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CLARiTI

ADRC Consortium for Clarity in ADRD Research Through Imaging

PET Technical Procedures Manual

Document Version History

Version	Date	Author	Description
1.12	Jan 21, 2022	Suzanne Baker	Replaced QuickStart Guide with PET checklist
1.2	July 22, 2022	Suzanne Baker	Added GE Disc ST reconstruction sheet
1.21	March 9, 2023	JiaQie Lee, Suzanne Baker, Brittany Hale	Adopted consistent language for Subject ID, PTID & NACCID; Updated PET Upload Form
1.22	April 5, 2023	Trevor Chadwick	Revised FDG and PI2620 acquisition times
1.23	June 22, 2023	Trevor Chadwick	Revised SCAN PET Checklist; Step 5 of Appendix D
1.24	May 6, 2024	Trevor Chadwick	Added GE Omni Legend PET/CT scanner, revised GE Discovery MI and GE Sigma scanner appendices
1.25	June 17, 2024	Trevor Chadwick	Added radiotracer Flutemetamol and preferred acquisition time for NAV4694, PI2620, and FDG
1.26	August 15, 2024	Wesley Thomas, Suzanne Baker	Updated Discovery 690 XT parameters Removed MK6240 and PI2620 non-preferred acquisition times. Added “allowable” for PIB and FDG non-preferred acquisition times. Included Clariti logo.
1.27	April 25, 2025	Trevor Chadwick	Added radiotracer RO948

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This Technical manual was originally developed for the SCAN project. The CLARiTI project uses the same PET imaging techniques as the CLARiTI project. Therefore, information about PET scanners, tracers, acquisition times and reconstruction are identical for the 2 studies. Please follow these methods for SCAN and CLARiTI and refer any questions to Suzanne Baker.

SCAN PET Checklist

About this checklist: This checklist is designed to serve as a roadmap

Step1. Identify SCAN Liaison(s) Responsible for Study Oversight and Submit Site Information

- Description of SCAN Liaison role:
  - Respond to queries from the SCAN team
  - Maintain list of site contacts for imaging site
  - Ensure protocol compliance
  - Submit PET contact information to SCAN via this form

Step2. Submit SCAN site information

- Submit Site and Contact Information team via Site Information Form noting:
  - Who will serve in the PET liaison role
  - All site contacts for imaging site (Technologists/Uploaders/PI's)

Step3. Prepare to participate in the SCAN Study

- Ensure regulatory compliance and institutional approval for data sharing
- Get ready to collect images:
  - Qualify your PET Scanner
  - Know how to order and allocate correct PET tracers
  - Review PET upload form with imaging center staff responsible for the protocol
- Identify participants that are eligible for the study:
  - All participants must have:
    - A NACC ID (NOTE: If the participant does not have an assigned NACC ID, the data upload will not be accepted)
    - Been scanned after Jan 1, 2021
    - PET data collected according to SCAN standards

Step4. Collect and upload data according to protocol

- Prepare for image collection:
  - Check-in with imaging center to review the following:
    - Protocol for data acquisition will be used
    - Protocol for image reconstruction will be used

- Technician acquires images:
  - Follow protocol for image acquisition tracer and dose
  - Ensure PET upload form is filled out during each scan
  - Reconstruct images as per scanner specifications (Appendix A)
- Upload images:
  - Ensure images are uploaded properly (Appendix D)
  - Make sure you have the filled-out PET upload form
  - After images are uploaded you will transfer PET upload form via web interface
- Troubleshooting:
  - Identify and correct any mistakes that are detected in image reconstruction or upload
  - Be aware of appropriate SCAN personnel available for questions/advice

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

Technical/QC questions:

koeppe@umich.edu (Robert A. Koeppe) 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 Koeppe, it will need to be qualified before imaging can be performed. Please contact Bob Koeppe (koeppe@umich.edu).

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

Hoffman Phantom Scans

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 (koeppe@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.

Regulatory

You must have institutional approval to share your data. 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.

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 your PTID or Subject ID (local Subject ID) which is a sequence of up to 10 characters. Formats vary by each center that you use for UDS (uniform dataset) identification internally. As a rule, enter the complete ID. However, you may leave off leading zeros if the format is all numeric digits. Also, either upper or lower case may be used for any alphabetic characters.

The Subject ID or PTID is different from the NACCID.

- Subject ID or PTID - this is the ADRC-managed participant ID, or "local ID". Formats vary by center.
- NACC ID - this is the NACC-managed participant ID. It is a string with the prefix ‘NACC’ followed by 6 digits.

PLEASE NOTE: If the participant does not have an affiliated NACCID assigned to the Subject ID or PTID you entered, the upload will not be accepted.

The tracer should be included in the Series Description:

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

Amyloid_PIB Tau_Flortaucipir

Amyloid_Florbetapir	Tau_MK6240
Amyloid_Florbetaben	Tau_PI2620
Amyloid_NAV	Tau_GTP1
Amyloid_Flutemetamol	Tau_RO948
FDG	

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.

ORDERING TRACER: Radiotracers are generally ordered from radio-pharmacies by the imaging center. Please be certain that your research participants will receive the correct tracer at the correct dose and be aware of the delivery time because the radioactivity will decay.

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 now acceptable (also preferred) for acquisition and reconstruction as long as it includes a preferred acquisition time. Example: If you acquire Flortaucipir from 75-115min post-injection (which is acceptable because it includes the preferred 80-100min acquisition time), we would rather you fill out the PET meta data form with the write-in start and stop times of 75 and 115 and upload 8x5min frames, instead of doing a special reconstruction that is only 80-100 min as 4x5min frames.

4. We are acquiring something different than what is listed for the acquisition times, what should we do?

- **If the protocol includes the acquisition start and stop time but collects more data, then whenever possible reconstruct only the preferred time:** ex if you are acquiring PIB 0-70min, we ask you upload the data from 50-70min only
- **If your current protocol does not fully encompass the acquisition start and stop times, then this is no longer considered SCAN compliant.**

Radiotracer Doses

Table 1: Radiotracer Doses, Acquisition times post-injection

	Suggested Target Dose ± 10%		Minimum injectable dose		Acquisition start-stop time post-injection (min)
Tracer	**mCi**	**MBq**	**mCi**	**MBq**	
AMYLOID TRACERS					
PIB	15	555	8	300	Preferred: 50-70 Allowed: 40-70, 40-60
Florbetapir	10	370	6	225	50-70
Florbetaben	8	295	5	185	90-110
NAV4694	8.1	300	6.5	240	50-70
Flutemetamol	5	185	4	150	90-110
TAU TRACERS					
Flortaucipir	10	370	6	225	80-100
MK6240	5	185	4	150	90-110
PI2620	5	185	4	150	45-75
GTP1	7	260	5	185	60-90
RO948	10	370	5	185	70-90
GLUCOSE METABOLISM TRACER					
FDG	5	185	4	150	Preferred: 30-60 Allowed: 30-45

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.

Preparing 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

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

- 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 '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 VPHD**S** or VPFX**S**). 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 VPHD**S** or VPFX**S**). 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.

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: 256 x **256** x **79**

FOV: 300 mm (results in voxel size of 1.17 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 30-60min 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; 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
Discovery ST - PET/CT scanners
(UCI)

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: Iterative if available (fully 3D Iter; not 3D FORE IR)
Only if fully iterative is not available, as in some older systems, is it ok to use 3D FORE IR.
4 iterations; 21 subsets* (* for older software versions having only 3D FORE IR, **24 subsets**)

Grid: 128 x **128 x 47**

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
Omni Legend PET/CT scanner

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

Reconstruction Parameters, phantom and all radiotracers:

Reconstruction Method: Iterative: VPHD (or VPFX): whichever you site normally uses, but NOT VPHDS or VPFXS
8 iterations; 12 subsets

Grid: 256 x 256 matrix

FOV: 25.6 cm (results in 1.0 mm voxels) Use Y-offset as needed to fit into this tighter FoV

Smoothing: **None** (there are 3 filters: in-plane, axial, and loop; all need to be **off**)

All corrections '**ON**'

GE Signa - PET/MR scanners
(Alabama, Stanford)

Acquisition Parameters:

Randoms Correction: Singles

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 30-60min 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: 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 30-60min 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; 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 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 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 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: 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 (SCAN only)

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:

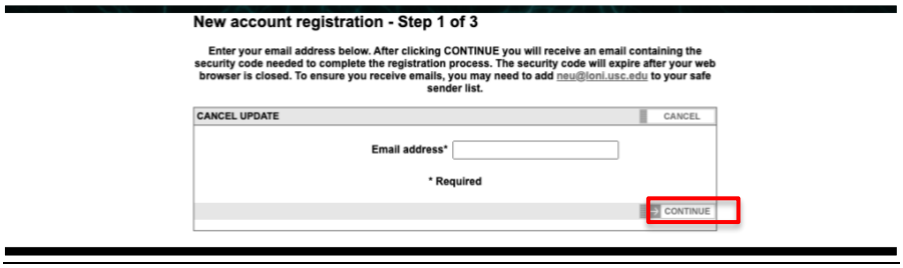
- a computer with Internet access
- newer web browser software (IE/Edge, Firefox, Chrome, Safari)
- a valid user account with upload access for SCAN and/or SCANQUAL
- installation of the IDA Uploader application

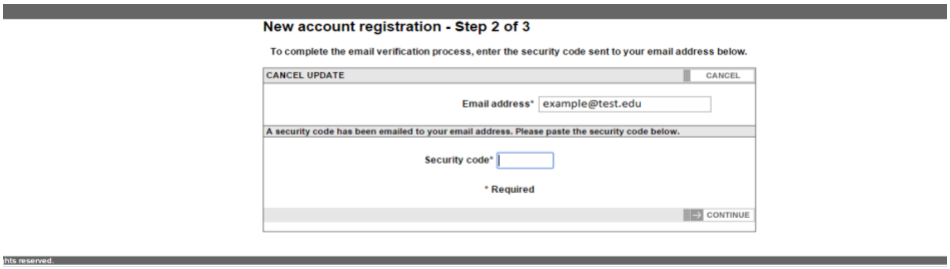
USER REGISTRATION *(Skip this step and go to Appendix C if you already have an IDA account)*

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).

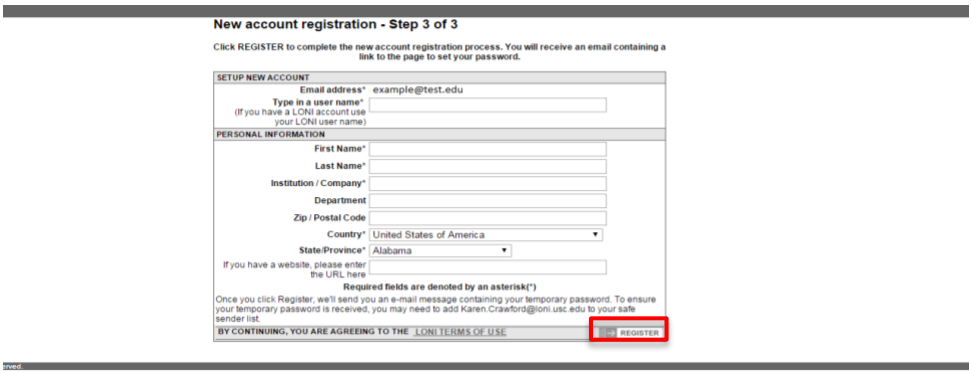
    a. Enter your email address and select "CONTINUE". A security code will be emailed to you.



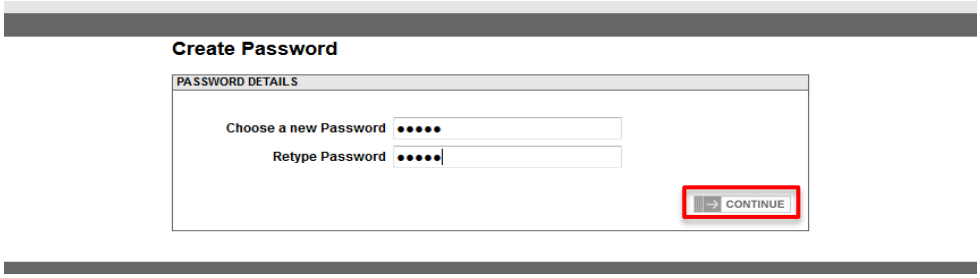


b. Enter the security code sent to your email and click “CONTINUE”.

c. 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”.



d. 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

a. Enter “SCAN Upload Access Request” or “SCANQUAL Upload Access Request” in the subject line of your email.
b. Provide the email address you used when creating your account, your site name and site number in your email request.

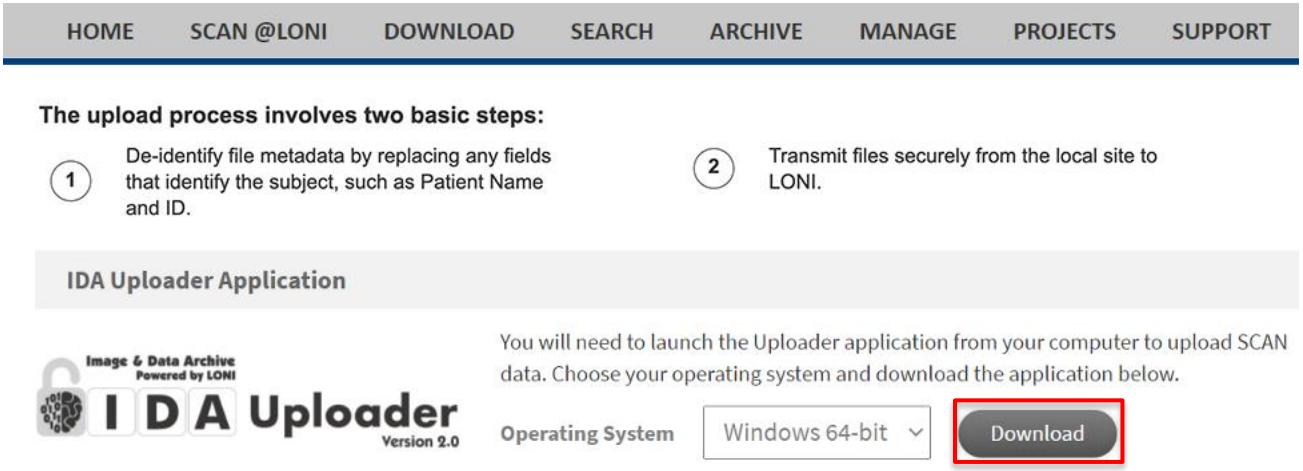
c. You will receive an email when your account access has been set, generally within one working day.

Appendix C:
Obtaining/Installing IDA-uploader (SCAN only)

OBTAINING AND INSTALLING THE IDA-UPLOADER

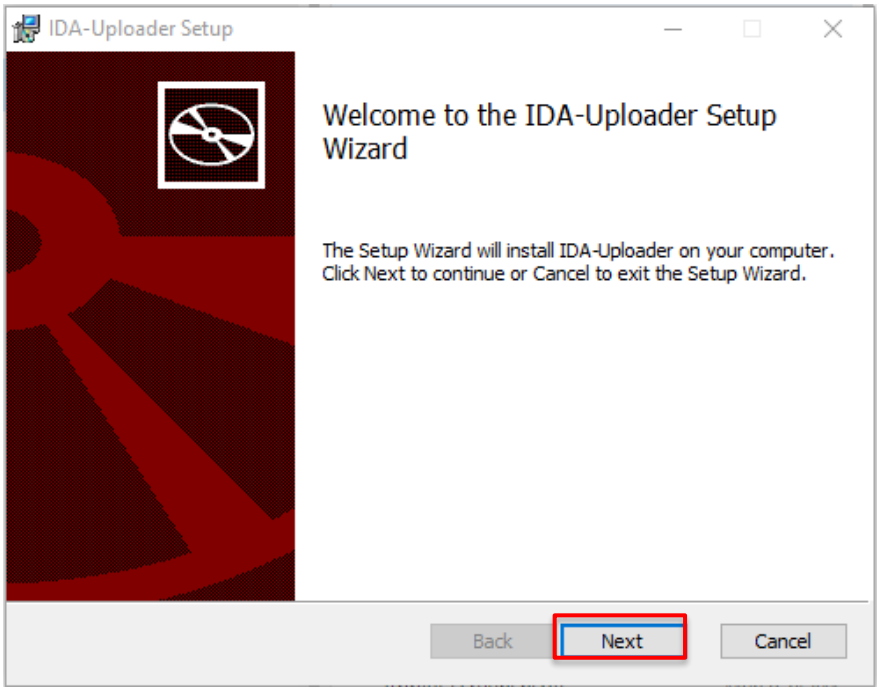
a. Installing the IDA-Uploader for Windows

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”.

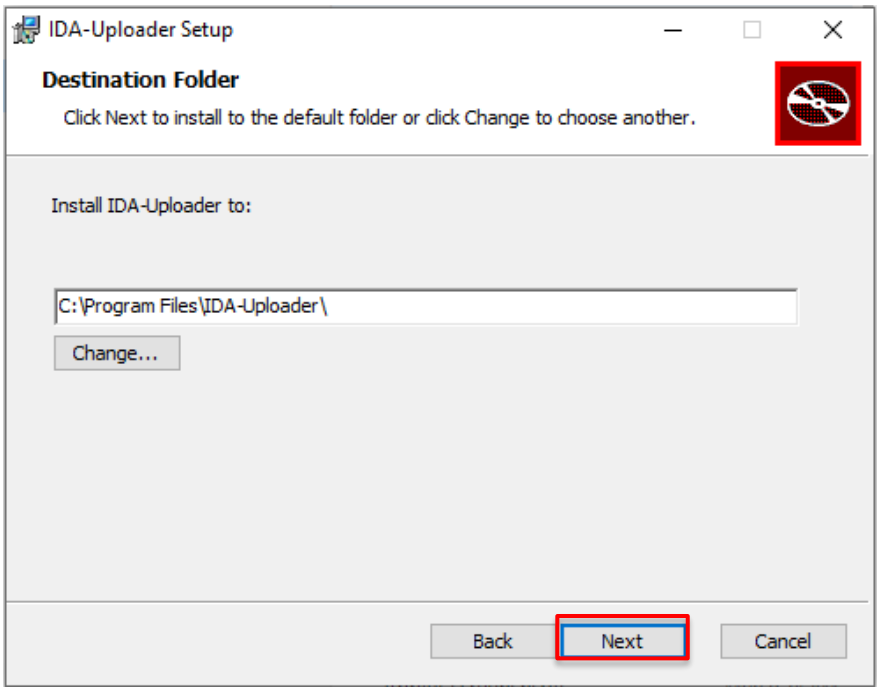


5. Open the application by clicking on the download in your browser or by locating the IDA-Uploader-2.0.msi application in the Downloads section of your File Explorer.

6. You will be taken to the IDA-Uploader Setup Wizard – click “Next” to continue.

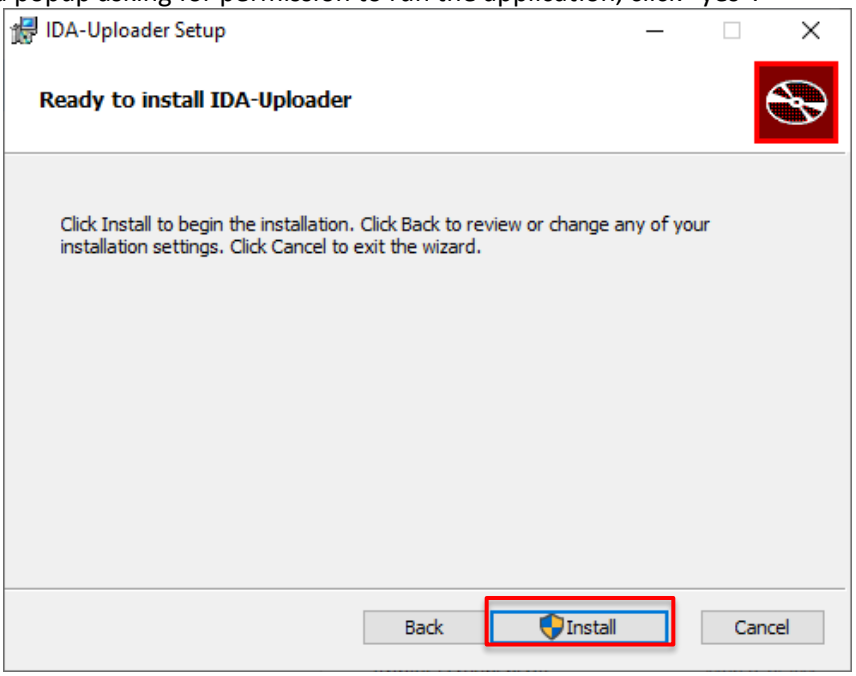


7. Choose your destination folder and click “Next”.

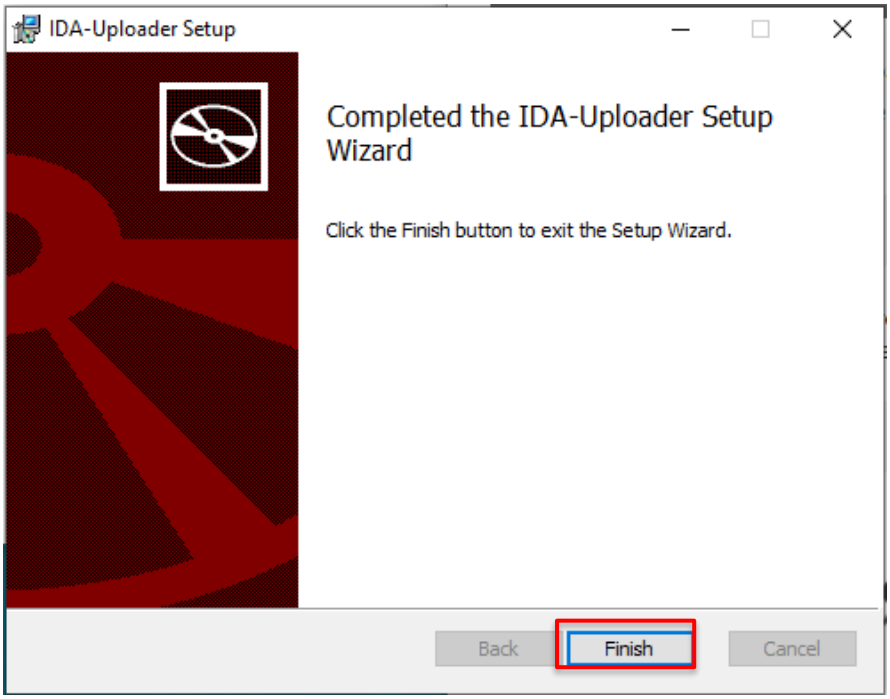


8. Click “Install”.

Note: If you receive a popup asking for permission to run the application, click “yes”.



9. Click “Finish” to exit the Setup Wizard.

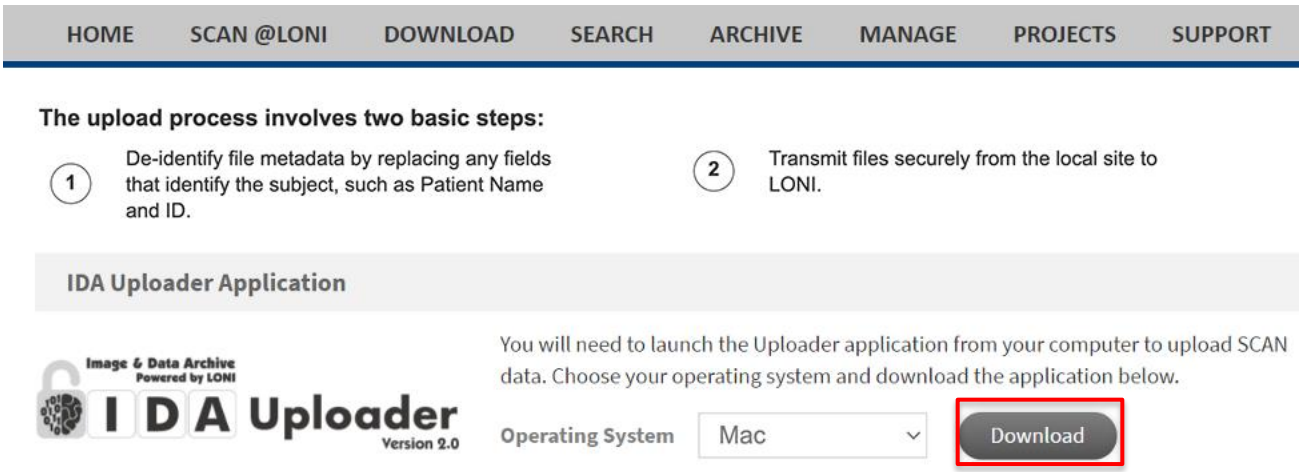


10. Locate the application on your device by typing in “IDA-Uploader” in the Windows Start Menu.

b. Installing IDA-Uploader for Mac

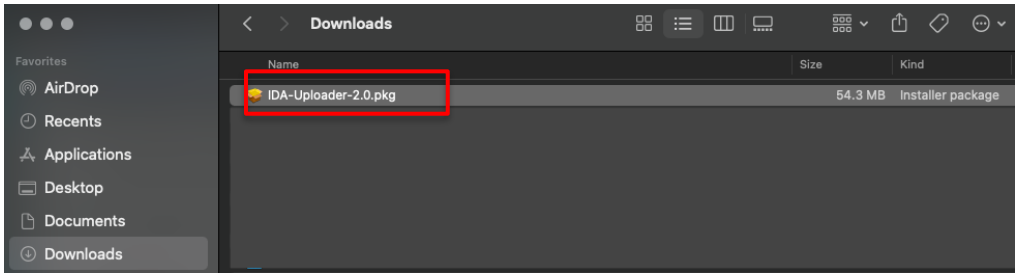
1. Log in to the IDA and select SCAN from the PROJECTS menu.

2. Click ARCHIVE from the Menu.
3. Select your operating system (Mac) from the dropdown menu.
4. Click “Download”.

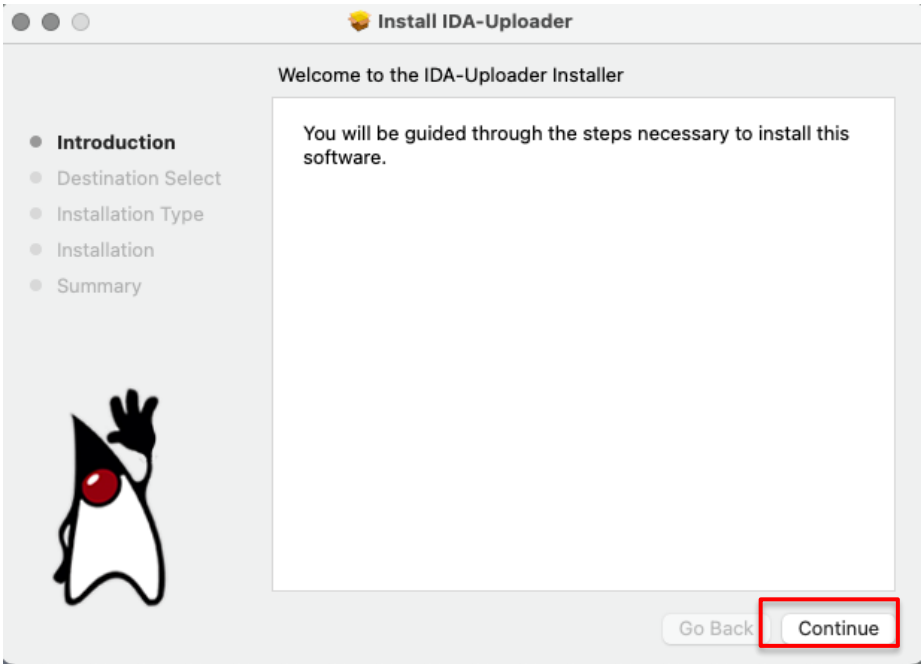


5. Open your Finder application, click Downloads, right-click ‘IDA-Uploader-2.0.pkg’ and select “Open”.

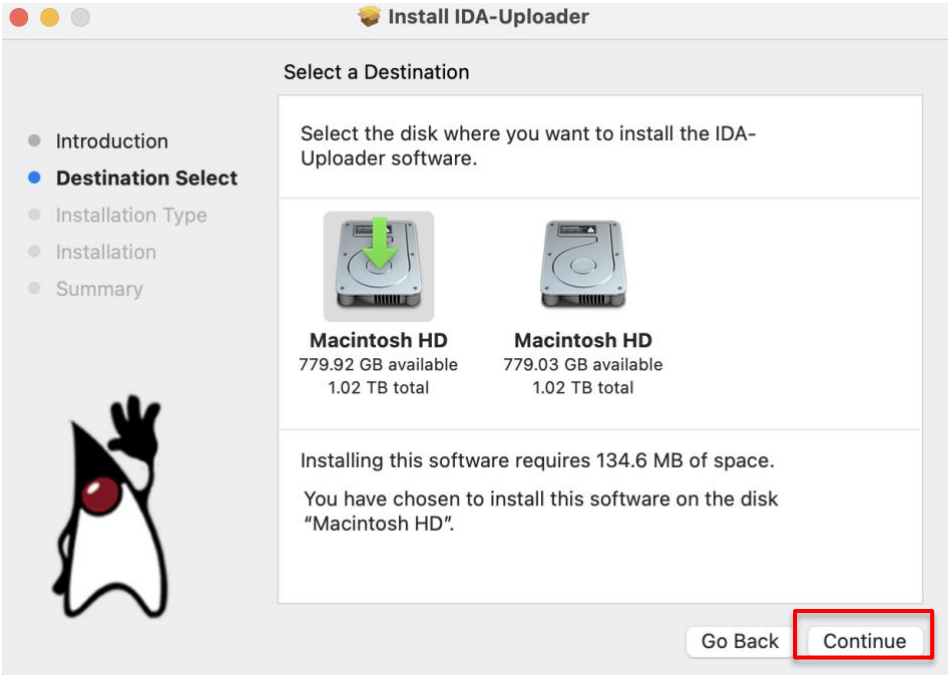
NOTE: If you try to install by double-clicking on ‘IDA-Uploader-2.0.pkg’, you may receive a message that it cannot be opened. Please ensure that you follow the instructions above to successfully open.



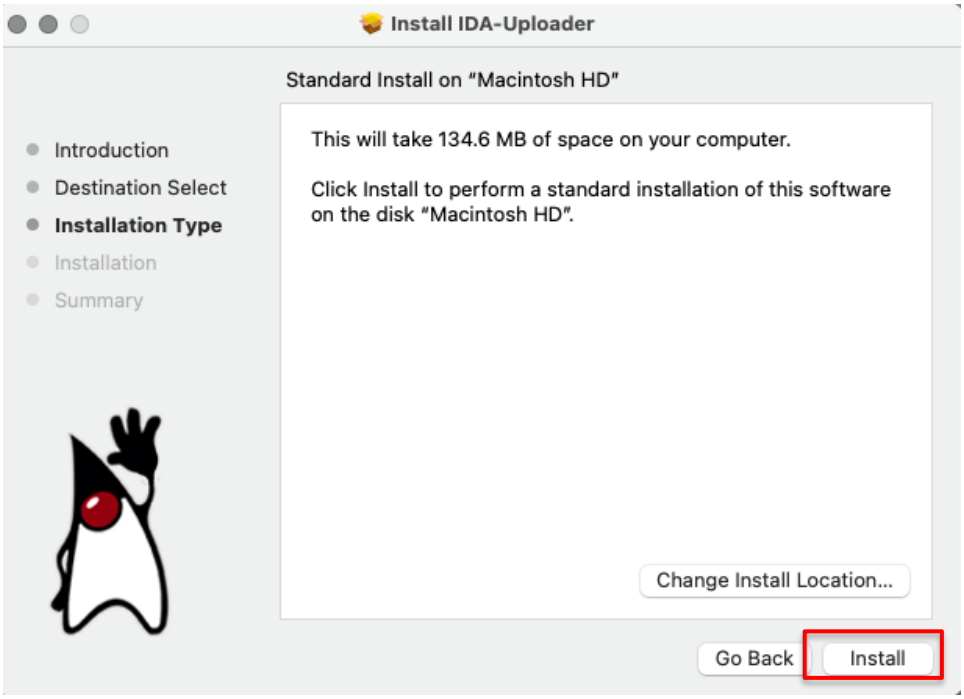
6. An Install IDA-Uploader window will appear. Click “Continue”.



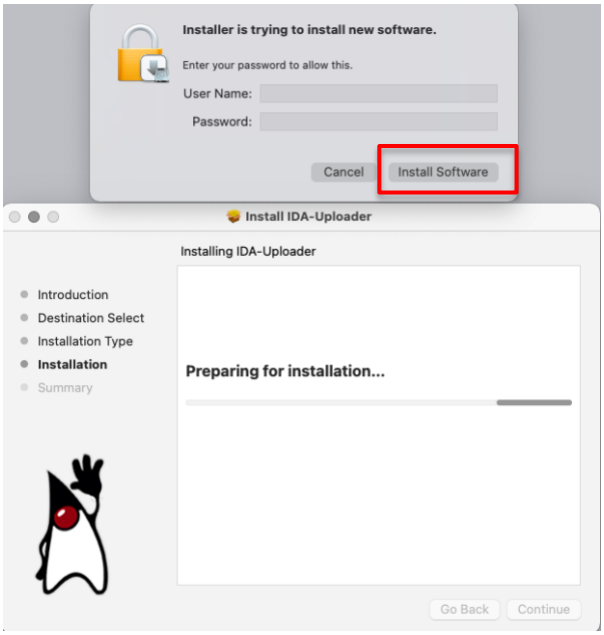
7. Next, choose a destination for the installation. Click “Continue”.



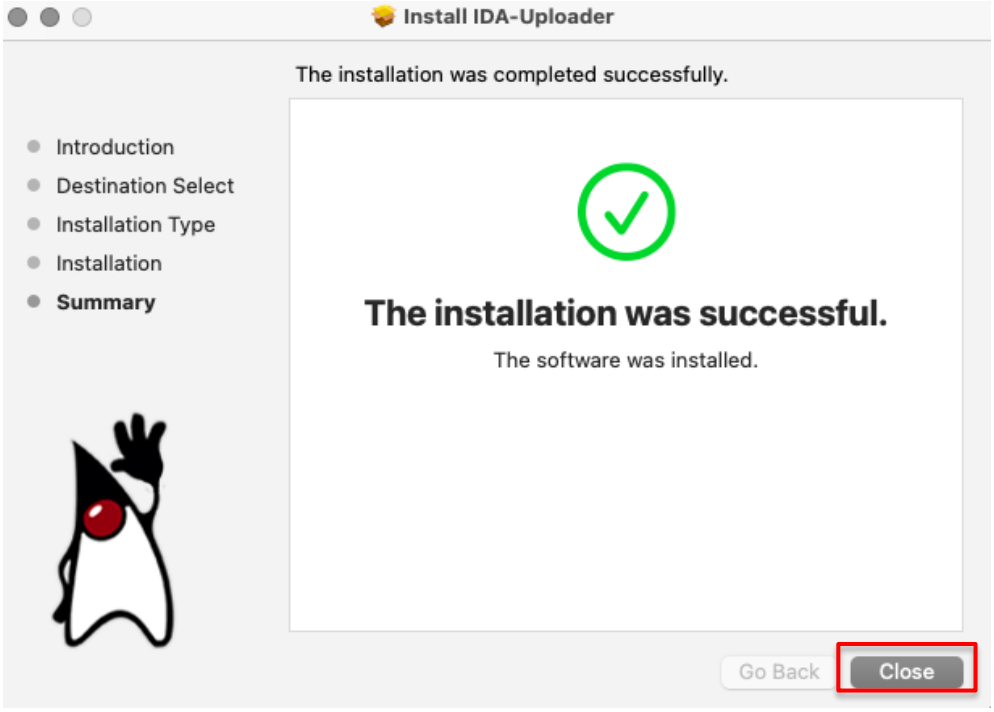
8. For Installation Type, you can review the details of the installation. Click “Install”.



9. During the installation, you will need to enter the User Name and Password for the computer. Click “Install Software”.



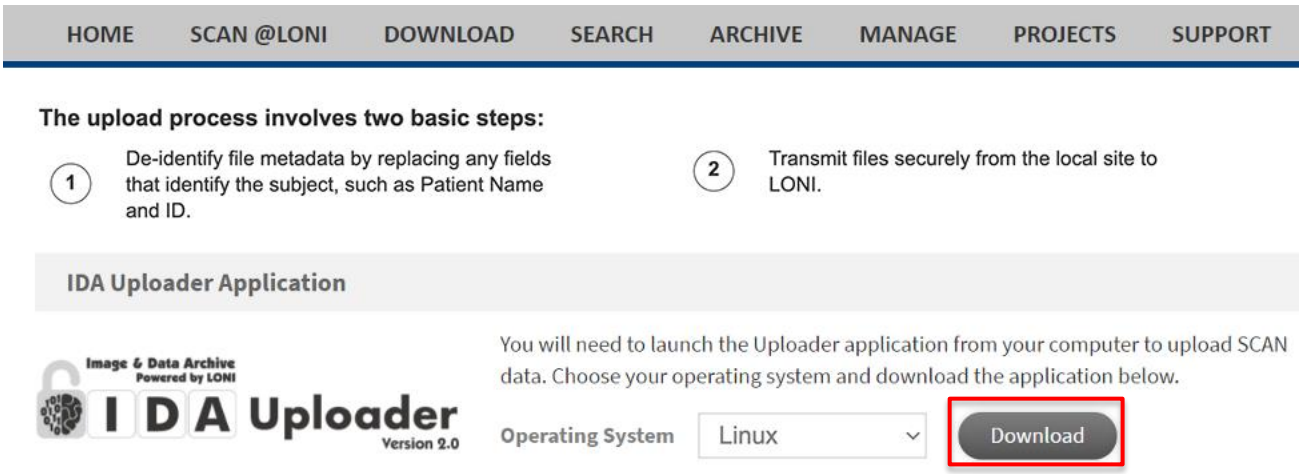
10. Once the installation is complete, the window will provide a summary of a successful installation. Click “Close”.
    NOTE: A window will appear to ask “Do you want to move the “IDA-Uploader” installer to the trash?”. You can choose Keep or Move to Trash.



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”.



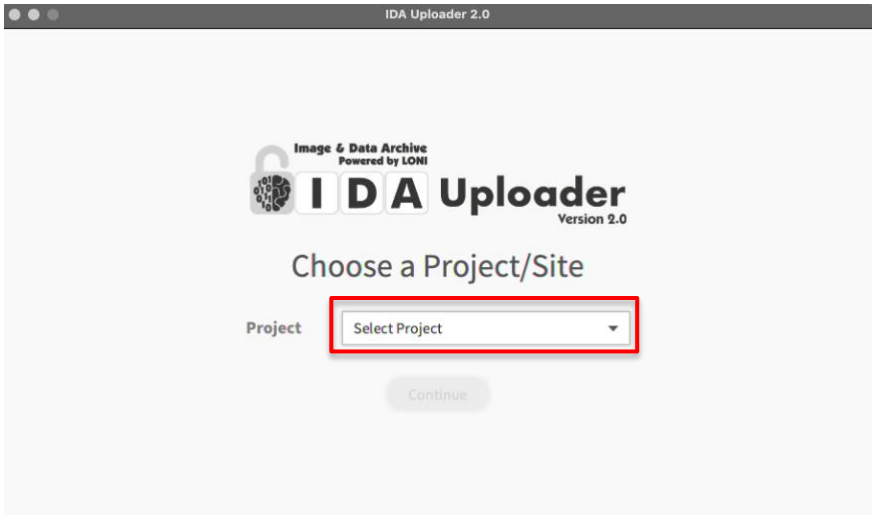
5. Please visit https://www.oracle.com/java/technologies/javase-downloads.html to download the latest Oracle JDK. NOTE: A minimum version of 15.0.1 is required to run IDA-Uploader-2.0.jar
6. Choose DEB, PRM or the compressed archive depending on your Linux Distribution.
7. Once you have completed the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

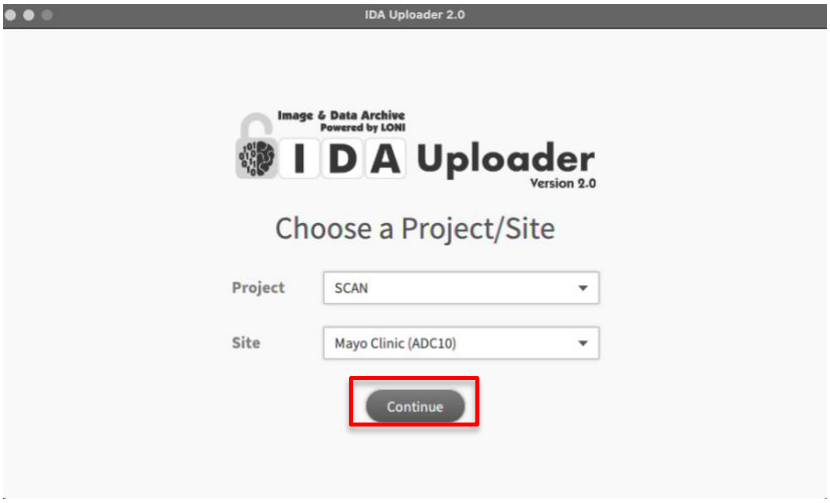
UPLOADING (ARCHIVING) TO SCAN

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”.



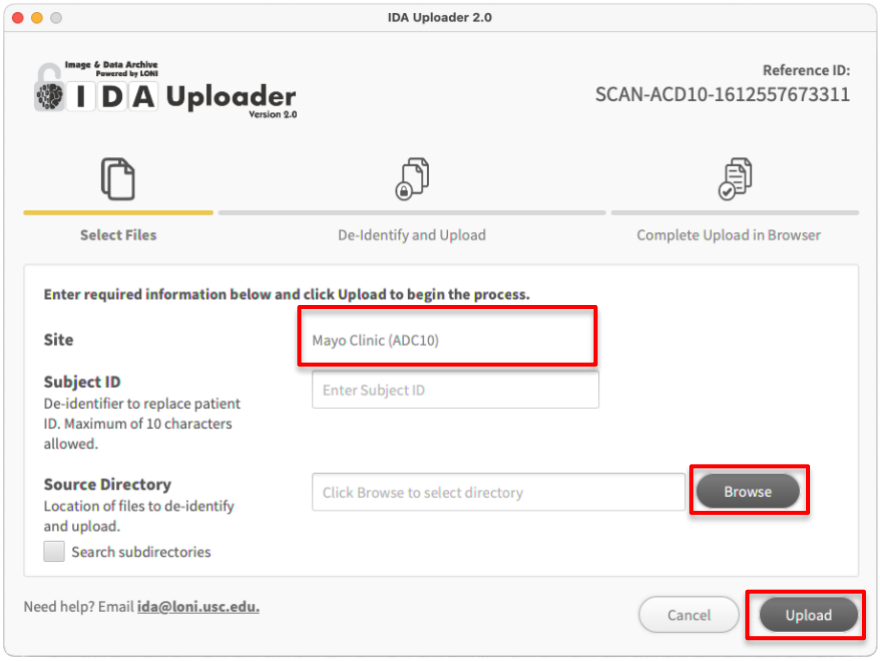
5. Enter the participants identifiers into the Subject ID field using the convention PTID+NACC ID, where the PTID and NACC ID are separated by the '+' character. As a rule, the user should enter the complete PTID and NACC ID and follow the formatting convention used for UDS data submission when applicable. Either upper or lower case may be used for any alphabetic characters. If the given PTID and NACC ID pair match the record present in the NACC database, the upload will be accepted. If not, the user will receive an error message indicating that the PTID and NACC ID combination are not valid, and the upload will not be allowed to continue.

   PLEASE NOTE: To upload data you must enter both the PTID and the NACC ID. To access your center's list of PTID and NACC ID pairs, you may work with your center UDS data manager to utilize the "PTID to NACC ID Map" tool available via the NACC portal: https://www.alz.washington.edu/MEMBER/portal.

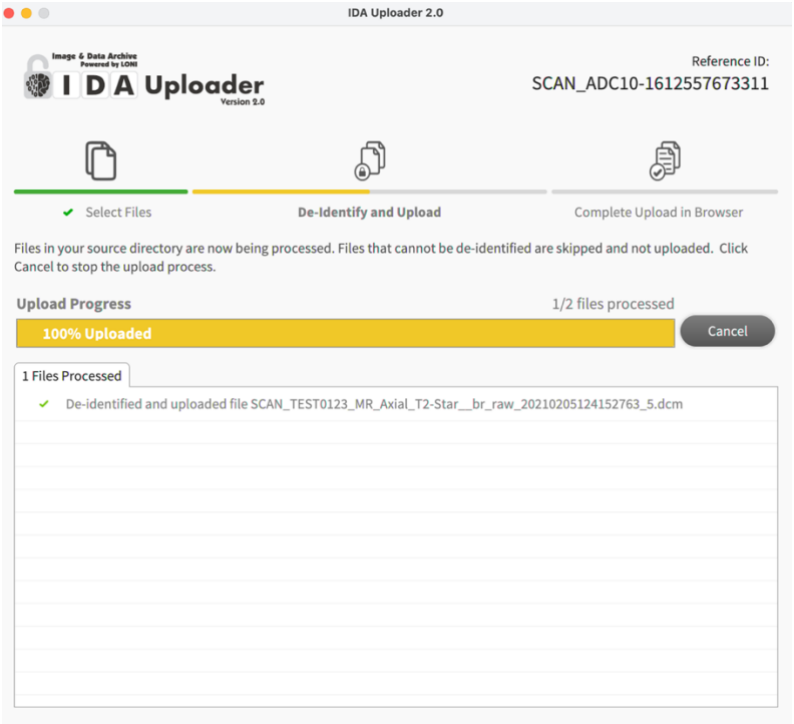
   Participant identifier terminology:
   - PTID (may be referred to as Subject ID or local ID). This is the ADRC-managed participant ID which is a sequence of up to 10 characters. Formats vary by each center; this is the ID used for UDS (uniform dataset) identification internally.
   - NACC ID: This is the NACC-managed participant ID. It is a string with the prefix 'NACC' followed by 6 digits.

6. Click “Browse” to select the Source Directory. Then click “Upload”.

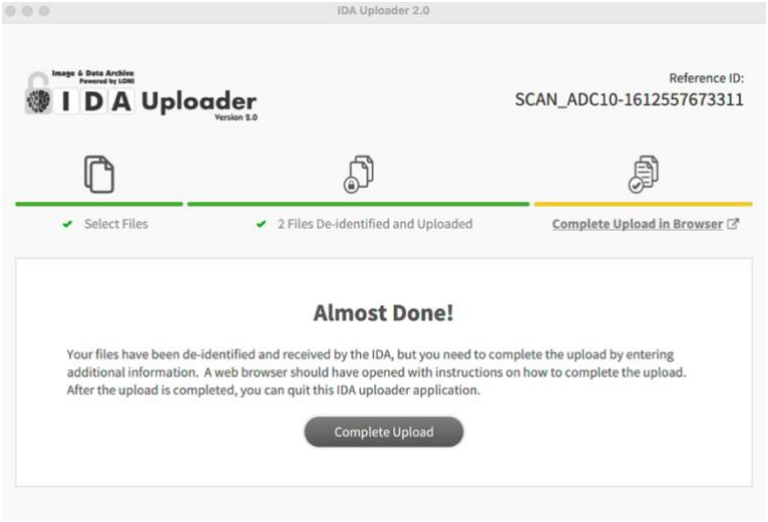
NOTE: The Source Directory is the directory containing the files to be uploaded. If your Source Directory contains subdirectories, choose to include/exclude those files by checking “Search subdirectories”.



7. You will be able to see the progress of your upload in the De-identify and Upload section.

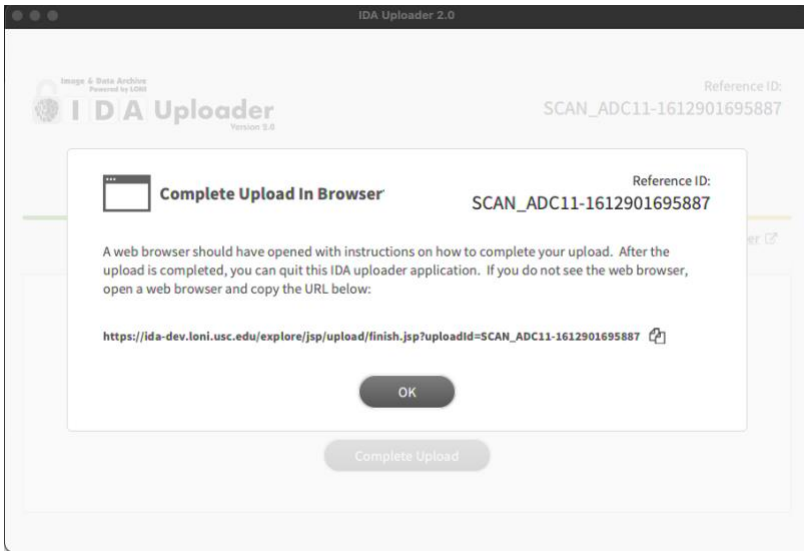


8. Once the files are de-identified and transferred to the IDA, you will need to complete the upload in your web browser.

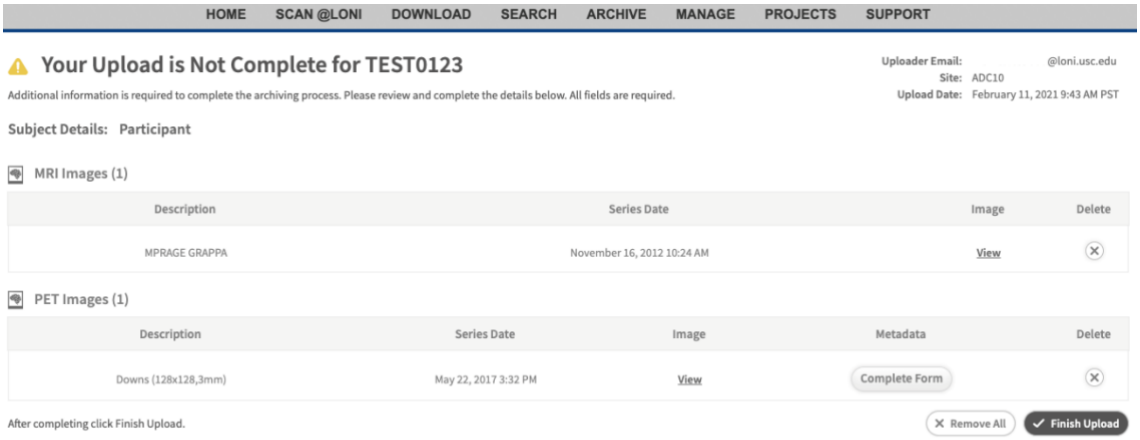


9. Your web browser should automatically open a new “Log In to Continue” page. Enter your IDA email and password. Click “Log In”.

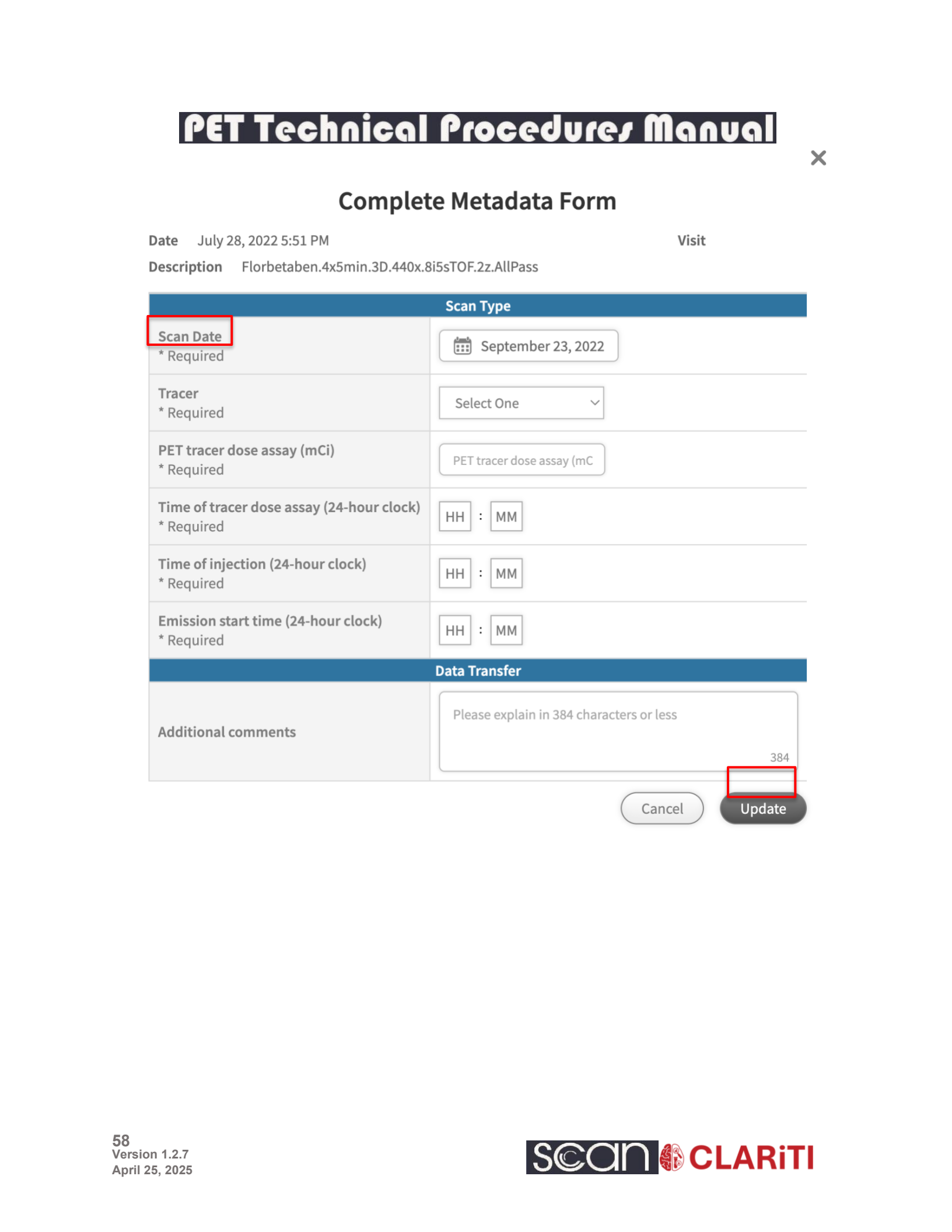
NOTE: If your web browser does not automatically open the “Log In to Continue” page, please click “Complete Upload” and you can copy-paste the link in your browser.



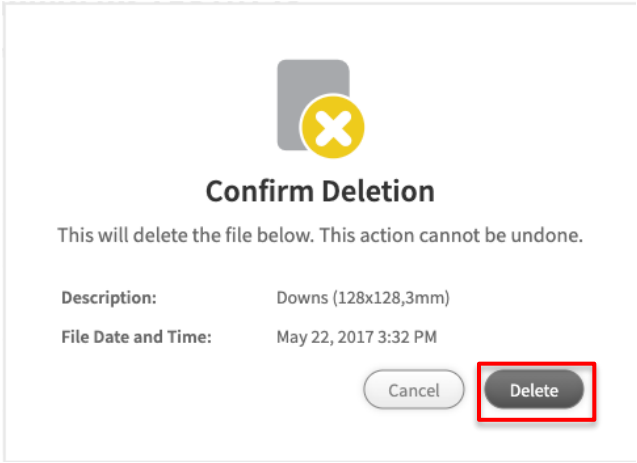
10. In the “Your Upload is Not Complete” page you can review the details of your upload.



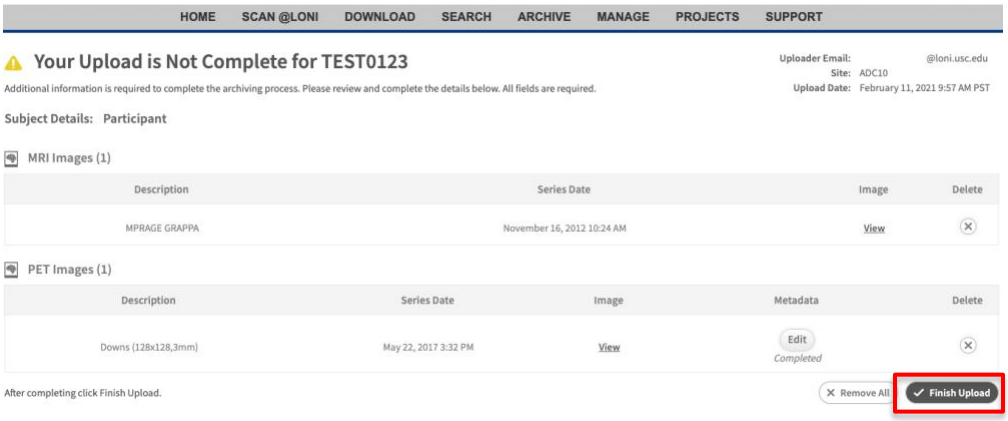
a. For PET image uploads, additional information is required in order to complete the upload.
   1. In the Metadata section, click “Complete Form”.
      NOTE: Fields marked (*Required) are required to complete the upload.
   2. Once the information is entered in the form, click “Update”.


Complete Metadata Form
Date July 28, 2022 5:51 PM
Visit
Description Florbetaben.4x5min.3D.440x.8i5sTOF.2z.AllPass
Scan Type
Scan Date
* Required
September 23, 2022
Tracer
* Required
Select One
PET tracer dose assay (mCi)
* Required
PET tracer dose assay (mC
Time of tracer dose assay (24-hour clock)
* Required
HH : MM
Time of injection (24-hour clock)
* Required
HH : MM
Emission start time (24-hour clock)
* Required
HH : MM
Data Transfer
Additional comments
Please explain in 384 characters or less
384
Cancel
Update

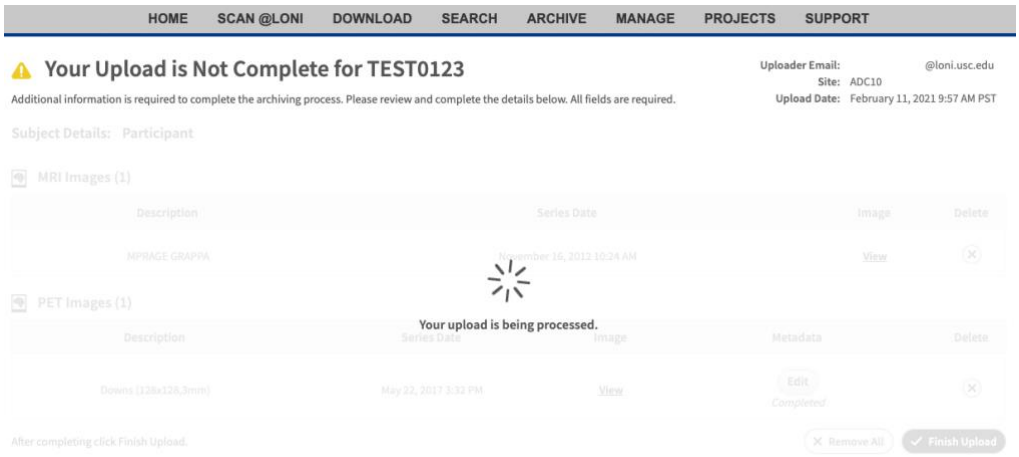
NOTE: If any data was mistakenly uploaded, you can click the “X” in the Delete column and it will be deleted from your upload. A window will appear to confirm the deletion. Click “Delete” to confirm file deletion or “Cancel”.



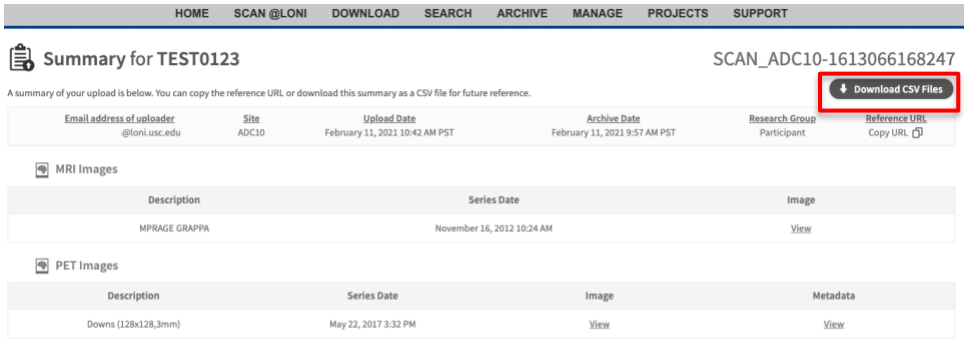
11. Once all required information has been entered, click “Finish Upload”.



12. You will see a screen that informs you that the upload is being processed.



13. 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.



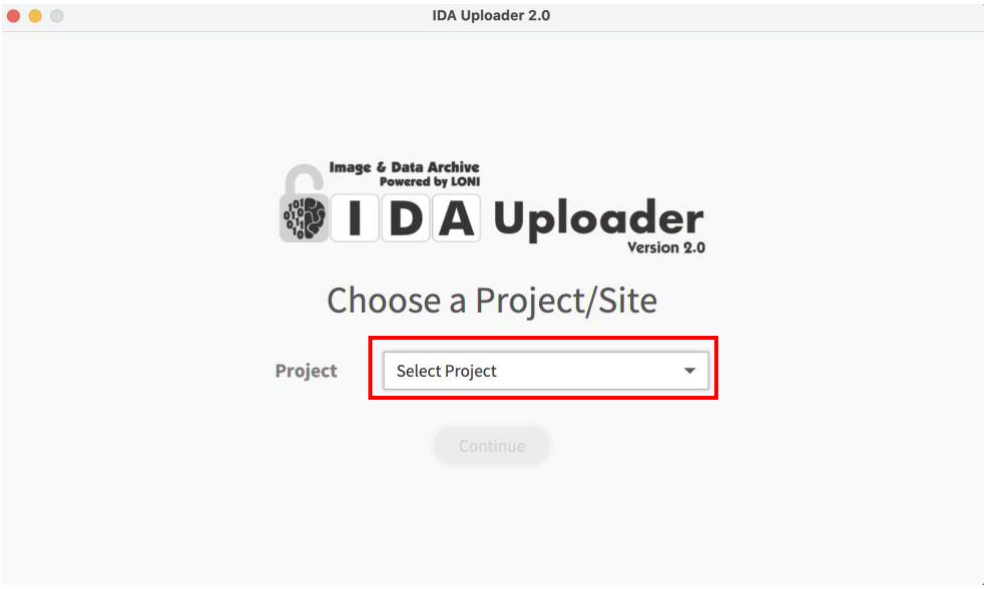
14. You can close the IDA-Uploader application or to upload images for another subject, click the “Upload More” button in the IDA-Uploader application.

Appendix E:
How to Upload PET Hoffman Phantom Data to SCANQUAL (SCAN only)

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.

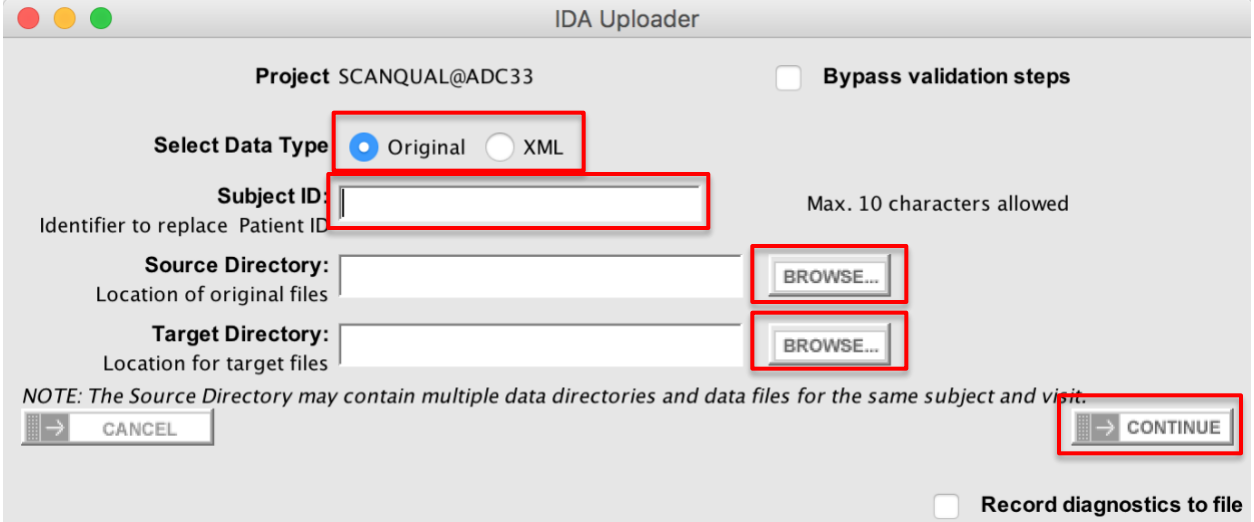


4. Click "Single Archive" or "Batch Archive".

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.



a. Click the type of data being uploaded – in this case," Original".
b. Enter the Phantom/Volunteer ID in the Subject ID field.

Phantom: 1_P_0001 (siteID_P_Number)
Volunteer: 1_V_0001 (siteID_V_Number)

Assign the Phantom/Volunteer ID in the Subject ID field as: "siteID_P_xxxx" or "siteID_V_xxxx", where siteID is your 1-3 digit Site ID and xxxx should count up for your site starting with 0001. Do not add leading zeros for siteID.

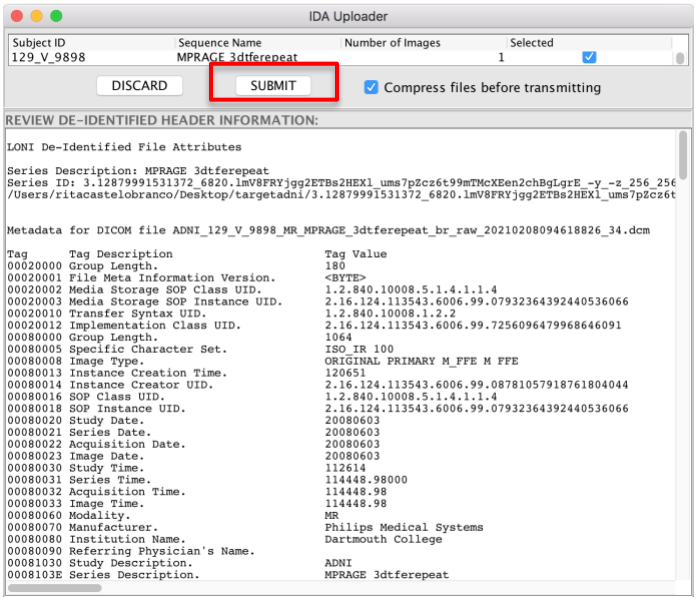
example, if your Site ID is ADC 13, you should fill in "13_P_0002" for the *second* phantom scan to be uploaded.

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

a. Deselect any image you do not want to be archived (if any) by unchecking the Selected checkbox.
b. Click "SUBMIT" to begin the transmission process.

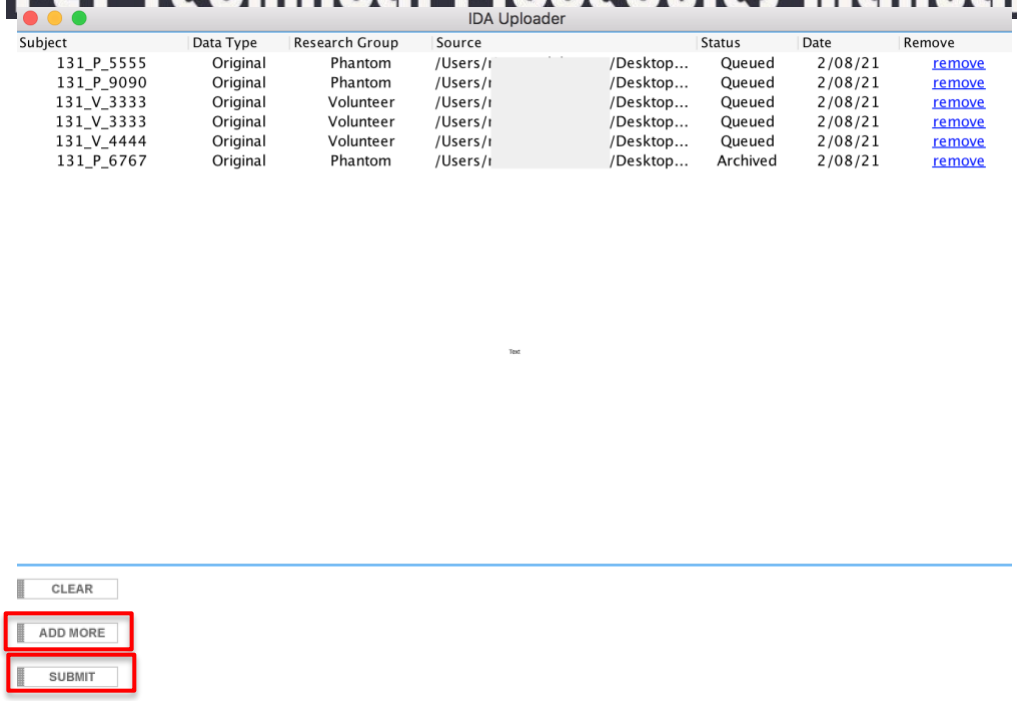
Note: This is not a feature during Batch Archive. Once the transmission has begun, a progress bar will show the status of the upload.



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.


IDA Uploader
Subject Data Type Research Group Source Status Date Remove
131_P_5555 Original Phantom /Users/ /Desktop... Queued 2/08/21 remove
131_P_9090 Original Phantom /Users/ /Desktop... Queued 2/08/21 remove
131_V_3333 Original Volunteer /Users/ /Desktop... Queued 2/08/21 remove
131_V_3333 Original Volunteer /Users/ /Desktop... Queued 2/08/21 remove
131_V_4444 Original Volunteer /Users/ /Desktop... Queued 2/08/21 remove
131_P_6767 Original Phantom /Users/ /Desktop... Archived 2/08/21 remove
CLEAR
ADD MORE
SUBMIT

Appendix F:
SCAN PET Upload Form (SCAN only)

PET Upload Form

Standardized Centralized Alzheimer's and Related Dementias Neuroimaging

v1.7 03/2023

Site: _____

PTID or Subject ID : _____

Scan date (mm/dd/yyyy): _____

PET tracer: _____

PET tracer dose assay (mCi): _____

Time of tracer dose assay (military time hh:mm): _____

Time of tracer injection (military time hh:mm): _____

Emission start time (military time hh:mm): _____

Possible PET tracers:

PIB	Flortaucipir	FDG
Florbetapir	MK6240	
Florbetaben	PI2620	
NAV4694	GTP1	