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**PET Quick Start guide:**

**Step 1.** Qualify your PET scanner for a multi-site study.

If you don’t know, contact Suzanne Baker (slbaker@lbl.gov).

If not qualified, you will need to do a Hoffman phantom scan. If you don’t have a Hoffman, contact Suzanne Baker to arrange borrowing a Hoffman phantom. Follow instructions on page 5-6 about scanning a Hoffman, follow instructions in Appendix A for reconstruction. If you do not have the IDA-uploader installed yet, register as a user (Appendix B), install the IDA-uploader (Appendix C) and upload the resulting Hoffman phantom scan using SCANqual (Appendix E). Then contact Bob Koeppe (koeppe@med.umich.edu) to get more information about whether your PET scanner has passed.

**Step 2.** Do you have data acquired after January 1, 2021 on NACC participants to upload?

Make sure the subject is appropriate and the images have been acquired/reconstructed according to SCAN protocols. Information on tracer and acquisition protocols can be found in Table 1. Scanner specific reconstruction parameters can be found in Appendix A.

**Step 3.** Are you acquiring new PET data?

Fill out PET upload form (Appendix F) for scheduling/scanning/reconstructing/uploading
Patient ID: use the local participant ID assigned by your center, not the NACC ID.
When acquiring PET data, the Series Description should include tracer information (see page 8). Check PET procedures and Table 1 for information about reconstruction start-stop time.

**Step 4.** Upload PET data.

Be sure to have PET upload form available, the information is required at the time of upload.

If you do not have the IDA-uploader installed yet, register as a user (Appendix B), install the IDA-uploader (Appendix C). Follow instructions on uploading data (Appendix D).

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Problems with scheduling Hoffman or PET questions: Suzanne Baker (slbaker@lbl.gov)
Problems with PET scanner qualification or PET questions: Bob Koeppe (koeppe@med.umich.edu)
Problems with IDA-uploader (registering, uploading subject data, uploading phantom data using SCANqual): data.coordinator@loni.usc.edu
General Information

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

- Imaging center training and setup process
- Image acquisition guidance (required image acquisition schedule, tracer, administration and recommended techniques)
- Submission of image data to the SCAN Data Portal

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.

Contact Information

Questions about Uploading SCAN data:

data.coordinator@ioni.usc.edu

(For questions/concerns regarding individual subjects contact the study coordinator at your referral site).

Technical/QC questions

koepepe@umich.edu (Robert A. Koepepe) or slbaker@lbl.gov (Suzanne L. Baker).

For questions regarding scanner specific acquisition and reconstruction parameters.

Site Qualification

It is preferable for sites to use existing qualified TRC-PAD, ADNI, LEADS, DIAN, DIAN-TU, Pointer, or NiAD scanners for PET imaging. If you are using a scanner that has not been qualified for one of these projects by Bob Koepepe, it will need to be qualified before imaging can be performed. Please contact Bob Koepepe (koepepe@umich.edu)

If you plan to acquire data for SCAN on a new PET scanner please contact Bob Koepepe. You will need to perform two Hoffman phantom scans and send images to Bob Koepepe prior to scanning any subjects on the new PET scanner.

Do you need to perform Hoffman phantom scans?:

Phantom scans will be performed during the site qualification process, to set up SCAN PET acquisition and reconstruction protocols and to validate their quality. It will also be required after a major hardware upgrade of your PET system, to detect any potential deviation due to the upgrade. Once the system is up and running again, please check the potential impact of the upgrade on the acquisition parameters and communicate
with Bob Koeppe (koepp@umich.edu) to find out what change is considered acceptable.

**NOTE:** If you are using a new scanner that is not listed in the appendix, then the University of Michigan PET QC Team will provide you with scanner specific instructions for your site’s PET scanner.

**Instructions on Hoffman phantom scans:**

1. **Filling Hoffman:**
   - **Radioactivity:** ~0.6 mCi F-18 at time of scan start.

   Fill the phantom carefully to remove air bubbles as much as possible. Mix thoroughly.

   **Tips for successful filling:**
   - **a)** Take out ~50 ml from a filled phantom, BEFORE putting in the radioactivity. It works best to use a spinal needle to inject the radioactivity. Be careful not to "stab" the plastic with the tip of the needle as this often creates a "hot" spot in the scan.
   - **b)** Next, fill the phantom with all but ~10 ml, and mix thoroughly.
   - **c)** Then put in all but the last ~1 ml, and mix again.
   - **d)** Finally, fill that last ml or so as best you can to get rid of the remaining air bubble and mix on last time. For mixing, it works well to put down absorbent pads and have two people roll the phantom back and forth for a half a minute to a minute, which allows less direct contact with the phantom, thus reducing personnel exposure. (One can even use the floor and their feet.)

2. **Scanning of the Hoffman phantom:**
   - The Hoffman phantom should be positioned in the scanner in the same manner as a subject laying on their back. The frontal cortex should be closer to the top of the scanner, occipital cortex to the floor.
   - **Acquisition:** The acquisition time for the Hoffman phantom scan should be four 5-min frames, for a total of 20 min. **Reconstruction:** The same reconstruction parameters should be used as the human scans.

3. **Upload Hoffman phantom reconstruction files:**
   - See Appendix B part D.

4. **Phantom scan evaluation and result:**
   - University of Michigan QC will examine the phantom data and determine if the correct parameters have been met and assure there are no other underlying problems with the scanning session. Your site will be notified by email if the phantom scans pass or fail, and whether your PET system has been certified for SCAN.
Sites must be appropriately licensed through appropriate state or federal agencies to receive and use all radiotracers prior to imaging.

Sites must also receive both IRB approval and radiation safety committee (RSC) or similar approval, before scanning any subjects. The human subjects protocol approved by the IRB must cover data sharing with SCAN.

**Continued Quality Monitoring of PET scanner**
To ensure scanner/ancillary equipment stability and quality, each site is required to perform ongoing quality control procedures.

**PET-only Scanner:**

- The PET scanner should have an up to date calibration and normalization on the date of each imaging session.

- A daily QC/blank 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:**

- The PET/CT 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.

**PET/MR Scanners**

- The PET/MR scanner should have an up to date calibration and normalization on the date of the imaging session.
• On the day of a scan, a daily normalization and detector setup should be completed before any subject scanning is performed. 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 MR QC should be performed as recommended by the specific vendor.

Ancillary Equipment:
• Quality control of the dose calibrator should be performed throughout the course of the study. This typically will include daily constancy, quarterly linearity checks and annual accuracy tests

PET General Information

Ambient Conditions

Standardization of the environment during the uptake period following tracer administration is not essential.

Naming convention

It is VERY important that each site follow standard file identification so that all scans can be easily identified.

When uploading data to SCAN, you will enter the local participant ID into the IDA Uploader (no site ID included). The IDA Uploader will pass the local participant ID and NACC site ID to NACC and receive from NACC either the existing NACC ID for the subject or a newly created one if necessary. The data in the SCAN database will automatically be identified by the NACC ID (same as SCAN ID).

The tracer should be included in the Series Description:

In the PET scan Series Description, include PET radiotracer used as follows:

- Amyloid_PIB
- Amyloid_Florbetapir
- Amyloid_Florbetaben
- Amyloid_NAV
- FDG

- Tau_Flortaucipir
- Tau_MK6240
- Tau_PI2620
- Tau_GTP1
Documentation
The study coordinator must ensure the PET Technologist has a copy of all PET Upload Form prior to each scan session, and that the PET scan information form matches the type of study being performed (amyloid, tau, or glucose metabolism). Be sure to complete the PET Upload form as the study is being acquired. A process should be established for transferring this form(s) back to the study coordinator.
PET Procedures

Be sure to have the PET scan upload form and fill out accordingly during the procedure. Considerations for acquisition and reconstruction:

1. **Reconstruction framing:** Any frames within the Acquisition start-stop time listed in Table 1 should be reconstructed as multiple 5 minute frames. *Examples:* for Florbetaben 90-110, this should be 4x5min frames; for MK6240 70-110 this should be 8x5min frames; for GTP1 this should be 6x5min frames.

2. **Are longer dynamic scans (emission started at time of injection) acceptable?**
   As long as the dynamic scan fully includes at least one of the start-stop times listed in Table 1 for that tracer, this is acceptable. You are encouraged to upload the reconstruction of the full dynamic dataset as long as the framing within the tracer-specific acquisition time is 5 minute frames. *Examples:* PIB 0-50min would not be acceptable, but a PIB scan from 0-60min would be acceptable where the framing from 0-40min should adhere to your site’s reconstruction protocols and framing within 40-60min must be 4x5min frames.

3. **Are longer static scans acceptable?** This is acceptable for acquisition, but not for SCAN-specific reconstruction. *Example:* If you acquire Flortaucipir from 75-115min post-injection, do not upload 8x5min frames, but instead upload data reconstructed from 80-100min as 4x5min frames.

4. **There are many Acquisition start-stop times listed for a tracer, which should we choose?**
   - **If you have a current protocol:** choose the start-stop time that adheres to your current protocol.
   - **If your current protocol covers multiple start-stop time options listed:** reconstruct/upload the longest option. *Examples:* If you are collecting MK6240 from 70-110min, reconstruct and upload 8x5min frames from 70-110min as a single reconstruction, not 70-90 or 90-110min. If you are acquiring PIB from 40-90min, reconstruct and upload 6x5min frames from 40-70min, not 40-60 or 50-70min. If you are acquiring PI2620 from 0-90min, reconstruct and upload the full dynamic data set where 0-45min can be framed as you see fit and 45-90min is 9x5min frames.
   - **If you do not have a current protocol, the preferred times for tracers with multiple options are:**
     - PIB 50-70min
     - MK6240 90-110min
     - PI2620 (AD) 60-90min
Table 1: Radiotracer Doses, Acquisition times post-injection

<table>
<thead>
<tr>
<th>Tracer</th>
<th>Suggested Target Dose ± 10%</th>
<th>Minimum injectable dose</th>
<th>Acquisition start-stop time post-injection (min)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>mCi</td>
<td>MBq</td>
<td>mCi</td>
</tr>
<tr>
<td>AMYLOID TRACERS</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PIB</td>
<td>15</td>
<td>555</td>
<td>8</td>
</tr>
<tr>
<td>Florbetapir</td>
<td>10</td>
<td>370</td>
<td>6</td>
</tr>
<tr>
<td>Florbetaben</td>
<td>8</td>
<td>295</td>
<td>5</td>
</tr>
<tr>
<td>NAV4694</td>
<td>8.1</td>
<td>300</td>
<td>6.5</td>
</tr>
<tr>
<td>TAU TRACERS</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Flortaucipir</td>
<td>10</td>
<td>370</td>
<td>6</td>
</tr>
<tr>
<td>MK6240</td>
<td>5</td>
<td>185</td>
<td>4</td>
</tr>
<tr>
<td>PI2620 (AD)</td>
<td>5</td>
<td>185</td>
<td>4</td>
</tr>
<tr>
<td>PI2620 (non-AD)</td>
<td>5</td>
<td>185</td>
<td>4</td>
</tr>
<tr>
<td>GTP1</td>
<td>7</td>
<td>260</td>
<td>5</td>
</tr>
<tr>
<td>GLUCOSE METABOLISM TRACER</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FDG</td>
<td>5</td>
<td>185</td>
<td>4</td>
</tr>
</tbody>
</table>

The above are suggested target doses +/-10%. We will accept data scanned with the above tracers as long as the amount injected does not fall below the minimum injectable dose and scans are acquired using the start-stop times listed under Acquisition time.
post-injection. If you are acquiring data using an acquisition time not listed, please contact Suzanne Baker (slbaker@lbl.gov).

Using aseptic technique and radiation shielding, draw of the radiotracer and assay with a dose calibrator. Record the assay time to the nearest minute. Do not add saline to the dose prior to administration. Adding saline could potentially lead to precipitation out of solution form.

**Prepare subject**

- Have the subject use the restroom and empty their bladder.
- Allow them to lie comfortably in a bed or reclining chair in a room. Supply them with blankets/pillows as needed to maximize their comfort.
- Obtain intravenous access using a small angiocath.

**Drawing up, assaying, and injection dose**

- Draw up sufficient tracer to achieve the target dose and assay with a dose calibrator.
- **Record the assay time to the nearest minute.** Do not q.s. (add saline) to the dose prior to administration. Adding saline could potentially lead to precipitation out of solution form.
- Inspect the radiopharmaceutical dose solution prior to administration and do not use it if it contains particulate matter or is discolored.
- Inject the radiotracer and follow the injection with an intravenous flush of 0.9% sterile sodium chloride. **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.
- If acquisition does not start with injection, allow the subject to rest comfortably in the room during the incorporation period until about 10-15 min prior to the start time for the particular radiotracer.
• 10-15 minutes before scanning, have the subject use the restroom and empty their bladder.

• For PET/CT scanners, the subject should be placed on the scanning table early enough to obtain a CT scan prior to the emission scan, and still be able to begin the emission acquisition at the appropriate start time. **PET-only systems will acquire a transmission scan following the emission acquisition**, so preparation of the subject can begin a few minutes later than if on a PET/CT system.

**Subject Positioning**

Proper subject positioning is a key aspect of the successful completion of the PET exams. It is important to take the time necessary to ensure not only that the subject is properly positioned but also can **comfortably** maintain that position throughout the duration of the scanning session. **Excessive motion and in particular a difference in the subjects’ position between the emission scan and the transmission or CT scan used for attenuation correction is the single most common cause of failed studies.**

• Have the subject remove any bulky items from their pockets such as billfolds, keys, etc.

• In addition, they should remove eyeglasses, earrings, and hair clips/combs if present. If possible, they should try and remove hearing aids also.

• Position the subject so that their head and 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 such that the PET scanning planes are parallel to the imaginary line between the external canthus of the eye and the external auditory meatus (orbitomeatal plane) and the head is centered in the sagittal plane. More important exact matching of the orbitomeatal plane is making sure the subject is comfortable, which will hopefully translate to less subject motion during the scan.

• Alignment marks should be put on the subject using the laser system, which can then be subsequently used to check alignment and reposition the subject as necessary.
• 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.

• Once the subject has been positioned foam pads can be placed alongside the head for additional support. Velcro straps and/or tape should also be used to secure the head position. Vacuum beanbags can also be used in this process.

• The subjects should be offered a “panic button” or be reassured that someone is watching or able to hear them at all times.

• Proper positioning of the subject to get the entire head in the field of view is critical to the success of the project.

Checking the subject positioning and readjusting (if possible) the position of the subjects’ head should be done often throughout the study.

**Attenuation Correction Procedures:**

**PET/CT Scanners**

• Standard CT acquisition parameters, but low effective mAs (~30 is typical)

• The subject must undergo the CT scan starting about 5 minutes prior to starting the PET scan. Be sure to prepare the subject so that you are ready to press “start” for the PET emission scan at the required time.

**PET-only Scanners**

• For dynamic PET scans (emission starts at injection), acquire the transmission scan for attenuation correction for 5-6 minutes before the emission scan. The subject should be repositioned “on their marks” prior to acquiring the emission scan.

• For static PET scans, acquire the transmission scan using rod sources for 5-6 minutes after the acquisition of the standard emission scan. The subject should be repositioned “on their marks” prior to acquiring the transmission scan.

• Segmentation and re-projection routines will be applied for attenuation correction.

**Emission acquisition procedures:**
Every effort should be made to make sure the acquisition time fully encompasses the target start-stop time from table 1. Scheduling scans very close in time following a clinical study (which could run late) is not an acceptable reason for starting a scan late. *Example: If you are only acquiring Flortaucipir data from 80-100min, every effort should be made to start the acquisition as close to 80min post-injection as possible.*

It is crucial that the subject’s position is checked several times throughout the PET scan. A good idea is to check the subject’s marks using the laser system at the end of each 5 min scan frame. The subject’s position should be returned as closely as possible to the original position just at the beginning of the next scan frame.

**Post PET Scan:**

- Reconstruct images using parameters specific to your site’s scanner (See Appendix A). The framing should always be multiple 5min frames within the start-stop time window in Table 1. Otherwise, the same reconstruction parameters should be used for all emission scans. Upon completion of the reconstruction, review all the images to assess for artifacts.

- Archive ALL raw and processed study data including copies of the attenuation correction-related files (transmission, CT, etc), normalization and blank scans. It is necessary to archive and store raw and processed data at the imaging site for the duration of the project and local guidelines (approximately 5 years).

- Upload PET data using IDA-Uploader (Appendix B)
Appendix A
PET scanner reconstruction parameters
GE Discovery MI - PET/CT scanners
(Arizona, Univ of Washington, Mayo)

Acquisition Parameters:

- **CT scan:**
  Low mAs scan acquired shortly before emission. Leave enough time to start emission acquisition promptly at start time given immediately above. Scans should never be started early.

- **Randoms Correction:**
  *Singles:* (not ‘real-time subtraction’ or ‘delays’)

Reconstruction Parameters:

- **For reconstruction framing, see Table 1:**
  Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60min start-stope time, 6x5min frames).
  If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

- **Reconstruction Method:**
  VPHD or VPFX (not VPHDS or VPFXS). Use VPHD or VPFX, which ever your site normally uses
  6 iterations; 16 subsets

- **Grid:** 192 x 192 x (53, 71, or 89) (depending on the Disc-MI model)

- **FOV:** 256 mm (results in voxel size of 1.333 mm)

- **Slice Thickness:** 2.79 mm

- **Smoothing Filter:** NONE or 0.0 (for all filter options: loop filter, post-filter and z-axis filter)

  All corrections ‘On’

- **Note:** Reconstruction offsets should be used to assure the head is fully in the in-plane FoV.
GE Discovery 600, 610, 690, 710, and MI DR - PET/CT scanners
(Wake Forest, Arizona, Oregon, Kansas, Boston)

Acquisition Parameters:

CT scan:
Low mAs scan acquired shortly before emission. Leave enough time to start emission acquisition promptly at start time given immediately above. Scans should never be started early

Randoms Correction:
Singles: (not ‘real-time subtraction’ or ‘delays’)

Reconstruction Parameters:

For reconstruction framing, see Table 1:
Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60min start-stope time, 6x5min frames).
If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

Reconstruction Method:
VPHD or VPFX (not VPHDS or VPFXS). Use VPHD or VPFX, which ever your site normally uses 4 iterations; 24 subsets (or as close to 24 subsets as the software allows)

Grid: 192 x 192 x 47

FOV: 256 mm (results in voxel size of 1.333 mm)

Slice Thickness: 3.27 mm

Smoothing Filter: NONE or 0.0 (for all filter options: loop filter, post-filter and z-axis filter)

All corrections ‘On’

Note: Reconstruction offsets should be used to assure the head is fully in the in-plane FoV.
GE Discovery 690-XT - PET/CT scanner
(Mayo)

Acquisition Parameters:

CT scan:
Low mAs scan acquired shortly before emission. Leave enough time to start emission acquisition promptly at start time given immediately above. Scans should never be started early.

Randoms Correction: Singles: (not real-time subtraction)

Reconstruction Parameters:

For reconstruction framing, see Table 1:
Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60min start-stope time, 6x5min frames).
If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

Reconstruction Method:
VPHD
4 iterations; 20 subsets

Grid: 192 x 192 x 79

FOV: 256 mm (results in voxel size of 1.333 mm)

Slice Thickness: 1.96 mm

Smoothing Filter: NONE or 0.0 (for all filter options: loop filter, post-filter and z-axis filter)

All corrections ‘On’

Note: Reconstruction offsets should be used to assure the head is fully in the in-plane FoV.

This scanner says Discovery 690 in the header, but the 79 (instead of 47) planes and 1.96mm slice thickness tells you it’s the XT
GE Discovery RX - PET/CT scanners
(Hopkins)

Acquisition Parameters:

CT scan:
Low mAs scan acquired shortly before emission. Leave enough time to start emission acquisition promptly at start time given immediately above. Scans should never be started early.

Randoms Correction:
Singles: (not real-time subtraction)

Reconstruction Parameters:

For reconstruction framing, see Table 1:
Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60min start-stope time, 6x5min frames).
If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

Reconstruction Method: 3D Iterative (fully 3D Iter; not 3D FORE IR):
4 iterations; 21 subsets

Grid: 128 x 128

FOV: 256 mm (results in voxel size of 2.0 mm)

Slice Thickness: 3.27 mm

Smoothing Filter: NONE or 0.0 (for all filter options: loop filter, post-filter and z-axis filter)

All corrections ‘On’

Note: Reconstruction offsets should be used to assure the head is fully in the in-plane FoV.
GE Discovery STE - PET/CT scanners
(UCSD, UCSF)

 Acquisition Parameters:

 **CT scan:**
 Low mAs scan acquired shortly before emission. Leave enough time to start emission acquisition promptly at start time given immediately above. Scans should never be started early.

 **Randoms Correction:**
 Singles: (not real-time subtraction)

 Reconstruction Parameters:

 **For reconstruction framing, see Table 1:**
 Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60 min start-stop time, 6x5 min frames).
 If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

 **Reconstruction Method:** 3D Iterative (fully 3D Iter; not 3D FORE IR):
 4 iterations; 20 subsets

 **Grid:** 128 x 128

 **FOV:** 256 mm (results in voxel size of 2.0 mm)

 **Slice Thickness:** 3.27 mm

 **Smoothing Filter:** NONE or 0.0 (for all filter options: loop filter, post-filter and z-axis filter)

 All corrections ‘On’

 **Note:** Reconstruction offsets should be used to assure the head is fully in the in-plane FoV.
GE Signa - PET/MR scanners
(Alabama, Stanford)

Acquisition Parameters:
  Randoms Correction: Singles: (not real-time subtraction)

Reconstruction Parameters:

For reconstruction framing, see Table 1:
Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60min start-stope time, 6x5min frames).
If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

  Reconstruction Method:
  VPHD
    4 iterations; 16 subsets

Grid: 192 x 192 x 89

FOV: 256 mm (results in voxel size of 1.333 mm)

Slice Thickness: 2.79 mm

Smoothing Filter: NONE or 0.0 (for all filter options: loop filter, post-filter and z-axis filter)

All corrections ‘On’

Note: Reconstruction offsets should be used to assure the head is fully in the in-plane FoV.
**Philips Vereos - PET/CT scanners (Vanderbilt)**

**Acquisition Parameters:**

**CT scan:**
Low mAs scan acquired shortly before emission. Leave enough time to start emission acquisition promptly at start time given immediately above. Scans should never be started early.

**Reconstruction Parameters:**

For reconstruction framing, see Table 1:
Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60min start-stope time, 6x5min frames).
If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

Reconstruction Method: OSEM 4 iterations; 21 subsets

Grid: 256 x 256 x 164

FOV: 256 mm (results in voxel size of 1.0 mm) Slice Thickness: 1.0 mm

Smoothing: Post-Gaussian filter should be 0 or OFF (no post-filtering)

The attenuation field should indicate “CTAC-SG” and the scatter field should indication “SS-Simul”.
Philips Ingenuity TF - PET/CT scanners
(Penn)

Acquisition Parameters:

CT scan:
Low mAs scan acquired shortly before emission. Leave enough time to start emission acquisition promptly at start time given immediately above. Scans should never be started early

Acquisition Protocol: Brain

Reconstruction Parameters:

For reconstruction framing, see Table 1:
Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60min start-stope time, 6x5min frames).
If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

Reconstruction Method: Blob-OS-TF

Grid: 128 x 128 x 90

FOV: 256 mm (results in voxel size of 2.0 mm) Slice Thickness: 2.0 mm

Smoothing: Set SMOOTHING parameter to ‘SHARP’

All other parameters should be set to defaults for the “Brain” protocol. All corrections ‘On’

For Blob-OS-TF reconstruction: The attenuation field should indicate “CTAC-SG” and the scatter field should indication “SS-Simul”.

Philips Gemini TF - PET/CT scanners  
(Penn, Rush, Florida: Univ of Miami, Cleveland)

Acquisition Parameters:

**CT scan:**
Low mAs scan acquired shortly before emission. Leave enough time to start emission acquisition promptly at start time given immediately above. Scans should never be started early

**Acquisition Protocol:** Brain Protocol

Reconstruction Parameters:

**For reconstruction framing, see Table 1:**
Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60 min start-stop time, 6x5 min frames). If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

**Reconstruction Method:** Iterative: LOR-Ramla

**Grid:** 128 x 128 x 90

**FOV:** 256 mm (results in voxel size of 2.0 mm)

**Slice Thickness:** 2.0 mm

**Smoothing:** Set SMOOTHING parameter to ‘SHARP’

All other parameters should be set to defaults for the “Brain” protocol. All corrections ‘On’

For LOR-Ramla reconstruction: The attenuation field should indicate “CTAC-SG” and the scatter field should indication “SS-Simul”.

Siemens BioGraph Horizon - mCT TrueV PET/CT scanners (Wisconsin)

Acquisition Parameters:

CT scan:
Low mAs scan acquired shortly before emission. Leave enough time to start emission acquisition promptly at start time given immediately above. Scans should never be started early.

Reconstruction Parameters:

For reconstruction framing, see Table 1:
Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60 min start-stop time, 6x5 min frames).
If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

Method: Iterative: OSEM-3D (do NOT use TrueX reconstruction)
4 iterations; 20 subsets

Grid: 360 x 360 x 81 (or 109 for the extended FoV model)

Zoom: 2.0 (results in voxel size of ~1.018 mm)

Smoothing Filter: NONE (All-pass or ‘0.0’)

Match CT slices: ‘Off’ or ‘No’ (results in PET slice thickness of ~2.027 mm)

All corrections ‘On’

I’ve seen 1 of 4 Horizon’s that shows a slice thickness of 2.025 instead of 2.027 ??
Siemens BioGraph mMR
(NYU, NY:Mount Sinai, Washington University)

Reconstruction Parameters:

For reconstruction framing, see Table 1:
Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60min start-stope time, 6x5min frames).
If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

Method:  Iterative: OSEM-3D (do NOT use TrueX reconstruction)
4 iterations; 21 subsets

Grid:  344 x 344 x 127

Zoom:  2.0  (results in voxel size of 1.04313 mm)

Smoothing Filter:  NONE  (All-pass or ‘0.0’)

Match CT slices:  ‘Off’ or ‘No’  (results in PET slice thickness of 2.03125 mm)

All corrections ‘On’

Note for BioGraphs:  1080, TruePoint (1093,1094), mCT, Horizon (possible mMR)
To reconstruction into a matrix >256 your site has to have purchased the high-resolution option.  Some have not, since it is actually pretty expensive.  256 is the best you can do.  Resolution tends to be close to 0.5mm lower.

As you probably know, Siemens recon interpolated the sinogram projections down to the recon grid first, which losses MUCH resolution if you go down to 128.  I know initially it was to speed up reconstruction, and then my (strong) guess is that at some point someone realized, when lets charge more for the ability to recon into large matrices and get the full resolution.
Siemens BioGraph Vision  PET/CT scanners  
(Indiana, Northwestern, New Mexico, UCSF, Washington University, Mayo)

Acquisition Parameters:

CT scan:
Low mAs scan acquired shortly before emission. Leave enough time to start emission acquisition promptly at start time given immediately above. Scans should never be started early

Reconstruction Parameters:

For reconstruction framing, see Table 1:
Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60min start-stope time, 6x5min frames).
If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

Method: Iterative: OSEM-3D  (do NOT use TrueX reconstruction)
  8 iterations; 5 subsets with ToF (time-of-flight)
  **ToF must be used**

Grid: 440 x 440 x 159

Zoom: 2.0  (results in voxel size of 0.825 mm)

Smoothing Filter: NONE  (All-pass or ‘0.0’)

Match CT slices: ‘Off’ or ‘No’  (results in PET slice thickness of ~1.645 mm)

All corrections ‘On’
Siemens BioGraph mCT - mCT TrueV PET/CT scanners
(UCDavis, New Mexico, Pittsburgh, Cleveland Clinic, USC, Florida: Univ of Florida, Columbia, Univ of Michigan, Yale)

Acquisition Parameters:

CT scan:
Low mAs scan acquired shortly before emission. Leave enough time to start emission acquisition promptly at start time given immediately above. Scans should never be started early.

Scans and scan duration:
LIST-MODE: If your scanner has list-mode capability:

NO LIST-MODE: ONLY If your scanner does not have list-mode capability:

*** Note that reducing motion artifacts, two separate emission scans will be acquired as closely together as possible. Do not repeat CT scan.

Reconstruction Parameters:

For reconstruction framing, see Table 1:
Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60min start-stope time, 6x5min frames).
If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

Method: Iterative: OSEM-3D (do NOT use TrueX or ToF reconstruction)
4 iterations; 24 subsets

Grid: 400 x 400 x 81 (or 109 for TrueV model)

Zoom: 2.0 (results in voxel size of ~1.018 mm)

Smoothing Filter: NONE (All-pass or ‘0.0’)

Match CT slices: ‘Off’ or ‘No’ (results in PET slice thickness of ~2.027 mm)

All corrections ‘On’
Siemens BioGraph HiRes – 81 slice PET/CT (Model 1080) (Florida: Mt Sinai)

Acquisition Parameters:

CT scan:
Low mAs scan acquired shortly before emission. Leave enough time to start emission acquisition promptly at start time given immediately above. Scans should never be started early

PET acquisition:
LIST-MODE: If your scanner has list-mode capability

NO LIST-MODE: ONLY If your scanner does not have list-mode capability

*** Note that to reduce motion artifacts, two separate emission scans will be acquired as closely together as possible. Do not repeat CT scan.

Reconstruction Parameters:

For reconstruction framing, see Table 1:
Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60 min start-stope time, 6x5 min frames).
If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

Method: Iterative: FORE / OSEM-2D
4 iterations; 16 subsets

Grid: 336 x 336 x 81

Zoom: 2.0 (results in voxel size of ~1.01567 mm)

Smoothing Filter: NONE (All-pass or ‘0.0’)

Match CT slices: ‘Off’ or ‘No’ (results in PET slice thickness of ~2.00 mm)

All corrections ‘On’
Siemens BioGraph TruePoint – and TruePoint TrueV
PET/CT scanners (Models 1093, 1094)
(Univ or Michigan, Washington University)

Acquisition Parameters:

CT scan:
Low mAs scan acquired shortly before emission. Leave enough time to start emission acquisition promptly at start time given immediately above. Scans should never be started early.

PET acquisition:
LIST-MODE: If your scanner has list-mode capability
NO LIST-MODE: ONLY If your scanner does not have list-mode capability

*** Note that reduce motion artifacts, two separate emission scans will be acquired as closely together as possible. Do not repeat CT scan.

Reconstruction Parameters:

For reconstruction framing, see Table 1:
Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60min start-stope time, 6x5min frames).
If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

Method: Iterative: OSEM-3D (do NOT use TrueX reconstruction)
4 iterations; 21 subsets

Grid: 336 x 336 x 81 (or 109 for TrueV (1094) model)

Zoom: 2.0 (results in voxel size of ~1.015 mm)

Smoothing Filter: NONE (All-pass or ‘0.0’)

Match CT slices: ‘Off’ or ‘No’ (results in PET slice thickness of ~2.027 mm)

All corrections ‘On’
Siemens ECAT Exact HR+ (BGO) 63-slice scanners
(Pittsburgh for PIB only)

Acquisition Parameters:

Transmission scan:
Five or six min 2-D scan acquired immediately post-emission scan; process with segmentation.

Reconstruction Parameters:

For reconstruction framing, see Table 1:
Framing within the start-stop time in Table 1 should be multiple 5 min frames (ex, for 30-60min start-stope time, 6x5min frames).
If dynamic data was acquired, uploading the reconstruction of the full dynamic dataset is encouraged as long as the frames within the start-stop time are reconstructed as multiple 5 min frames.

Method: Iterative: (FORE / OSEM-2D) 4 iterations; 16 subsets

Grid: 128 x 128 x 63

Brain Mode: ON

Zoom: 2.0

Smoothing Filter: NONE (software version 7.2 says ‘All Pass (Ramp)’)

Axial filtering: NONE (software version 7.2 says ‘Off’)

All corrections ‘On’
Appendix B
IDA Uploader introduction and user registration
INTRODUCTION
This document provides instructions for account registration and uploading images for the SCAN project in the Laboratory of Neuro Imaging's Image & Data Archive (IDA). For sites needing to upload site qualification scans, instructions for uploading to the SCANQUAL project are also included. The IDA utilizes a data de-identification process and encrypted file transmission to help ensure compliance with subject-privacy regulations.

SYSTEM REQUIREMENTS
The IDA system requires the following:
- a computer with Internet access
- newer web browser software (IE/Edge, Firefox, Chrome, Safari)
- a valid user account with upload access for SCAN and/or SCANQUAL
- installation of the IDA Uploader application

USER REGISTRATION (Skip this step and go to Step B if you already have an IDA account)
1. To register for a user account, go to the Image & Data Archive Log-In website (https://ida.loni.usc.edu) and select “Instant free signup” in the top right corner.
2. Complete New account registration (3 steps).
   a. Enter your email address and select “CONTINUE”. A security code will be emailed to you.
b. **Enter the security code sent to your email and click “CONTINUE”**.

![Security Code Form]

- Enter the security code sent to your email and click “CONTINUE”.
- Complete the New account registration form and click “REGISTER”. A link to set your password will be emailed to you with subject line “Welcome to the LONI Image & Data Archive”.
- Create a password and click “CONTINUE”.

3. Your account is created, if you need upload access to SCAN or SCANQUAL, please send an email to the appropriate contact following the steps below:

   For access to SCAN or SCANQUAL, email data.coordinator@loni.usc.edu
   
   - Enter “SCAN Upload Access Request” or “SCANQUAL Upload Access Request” in the subject line of your email.
   - Provide the email address you used when creating your account, your site name and site number in your email request.
   - You will receive an email when your account access has been set, generally within one working day.
Appendix C
Obtaining/installing IDA-uploader
OBTAINING AND INSTALLING THE IDA-UPLOADER

a. Installing the IDA-Uploader for Windows
b. Installing the IDA-Uploader for Mac
c. Installing the IDA-Uploader for Linux

a. Installing the IDA-Uploader for Windows
1. Log in to the IDA and select SCAN from the PROJECTS menu.
2. Select the ARCHIVE Menu option.
3. Select your operating system (Windows 32-bit or 64-bit) from the dropdown menu.
4. Click “Download”.

5. Open the application by clicking on the download in your browser or by locating the IDA-Uploader-2.0.msi application in the Downloads section of your File Explorer.
6. **You will be taken to the IDA-Uploader Setup Wizard – click “Next” to continue.**

![Image of IDA-Uploader Setup Wizard]

7. Choose your destination folder and click “Next”.

![Image of destination folder selection in IDA-Uploader Setup Wizard]
8. **Click “Install”**.
   Note: If you receive a popup asking for permission to run the application, click “yes”.

9. Click “Finish” to exit the Setup Wizard.
10. Locate the application on your device by typing in “IDA-Uploader” in the Windows Start Menu.

b. **Installing IDA-Uploader for Mac**

1. Log in to the IDA and select SCAN from the PROJECTS menu.
2. Click ARCHIVE from the Menu.
3. Select your operating system (Mac) from the dropdown menu.
4. Click “Download”.

<table>
<thead>
<tr>
<th>HOME</th>
<th>SCAN @LONI</th>
<th>DOWNLOAD</th>
<th>SEARCH</th>
<th>ARCHIVE</th>
<th>MANAGE</th>
<th>PROJECTS</th>
<th>SUPPORT</th>
</tr>
</thead>
</table>

The upload process involves two basic steps:

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

### IDA Uploader Application

You will need to launch the Uploader application from your computer to upload SCAN data. Choose your operating system and download the application below.

5. **Open your Finder application, click Downloads, right-click ‘IDA-Uploader-2.0.pkg’ and select “Open”**.

NOTE: If you try to install by double-clicking on ‘IDA-Uploader-2.0.pkg’, you may receive a message that it cannot be opened. Please ensure that you follow the instructions above to successfully open.
6. An Install IDA-Uploader window will appear. Click “Continue”.

7. Next, choose a destination for the installation. Click “Continue”.

Select the disk where you want to install the IDA-Uploader software.

- Macintosh HD 779.92 GB available 1.02 TB total
- Macintosh HD 779.03 GB available 1.02 TB total

Installing this software requires 134.6 MB of space.
You have chosen to install this software on the disk "Macintosh HD".
8. For Installation Type, you can review the details of the installation. Click “Install”.

9. During the installation, you will need to enter the User Name and Password for the computer. Click “Install Software”.
10. Once the installation is complete, the window will provide a summary of a successful installation. Click “Close”.
   NOTE: A window will appear to ask “Do you want to move the “IDA-Uploader” installer to the trash?”. You can choose Keep or Move to Trash.

11. Locate the application in your computer by opening your Finder application. Click on Applications and double-click IDA-Uploader.
c. **Installing IDA-Uploader for Linux**

1. Log in to the IDA and select SCAN from the PROJECTS menu.
2. **Select the ARCHIVE Menu option.**
3. **Select your operating system (Linux) from the dropdown menu.**
4. Click “Download”.

   The upload process involves two basic steps:
   - 1️⃣ **De-identify file metadata by replacing any fields that identify the subject, such as Patient Name and ID.**
   - 2️⃣ **Transmit files securely from the local site to LONI.**

5. **Please visit [https://www.oracle.com/java/technologies/javase-downloads.html](https://www.oracle.com/java/technologies/javase-downloads.html)** to download the latest Oracle JDK. **NOTE:** A minimum version of 15.0.1 is required to run IDA-Uploader-2.0.jar
6. **Choose DEB, PRM or the compressed archive depending on your Linux Distribution.**
7. **Once you have completed the installation, open the terminal and run:** `java -jar IDA-Uploader-2.0.jar`
Appendix D

How to upload PET data to SCAN using IDA-uploader
UPLOADING (ARCHIVING) TO SCAN
1. Open the IDA-Uploader application.
2. Enter your email and password, then click “Log In”.
3. Select SCAN from the Project dropdown menu.
4. Then, select your site from the Site dropdown menu. Click “Continue”.

5. Enter your local Subject ID (do not precede with “ADRC”). Click “Browse” to select the Source Directory. Then click “Upload”.

NOTE: The Source Directory is the directory containing the files to be uploaded. If your Source Directory contains subdirectories, choose to include/exclude those files by checking “Search subdirectories”.
6. You will be able to see the progress of your upload in the De-identify and Upload section.

![Image of IDA Uploader interface](image1.png)

7. Once the files are de-identified and transferred to the IDA, you will need to complete the upload in your web browser.

![Image of IDA Uploader interface](image2.png)
8. Your web browser should automatically open a new “Log In to Continue” page. Enter your IDA email and password. Click “Log In”.

NOTE: If your web browser does not automatically open the “Log In to Continue” page, please click “Complete Upload” and you can copy-paste the link in your browser.
9. **In the “Your Upload is Not Complete” page you can review the details of your upload.**

![Image of Your Upload is Not Complete page]

a. **For PET image uploads, additional information is required in order to complete the upload.**
   1. **In the Metadata section, click “Complete Form”.**
      
      NOTE: Fields marked (*Required) are required to complete the upload.
   2. **Once the information is entered in the form, click “Update”.**
NOTE: If any data was mistakenly uploaded, you can click the “X” in the Delete column and it will be deleted from your upload. A window will appear to confirm the deletion. Click “Delete” to confirm file deletion or “Cancel”.

![Confirm Deletion](image)

Description: Downs (128x128mm)
File Date and Time: May 22, 2017 3:32 PM
10. Once all required information has been entered, click “Finish Upload”.

11. You will see a screen that informs you that the upload is being processed.
12. Once the upload is processed, a summary page for the upload will be displayed. Please note that you have the option of clicking “Download CSV Files” to keep a record of the upload.

13. You can close the IDA-Uploader application or to upload images for another subject, click the “Upload More” button in the IDA-Uploader application.
Appendix E
How to upload PET Hoffman phantom data to SCANqual
UPLOADING (ARCHIVING) TO SCANQUAL

1. Open the IDA-Uploader application.
2. Enter your email and password, then click “Log In”.

3. Select SCANQUAL from the dropdown menu. Once you select SCANQUAL, a dropdown with the sites will appear. Select your site and click Continue.
4. Click “Single Archive” or “Batch Archive”.

**a. Single Archive**

Use the Single Archive process to upload one or more files from a single subject.

1. **After clicking “Single Archive” the De-Identification page will be displayed.**

   ![Image of IDA Uploader](https://via.placeholder.com/150)

   a. **Click the type of data being uploaded – in this case, “Original”.**
   
   b. **Enter the Phantom/Volunteer ID in the Subject ID field.**
      
      assign phantom ID in subject ID field as : siteID_P xxxx
      
      where siteID is your 1-3 digit site ID and xxxx should count up for your site starting with 0001.
   
   c. **Select the Source Directory in which the original files are located.**
   
      d. Select the Target Directory for de-identified files to be written to.
   
      e. Click “CONTINUE” to begin the de-identification process.

2. **On the Verify and Submit page**
b. Batch Archive

The Batch Archive process is similar to Single Archive, except that multiple subjects and image series can be submitted in a batch. Batches can be of the same or different modalities. However, users cannot review the results of the de-identification process prior to the batch upload.

1. Proceed to follow the De-identification steps in the Single Archive section.
2. The Batch Archive will skip the Verify and Submit step that is available in Single Archive, and direct you to the Image Database Batch Queue page.
3. Click “ADD MORE” to add more images to the Batch. Repeat this process until you have added everything you intend to archive.
4. Click “SUBMIT” to begin both the de-identification and transmission processes.
<table>
<thead>
<tr>
<th>Subject</th>
<th>Data Type</th>
<th>Research Group</th>
<th>Source</th>
<th>Status</th>
<th>Date</th>
<th>Remove</th>
</tr>
</thead>
<tbody>
<tr>
<td>131_P_5555</td>
<td>Original</td>
<td>Phantom</td>
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<td>remove</td>
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<td>Phantom</td>
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<td>2/08/21</td>
<td>remove</td>
</tr>
<tr>
<td>131_V_3333</td>
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<td>Volunteer</td>
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<td>2/08/21</td>
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<td>/Desktop/...</td>
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<td>2/08/21</td>
<td>remove</td>
</tr>
</tbody>
</table>
Appendix F
SCAN PET upload form
To be completed by Study Coordinator

Study Coordinator Name: ____________________________

Telephone #: ( ) _________ Schedule date: mm/dd/yyyy

To be completed by PET technologist

(PET tech initials)

1. Tracer (select one)
   □ Forbetapir  □ PIB  □ Florbetaben
   □ Flortaucipir  □ MK6240  □ PI2620
   □ GTP1  □ FDG

2. Reconstruction Start-Stop times (min) (select one)
   □ 0-end  □ 50-70
   □ 40-60  □ 40-70  □ 50-70
   □ 90-110
   □ 80-100
   □ 70-90  □ 70-110  □ 90-110
   □ 45-75  □ 45-90  □ 60-90
   □ 30-60 (non-AD subjects)
   □ 60-90
   □ 60-90
   □ 50-70
   □ 0-end
   □ 5-8
   □ 5-10
   □ 4-5
   □ 4-5
   □ 5-7
   □ 4-5

3. Scan date: mm/dd/yyyy

4. Time of today's scanner QC: hh:mm

5. PET tracer dose assay (mCi): ____________

6. Time of tracer dose assay: hh:mm

7. Time of tracer injection: hh:mm
   (military time)

8. Residual PET tracer dose assay: ____________
   (mCi)

9. Time of residual tracer dose assay: hh:mm
   (military time)

10. Emission start time: hh:mm
    (military time)

11. Attenuation Correction: □ CT  □ MRI  □ $^{68}$Ge+segmentation  □ $^{137}$Cs+segmentation

12. Any variations from protocol during uptake? □ No  □ Yes, if yes, explain: ____________

continue on next page
13. Any start time variation from protocol? □ No □ Yes, if yes, explain: ________________

14. Any other variations from protocol? □ No □ Yes, if yes, explain: ________________

### Reconstruction:

<table>
<thead>
<tr>
<th>Method</th>
<th>GE scanners</th>
<th>Philips scanners</th>
<th>Siemens scanners</th>
</tr>
</thead>
<tbody>
<tr>
<td>15.</td>
<td>□ VPHD</td>
<td>□ OSEM</td>
<td>□ OSEM-3D</td>
</tr>
<tr>
<td></td>
<td>□ VPFX</td>
<td>□ Blob-OS-TF</td>
<td>□ FORE/OSEM-2D</td>
</tr>
<tr>
<td></td>
<td>□ 3D Iterative</td>
<td>□ LOR-Ramla</td>
<td>□ 3D OSEM + ToF</td>
</tr>
<tr>
<td></td>
<td>□ FORE Iterative</td>
<td></td>
<td></td>
</tr>
<tr>
<td>16. Smoothing</td>
<td>□ 0.0 or None</td>
<td>□ 0.0, None, All-pass</td>
<td>□ 0.0, None, All-pass</td>
</tr>
<tr>
<td></td>
<td></td>
<td>□ SHARP (Gemini TF, Ingenuity TF)</td>
<td>□ 2mm Gaussian (HRRT)</td>
</tr>
<tr>
<td>17. Other corrections:</td>
<td>□ On</td>
<td>□ On</td>
<td>□ On</td>
</tr>
</tbody>
</table>

18. Iterations: □ 4 □ 6 □ 8
19. Subsets: □ 5 □ 12 □ 16 □ 20 □ 21 □ 24

**To be completed by person uploading data**

20. Date of upload: mm/dd/yyyy

21. Was all raw PET data archived locally to be able to do complete reconstruction of PET scan if needed?
   - □ Yes, what was archive medium?: ____________________________
   - □ No, if no, explain: ____________________________

22. Additional comments: ____________________________________________