

Data Archive - ADNI and RADC

ADNI

Downloading New ADNI Data

- Visit the ADNI Website: <http://adni.loni.usc.edu/> and select the 'Access Data Samples' in the Data and Samples dropdown menu.

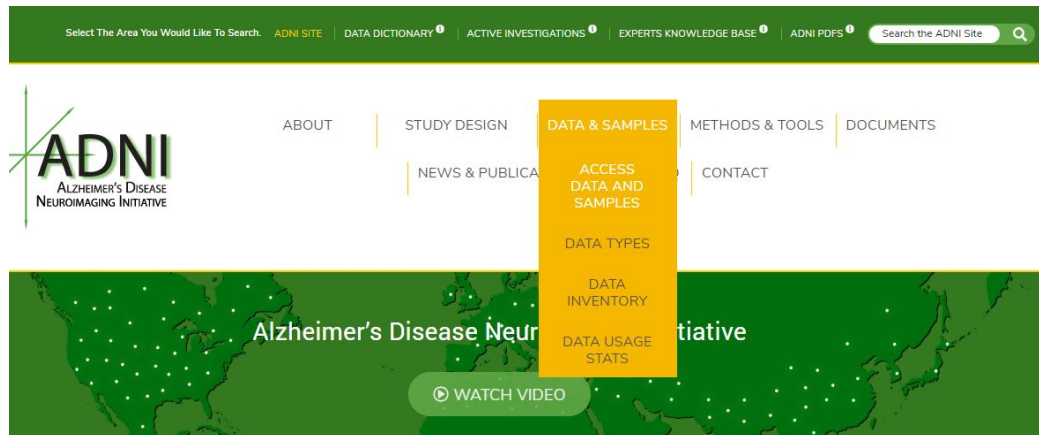


Fig: Accessing ADNI Data Samples

- A login screen will appear. If you do not already have personal access to ADNI data, an application for the same can be made here:
<https://ida.loni.usc.edu/collaboration/access/appLicense.jsp;jsessionid=18F0EC9091160BBE877B07EE41C4A8F6>

ACCESS DATA AND SAMPLES

A screenshot of the 'Data Archive Login' screen. The background is green. At the top, it says 'Data Archive Login'. Below that, a message states: 'If you have already received approval to access ADNI data, you can login to search and download data from the repository. To request approval, see below.' There are two input fields: 'EMAIL' with the value 'shreyakr96@gmail.com' and 'PASSWORD' with masked characters '.....'. A green 'SUBMIT' button is at the bottom.

Fig: Logging into the ADNI Database

- This takes you to the ADNI database page. Under the download tab, there are 3 options:
- **Study Data:** This contains a collection of spreadsheets with different kinds of subject data. This includes test scores, demographic information, diagnosis information etc.
 - **Image Collections:** This contains all subject scans. This includes structural, functional, diffusion imaging and PET data.
 - **Genetic Data:** Contains Genome Wide Association Studies (GWAS) and Whole Genome Sequencing (WGS) data for ADNI1, ADNIGO/2 Cohorts.

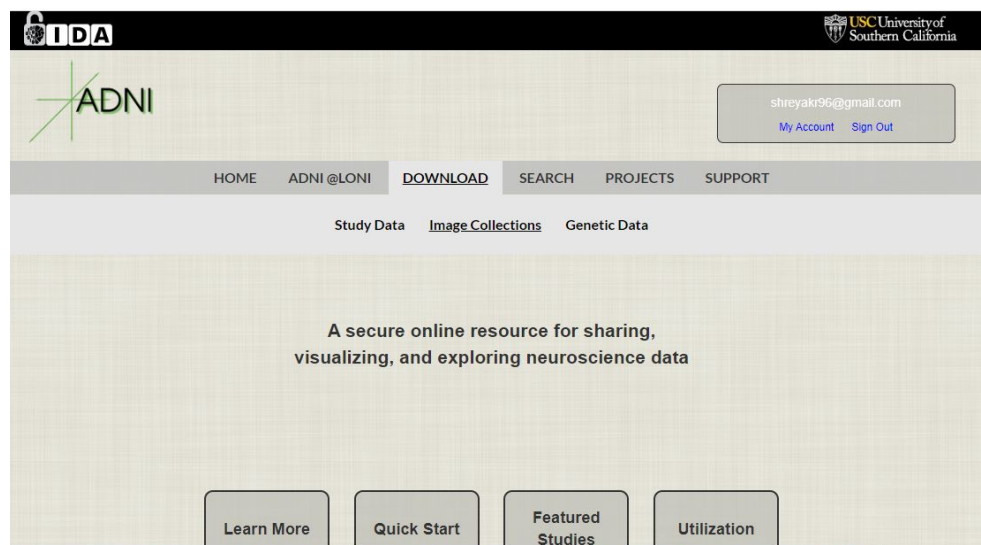


Fig: Navigating the ADNI Data Download Page

- **Navigating the Study Data Collection:**
 - The list in the left column contains the categories under which spreadsheets are arranged.
 - The most important table which contains all key ADNI tables merged into one, is present in the **Study Info** Category.
 - Select two items - **Key ADNI tables merged into one** (ADNIMERGE table) and the corresponding **Dictionary** and press the Download button on the top right corner.
 - The former - ADNIMERGE table - contains a compilation of several entries - **demographic information** like age, gender etc., **Diagnosis** - Normal, MCI, AD, **Several test scores** like MMSE, ADAS etc. for all subjects in all 3 ADNI cohorts.

- The latter contains expansions of the column names present within the **ADNIMERGE** table.
- If specific test scores or neuropathological entries not included in the ADNIMERGE table are required for analysis, they can be downloaded as **separate tables** and must be sought out from the categories present in the left column.

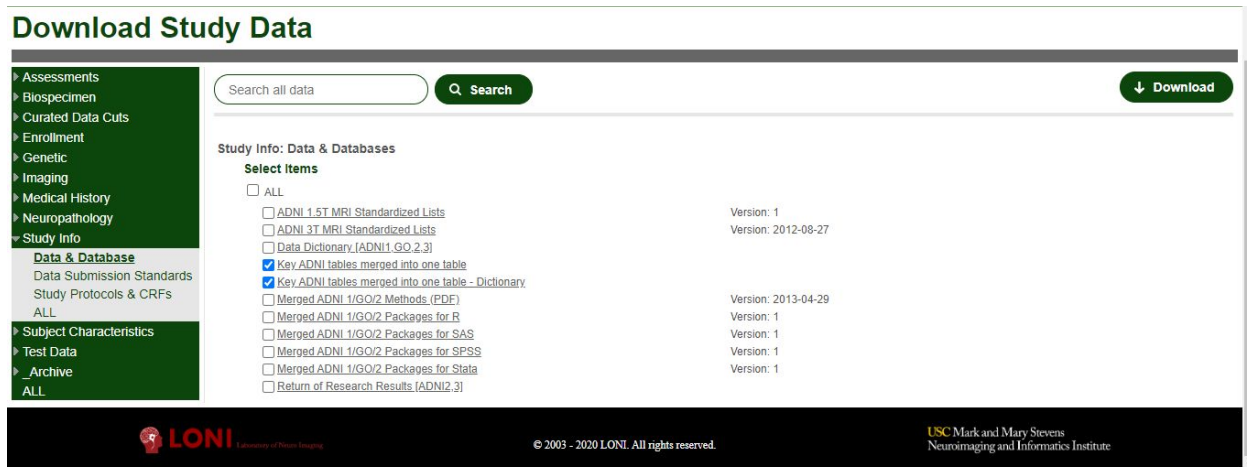


Fig: Downloading the ADNIMERGE table and the dictionary from the Study Data Page

- **Navigating the Imaging Database:**

- Toggle to the '**Advanced Search**' Option in Image Collections Window. (See figures below)
- On the left, there are search options that you might want to narrow in on, while downloading subjects' image data.
- Some important fields to check are:
 - **Project Phase:** This allows you to select the cohorts - ADNI1, ADNIGO, ADNI2 and ADNI3 - you want to restrict your subject selection to. The factors to be taken into consideration here are the scanner strength for that cohort, availability of certain modalities etc.
 - **Subject:** This can be used to look for imaging data of **only a specific subject** if the ID is previously known. It can also be used to look for **subjects of a specific age or gender**. What this field is most commonly used for is to identify a group of subjects that had **the same initial diagnosis (at their baseline visit)**.
 - **Image:** This allows you to select the modalities you wish to download from **PET, MRI, FMRI and DTI**

- **Imaging Protocol:** This is primarily used to select a particular scanner manufacturer, as there might be differences in preprocessing steps depending on the manufacturer.

Options

Exclude Previous Downloads

SEARCH SECTION

Project/Phase

Subject

Subject Specific Information

Assessments

Study/Visit

Image

Imaging Protocol

Image Status

Image Processing

IMAGE TYPES

Original

Pre-processed

Post-processed

Options

Subject ID

Search Criteria

Specify selection criteria using the checkboxes on the left. Wild cards (*) are permitted in fields marked with a star below. For example, "rest*" returns results that begin with "rest."

PROJECT/PHASE

Projects (ADNI) ☒ ADNI ☐ HCP ☐ ADNI GO ☐ ADNI 1 ☐ ADNI 2 ☐ ADNI 3

SUBJECT

Subject ID * Separate multiple Subject ID's by commas

Age (years) Equals

Sex Both

Weight (kgs) Equals

Research Group ☐ MCI ☐ EMCI ☐ LMCI ☐ Patient ☐ AD ☐ Phantom ☐ SMC ☐ Volunteer ☐ CN

STUDY/VISIT

Study Date Equals

Archive Date Equals

(ADNI) ☐ ADNI Screening ☐ ADNI Baseline ☐ ADNI1/GO Month 6 ☐ ADNI1/GO Month 12 ☐ ADNI1/GO Month 18 ☐ ADNI1/GO Month 24 ☐ ADNI1/GO Month 30 ☐ ADNI1/GO Month 36 ☐ ADNI1/GO Month 42 ☐ ADNI1/GO Month 48 ☐ Unscheduled ☐ No Visit Defined ☐ ADNI/GO Screening MRI ☐ ADNI/GO Month 3 MRI ☐ ADNI/GO Month 54 ☐ ADNI/GO Month 60 ☐ ADNI/GO Month 66 ☐ ADNI/GO Month 72 ☐ ADNI/GO Month 78 ☐ ADNI2 Screening-New Pt

☒ OR ☐ AND
Subject has at least one

Fig: ADNI Imaging Database Advanced Search Options - Part I

IMAGE

Image Description *

Image ID Separate multiple Image ID's by commas (eg. 1123,1456,... or 123,456,...)

Modality ☐ DTI ☒ MRI ☐ PET ☐ fMRI ☐ OR ☐ AND
Subject has at least one

IMAGING PROTOCOL

(MRI) ☐ AXIAL ☐ CORONAL ☐ SAGITTAL

Acquisition Type ☐ 2D ☐ 3D

Field Strength (tesla) Equals

Manufacturer ☐ GE MEDICAL SYSTEMS ☐ Philips ☐ Philips Healthcare ☐ Philips Medical Systems ☐ SIEMENS ☐ SIEMENS/PixelMed

Matrix Z Equals

Mfg Model ☐ Achieva ☐ Achieva dStream ☐ Aera ☐ Allegra ☐ Avanto ☐ Biograph_mMR ☐ DISCOVERY MR750 ☐ DISCOVERY MR750w ☐ Espree ☐ GEMINI ☐ GENESIS_SIGNA ☐ Gyroscan Intera ☐ Gyroscan NT ☐ Ingenia ☐ Ingenia Elition X ☐ Ingenuity ☐ Intera ☐ Intera Achieva ☐ MAGNETOM VISION ☐ NUMARIS/4 ☐ Obelix ☐ Prisma ☐ Prisma_fit ☐ SIGNA EXCITE ☐ SIGNA HDx ☐ Signa HDxt ☐ SIGNA Premier ☐ Skyra ☐ Skyra_fit ☐ Skyra/DicomCleaner ☐ Sonata ☐ SonataVision ☐ Symphony ☐ SymphonyTim ☐ Trio ☐ TrioTim ☐ Verio

Slice Thickness (mm) Equals

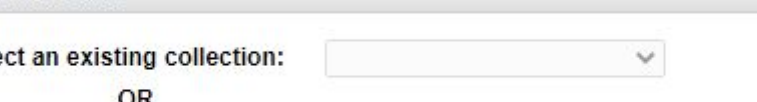
Weighting ☐ PD ☐ T1 ☐ T2

RESET ALL **SEARCH**

Fig: ADNI Imaging Database Advanced Search Options - Part II

- **Moving Selected Subjects to Collection:**
 - Once the search criteria are defined, the search results throw up all images that match the criteria.
 - This often includes more than one visit for each subject.

- | Search | Advanced Search (beta) | Advanced Search Results | Data Collections | | | | | | | | |
|---|------------------------|-------------------------|--------------------------|-------|-------------------------------------|----------------------|-----------------------------|--|--|--|--|
| <div> <div> <div>Your Current Search</div> <div>Project Phase</div> <div>ADNI 3</div> <div>Research Group</div> <div>MCI</div> <div>Image Modality - OR</div> <div>MR</div> <div>fMRI</div> <div>Refine Your Search</div> <div>Subject Age</div> <div>50-75 years (2384)</div> <div>75-100 years (1883)</div> <div>Subject Sex</div> <div>Male (2408)</div> <div>Female (1819)</div> </div> <div> <div>Displaying Results 1-20 of 4227</div> <div>4 images selected</div> <div> <input type="checkbox"/> Select All <input type="button" value="Add To Collection"/> <input type="button" value="CSV Download"/> </div> </div> </div> | | | | | | | | | | | |
| SUBJECT | | STUDY | | IMAGE | | | | | | | |
| Select | Subject ID ▼ | Sex | Select | Age | Select | View | Description | | | | |
| <input type="checkbox"/> | 002_S_1155 | M | <input type="checkbox"/> | 68.2 | <input type="checkbox"/> | VIEW | Axial 3D PAST (Eyes Open) | | | | |
| | | | | | <input type="checkbox"/> | VIEW | Perfusion_Weighted | | | | |
| | | | | | <input type="checkbox"/> | VIEW | Accelerated Sagittal MPRAGE | | | | |
| | | | | | <input type="checkbox"/> | VIEW | Axial T2 STAR | | | | |
| | | | | | <input checked="" type="checkbox"/> | VIEW | Field Mapping | | | | |
| | | | | | <input checked="" type="checkbox"/> | VIEW | Field Mapping | | | | |
| | | | | | <input type="checkbox"/> | VIEW | Sagittal 3D FLAIR | | | | |
| | | | | | <input type="checkbox"/> | VIEW | HighResHippocampus | | | | |
| | | | | | <input checked="" type="checkbox"/> | VIEW | Field Mapping | | | | |
| | | | | | <input checked="" type="checkbox"/> | VIEW | Axial rsfMRI (Eyes Open) | | | | |
| | | | <input type="checkbox"/> | 69.3 | <input type="checkbox"/> | VIEW | Accelerated Sagittal MPRAGE | | | | |
| | | | | | <input type="checkbox"/> | VIEW | Axial 3D PAST (Eyes Open) | | | | |
| | | | | | <input type="checkbox"/> | VIEW | Perfusion_Weighted | | | | |
| | | | | | <input type="checkbox"/> | VIEW | Axial T2 STAR | | | | |
| | | | | | <input type="checkbox"/> | VIEW | Field Mapping | | | | |
| | | | | | <input type="checkbox"/> | VIEW | Field Mapping | | | | |
| | | | | | <input type="checkbox"/> | VIEW | Sagittal 3D FLAIR | | | | |
| | | | | | <input type="checkbox"/> | VIEW | HighResHippocampus | | | | |
| | | | | | <input type="checkbox"/> | VIEW | HighResHippocampus | | | | |
| | | | | | <input type="checkbox"/> | VIEW | Field Mapping | | | | |



Add To Collection

Select an existing collection:

OR

Enter a name for the collection:

Optional collection description:

OK Cancel

- **Downloading the Selected Images:**
 - Navigate to the Data Collections Tab.
 - Select the Collection you have stored the data in, which is 'Tutorial' in our example (**see figure below**).
 - Select all the scans you wish to download from this collection. Select the '**As Archived**' option to download in the **DICOM format**, if the fMRI data is to be preprocessed using fMRIPrep.
 - Click on the '**1-Click Download**' option, and download the Zip file (**see figure below**)

Search | Advanced Search (beta) | Advanced Search Results | Data Collections

COLLECTIONS

REFRESH COUNTS

My Collections

- + AD Subjects (118)
- + AD adn13 (15)
- + ADNI3_missing16sMRI (16)
- + ADNI3_rsfmri (83)
- + ADNI3_sMRI (111)
- + ADNI3_MCI (233)

Collection: Tutorial

CSV

As Archived ☐ NIFTI ☐ MINC ☐ ANALYZE

1-CLICK DOWNLOAD | ADVANCED DOWNLOAD

4 items selected

REMOVE | REGROUP

Subject	Group	Sex	Age	Visit	Modality	Description	Type	Acq Date	Format	Downloaded	All
002_S_1155	MCI	M	68	101	fMRI	Axial rsfMRI (Eyes Open)	Original	4/24/2017	DCM	12/16/2019	<input checked="" type="checkbox"/>
002_S_1155	MCI	M	68	101	MRI	Field Mapping	Original	4/24/2017	DCM	12/16/2019	<input checked="" type="checkbox"/>
002_S_1155	MCI	M	68	101	MRI	Field Mapping	Original	4/24/2017	DCM	12/16/2019	<input checked="" type="checkbox"/>

Fig: Selecting Images from the Collection to download

1-Click Download

• This download will stop if your connection is interrupted or session expires.
 • For more download options, close this window and then click the Advanced Download button on the Collections page.

Download Zip File

Size: 51.70 MB Time estimate: about 10 mins

[Download Metadata](#)

CLOSE WINDOW

Fig: 1-Click Download Option

Accessing Already Downloaded, Preprocessed and Parcellated ADNI Data:

- Downloaded ADNI Raw Data** can be found in Z Drive under the following folder: **Z:\zSturfiData\Raw\ADNI**. This folder contains subfolders which contain MC1c and MC1s subject scans.
 - MC1c** corresponds to subjects who were in MCI and then converted to AD, as seen from their longitudinal data. These scans are taken from visits when these subjects were still in the MCI state.
 - The MC1c subjects are further categorized **MC1c-12**, **MC1c 12-24**, and **MC1c -24** in these subfolders, which indicates how many months prior to conversion to AD those scans were taken at. This detail might or might not be relevant to your analysis.

- There are also **MCIs folders** which contain subjects who have stayed in MCI state for at least two years, and never converted to AD until the last known scan.

%% This Data has been preprocessed using the Old Lab pipeline, with a different set of steps, and a different order than what we plan to do in the future with dcm2bids + fmrippep.

- **Preprocessed fMRI data:** Data which has been preprocessed using the old lab fMRI preprocessing pipeline can be found here: **Z:\zSturfiData\PreProcessed\ADNI** under MCIC and MCIs subfolders.
 - This pipeline did not include susceptibility distortion correction, and there might be errors in slice timing correction. All other standard steps have been applied.
- **Parcellated fMRI data:** Data which has been parcellated following the above preprocessing pipelines can be found here:
 - Willard 90 Parcellated Data is present in the hard drive labelled **Hard Drive 6** in the following folder **F:\Parcellation\Will_90\ADNI** containing subfolders **MCIC** and **MCIs**.
 - **Power 264, Willard 14** present in **RADC Hard drive** (*will add links when I have access to it*)
 - **Parcellation Scripts** are present Hard Drive 6: **F:\Parcellation\Parcellation**

RADC Data

All RADC DICOM and NIFTI information, and their demographic information and visit wise scores have been uploaded to a G-Suite Shared Drive. If you require access, please contact Dr. Sridhar:

<https://drive.google.com/drive/folders/16QaAzwSfWCa0aH4rB8K5kp4bX3O10w5X?usp=sharing>

Other Backup Locations:

- RADC Raw Data is stored in two hard drives. One labelled RADC and the other labelled Hard Drive 6.
- In the RADC harddrive, the path to the **zipped raw data** is: **E:\MRI_DEVARAJAR**
- In hard drive 6, the path to **unzipped** RADC raw data is:
F:\MRI_DEVARAJAR\Unzipped
- Within each of these folders, there are sub-folders MG, BCK and UC for 3 different centres at which scans are collected.
- Some subjects from the MG and BCK center had **missing .bvec and .bval files** that were separately requested later. These can be found in **Hard Drive 6** in this path:
F:\MRI_DEVARAJAR\New_Scores\bfiles
- Subject Information is stored in: **F:\MRI_DEVARAJAR\New_Scores** in **Hard Drive 6**
















Subject Information:

- Subject information is present in the following two spreadsheets in the path attached, in Hard Drive 6 - **F:\MRI_DEVARAJAR\New_Scores** :
 - **Dataset_611_basic_04-23-2019**: This contains information for all subjects included in the study, that **stay constant across multiple visits** of the same subject. This includes factors like **age, gender, race, education level, genetic information like tau tangles, age of death etc.**
 - **Dataset_611_long_04-23-2019**: This sheet contains factors that vary across visits. This includes **diagnosis, several cognitive scores, physiological factors like hemoglobin levels, and mental health metrics.**
 - **RADC_codebook_data_set_611_04-23-2019**: This **codebook** contains expansions of the column names in both the spreadsheets above. It also contains **details of the cognitive tests** performed whose scores are reported in the above sheets.

RADC Raw Data - Important Details

- As RADC does not share raw data in the DICOM format, some important parameters required for preprocessing which are not present in NIfTI headers can be found in the scanner protocols.
- These protocols can be found on their official website at the attached link:
<https://www.radc.rush.edu/docs/var/scannerProtocols.htm>
- The parameters that have to be determined from the above links include **Time of Echo (TE), slice acquisition order, and the two times of echo for GRE field mapping.**
- The protocols for each scanner at each of the different locations is **different.**
- We have primarily used only the **MG centre's** data so far because **BCK center uses a 1.5T Tesla scanner**, and **UC does not contain MCI data.**
- The **UC Center does not have fMRI or Fieldmap Data.**
- All fMRI data follows a **sequential interleaved slice acquisition.**
- **MG Center** data has **GRE fieldmaps** - 2 Magnitude images and 1 phase difference images.

MG Center Raw Data Example:

Name	Date modified	Type	Size
 DIFFDTI45directions.nii	8/20/2014 5:40 AM	NII File	73,256 KB
 DIFFDTI45directionsA.nii	8/20/2014 5:40 AM	NII File	1,593 KB
 DIFFDTI45directionsB.nii	8/20/2014 5:40 AM	NII File	1,593 KB
 DIFFDTI45directionsC.nii	8/20/2014 5:40 AM	NII File	1,593 KB
 DIFFDTI45directionsD.nii	8/20/2014 5:40 AM	NII File	2,390 KB
 ep2dfidbasicbold.nii	8/20/2014 5:40 AM	NII File	45,601 KB
 FLAIRAxialTE150.nii	8/20/2014 5:40 AM	NII File	4,481 KB
 FLAIRAxialTE150A.nii	8/20/2014 5:40 AM	NII File	4,481 KB
 grefieldmapping.nii	8/20/2014 5:40 AM	NII File	4,161 KB
 grefieldmappingA.nii	8/20/2014 5:40 AM	NII File	2,081 KB
 t1mprnssagpat2iso.nii	8/20/2014 5:40 AM	NII File	22,529 KB
 t1mprnssagpat2isoA.nii	8/20/2014 5:40 AM	NII File	22,529 KB
 t2f13dtraNoSWI.nii	8/20/2014 5:40 AM	NII File	61,441 KB
 t2f13dtraNoSWIA.nii	8/20/2014 5:40 AM	NII File	61,441 KB
 T2mapping.nii	8/20/2014 5:40 AM	NII File	102,001 KB

- **fMRI file:** [ep2dfidbasicbold.nii](#)
- **Structural File:** [t1mprnssagpat2iso.nii](#)
- **GRE fieldmap - Magnitude File:** [grefieldmapping.nii](#) (contains 2 volumes - each is one magnitude image at a different TE)
- **GRE Fieldmap - Phase Difference Image:** [grefieldmappingA.nii](#)

Preprocessed and Parcellated RADC Data Locations:

%% The following data has been preprocessed with the old lab pipeline with a different set and order of steps than dcm2bids + fmriprep

Preprocessed RADC Data:

- It is stored in Z drive in the following location: [Z:\zSturfData\PreProcessed\RADC](#)
- This folder contains subfolders which contain MCIC and MCIs subject scans.
 - **MCIC** corresponds to subjects who were in MCI and then converted to AD, as seen from their longitudinal data. These scans are taken from visits when these subjects were still in the MCI state.
 - The MCIC subjects are further categorized **MCIC-12**, **MCIC 12-24**, and **MCIC -24** in these subfolders, which indicates how many months prior to conversion to AD those scans were taken at. This detail might or might not be relevant to your analysis.

- There are also **MCIs folders** which contain subjects who have stayed in MCI state for at least two years, and never converted to AD until the last known scan.
- This data has been preprocessed using the **old lab fMRI pipeline**
- This pipeline did not include susceptibility distortion correction, and there might be errors in slice timing correction. All other standard steps have been applied.

Parcellated RADC Data:

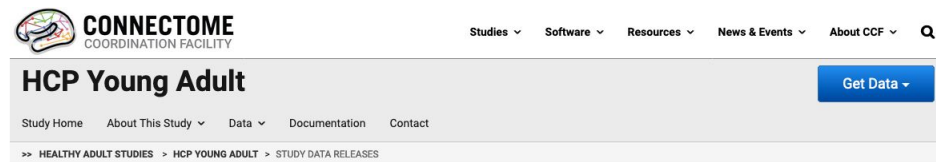
- **Parcellation Scripts** are present Hard Drive 6: [F:\Parcellation\Parcellation](#)
- **Parcellated data locations to be added.**

Human Connectome Project (HCP) Data

Registering on the ConnectomeDB System and Amazon Web Services

- Visit the Connectome Coordination Facility that will direct you to the Connectome DB database management system.

<https://www.humanconnectome.org/study/hcp-young-adult/data-releases>



Current Data Releases



S1200 Extensively Processed fMRI Data

Released on 07/21/2017

High-level extensively processed data for the 1200 Subjects release including group average structural and fMRI data, group average functional connectivity, and Group ICA-based parcellation + timeseries + netmats datasets.

[View Data Release Documentation](#)

[Get Data: Download Data on ConnectomeDB](#)

"Let me explore the dataset"



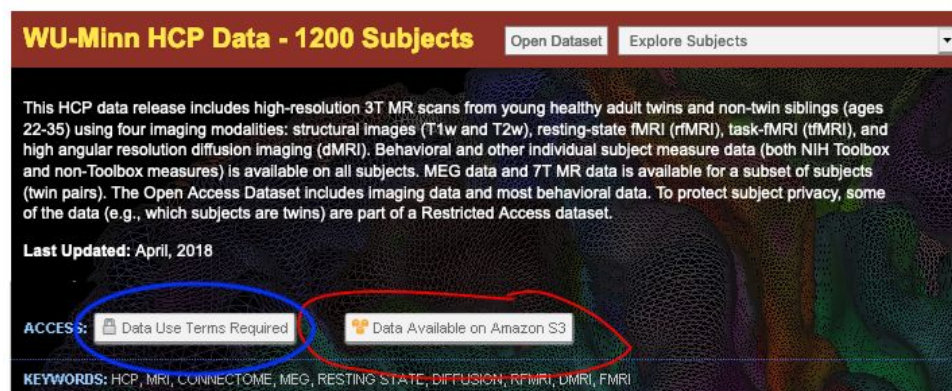
All HCP data can be downloaded from ConnectomeDB, including a variety of convenient packaged downloads for groups of unrelated subjects. You can explore the full protocol before downloading with our online data archive.

[Log in to ConnectomeDB](#)

- Click on the “Get Data” button on the top right and choose “Download from Connectome DB”.
- Create your own account by registering.
- Once you login, you will see the following page with all the datasets such as the following:

Public Connectome Data

Updated April 2018: All 7T functional MR data (184 subjects) re-preprocessed to remove unwarping bug. FIX-cleaned retinotopy fMRI data now available (183 subjects). NIH Toolbox Cognition composite scores added.



- Accept the Data Use Terms by clicking on the tab circled in blue shown above.
- Next, you must get access to the Amazon S3 browser. For this you need AWS credentials. Click on the “Data Available on Amazon S3” tab circled in red shown above and follow the steps provided [here](#) to create your credentials. Please remember to safely save your username, access key ID and secret access key for future reference.
- Download the S3 browser for Windows [here](#).
 - Once you launch the S3 browser, you should be prompted to create an account. Enter your access key ID and secret access key that you obtain with your credentials in the previous step.

Edit Account
Edit account details and click Save changes

Account Name:
whdev
You can assign any name to your account. S3 Browser uses it to distinguish one account from another.

Storage Type:
Amazon S3 Storage
Choose the storage you want to work with. Default value is Amazon S3 Storage.

Access Key ID:
AKIAJHISMFYRI52ATWAA
Access Key ID can be found here: https://console.aws.amazon.com/iam/home?#security_credential

Secret Access Key:
.....
Secret Access Key can be found here: https://console.aws.amazon.com/iam/home?#security_credential

☐ Encrypt Access Keys with a password:
Turn this option on if you want to protect your Access Keys with a master password.

[Click here to sign up for Amazon S3.](#) Save changes Cancel

- Once done, you should be able to see the HCP datasets as shown below:

File	Size	Type	Last Modified	Storage Class
HCP/				

- For Linux, using the AWS Command Line Interface is an easier approach. You can follow the instructions [here](#) to install the **awscli** package for your system based on your OS and version of Python.

- Once installed, open a new terminal window and type

\$ aws configure

- You will be prompted to enter your access key ID and secret access key that you obtain with your credentials in the previous step. Once you enter these, you're good to go. Close the terminal
- To test if **awscli** has been installed correctly, type in a new terminal window

\$ aws s3 ls

- You should be able to see the HCP database as follows:

```
varsha@dti:~$ aws s3 ls
2018-11-05 16:53:55 hcp-openaccess
2018-07-26 02:49:34 hcp-openaccess-logfiles
2018-04-20 21:18:28 hcp-openaccess-logs-temp
2018-06-08 21:45:19 hcp-openaccess-logstorage-temp
2018-06-29 18:47:03 hcp-openaccess-test
2018-04-20 21:13:24 hcp-openaccess-trail-temp
```

- Detailed instructions can be found here and other information can be found [here](#).

Downloading HCP data from using Amazon S3

- **Windows**

- Launch the S3 browser, enter the folder called HCP/
- You will see a list of all the subjects whose data is available. Enter the folder for a subject and select the file to download. Click the download button at the bottom. You will be prompted to choose a download location. Navigate to your folder of choice and commence download.

- **Linux**

- Open a new terminal.
- To view the all the subjects' data available type
\$ aws s3 ls s3://hcp-openaccess/HCP_1200/
- You should see a list something like this:

```
varsha@dti:~$ aws s3 ls s3://hcp-openaccess/HCP_1200/
PRE 100206/
PRE 100307/
PRE 100408/
PRE 100610/
PRE 101006/
PRE 101107/
PRE 101309/
PRE 101410/
PRE 101915/
PRE 102008/
PRE 102109/
PRE 102311/
PRE 102513/
PRE 102614/
PRE 102715/
PRE 102816/
PRE 103010/
```

- Next, to view all the data for a given subject, say 100206, type
\$ aws s3 ls s3://hcp-openaccess/HCP_1200/100206/

```
varsha@dti:~$ aws s3 ls s3://hcp-openaccess/HCP_1200/100206/
PRE .xdlm/
PRE MNINonLinear/
PRE T1w/
PRE release-notes/
PRE unprocessed/
varsha@dti:~$
```


- To download a file, say for example the T1-weighted image which is in the T1w folder, type

```
$ aws s3 cp s3://hcp-openaccess/HCP_1200/100206/foldername/...  
filename path_to_destination
```

- To download the entire folder, type

```
$ aws s3 cp s3://hcp-openaccess/HCP_1200/100206/foldername/...  
path_to_destination --recursive
```

Where to find minimally preprocessed DTI data

What you will need:

1. T1-weighted image: T1w_acpc_dc_restore_brain.nii.gz (brain extracted image)
2. DTI data: data.nii.gz, bvals, bvecs
3. Optional: nodiff_brain_mask.nii.gz (brain mask), grad_dev.nii.gz
4. Freesurfer data: parcellations and segmentations

Where will you find it:

1. s3://hcp-openaccess/HCP_1200/subject_id/T1w/
2. s3://hcp-openaccess/HCP_1200/subject_id/T1w/Diffusion/
3. s3://hcp-openaccess/HCP_1200/subject_id/T1w/Diffusion/
4. s3://hcp-openaccess/HCP_1200/subject_id/T1w/subject_id/

It is recommended that you download the entire “Diffusion” folder. This will cover #2-3. For #4, there must be subfolders by the name **label/**, **mri/**, **surf/**, **stats/**, **touch/**. It is advised that you download all the subfolders.

Where to find minimally preprocessed fMRI data

What you will need:

1. T1-weighted image: T1w_acpc_dc_restore_brain.nii.gz (brain extracted image)
2. fMRI data: files for 2 rest scans and 7 task scans, each in L>>R and R>>L phase-encoding (total of 18 datasets)
3. Movement regressors and derivatives (optional): corresponding to each fMRI dataset

What will you find it:

1. s3://hcp-openaccess/HCP_1200/subject_id/T1w/
2. s3://hcp-openaccess/HCP_1200/100206/MNINonLinear/Results/rfMRI_REST1_LR/rfMRI_REST1_LR.nii.gz (first run of rest fMRI, say). There is one folder corresponding to each of the 18 datasets.
3. s3://hcp-openaccess/HCP_1200/100206/MNINonLinear/Results/rfMRI_REST1_LR/Movement_Regressors.txt, Movement_Regressors_dt.txt.