invalid, an error message will be displayed.</p>
[Apply & Quit]	 <p>Closes the export configuration panel, applying the new configuration.</p>
Export Panel	
Select Data to be Exported	 <p>Select the datasets of the first study to be exported.</p> <p>The datasets in the Listing Window can be sorted via the Sort By drop-down menu which includes the following sorting options:</p> <ul style="list-style-type: none"> • Patient ID • Series ID • Dataset Name <p>Information pertaining to the 1st selected study is displayed below the Listing Window with a default File Name to Export to.</p> <p>You can change the default file name by overwriting it (up to 8 characters).</p>

Export Panel (Continued)		
[Export]		<p>Exporting of the first study in the Listing Window is initiated. The progress of the export operation is displayed. If a remote station was selected, a connection to this station is established. Note: datasets currently in use can not be exported.</p>
Export Log		<p>When file conversion is completed, check the Export Log, which displays an entry for each dataset exported to the 1st file. The Status field indicates a successful conversion as "completed" and a non-successful conversion as "Failed".</p>
[Export]		<ul style="list-style-type: none"> • Click on the 2nd study to be exported. • If necessary, change the default file name to Export to. • Click [Export]. The second study is exported as shown in the Export Log. <p>Repeat this procedure for each study to be exported.</p>
[Clear Log]		<p>When all the studies were exported, clear the Export Log.</p>

Philips Allegro

For Philips Allegro systems, the native image file format is PETVIEW. In order to send the image files to LONI, they must be converted to DICOM format. Use the ***DICOM Send*** option to do this. The following is an excerpt from chapter 17 of the Allegro Imaging System User's Manual which explains how to convert the images to DICOM format.

Allegro Imaging System User's Manual

Sending Images

To send PETVIEW images in DICOM format:

1. Highlight one or more images from the *Study Files* window.



If you have edited patient information in the database file, be sure to edit the information in the Mainheader of each image (.img), sinogram (.scn), and syntegra (.syn) file within the study accordingly. This is critical, because the information in the Mainheader displays in all image display applications and is sent during a DICOM translation of image (.img) files. (Refer to *Edit Mainheader/Subheader* in *Chapter 5* for specific procedures.) Failure to correct all files before DICOM translation may result in the propagation of incorrect patient information and/or misdiagnosis.

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.

Philips Gemini

For Philips Gemini systems, the native image file format is PETVIEW. In order to send the image files to LONI, they must be converted to DICOM format. Use the **DICOM Send** option to do this. The following is an excerpt from chapter 5 of the GEMINI Dual-Slice EXP PET/CT System documentation which explains how to export the images in DICOM format.

Exporting Images

You can send images to other systems or you can export them to a directory. If you send the image to a directory, the file is stored as a DICOM part-10 format file. You can export *.img and *.syn files.

NOTE: To export .syn files, the original DICOM (.dcm) files need to be in the patient directory. If the files have been deleted, the export of the .syn files fails.

To export images to other systems using DICOM:

1. In the File Management System window, open the patient directories that contain the images you want to export. You can choose one or multiple patient studies.

NOTE: Refer to *Managing PET Studies and Files* to open study files or if an error message displays.

The Study Files window displays.

2. Select all the patient images you want to export.

For example, files that have *.img or *.syn extensions.

3. From the menu, select **Options > DICOM Send**.

The DICOM Export window displays. The image files you selected are listed in this window.

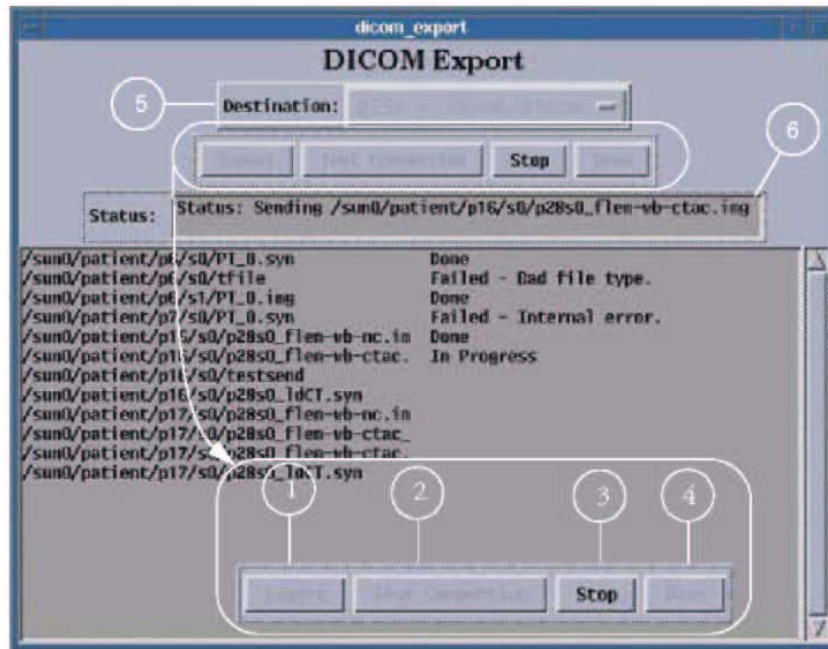


Figure 5-1 DICOM Export Window

4. Click and hold the button next to Destination: (5) to bring up a list of possible destinations in the configuration file.
5. Select the destination where you want to send the image(s).
Destinations can be other workstations, personal OD/CDs, or local file folders (i.e. writing DICOM files).
6. To test the destination connection and make sure it is active, click **Test Connection** (2).
If you chose a directory destination, the **Test Connection** button is not active.
A message displays in the **Status** field (6) when the destination you chose is active. When the destination is not active, the message indicates it failed to connect. If a destination is not active, then choose a different destination or determine why the destination you chose did not work.
7. When you have verified the destination as active, click **Export** (1).
In the DICOM Export window, text displays next to each file listed indicating the transmission progress.

After the image file is sent, the `In Progress` status changes to `Done`.

If there is any failure, `Failed` displays with the reason for the failure. Refer to [Investigating Failed Export of DICOM Files](#) to investigate a failed file export.

NOTE: To stop the export process, refer to [Stopping and Restarting Export](#).

8. If you want to export the same files to a different location, change the destination in the **Destination** list and click **Export**.

The Status history from the previous export is cleared and the files are exported to the new destination.

9. When you are finished exporting, click **Done** (4)

The DICOM Export window closes.

B. Uploading Reconstructed Images to LONI*

*The following are instruction taken from the May 24th, 2005 Version 1 of the LONI Image Data Archive Instructions (IDA Instruction Manual). Please visit the LONI website at <http://www.loni.ucla.edu/ADNI/Data/index.shtml> for the most current version.

i. IMAGE DATA ARCHIVE OVERVIEW

The LONI Image Data Archive (IDA) provides an integrated environment for safely archiving, querying and visualizing neuroimaging data utilizing a web-browser interface. The archive protects data from unauthorized access while providing the ability to share data among collaborative investigators.

For questions or problems with the IDA please send email to dba@loni.ucla.edu

ii. SYSTEM REQUIREMENTS

The IDA requires a newer web browser (IE, Netscape, Mozilla) with the Java 1.4.2 (or higher) plug-in. The version of Java Plug-in installed can be verified at <http://javatester.org/version.html>.

iii. USER REGISTRATION

- From the ADNI home page at <http://www.loni.ucla.edu/ADNI/> click the data management link.



GOAL

The Alzheimer's Disease Neuroimaging Initiative (ADNI) is a 5-year public-private partnership to test whether serial magnetic resonance imaging (MRI), positron emission tomography (PET), other biological markers, and clinical and neuropsychological assessment can be combined to measure the progression of mild cognitive impairment and early Alzheimer's disease. There are three major goals of ADNI. The first goal is to develop improved methods, that will lead to uniform standards for acquiring longitudinal, multi-site MRI and PET data on patients with Alzheimer's disease, mild cognitive impairment, and elderly controls. The second goal is to create a generally accessible data repository that describes longitudinal changes in brain structure and metabolism while acquiring clinical, cognitive and biomarker data for validation of imaging surrogates. The final goal is to determine those methods, that provide maximum power to determine treatment effects in trials involving these patient groups. It is expected that ADNI will provide extensive new data concerning the natural history of brain changes which occur during the transition from normal aging to MCI to AD that can be used for future design and power of clinical trials and extensive information about the relationship between brain imaging changes and changes in biomarkers obtained from blood and CSF.

[READ MORE ABOUT ADNI](#) ...

[↑ Back to Top](#)

IN THIS SECTION:

[About ADNI](#)

[Research](#)

[Data Management](#)

[Billboard](#)

[Contacts](#)

[January 30 Steering Committee Meeting](#)



- Click the Login button to archive files or query the database.

ADNI Alzheimer's Disease Neuroimaging Initiative

HOME ABOUT ADNI RESEARCH DATA MANAGEMENT BILLBOARD LONI HOME

LONI > ADNI

Data Management

DATA ARCHIVE LOG IN

The LONI data archive provides an integrated environment for safely archiving, querying and visualizing imaging data utilizing a web-browser interface. The archive protects data from unauthorized access while providing the ability to share data among collaborative investigators. The various components of the data archive are described in the following sections.

ARCHIVE

The archival process involves de-identifying the header file and securely transmitting the image data from the local site to LONI. The purpose of de-identification is to remove or replace any fields in the header file that have to do with the identity of the subject, such as the Patient Name and ID fields.

DATABASE QUERIES

The query interface allows individuals to browse archived data at varying levels, according to their role within the project. Those with sufficient authorization may view, download and create collections of images.

Follow this link for up-to-date statistics on archived images

IN THIS SECTION:

- [DOJ Protection of Human Subjects](#)
- [DHHS Privacy Rule](#)
- [Subject Privacy Links \(PDF\)](#)
- [LONI Policy \(PDF\)](#)
- [IDA Instruction Manual](#)

RELATED SITES:

- [ADCS Database](#)

- Click “Please follow this link to setup your account” to complete the user registration.

LONI Laboratory of Neuro Imaging, UCLA

HOME ABOUT LONI RESEARCH VISUALIZATION NEWS & EVENTS

LONI > About LONI > Resources

Image Data Archive - Sign In

RETURNING USERS SIGN IN

E-mail

Password

[Forgot your password?](#)

SIGN IN

Java 1.4.2 plugin is required.

NEW USERS

Create a new account.
Please follow this link to setup your account

Benefits:

- Establish an account to create access to web resources
- Highly secure and very convenient

BENEFITS

- De-identification**
Addresses government regulations for protection of human subject privacy
- Data Transmission**
Data is transmitted over the internet using Hyper-Text Transfer Protocol with SSL encryption (HTTPS)
- Storage**
Data is archived on a fault-tolerant storage area network (SAN), providing near 24/7 availability

RELATED LINKS

- [DOJ Protection of Human Subjects >](#)
- [DHHS Privacy Rule >](#)
- [LONI De-Identification Policy >](#)
- [LONI Policy \(PDF\) >](#)

OVERVIEW

The LONI Image Data Archive was constructed to provide a simple, yet effective means of securely storing neuroimaging data on the LONI storage network. The easy-to-use web browser interface provides complete data de-identification and data transmission functionality. The Java applet that performs data de-identification travels to the user's local workstation where the de-identification process occurs. This approach ensures that no identifiable patient information crosses the network. The user may review the results of the de-identification process prior to initiating data transmission, further ensuring the integrity of the data.

The **LONI Image Data Archive System** provides a secure system for the archival of collaborator collected image data, ensuring confidentiality, and restricting access to authorized users. Read our [Privacy Notice](#).

© 2005 LONI. All rights reserved. TERMS OF USE SITEMAP CONTACT

- Complete the New Account form then press the Register button. Notify the LONI administrator (dba@loni.ucla.edu) when you have registered so your access level can be set. You will receive an e-mail when this process is complete (within one business day).

The screenshot shows the LONI website's registration page. At the top is a blue header with the LONI logo and 'Laboratory of Neuro Imaging, UCLA'. A search bar is in the top right. Below the header is a navigation menu with links for HOME, ABOUT LONI, RESEARCH, VISUALIZATION, and NEWS & EVENTS. The main content area is titled 'Create New Account' and is divided into two sections: 'SETUP NEW ACCOUNT' and 'PERSONAL INFORMATION'. The 'SETUP NEW ACCOUNT' section contains two required text input fields: 'Type in your E-mail address*' and 'Type in a user name*'. A note below the second field states: 'If you have a LONI account use your LONI user name'. The 'PERSONAL INFORMATION' section contains several required text input fields: 'First Name*', 'Last Name*', 'Institution / Company*', 'Department*', 'Zip / Postal Code*', and 'Country*'. There is also an optional field: 'If you have a website, please enter the URL here'. Below these fields is a note: 'Once you click Register, we'll send you an e-mail message containing your temporary password.' and a note: 'Required fields are denoted by an asterisk(*)'. At the bottom of the form is a blue bar with the text 'BY CONTINUING, YOU ARE AGREEING TO THE LONI TERMS OF USE' and a 'REGISTER' button. The footer of the page contains copyright information: '© 2004 LONI. All rights reserved.' and links for 'TERMS OF USE', 'SITEMAP', and 'CONTACT'.

iv. IDA LOG IN

- From the ADNI home page <http://www.loni.ucla.edu/ADNI/Data>, enter your e-mail address and password, then click the Sign-In button. New users, please refer to the user registration section for instructions on how to register as a user

The screenshot shows the LONI (Laboratory of Neuro Imaging, UCLA) website's sign-in interface. At the top, there is a navigation bar with links for HOME, ABOUT LONI, RESEARCH, VISUALIZATION, and NEWS & EVENTS. The main heading is "Image Data Archive - Sign In". Below this, there are two sections: "RETURNING USERS SIGN IN" and "NEW USERS".

RETURNING USERS SIGN IN

E-mail:
Password:
Forgot your password? [\[?\]](#) SIGN-IN
Java 1.4.2 plugin is required.

NEW USERS

Create a new account:
Please follow this link to setup your account [\[link\]](#)

Benefits:

- Establish an account to create access to web resources
- Highly secure and very convenient

BENEFITS

- **De-identification**
Addresses government regulations for protection of human subject privacy
- **Data Transmission**
Data is transmitted over the internet using Hyper-Text Transfer Protocol with SSL encryption (HTTPS)
- **Storage**
Data is archived on a fault-tolerant storage area network (SAN), providing near 24/7 availability

RELATED LINKS

- [DOJ Protection of Human Subjects >](#)
- [DHHS Privacy Rule >](#)
- [LONI De-Identification Policy >](#)
- [LONI Policy \(PDF\) >](#)

OVERVIEW

The LONI Image Data Archive was constructed to provide a simple, yet effective means of securely storing neuroimaging data on the LONI storage network. The easy-to-use web browser interface provides complete data de-identification and data transmission functionality. The Java applet that performs data de-identification travels to the user's local workstation where the de-identification process occurs. This approach ensures that no identifiable patient information crosses the network. The user may review the results of the de-identification process prior to initiating data transmission, further ensuring the integrity of the data.

The LONI Image Data Archive System provides a secure system for the archival of collaborator collected image data, ensuring confidentiality, and restricting access to authorized users. Read our [Privacy Notice](#).

© 2005 LONI. All rights reserved. | [TERMS OF USE](#) | [SITEMAP](#) | [CONTACT](#)

- From the IDA Data Management Menu page, click the Query button to view or download images, or the Archive Files button to upload images to the data archive.

The screenshot shows the LONI (Laboratory of Neuro Imaging, UCLA) website's IDA Data Management Menu page. At the top, there is a navigation bar with links for HOME, ABOUT LONI, RESEARCH, VISUALIZATION, and NEWS & EVENTS. The main heading is "IDA Data Management Menu".

RELATED LINKS

- [DOJ Protection of Human Subjects >](#)
- [DHHS Privacy Rule >](#)
- [LONI De-Identification Policy >](#)
- [LONI Policy \(PDF\) >](#)

Select an option from the menu below or click Logout to end your session. [\[?\]](#) LOG OUT

[\[?\]](#) QUERY Select QUERY to access the query interface, view images, form collections of images or download images.

[\[?\]](#) ARCHIVE FILES Select ARCHIVE to upload new images into the Image Data Archive.

© 2005 LONI. All rights reserved. | [TERMS OF USE](#) | [SITEMAP](#) | [CONTACT](#)

v. IMAGE ARCHIVE OVERVIEW

The two steps that comprise the image archive process are de-identification and file transmission. The image files are de-identified at the user's local workstation, in accordance with HIPAA regulations and ensuring that no identifiable patient information crosses the network. Then, the de-identified files are securely transmitted to LONI and stored in the data archive.

PROCESS

Following user authentication, the user chooses the data to be archived by selecting the directory where the data are located and chooses a directory where the de-identified files will be written. Next, a Java applet de-identifies the files, inserting the user-supplied subject identifier and removing or replacing other potentially identifying information. The user is given the opportunity to validate the de-identification results, prior to transmitting the images. Once the results of the de-identification process have been validated, the files are transmitted from the user's local computer to LONI. Upon arrival at LONI, the data are stored in a fault-tolerant storage area network and the database is populated with relevant metadata attributes.

v. ARCHIVE INSTRUCTIONS FOR ORIGINAL FILES

The Archive and Review page is the starting point for uploading new images. The bottom portion of the page lists the last 10 images uploaded by the user.

SYSTEM REQUIREMENTS: The IDA requires a newer web browser (IE, Netscape, Mozilla) with the Java 1.4.2 (or higher) plug-in. The version of the Java Plug-in installed can be verified at <http://javatester.org/version.html>.

ASSUMPTIONS:

- The source directory may contain subdirectories, as long as all data beneath the highest level folder belongs to a single subject.
- An empty directory exists for holding the de-identified files (or a new, empty directory can be created).

LOGGING IN:

The archive log in page is available by clicking the Log In button on the ADNI Data Management page <http://www.loni.ucla.edu/ADNI/Data>.

On the Sign-In page, enter your e-mail address and password, then click the Sign-In button.

New users, please refer to the user registration section for instructions on how to register.

LONI Laboratory of Neuro Imaging, UCLA

HOME ABOUT LONI RESEARCH VISUALIZATION NEWS & EVENTS

LONI > About LONI > Resources

Image Data Archive - Sign In

RETURNING USERS SIGN IN

E-mail:

Password:

Forgot your password?

Java 1.4.2 plugin is required.

NEW USERS

Create a new account:
Please follow this link to setup your account

Benefits:

- Establish an account to create access to web resources
- Highly secure and very convenient

BENEFITS

- **De-identification**
Addresses government regulations for protection of human subject privacy
- **Data Transmission**
Data is transmitted over the internet using Hyper-Text Transfer Protocol with SSL encryption (HTTPS)
- **Storage**
Data is archived on a fault-tolerant storage area network (SAN), providing near 24/7 availability

RELATED LINKS

- DOJ Protection of Human Subjects >
- DHHS Privacy Rule >
- LONI De-identification Policy >
- LONI Policy (PDF) >

OVERVIEW

The LONI Image Data Archive was constructed to provide a simple, yet effective means of securely storing neuroimaging data on the LONI storage network. The easy-to-use web browser interface provides complete data de-identification and data transmission functionality. The Java applet that performs data de-identification travels to the user's local workstation where the de-identification process occurs. This approach ensures that no identifiable patient information crosses the network. The user may review the results of the de-identification process prior to initiating data transmission, further ensuring the integrity of the data.

The LONI Image Data Archive System provides a secure system for the archival of collaborator collected image data, ensuring confidentiality, and restricting access to authorized users. Read our Privacy Notice.

© 2005 LONI. All rights reserved. | TERMS OF USE | SITEMAP | CONTACT

On the IDA Data Management Menu page, click the Archive button.



[LONI](#) Laboratory of Neuro Imaging, UCLA SEARCH

[HOME](#) [ABOUT LONI](#) [RESEARCH](#) [VISUALIZATION](#) [NEWS & EVENTS](#)

[LONI > About LONI > Resources](#)

IDA Data Management Menu

RELATED LINKS

- [DOJ Protection of Human Subjects >](#)
- [DHHS Privacy Rule >](#)
- [LONI De-Identification Policy >](#)
- [LONI Policy \(PDF\) >](#)

Select an option from the menu below or click Logout to end your session. LOG OUT

QUERY Select QUERY to access the query interface, view images, form collections of images or download images.

ARCHIVE FILES Select ARCHIVE to upload new images into the Image Data Archive.

© 2005 LONI. All rights reserved. | [TERMS OF USE](#) | [SITEMAP](#) | [CONTACT](#)

On the Archive and Review page, select your Project/Site from the drop down menu and click the Archive Files button. Do not open multiple IDA browser windows while archiving data.



[LONI](#) Laboratory of Neuro Imaging, UCLA SEARCH

[HOME](#) [ABOUT LONI](#) [RESEARCH](#) [VISUALIZATION](#) [NEWS & EVENTS](#)

[LONI > About LONI > Resources](#)

Archive and Review

LOG OUT

PROJECT INFORMATION:

Select Project:

You can de-identify and archive files for the project and site shown above by selecting the ARCHIVE FILES button, query the database by clicking the QUERY button below, or review previously uploaded files in the VIEW RECENTLY ARCHIVED VOLUMES section below.

QUERY

ARCHIVE FILES:

The data archival process involves two basic steps:

1. De-identify the header file by replacing any fields that identify the subject, such as Patient Name and ID, and
2. Transmit image data securely from the local site to LONI.

NOTE: Do not open multiple IDA browser windows while archiving data.

ARCHIVE FILES

VIEW RECENTLY ARCHIVED VOLUMES:

Click on the VIEW button to visualize the volumetric representation of your uploaded files.
Click on the REFRESH button to update the volume list.

REFRESH

Subject ID	Series Description	No of Images	Date ▲	View	Download
PET_2	p640s0_LIM-NS-BR.img: 3D-RAMLA	90	Mon, 05/23/2005	<input type="button" value="VIEW"/>	<input type="button" value="DOWNLOAD"/>
PET_1	Hoffman 3D phantom seb AC	210	Mon, 05/23/2005	<input type="button" value="VIEW"/>	<input type="button" value="DOWNLOAD"/>

Step 1:

Select the data type: choose **Original**.

Complete the required information on the De-Identify page, making sure that a proper research identifier is supplied for the subject, then click the De-Identify button.

Choosing “Bypass Validation Steps” allows you to skip the validation of header attributes, and upload all series without further interaction, however the browser must remain open for the duration of the upload process.

Note: The directory containing the original data files may contain multiple series; however all data within the directory must be from a single subject.

The screenshot shows the LONI Laboratory of Neuro Imaging, UCLA website. The main navigation bar includes links for HOME, ABOUT LONI, RESEARCH, VISUALIZATION, and NEWS & EVENTS. The current page is titled "De-identify" under the "Resources" section. A sidebar on the right lists the steps: 1: De-Identify, 2: Verify & Submit Data, and 3: Confirmation. The main content area features a large "1" in a box next to the heading "STEP ONE: DE-IDENTIFY". Below this, a paragraph explains the de-identification process. A bulleted list provides instructions: select data type (Original, Synthetic, or Derived), enter a Subject ID, choose source and target directories, and check the "Bypass Validation steps" checkbox. A form below these instructions contains fields for Project (ADNI@UCLA), Select Data Type (radio buttons), Research Group (dropdown), Visit Number (text input), Subject ID (text input), Source Directory (text input with BROWSE... button), and Target Directory (text input with BROWSE... button). A note at the bottom of the form explains the requirements for source and target directories. At the bottom of the page, there are links for CANCEL and DE-IDENTIFY, and a footer with copyright information and other site links.

1 **STEP ONE: DE-IDENTIFY**
The de-identification process removes certain data elements from the file header and replaces the patient id with an alternate subject identifier provided by the user.

- Select the type of data to be uploaded then complete the form entries.
- The Subject ID entered below replaces the existing Patient ID in the image file(s). It is recommended that the user keep a separate cross reference of original and replacement subject identifiers.
- Choose source directory (directory in which the original files are located & containing only image files).
- Choose target directory (an empty directory which will contain the new, de-identified files).
- Click the De-identify button to begin de-identification process.
- Check the Bypass validation steps checkbox, to upload files without validating.

PLEASE FOLLOW THE INSTRUCTIONS OUTLINED ABOVE:

Project ADNI@UCLA

Select Data Type Original Synthetic Derived Bypass Validation steps

Research Group Patient

Visit Number Max. 3 characters allowed

Subject ID: Max. 10 characters allowed
Identifier to replace: Patient ID

Source Directory: BROWSE...
Location of original files

Target Directory: BROWSE...
Location for target files

NOTE: Source Directory for file formats that are considered headered (DICOM, GE, etc) may contain multiple series from a single subject. Source Directory for headerless file formats (TIFF, TGA, etc) may contain a single series for a single subject and must have a file name which contains a slice or sequence number (eg subject100_niss1__001.TIFF). ANALYZE files are assumed to be in SPM orientation.

© 2005 LONI. All rights reserved. TERMS OF USE SITEMAP CONTACT

Step 3:

During file transmission, the progress bar will continually show the progress of the file transfer process. When the transmission is complete choose to Return to Menu, Review Uploaded Files, Archive More files or Log Out.

The screenshot displays the LONI Laboratory of Neuro Imaging, UCLA website. The top navigation bar includes links for HOME, ABOUT LONI, RESEARCH, VISUALIZATION, and NEWS & EVENTS. A search bar is located in the top right corner. The main content area is titled "Confirmation" and includes a breadcrumb trail: LONI > About LONI > Resources. A "LOG OUT" button is visible. A list of steps in this section is provided: 1: De-Identify, 2: Verify & Submit Data, and 3: Confirmation (highlighted in red). A large number "3" is displayed in a box. The "CONFIRMATION" section states: "The files listed below have been transmitted to the LONI Archive." and provides instructions: "Please print and retain the LogFile specified in the TRANSMISSION RESULTS window," "To archive additional image data, click the ARCHIVE MORE button," and "To complete the data archival process, click the LOGOUT button." Below this is the "TRANSMISSION RESULTS" section, which shows a progress bar at 100% and a connection speed of 829.0 KB/s. A table lists connection options: Modem, DSL, T1, and LAN. A log window displays the following text: "Completed at 815 KB/s.", "Uploading file 210/210 ADNI_PET_1_PT_Hoffman_3D_phantom_seb_AC__br_raw_20050523 153937484_210.dcm ...", "Completed at 815 KB/s.", and "Mon May 23 15:41:42 PDT 2005 Finished upload at 829.0 KB/s." At the bottom of the transmission results section are buttons for "Return to Menu", "Review Uploaded Files", "ARCHIVE MORE", and "CANCEL". The footer contains copyright information: "© 2005 LONI. All rights reserved." and links for "TERMS OF USE", "SITEMAP", and "CONTACT".

vii. QUERY AND DOWNLOAD INSTRUCTIONS

Overview: The query interface allows the user to search for images based on subject and image-related criteria, view images, form image collections and download images in a number of file formats.

From the ADNI Data Management page, <http://www.loni.ucla.edu/ADNI/Data>, click the Login In button. Enter your e-mail address and password, then click the Sign-In button. From the IDA Data Management Menu page, click the Query button.

The screenshot shows the LONI Laboratory of Neuro Imaging, UCLA website. The header includes the LONI logo and a search bar. A navigation menu contains links for HOME, ABOUT LONI, RESEARCH, VISUALIZATION, and NEWS & EVENTS. The main content area is titled "IDA Data Management Menu" and includes a breadcrumb trail: LONI > About LONI > Resources. Below the title, there is a "SELECT AN OPTION FROM THE MENU BELOW OR CLICK LOGOUT TO END YOUR SESSION." instruction. Two menu items are listed: "QUERY" (with a description: "Select QUERY to access the query interface, view images, form collections of images or download images.") and "ARCHIVE FILES" (with a description: "Select ARCHIVE to upload new images into the Image Data Archive."). A "LOG OUT" button is also present. To the right, under "RELATED LINKS", there are four links: "DOJ Protection of Human Subjects >", "DHHS Privacy Rule >", "LONI De-Identification Policy >", and "LONI Policy (PDF) >". The footer contains copyright information: "© 2005 LONI. All rights reserved." and links for "TERMS OF USE", "SITEMAP", and "CONTACT".

To perform a query, enter search criteria in the fields provided, and then click the “Search” button. Data can be queried based on a combination of subject- and image-related attributes.

SEARCH

LONI
Laboratory of Neuro Imaging, UCLA

HOME
ABOUT LONI
RESEARCH
VISUALIZATION
NEWS & EVENTS

LONI > About LONI > Resources

Image Database Search

LEGEND: [Projects](#) | [Research Groups](#) | [Modalities](#) | [Help](#) | [View Collections](#) | [Manage Users](#) LOG OUT

Enter your selection criteria using the form below:

SUBJECT INFORMATION	IMAGE INFORMATION
<p>Subject ID: <input type="text"/> <small>Leave blank unless searching for a specific subject.</small></p> <p>Species: <input type="text" value="Both"/></p> <p>Research Group: <input type="text" value="Both"/></p> <p>Sex: <input type="text" value="Both"/></p> <p>Age: <input type="text" value="="/> <input type="text"/> <input type="text" value=">"/> <input type="text"/> Years</p> <p>Weight: <input type="text" value="="/> <input type="text"/> <input type="text" value=">"/> <input type="text"/> Kg</p>	<p>Modality: <input type="text" value="PET"/></p> <p>Series Description: <input type="text"/></p> <p>Weighting: <input type="text" value="Select Value"/></p> <p>Pulse Sequence: <input type="text" value="Select Value"/></p> <p>Slice Thickness: <input type="text" value="="/> <input type="text"/> <input type="text" value=">"/> <input type="text"/> mm</p> <p>Acquisition Plane: <input type="text" value="Select Value"/></p> <p style="text-align: right;"><input type="button" value="RESET"/></p>
Aggregate Results:	Search Results:
Group By: <input type="text"/> and <input type="text"/>	Order By: <input type="text"/> and then by: <input type="text"/>
<input type="button" value="AGGREGATE"/>	<input type="button" value="SEARCH"/>

© 2005 LONI. All rights reserved.
TERMS OF USE
SITEMAP
CONTACT

Query results can be either aggregated and grouped or individually displayed and ordered as shown below.

[HOME](#) | [ABOUT LONI](#) | [RESEARCH](#) | [VISUALIZATION](#) | [NEWS & EVENTS](#)

[LOG OUT](#)

Image Database Search Results

LEGEND: [Projects](#) | [Research Groups](#) | [Modalities](#) | [Help](#) | [View Collections](#)

72 image sets match your criteria: Sex = M, Modality = MRI, Weighting = T1.

Your access level: Member (CBM, SFC)
 Access to data is controlled by each project's leader. Click the Projects link above for additional information.

Subject	Species	Project	Research Group	Sex	Age	Modality	Series Description	View*	Select
3_S_547162	Human	SFC	Control	M	0.6	MRI	3DSPGR	<input type="button" value="VIEW"/>	<input type="checkbox"/>
3_S_622255	Human	SFC	Control	M	0.6	MRI	3DSPGR	<input type="button" value="VIEW"/>	<input type="checkbox"/>
3_S_623166	Human	SFC	Control	M	0.6	MRI	3DSPGR	<input type="button" value="VIEW"/>	<input type="checkbox"/>
					0.6	MRI	fallback T1	<input type="button" value="VIEW"/>	<input type="checkbox"/>
					1.0	MRI	3DSPGR	<input type="button" value="VIEW"/>	<input type="checkbox"/>
3_S_658300	Human	SFC	Control	M	0.5	MRI	3DSPGR	<input type="button" value="VIEW"/>	<input type="checkbox"/>
3_S_626143	Human	SFC	Control	M	0.5	MRI	3DSPGR	<input type="button" value="VIEW"/>	<input type="checkbox"/>
					1.0	MRI	3DSPGR	<input type="button" value="VIEW"/>	<input type="checkbox"/>
3_S_827145	Human	SFC	Control	M	0.5	MRI	3DSPGR	<input type="button" value="VIEW"/>	<input type="checkbox"/>
3_S_831296	Human	SFC	Control	M	0.5	MRI	3DSPGR	<input type="button" value="VIEW"/>	<input type="checkbox"/>
3_S_913340	Human	SFC	Control	M	0.5	MRI	3DSPGR	<input type="button" value="VIEW"/>	<input type="checkbox"/>
4_S_101093	Human	SFC	Control	M	0.6	MRI	GE 3D T1W	<input type="button" value="VIEW"/>	<input type="checkbox"/>

To select an individual data set, click the corresponding select box or click here to select all data sets:

Previous 1 2 3 4 5 6 Next

*Clicking the view icon launches the LONI Image Viewer. The viewer requires a Java-enabled browser with [Java Plug-in 1.4.2](#) or newer installed.

Users may form collections of images for downloading. To create a collection, click the select box beside the desired image(s), and then click the “Add to Collection” button. When prompted, enter the collection name. A new window displaying the data collection will open. To download images, select the desired files and click the “Download” button.

[HOME](#) | [ABOUT LONI](#) | [RESEARCH](#) | [VISUALIZATION](#) | [NEWS & EVENTS](#)

[LOG OUT](#)

Image Database Collection

LEGEND: [Projects](#) | [Research Groups](#) | [Modalities](#) | [Help](#) | [View Collections](#) | [Manage Users](#)

Collection	Subject ID	Group	Sex	Age	Modality	Sequence	Format	Downloaded	View*	Select
PET_collection	PET_1	Control	M	0.0	PET	Hoffman 3D phantom seb AC	DICOM		<input type="button" value="VIEW"/>	<input type="checkbox"/>
	PET_2	Patient	F	0.0	PET	p640s0_LIM-NS-BR.img: 3D-RAMLA	DICOM		<input type="button" value="VIEW"/>	<input type="checkbox"/>
	PET_3	Patient	X	0.0	PET		DICOM		<input type="button" value="VIEW"/>	<input type="checkbox"/>

To select an individual data set, click the corresponding select box or click here to select all data sets:

Previous 1 Next

As Archived Minc Analyze

*VIEWING: Clicking the view icon launches the LONI Image Viewer. The viewer requires a Java-enabled browser with [Java Plug-in 1.4.2](#) or newer installed.
*DOWNLOADING: Select desired file format then click the Download button. All selected files will be downloaded into a single directory.

© 2005 LONI. All rights reserved. | [TERMS OF USE](#) | [SITEMAP](#) | [CONTACT](#)

Appendix C - Quantitative PET Imaging Protocol

Pre-Visit Preparation Specific to Quantitation:

- Cross-Calibration procedure between the PET scanner and well counter needs to be performed prior to the patient exam. Refer to the procedure in Appendix D.
- Synchronize the clocks/timers on the PET Scanner, well counter and/or equipment recording blood draw times.
- Ancillary Equipment and Supplies
 - 10 3 cc syringes
 - 5 18-gauge needles
 - 5 2-ml labeled blood sample containers
 - 10 small (5-7 ml) test tubes in which the plasma from the venous samples will be dispensed using a pipette
 - Red Biohazard Bucket
 - Glucose meter and test strips
 - 3-4 10 cc saline flushes
 - 3-way stopcock
 - 3-way stopcock w/6" extension
 - Small cup of ice.

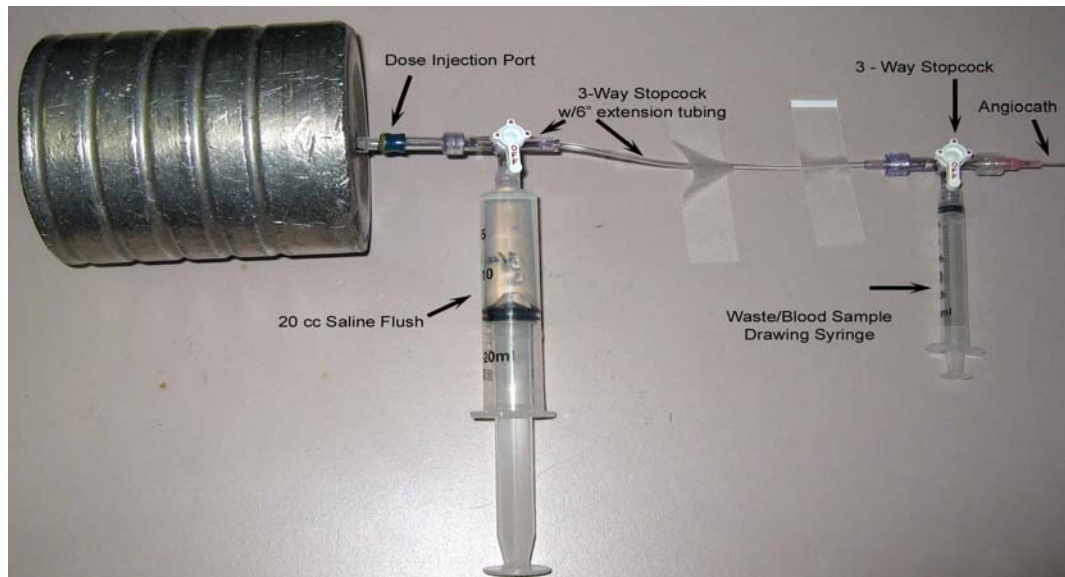
Procedure

- Upon arrival to the imaging center, compliance to the dietary requirements should be confirmed. If they have not complied with the preparation instructions then the following procedures should apply:
 - If < 2 hours have elapsed food/drink, wait until 2 hours have elapsed from last ingestion
 - Once >2 hour have elapsed since last ingestion, measure the blood glucose levels. If the blood glucose level is <180 mg/dL (9.9 mmol/L) then proceed with the scan. If not, the subject will need to wait an additional amount of time until the blood glucose levels meet the above criteria or reschedule.
 - The fasting blood sugar level can be checked at the time of IV insertion if the subject has complied with the dietary prep instructions.
- Have the patient use the restroom and empty their bladder.

- Lay the patient on the imaging table and make him/her as comfortable as possible. Establish an IV line using at least a 22g angiocath. An 18g or 20g angiocath is preferred. Ensure the IV site will be readily accessible for injection once the patient is positioned in the scanner. It is preferable to have the catheter placed in the antecubital fossa if possible.

IMPORTANT: An 18 gauge or 20 gauge angiocath is preferred as it is imperative that venous samples be easily and quickly obtained. If this condition is not obtained with the placement of the first IV another IV must be placed!)

- The following tubing configuration should be used to prevent contamination of the dose into the later venous draws:
 - Angiocath --> 3-way stopcock --> 6" tubing with 3-way stopcock



Recommended Tubing Configuration

- On the 6" line/stopcock, one port of the stopcock should have a hep-lock adaptor and the other should contain a 20 cc flush. All blood draws should be performed from the stopcock attached directly to the angiocath. Since the potential of contamination from the dose to venous samples is high on this technique, it is advisable not to use a reflux valve on the angiocath.

IMPORTANT: All blood draws should be performed from the stopcock attached directly to the angiocath. Since the potential of contamination from the dose to venous samples is high on this technique, it is advisable not to use a reflux valve on the angiocath.

- Position and secure the subject in the scanner using methods previously described.
- Draw 5 ± 0.5 mCi (185 MBq) of [^{18}F]-FDG and assay with a dose calibrator. **The total dose volume should be diluted with normal saline to a final volume of 5 cc's.** Record the assay time to the nearest minute.
- **SIMULTANEOUSLY** inject the patient with [^{18}F]-FDG and begin the 3D dynamic acquisition using framing rate below. Immediately follow with a 20 cc dose of normal saline to flush the line. **DO NOT FLUSH THE DOSE SYRINGE** Record the injection time.

IMPORTANT: Dynamic Framing Rate for Quantitative PET

- (1 frame @ 10 seconds)
- (12 frames @ 5 seconds)
- (2 frames @ 10 seconds)
- (3 frames @ 30 seconds)
- (3 frames @ 60 seconds)
- (2 frames @ 120 seconds)
- (10 frames @ 300 seconds)

33 frames total – 3600 seconds/ 60 minutes

- Re-assay the dose syringe. If residual activity is present, correct the amount of the injected dose for the residual activity.
- Venous blood samples should be drawn according to the following schedule. **A waste syringe should be used to withdraw any saline/residual blood in the line before the actual sample is drawn.** Once samples are drawn they should be dispensed into the pre-labeled tubes, exact draw time recorded, and placed on ice. A small amount of the sample is used to determine the blood glucose level.

IMPORTANT: Venous Sampling Schedule

<u>Sample Number</u>	<u>Draw Time</u> <u>(minutes post FDG Injection)</u>
1	8:00
2	12:00
3	20:00
4	25:00
5	45:00

- All images will need to be corrected using measured attenuation.
 - PET Only Scanners
 - Acquire a post-injection attenuation correction scan using rod sources for 6 minutes upon completion of the dynamic emission scan.
 - Segmentation and re-projection routines will be applied for attenuation correction.
 - GE Scanners may also require a short 2D emission scan to correct the transmission scan
 - PET/CT Scanners
 - Standard CT acquisition parameters
- Upon completion the subject can be removed from the scanner and encouraged to void. The subject should also be instructed to drink plenty of fluids and void frequently throughout the day to help reduce radiation exposure.
- Reconstruct images using parameters specific to the system used for scanning. (See Appendix A in this document).
- Upon completion of the reconstruction, review all the images to assess for artifacts and motion.
- Determine radioactivity concentrations in venous blood samples.
 - Centrifuge all blood samples for 10 minutes at 3000 rpm.
 - Pipette 200 uL of plasma in duplicate and transfer it to the respective labeled test tube.
 - Count each of the samples in the well counter for 60 sec using a 460 - 562 keV window. Window values should be set to this range as closely as possible. It is important to ensure the same energy range is used for both the determination of the scanner/well counter cross calibration as is used in the counting of the subject blood samples. The sample activity in cpm and sample count time should be recorded.
- Archive all raw and processed study data including copies of the normalization and blank scans.
- Transfer image data to LONI using the procedure detailed in Appendix B

Appendix D Scanner – Well Counter Cross-Calibration Procedure

This procedure is used to establish a cross calibration factor between the scanner and well counter; the latter of which is used to count blood samples for the creation of an arterial or venous input function. The procedure can be performed with either an ^{18}F aqueous source or a ^{68}Ge solid source.

^{18}F Method

- 1) Synchronize the PET scanner and well counter times prior to performing the procedures if necessary.
- 2) Fill a uniform cylindrical phantom with deionized water (if necessary). Eliminate as many air bubbles as possible.
- 3) Obtain approximately 0.5 mCi ^{18}F in any form. Assay the activity and record the time.
- 4) Withdraw approximately 60 cc of fluid from the phantom using a large syringe and an 18 gauge needle.
- 5) Add the ^{18}F into the phantom and rinse the syringe thoroughly. Seal the phantom and repeatedly invert to mix the solutions. Re-assay the syringe and record any residual activity and the assay time.
- 6) Replace the 60 cc of fluid previously withdrawn from the phantom. Re-seal and invert several times.
- 7) Pipette 2-200uL samples from the 1 cc of solution previously withdrawn from the phantom into two separate test tubes to be counted later in the well counter.
- 8) Reseal the phantom and position in the center of the gantry using the phantom holder supplied with the scanner.
- 9) Execute a 15 minute static scan using identical acquisition and reconstruction parameters used for the ADNI patient acquisitions.
- 10) Using the activities recorded in steps 3 and 5, determine the actual activity added to the phantom at the time the scan was started.
- 11) Upon completion of the image reconstruction measure the average activity by drawing a large circular ROI, on one plane and then copying that ROI, to all planes. Obtain the mean activity for all the ROI's throughout the phantom volume in units of counts.

- 12) Pipette 2-200uL samples from the 1 cc of solution previously withdrawn from the phantom into two separate test tubes. Place them in the well counter and count for 60 seconds using a counting window of 460 - 562 keV. Obtain counts from a background sample under the same counting conditions. Correct the samples for background, decay correct them to the scan start time and average the two values. Record the average, decay-corrected aliquot counts per minute.
- 13) Using the EXCEL spreadsheet provided, enter the data from the above procedure to compute the cross-calibration factor.

⁶⁸Ge Method

- 1) This procedure uses a ⁶⁸Ga/⁶⁸Ge phantom that many manufacturers supply with the PET scanners. **It requires that a small aliquot of the material used to fill the phantom has been used to create a rod source identical in concentration for counting in the well counter. If this is not available you must use the ¹⁸F method to compute the cross-calibration factor.**
- 2) Synchronize the PET scanner and well counter times prior to performing the procedures if necessary.
- 3) Position the phantom in the center of the gantry using the phantom holder supplied with the scanner.
- 4) Execute a 15 minute static scan using identical acquisition and reconstruction parameters used for the ADNI patient acquisitions. Record the scan start time
- 5) Upon completion of the image reconstruction measure the reconstructed activity by drawing a large circular ROI on one plane and then copying that ROI to all other planes. Obtain the mean activity for all the ROI's throughout the phantom volume in units of counts.
- 6) Count the ⁶⁸Ga/⁶⁸Ge aliquot as well as a background sample in the well counter and count for 60 seconds using a counting window of 460 - 562 keV. Record the background corrected aliquot counts per minute.
- 7) Using the EXCEL spreadsheet, enter the data from the above procedure to compute the cross-calibration factor. You will also need to know the original phantom activity and date of calibration to compute the phantom activity at the time of the scan.