

Quick guide to A4 and LEARN imaging data on LONI

First, remember that all available data are from screening/baseline, prior to randomization in the clinical trial. No additional data for these participants will be available until the study concludes.

Research Groups:

amyloidE: these are participants who were found to have **elevated** (E) amyloid on Florbetapir amyloid imaging and were potentially eligible to continue in screening for A4 randomization (N=1323). The “elevated amyloid” determination was done via an algorithm using both quantitative and qualitative assessments (see Sperling et al *JAMA Neurology* 2020). Not all of the elevated amyloid participants were ultimately randomized into the clinical trial. The majority of these “amyloidE” participants also have screening MRI data (N=1251) and a subset (N=392) have Flortaucipir PET imaging.

LEARN amyloidNE: these are participants who were found to have **not elevated** (NE) amyloid on Florbetapir imaging, and were screened for the LEARN observational study (N=567). These subjects are not enrolled in the A4 clinical trial and do not receive any treatment. Not all of these participants were ultimately enrolled into LEARN, but those who were are followed longitudinally with the same imaging and clinical assessments as in the A4 Study clinical trial. Like the “amyloidE” group, the majority of these LEARN amyloidNE participants have MRI data (N=542), and a subset (N=55) underwent Flortaucipir PET imaging.

amyloidNE: these are participants who were found to have **not elevated** (NE) amyloid on screening Florbetapir imaging and were not screened for the LEARN observational study (N=2596). These participants have screening cognitive assessments and Florbetapir-PET imaging. None of these subjects have MRI data or Flortaucipir imaging. No further data will be collected on these participants.

Visit codes:

SCV2: This is the Florbetapir (amyloid) PET visit.

SCV4: This is the MRI visit and the Flortaucipir (tau) PET visit.

Image Formats:

For consistency, anonymization, and ease of use, all data being shared are in NIFTI-1 format. This was done to ensure deidentification of data, to help clarify which sequences/reconstructions should be used, to eliminate any issues with DICOM conversion, and to enable the implementation of face blinding for high contrast/resolution MRI data.

PET data: each session has one and only one nifti file that is shared, and this is the file that should be used for analysis.

Florbetapir (amyloid PET) data was collected from 50-70 minutes post-injection and was generally reconstructed in 4x5-minute frames. There are some exceptions to this (e.g. some sites reconstructed the 50-70 minute data into a single frame); our advice is to use the data as provided. Realignment of frames followed by mean/sum over the frames into a single 3D image which is then suitable for SUVR analysis.

Flortaucipir (tau PET) data was collected from 80-110 minutes post-injection and was generally reconstructed in 6x5-minute frames. There are some exceptions to this (i.e. some sites reconstructed the 80-110 minute data into a single frame). Our advice is to use the data as provided. Realignment and mean/sum over the frames into a single 3D image which is then suitable for SUVR analysis.

MRI data consists of six sequences; T1 MPRAGE, FLAIR, T2 SE, T2 star, DWI, and resting state fMRI. The T1 MPRAGE, FLAIR, and T2 Fast/Turbo SE sequences were found to have sufficiently high resolution and contrast for facial reconstruction. Consequently, all three of these MR sequences were de-identified using *mri_reface*, which uses an average MRI and face template to replace image regions in the face, ears, and surrounding air that could potentially be re-identified (<https://dx.doi.org/10.1056/NEJMc1908881>). Compared to other MRI face-deidentification techniques, this method reduces effects on brain volume measurements from de-identified scans (<https://doi.org/10.1016/j.neuroimage.2021.117845>). Trained image analysts validated that face imagery was successfully replaced in all images. For T1 MPRAGE, gradient nonlinearity correction was applied when necessary. T2 star, DWI, and fMRI sequences were converted directly from DICOM without face blinding. Spreadsheets with BIDS style information on sequence parameters for DWI and fMRI are provided in the *StudyData -> Imaging* portion of the Downloads section. Keep in mind that due to a variety of reasons, not every subject has an image for every sequence. Additionally, some subjects have repeat scans for a given sequence type. If the sequence passed QA, it was converted to nifti and provided in the dataset.

Guide to downloading image data

In order to download imaging data, you will need to select the flag for “pre-processed” data. You can then use the Research Groups “amyloidE”, “amyloidNE”, and “LEARN amyloidNE” to select specific groups of subjects (see above). Since the only data available are the nifti files we were able to regularize the image descriptions for all available data. The image descriptions are listed below (*italics* denotes information that is not present for all instances):

Sequences	Image Description	Suggested Search Term
FBP amyloid PET:	“Florbetapir”	Florbetapir

FTP tau PET:	"Flortaucipir"	Flortaucipir
T1 MPRAGE:	"T1; <i>GradWarp</i> ; DeFaced"	T1*
FLAIR:	"FLAIR; DeFaced"	FLAIR*
T2 spin echo:	"T2_SE; DeFaced"	T2_SE*
T2*:	"T2_star"	T2_star
Diffusion imaging:	"DWI"	DWI
Resting state fMRI:	"fMRI_rest"	fMRI_rest

We recommend selecting both visits and all imaging modalities and then using the Research Groups and the Image Description to accurately select the images you want to download. For example, if you wanted to download Flortaucipir data, you could select all research groups and all visits, then enter "Flortaucipir" into the image description. Downloading the resulting spreadsheet would then allow you to create a comma separated list of participants. Adding that to the "Subject ID" field and entering "T1*" into the image description field would then allow you to select the structural MPRAGE data for only the participants with Flortaucipir data.