

## ADNI Data Training Part 2

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Department of Public Health Sciences

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# Outline

## Today's Presentation Outline

- Data overview
- Commonly used data (tables)
- Helpful tips about working with data
- Cross-validation
- IDA image data

## About ADNI Data

### Data organization

- RID: Participant roster ID.
- In general, data is 'long' format
  - ✓ One row per each visit (VISCODE)
  - ✓ Multiple rows belonging to same subject.

	A	B	C	D	E	F	G
1	ID	RID	SITEID	VISCODE	USERDATE	USERDATE	EXAMDAT
2	9216365	2	107	bl	1/17/2012		9/8/20C
3	9216367	2	107	m06	1/17/2012		3/6/20C
4	9216369	2	107	m36	1/17/2012		8/27/20C
5	9216371	3	107	bl	1/17/2012		9/12/20C
6	9216373	3	107	m06	1/17/2012		3/13/20C
7	9216375	3	107	m12	1/17/2012		9/12/20C
8	9216377	3	107	m24	1/17/2012		9/12/20C

# About ADNI Data

## Data organization

- Some exceptions in image data.

- ✓ ADNI1:

- Some MRI files have both 1.5T and 3T scans (FLDSTRENG or MRFIELD).
- Stroke, WMH file has one row per stroke (STROKESUM\_V2.csv and MRI\_INFARCTS.csv)
- FDG-PET: UC Berkeley has 5 different regions, one per row, for each visit.

- ✓ ADNIGO2:

- MRI files may include both accelerated and non-accelerated scans.
- MAYOADIRL\_MRI\_MCH.csv has one row per MR finding.

## About ADNI Data

### Visit code

- VISCODE
  - ✓ ADNI2 uses different convention.
  - ✓ ADNI2\_VISITID table links VISCODE to VISCODE2.
- VISCODE2
  - ✓ All phases use same convention(i.e. sc, bl, m06)
  - ✓ Not all data contains VISCODE2.

### Phase

- PHASE or COLPROT: ADNI1, GO or 2.
- Some files do not contain this variable. (i.e. PET data, MRI data)

## About ADNI Data

### Date variables

- EXAMDATE: date of the exam.
  - ✓ Most clinical data files do not have EXAMDATE for ADNI2.
  - ✓ Please extract EXAMDATE from REGISTRY table using RID and VISCODE.
- USERDATE: date of data entry (maybe very different from EXAMDATE).

### Missing values

- Missing data is coded with -1 and -4.
  - ✓ -4: 'passively' missing or not applicable.
  - ✓ -1: confirmed missing at point of data entry

# LONI: Download Data

You can download data from the **Download Study Data** page.

ADNI

ADNI @ LONI PROJECTS SEARCH DOWNLOAD EXPLORE LONI Home

Study Data Image Collections

## Download Study Data

Filter(s)

☐ Only include data that is new/changed since

☐ Select ALL tabular data (csv format)

☐ Select ALL documents and zip files (30.0 GB)

☐ Assessments

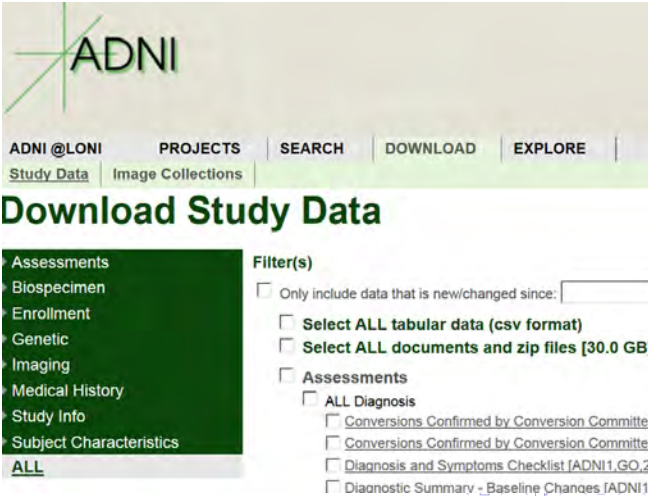
☐ ALL Diagnosis

- ☐ Conversions Confirmed by Conversion Committee (ADN11)
- ☐ Conversions Confirmed by Conversion Committee (ADN11)
- ☐ Diagnostic and Symptom Checklist (ADN11.G0.2)
- ☐ Diagnostic Summary - Baseline Changes (ADN11.G0.2)
- ☐ Diagnostic Summary (ADN11.G0.2)

☐ ALL Neuropsychological

- ☐ ADAS Sub-Scores and Total Scores (ADN11)
- ☐ Alzheimer's Disease Assessment Scale (ADAS) (ADN11)
- ☐ Alzheimer's Disease Assessment Scale (ADAS) (ADN11.G0.2)
- ☐ Clinical Dementia Rating Scale (CDR) (ADN11.G0.2)
- ☐ Everyday Cognition - Participant Self Report (ADN11.G0.2)
- ☐ Functional Activities Questionnaire (FAQ) (ADN11.G0.2)
- ☐ Genetic Depression Scale (GDS) (ADN11.G0.2)
- ☐ Item Level Data (ADAS-Cog, ANART, MMSE, etc)
- ☐ Item Level Data Dictionary
- ☐ Mini-Mental State Examination (MMSE) (ADN11.G0.2)
- ☐ Modifiedmachinski Ischemia Scale (ADN11.G0.2)
- ☐ Montreal Cognitive Assessment (MoCA) (ADN11.G0.2)

# Commonly Used Data



The screenshot shows the ADNI website interface. At the top is the ADNI logo. Below it is a navigation bar with links: ADNI @LONI, PROJECTS, SEARCH, DOWNLOAD, and EXPLORE. Under 'ADNI @LONI' are sub-links for 'Study Data' and 'Image Collections'. The main heading is 'Download Study Data'. On the left is a green sidebar menu with categories: Assessments, Biospecimen, Enrollment, Genetic, Imaging, Medical History, Study Info, Subject Characteristics, and ALL (which is highlighted). To the right of the sidebar is the 'Filter(s)' section. It includes a checkbox for 'Only include data that is new/changed since:' followed by an empty text box. Below that are two checkboxes: 'Select ALL tabular data (csv format)' and 'Select ALL documents and zip files [30.0 GB]'. There is also a checkbox for 'Assessments', which is expanded to show a list of data types: 'ALL Diagnosis', 'Conversions Confirmed by Conversion Committee' (two instances), 'Diagnosis and Symptoms Checklist [ADNI 1.GO.2]', and 'Diagnostic Summary - Baseline Changes [ADNI 1.1]'. At the bottom right of the filters are icons for a list, search, and refresh.

ADNI

ADNI @LONI PROJECTS SEARCH DOWNLOAD EXPLORE

Study Data Image Collections

## Download Study Data

- Assessments
- Biospecimen
- Enrollment
- Genetic
- Imaging
- Medical History
- Study Info
- Subject Characteristics
- ALL**

Filter(s)

☐ Only include data that is new/changed since:

☐ Select ALL tabular data (csv format)

☐ Select ALL documents and zip files [30.0 GB]

☐ Assessments

- ☐ ALL Diagnosis
  - ☐ Conversions Confirmed by Conversion Committee
  - ☐ Conversions Confirmed by Conversion Committee
  - ☐ Diagnosis and Symptoms Checklist [ADNI 1.GO.2]
  - ☐ Diagnostic Summary - Baseline Changes [ADNI 1.1]



# Commonly Used Data: Assessments

Assessments > Diagnosis

The screenshot shows the ADNI website interface. At the top, there is a navigation bar with links: ADNI @LONI, PROJECTS, SEARCH, DOWNLOAD, and EXPLORE. Below this, there are tabs for 'Study Data' and 'Image Collections'. The main heading is 'Download Study Data'. On the left, there is a sidebar menu under the heading 'Assessments'. The menu items are: Diagnosis (highlighted), Neuropsychological, ALL, Biospecimen, Enrollment, Genetic, Imaging, Medical History, Study Info, Subject Characteristics, and ALL. The main content area is titled 'Assessments: Diagnosis'. It includes a 'Filter(s)' section with a checkbox for 'Only include data that is new/changed since:' followed by a text input field. Below this is a 'Select Items' section with a checkbox for 'ALL' and a list of items with checkboxes: 'Conversions Confirmed by Conversion Committee Dictionary [ADNI1]', 'Conversions Confirmed by Conversion Committee [ADNI1]', 'Diagnosis and Symptoms Checklist [ADNI1.GO.2]', 'Diagnostic Summary - Baseline Changes [ADNI1.GO.2]', and 'Diagnostic Summary [ADNI1.GO.2]'. At the bottom left, there is a copyright notice: '© 2013 LONI. All rights reserved.'

## Commonly Used Data: Assessments

Assessments > Diagnosis

### Diagnostic Summary (DXSUM\_PDXCONV\_ADNIALALL.csv)

- Diagnosis by each visit code.
- ADNI1 and ADNIGO2 use different variables for diagnosis.
  - ✓ ADNI1: DXCURREN, DXCONV, DXREV, DXCONTYP.
  - ✓ ADNIGO2: DXCHANGE.
- If you use ADNIMERGE package, DXCHANGE is the only diagnosis variable.
- We will discuss more in the Working with Data section.

# Commonly Used Data: Assessments

Assessments > Neuropsychological

## Download Study Data

- Assessments
  - Diagnosis
  - Neuropsychological
  - ALL
- Biospecimen
- Enrollment
- Genetic
- Imaging
- Medical History
- Study Info
- Subject Characteristics
- ALL

### Assessments: Neuropsychological

#### Filter(s)

☐ Only include data that is new/changed since:

#### Select Items

☐ ALL

- ☐ ADAS Sub-Scores and Total Scores [ADNI1]
- ☐ Alzheimer's Disease Assessment Scale (ADAS) [ADNI1]
- ☐ Alzheimer's Disease Assessment Scale (ADAS) [ADNIGO.2]
- ☐ Clinical Dementia Rating Scale (CDR) [ADNI1.GQ.2]
- ☐ Everyday Cognition - Participant Self Report [ADNIGO.2]
- ☐ Functional Activities Questionnaire (FAQ) [ADNI1.GQ.2]
- ☐ Geriatric Depression Scale (GDS) [ADNI1.GQ.2]
- ☐ Item Level Data (ADAS-Cog, ANART, MMSE, etc)
- ☐ Item Level Data Dictionary
- ☐ Mini-Mental State Examination (MMSE) [ADNI1.GQ.2]
- ☐ Modified Hachinski Ischemia Scale [ADNI1.GQ.2]
- ☐ Montreal Cognitive Assessment (MoCA) [ADNIGO.2]
- ☐ Neuropsychiatric Inventory (NPI) [ADNI2]
- ☐ Neuropsychiatric Inventory Questionnaire (NPI-Q) [ADNI1.GQ.2]

## Commonly Used Data: Assessments

Assessments > Neuropsychological

### **ADAS Sub-Scores and Total Scores[ADNI1] (ADASSCORES.csv)**

- ADAS-cog sub and total scores in ADNI1.
- Key variables:
  - ✓ TOTAL11: 11 items score
  - ✓ TOTALMOD: 13 items score

### **Alzheimer's Disease Assessment Scale (ADAS)[ADNIGO,2] (ADAS\_ADNIGO2.csv)**

- ADAS-cog total scores in ADNIGO/2.
- Key variables:
  - ✓ TOTSCORE: 11 items score
  - ✓ TOTAL13: 13 items score

## Commonly Used Data: Assessments

Assessments > Neuropsychological

### Clinical Dementia Rating Scale(CDR) (CDR.csv)

- 6 domains and global scores are available.
  - ✓ CDMEMORY: memory , CDORIENT: orientation , CDJUDGE: judgement & problem solving , CDCOMMUN: community affairs , CDHOME: home and hobbies , CDCARE: personal care , CDGLOBAL: Global CDR

#### SAS example code to create CDRsum score

```
array cdr {*}cdmemory cdorient cdjudge cdcommun cdhome cdcare ;  
do j=1 to dim(cdr) ;  
  if cdr{j} in ( -1, -4 ) then cdr{j} = . ;  
end;  
if nmiss(of cdr{*})=0 then cdrsum = sum(of cdr{*}) ;  
label cdrsum = "Clinical Dementia Rating Sum " ;
```

## Commonly Used Data: Assessments

Assessments > Neuropsychological

### Everyday Cognition-Participant Self Report[ADNIGO,2] (ECOGPT.csv)

- Create each domain score by taking average (at least half of the items are not missing for each domain)
  - ✓ memory 8 items (memory1-memory8)
  - ✓ language 9 items (lang1-lang9)
  - ✓ visuo-spatial 7 items (visspat1-visspat4, visspat6-visspat8 : visspat5 is a duplicated field (see DATADIC.csv))
  - ✓ planning 5 items (plan1-plan5)
  - ✓ organization 6 items (organ1-organ6)
  - ✓ divided attention 4 items (divatt1-divatt4)
  - ✓ total score 39 items

## Commonly Used Data: Assessments

Assessments > Neuropsychological

### Functional Activities Questionnaires (FAQ.csv)

- FAQ item and total score.
  - ✓ FAQTOTAL: FAQ total score.

### Mini-Mental State Examination (MMSE.csv)

- MMSE item and total score.
  - ✓ MMSCORE: MMSE total score.

### Neuropsychological Battery (NEUROBAT.csv)

- All remaining neuropsychological test scores.

# Commonly Used Data: Biospecimen

## Biospecimen > Biospecimen Results



### Biospecimen: Biospecimen Results

#### Filter(s)

☐ Only include data that is new/changed since:

#### Select Items

☐ ALL

- ☐ ADNI Biomarker Core Laboratory, Baseline Isoprostanes Data Dic
- ☐ ADNI Biomarker Core Laboratory, Baseline Isoprostanes Data [AC
- ☐ ApoE - Results [ADNI1.GO.2]
- ☐ Biomarker Samples [ADNI1.GO.2]
- ☐ Biomarkers Consortium ADNI CSF BACE ACTIVITY and sAPPbe
- ☐ CSF - Local Lab Results [ADNI1.GO]
- ☐ CSF Multiplex Proteomics (Zip File)
- ☐ Homocysteine - Results [ADNI1.GO]
- ☐ Redox reactive autoantibodies
- ☐ Redox reactive autoantibodies Data Dictionary
- ☐ Redox reactive autoantibodies Methods (PDF)
- ☐ Rules Based Medicine Plasma Multiplex Data (Zipped file) [ADNI1
- ☐ Rules Based Medicine Plasma Multiplex QC Data Dictionary [ADN
- ☐ Rules Based Medicine Plasma Multiplex QC Data [ADNI1]
- ☐ Rules Based Medicine Plasma Multiplex Raw Data Dictionary [AD
- ☐ Rules Based Medicine Plasma Multiplex Raw Data [ADNI1]
- ☐ Serum Autoantibody Data - Set 1 of 1 (Zip file)



## Commonly Used Data: Biospecimen

Biospecimen > Biospecimen Results

### ApoE-Results (APOERES.csv)

- ApoE Genotyping Results
  - ✓ APGEN1: Genotype - Allele 1 (2,3, or 4)
  - ✓ APGEN2: Genotype - Allele 2 (2,3, or 4)
- PHASE: it has either 'ADNI1' or 'ADNIGO2'
- For ADNIGO2, it has missing values on VISCODE, SITEID, and APTESTDT(examdate) as of June 2013.

## Commonly Used Data: Biospecimen

Biospecimen > Biospecimen Results

### **UPENN CSF Data (ABETA, TAU, PTAU)**

- ✓ 4 sets of data from ADNI1, one dataset from ADNIGO/2, and one dataset from ADNI1/GO/2.
- ✓ Each data contains results of each analytical runs, so two data could have different values for the same subject at the same visit time..
- ✓ Researchers should only use values within the same file. (see LONI website Data FAQs)
- ✓ UPENNBIOMK5.csv file will be updated soon (from LONI Biomarker Core News as of July 23, 2013): Biomarker Core is re-anchoring the 2012 results using most recent data.

## Commonly Used Data: Biospecimen

Biospecimen > Biospecimen Results

### **UPENN-Biomarker Data (UPENNBIOMK.csv):**

- baseline abeta, tau, ptau for 415 ADNI1 subjects (+1 screening failed subject: RID=975)

### **UPENN-Longitudinal Data (UPENNBIOMK2.csv):**

- baseline&m12 abeta and tau for 417 ADNI1 subjects (92 subjects have missing value on m12)

### **UPENN-Longitudinal Data(3yr) (UPENNBIOMK3.csv):**

- baseline(n=103), m12(n=101), m24(n=87)&m36(n=23) abeta, tau, ptau for ADNI1 subjects.

## Commonly Used Data: Biospecimen

### **UPENN-Longitudinal Data(4yr) (UPENNBIOMK4.csv):**

- baseline(n=141), m12(n=138), m24(n=102), m36(n=78)&m48(n=33) abeta, tau, ptau for ADNI1 subjects (+1 screen failed subjects have bl,m12,m36: RID=975).

### **UPENN-CSF Biomarkers[ADNIGO2](UPENNBIOMK5.csv):**

- baseline abeta, tau, and ptau for 117 ADNIGO subjects and 271 ADNI2 subjects (+1 screen failed subject: RID=4124)
- This file will be available soon (as of Jul 23, 2013).

### **Second batch analysis of CSF (UPENNBIOMK6.csv):**

- longitudinal abeta, tau, ptau for 82 ADNI1 subjects (up to m84: 4 subjects), bl and m24 for 32 ADNIGO subjects(n=5 have missing bl), and baseline for 309 ADNI2 subjects.

## Commonly Used Data: Biospecimen

Biospecimen > Lab Collection Procedures

### Laboratory Data (LABDATA.csv)

- Screening clinical lab results (i.e. urine, chemistry panel).
- Data contains some character coding (i.e. SCC09: No specimen received ), and they can be treated as missing data.
- Currently, ADNI1/GO lab results are available on LONI. (ADNIMERGE package contains ADNI2 lab results also.)

# Commonly Used Data: Enrollment

Enrollment > Enrollment

The screenshot shows the ADNI website interface. At the top, there is a navigation bar with links: ADNI@LONI, PROJECTS, SEARCH, DOWNLOAD, and EXPLORE. Below this, there is a sub-navigation bar with links: Study Data and Image Collections. The main heading is 'Download Study Data'. On the left, there is a sidebar menu with categories: Assessments, Biospecimen, Enrollment (selected), Genetic, Imaging, Medical History, Study Info, Subject Characteristics, and ALL. Under the 'Enrollment' category, there is a sub-menu with the following items: Additional Comments [ADNI1.GO.2], ADNI 2 Visit Codes Assignment Methods (PDF), ADNI 2 Visit Codes Lookup [ADNI2], Arm [ADNI1.GO.2], Early Discontinuation and Withdrawal [ADNI1.GO.2], Exclusion Criteria [ADNI1], Inclusion Criteria [ADNI1], Registry [ADNI1.GO.2], Roster [ADNI1.GO.2], and Visits [ADNI1.GO.2]. The 'Enrollment: Enrollment' section is active, showing a 'Filter(s)' section with a checkbox for 'Only include data that is new/changed since:' followed by an empty text box. Below this is a 'Select Items' section with a checkbox for 'ALL' and a list of items with checkboxes: Additional Comments [ADNI1.GO.2], ADNI 2 Visit Codes Assignment Methods (PDF), ADNI 2 Visit Codes Lookup [ADNI2], Arm [ADNI1.GO.2], Early Discontinuation and Withdrawal [ADNI1.GO.2], Exclusion Criteria [ADNI1], Inclusion Criteria [ADNI1], Registry [ADNI1.GO.2], Roster [ADNI1.GO.2], and Visits [ADNI1.GO.2].

## Commonly Used Data: Enrollment

Enrollment > Enrollment

### ADNI2 Visit Codes Lookup[ADNI2] (ADNI2\_VISITID.csv)

- Visit code assignment for each ADNI2 subjects.

### ARM[ADNI1, GO, 2] (ARM.csv)

- Arm assignment
- EMCI and SMC information can be obtained.
  - ✓ ARM: 1=NL(ADNI1 1.5T only), 2=LMCI(ADNI1 1.5T only) ,  
3=AD(ADNI1 1.5T only) , 4=NL(ADNI1 PET+1.5T) ,  
5=LMCI(ADNI1 PET+1.5T) , 6=AD(ADNI1 PET+1.5T) ,  
7=NL(ADNI1 3T+1.5T) , 8=LMCI(ADNI1 3T+1.5T) ,  
9=AD(ADNI1 3T+1.5T) , 10=EMCI , 11=SMC

### Early Discontinuation and Withdrawal(TREATDIS.csv)

- list of subjects who discontinued from the study.

## Commonly Used Data: Enrollment

Enrollment > Enrollment

### Registry[ADNI1,GO,2](REGISTRY.csv)

- Contains important key variables.
  - ✓ EXAMDATE: date of assessment (clinical data for ADNIGO/2 do not include this field, so you need extract EXAMDATE from this table)
  - ✓ RGCONDCT: whether this visit was conducted (ADNI1)
  - ✓ PTSTATUS: whether active or discontinued from follow up.
  - ✓ RGSTATUS: whether screening visit was performed

### Roster[ADNI1,GO,2](ROSTER.csv)

- List for RID and PTID(ADNI subject ID: form of 123\_S\_5678)

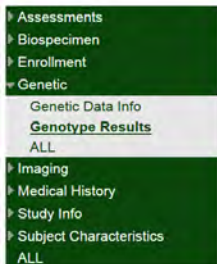
### Visits[ADNI1,GO,2](VISITS.csv)

- Dictionary of VISCODE. (ADNI2 use different convention.)



# Commonly Used Data: Genetic

## Genetic > Genetic Results



### Genetic: Genotype Results

#### Filter(s)

☐ Only include data that is new/changed since:

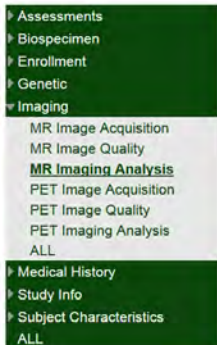
#### Select Items

☐ ALL

- ☐ ADNI 1 SNP genotype data - set 01 of 11 (CSV Format)
- ☐ ADNI 1 SNP genotype data - set 02 of 11 (CSV Format)
- ☐ ADNI 1 SNP genotype data - set 03 of 11 (CSV Format)
- ☐ ADNI 1 SNP genotype data - set 04 of 11 (CSV Format)
- ☐ ADNI 1 SNP genotype data - set 05 of 11 (CSV Format)
- ☐ ADNI 1 SNP genotype data - set 06 of 11 (CSV Format)
- ☐ ADNI 1 SNP genotype data - set 07 of 11 (CSV Format)
- ☐ ADNI 1 SNP genotype data - set 08 of 11 (CSV Format)
- ☐ ADNI 1 SNP genotype data - set 09 of 11 (CSV Format)
- ☐ ADNI 1 SNP genotype data - set 10 of 11 (CSV Format)
- ☐ ADNI 1 SNP genotype data - set 11 of 11 (CSV Format)
- ☐ ADNI GO/2 SNP genotype data - set 1 of 9 (CSV Format)
- ☐ ADNI GO/2 SNP genotype data - set 2 of 9 (CSV Format)
- ☐ ADNI GO/2 SNP genotype data - set 3 of 9 (CSV Format)
- ☐ ADNI GO/2 SNP genotype data - set 4 of 9 (CSV Format)
- ☐ ADNI GO/2 SNP genotype data - set 5 of 9 (CSV Format)
- ☐ ADNI GO/2 SNP genotype data - set 6 of 9 (CSV Format)

# Commonly Used Data: Imaging

## Imaging > MR Imaging Analysis



### Imaging: MR Imaging Analysis

#### Filter(s)

☐ Only include data that is new/changed since:

#### Select Items

☐ ALL

- ☐ Banner Alzheimer's Institute MRI NMRC Summaries Dictionary [A
- ☐ Banner Alzheimer's Institute MRI NMRC Summaries [ADNI1]
- ☐ Fox Lab BSI Measures Dictionary [ADNI1,GO,2] 1May2013
- ☐ Fox Lab BSI Measures Methods (PDF)
- ☐ Fox Lab BSI Measures [ADNI1,GO,2] 1May2013
- ☐ Mayo (Jack Lab) - Default Mode Network Connectivity 09May201
- ☐ Mayo (Jack Lab) - Default Mode Network Connectivity Dictionary
- ☐ Mayo (Jack Lab) - Task-Free fMRI Summary Metric of DMN ROIs
- ☐ Mayo (Jack Lab) - TBM-SyN Based Scores
- ☐ Mayo (Jack Lab) - TBM-SyN Based Scores Dictionary
- ☐ Mayo (Jack Lab) - TBM-SyN Based Scores Methods (PDF)
- ☐ Stroke Summary Dictionary Version 2 [ADNI1]
- ☐ Stroke Summary Version 2 [ADNI1]
- ☐ UA - MRI SPM Voxel Based Morphometry (VBM) Analysis Diction
- ☐ UA - MRI SPM Voxel Based Morphometry (VBM) Analysis [ADNI1
- ☐ UCD - Total Cranial Vault Segmentation Dictionary [ADNI1]
- ☐ UCD - Total Cranial Vault Segmentation Method and Grading Rub

## Commonly Used Data: Imaging

### Imaging > MR Imaging Analysis

- Data comes with its data dictionary and method paper.

Imaging: MR Imaging Analysis

**Filter(s)**

☐ Only include data that is new/changed since:

**Select Items**

☐ ALL

☐ Banner Alzheimer's Institute MRI NMRC Summaries Dictionary [ADNI1]

☐ Banner Alzheimer's Institute MRI NMRC Summaries [ADNI1]

**Data Dictionary**

**Method Paper**

**Data**

Lab BSI Measures Dictionary [ADNI1,GO,2] 1May2013

Fox Lab BSI Measures Methods (PDF)

Fox Lab BSI Measures [ADNI1,GO,2] 1May2013

Stroke Summary Dictionary Version 2 [ADNI1]

Stroke Summary Version 2 [ADNI1]

UA - MRI SPM Voxel Based Morphometry (VBM) Analysis Dictionary [ADNI1]

UA - MRI SPM Voxel Based Morphometry (VBM) Analysis [ADNI1]

# Commonly Used Data: Imaging

## Imaging > PET Imaging Analysis



### Imaging: PET Imaging Analysis

#### Filter(s)

☐ Only include data that is new/changed since:

#### Select Items

☐ ALL

- ☐ Banner Alzheimer's Institute NMRC Summaries Dictionary [ADNI:]
- ☐ Banner Alzheimer's Institute NMRC Summaries [ADNI1]
- ☐ Banner Alzheimer's Institute PET NMRC Summaries
- ☐ Banner Alzheimer's Institute PET NMRC Summaries Dictionary
- ☐ Banner Alzheimer's Institute PET NMRC Summaries Methods (PDF)
- ☐ Cross-Validation Dictionary [ADNI1]
- ☐ Cross-Validation [ADNI1]
- ☐ NYU FDG-PET Hippocampus (pons normalized)
- ☐ NYU FDG-PET Hippocampus (pons normalized) Dictionary
- ☐ NYU FDG-PET Hippocampus (pons normalized) Methods (PDF)
- ☐ sPAP Avid ADNI Florbetapir summaries
- ☐ sPAP Avid ADNI Florbetapir summaries dictionary
- ☐ sPAP Avid ADNI Florbetapir summaries Methods (PDF)
- ☐ UC Berkeley - AV45 analysis Dictionary [ADNIGO/2]
- ☐ UC Berkeley - AV45 analysis [ADNIGO/2]
- ☐ UC Berkeley - FDG Analysis 03Mar2013 [ADNI1, GO,2]
- ☐ UC Berkeley - FDG Analysis Dictionary 03Mar2013 [ADNI1, GO,2]

# Commonly Used Data: Study Info

## Study Info > Data & Database

The screenshot displays the 'Download Study Data' interface. At the top, there are two tabs: 'Study Data' (selected) and 'Image Collections'. Below the tabs, the main heading is 'Download Study Data'. On the left side, there is a vertical navigation menu with several categories: 'Assessments', 'Biospecimen', 'Enrollment', 'Genetic', 'Imaging', 'Medical History', 'Study Info' (highlighted in green), 'Data & Database' (sub-category of Study Info), 'Data Submission Standards', 'Study Protocols & CRFs', 'ALL' (sub-category of Study Info), 'Subject Characteristics', and 'ALL' (sub-category of Subject Characteristics). The main content area on the right is titled 'Study Info: ALL'. It contains a list of links, each preceded by a checkbox. The first checkbox is 'Select ALL'. Below this, there is a section titled 'Data & Databases' which contains a list of links, each preceded by a checkbox: 'ALL Data & Databases', 'ADNI 1.5T MRI Standardized Lists', 'ADNI 3T MRI Standardized Lists', 'Data Dictionary [ADNI1.GO.2]', 'Key ADNI tables merged into one table', 'Key ADNI tables merged into one table - Dictionary', 'Merged ADNI 1/GO/2 Methods (PDF)', 'Merged ADNI 1/GO/2 Packages for R', 'Merged ADNI 1/GO/2 Packages for SAS', 'Merged ADNI 1/GO/2 Packages for SPSS', 'Merged ADNI 1/GO/2 Packages for Stata', and 'Return of Research Results'. Below this list is a section titled 'Data Submission Standards' which contains a list of links, each preceded by a checkbox: 'ALL Data Submission Standards', 'ADNI Methods Template (DOCX)', and 'Data Submission Metadata Standard (PDF)'. At the bottom of the main content area is a section titled 'Study Protocols & CRFs'.

Study Data | Image Collections

## Download Study Data

- Assessments
- Biospecimen
- Enrollment
- Genetic
- Imaging
- Medical History
- Study Info
  - Data & Database
  - Data Submission Standards
  - Study Protocols & CRFs
  - ALL
- Subject Characteristics
  - ALL

Study Info: ALL

- ☐ Select ALL

Data & Databases

- ☐ ALL Data & Databases
  - ☐ ADNI 1.5T MRI Standardized Lists
  - ☐ ADNI 3T MRI Standardized Lists
  - ☐ Data Dictionary [ADNI1.GO.2]
  - ☐ Key ADNI tables merged into one table
  - ☐ Key ADNI tables merged into one table - Dictionary
  - ☐ Merged ADNI 1/GO/2 Methods (PDF)
  - ☐ Merged ADNI 1/GO/2 Packages for R
  - ☐ Merged ADNI 1/GO/2 Packages for SAS
  - ☐ Merged ADNI 1/GO/2 Packages for SPSS
  - ☐ Merged ADNI 1/GO/2 Packages for Stata
  - ☐ Return of Research Results

Data Submission Standards

- ☐ ALL Data Submission Standards
  - ☐ ADNI Methods Template (DOCX)
  - ☐ Data Submission Metadata Standard (PDF)

Study Protocols & CRFs

## Commonly Used Data: Study Info

Study Info > Data & Database

**ADNI 1.5T MRI Standardized Lists**  
(ADNI\_1.5T\_MRI\_Standardized\_Lists.zip)

**ADNI 3T MRI Standardized Lists**  
(ADNI\_3T\_MRI\_Standardized\_Lists.zip)

- Standardized analysis sets of volumetric scans from ADNI1.

**Data Dictionary[ADNI1,GO,2] (DATADIC.csv)**

- Data dictionary of most of data on LONI.

## Commonly Used Data: Study Info

Study Info > Data & Database

### Key ADNI tables merged into one table (ADNIMERGE.csv)

- contains some of the key variables in one table.

### Merged ADNI1/GO/2 Packages

- ADNI Merge packages for R, SAS, SPSS, and Stata. (we will talk more about ADNIMERGE packages later)

# Commonly Used Data: Subject Characteristics

## Subject Characteristics

ADNI @LONI PROJECTS SEARCH DOWNLOAD EXPLORE

[Study Data](#) | Image Collections

## Download Study Data

- Assessments
- Biospecimen
- Enrollment
- Genetic
- Imaging
- Medical History
- Study Info
- Subject Characteristics**
  - Family History
  - Subject Demographics
  - ALL
  - ALL

Subject Characteristics: ALL

**Filter(s)**

☐ Only include data that is new/changed since:

☐ **Select ALL**

**Family History**

☐ ALL Family History

☐ Family History Questionnaire Subtable [ADNI1.GO.2]

☐ Family History Questionnaire [ADNI1.GO.2]

**Subject Demographics**

☐ Subject Demographics [ADNI1.GO.2]

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# Commonly Used Data: Subject Characteristics

## Subject Characteristics

### Family History Questionnaire (FHQ.csv)

- information of parents and if they have siblings.
- yes=1/no=0/don't know=2 if their mother or father have dementia or having AD.

### Family History Questionnaire Subtable (RECFHQ.csv)

- information of siblings (if they have siblings in FHQ.csv).
- yes=1/no=0/don't know=2 if they have dementia or having AD (one row per each sibling).

### Subject Demographics (PTDEMOG.csv)

- Demographic information at screening (for each phase).

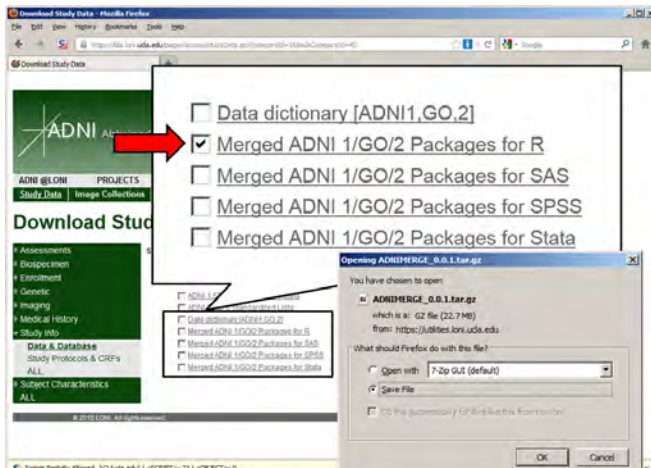
## ADNIMERGE Packages

What is the ADNIMERGE package?

- This loads all ADNI data (except genetic data).
- R, SAS, Stata and SPSS versions are available.
- Mike Donohue from UC San Diego wrote R code to store R dataframes in SAS, Stata, and SPSS.
- It includes 'adnimerge' data which contains commonly used variables. This single csv file is also available to download. (i.e. demographic, clinical exam, MRI and PET variables)
- Labels & formatting have been incorporated in R, SAS, Stata.
- ADNIMERGE packages are updated daily.

## ADNIMERGE: R users

Download ADNIMERGE\_0.0.1.tar.gz

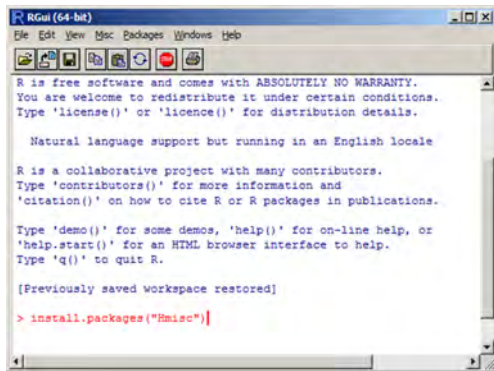


## ADNIMERGE: R users

Open R.

Install Hmisc package if it is not installed already.

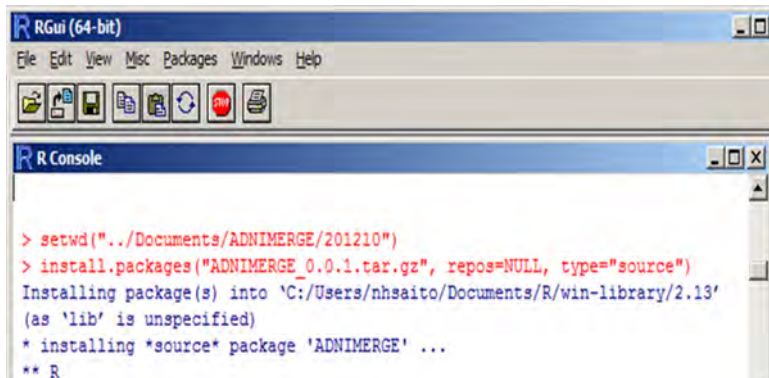
```
install.packages("Hmisc")
```



## ADNIMERGE: R users

Install the ADNIMERGE package which you have downloaded.

```
install.packages("../your path/ADNIMERGE_0.0.1.tar.gz",  
repos=NULL, type="source")
```



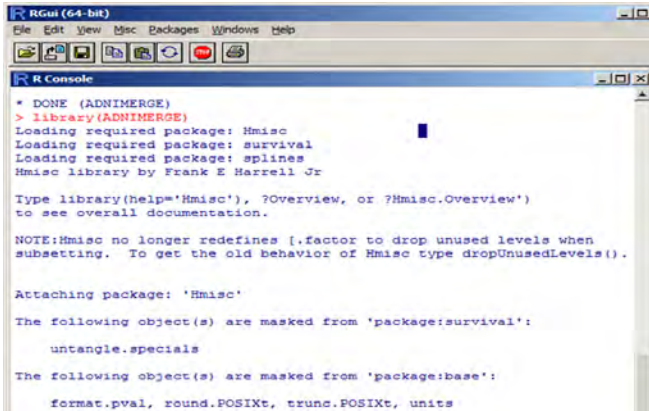
The screenshot shows the RGui (64-bit) window. The menu bar includes File, Edit, View, Misc, Packages, Windows, and Help. Below the menu bar is a toolbar with icons for file operations and package management. The R Console window is open, displaying the following text:

```
> setwd("../Documents/ADNIMERGE/201210")  
> install.packages("ADNIMERGE_0.0.1.tar.gz", repos=NULL, type="source")  
Installing package(s) into 'C:/Users/nhsaito/Documents/R/win-library/2.13'  
(as 'lib' is unspecified)  
* installing *source* package 'ADNIMERGE' ...  
** R
```

## ADNIMERGE: R users

To load the ADNIMERGE package.

```
library(ADNIMERGE)
```



```
RGui (64-bit)
File Edit View Misc Packages Windows Help

R Console

* DONE (ADNIMERGE)
> library(ADNIMERGE)
Loading required package: Hmisc
Loading required package: survival
Loading required package: splines
Hmisc library by Frank E Harrell Jr

Type library(help='Hmisc'), ?Overview, or ?Hmisc.Overview')
to see overall documentation.

NOTE:Hmisc no longer redefines [.factor to drop unused levels when
subsetting. To get the old behavior of Hmisc type dropUnusedLevels().

Attaching package: 'Hmisc'

The following object(s) are masked from 'package:survival':

    untangle.specials

The following object(s) are masked from 'package:base':

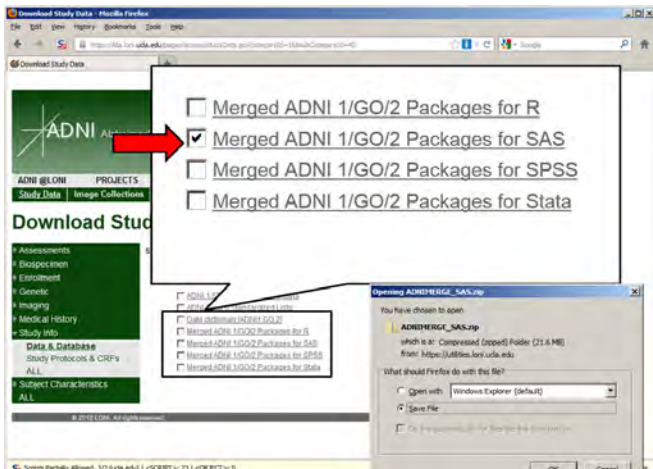
    format.pval, round.POSIXt, trunc.POSIXt, units
```

## ADNIMERGE: R users

- To see the documentation, `help(package="ADNIMERGE")`.
- ADNIMERGE package loads all ADNI data, so you can start working with individual tables.
  - ✓ One of the loaded items is the `adnimerge` dataframe which contains commonly used variables. (i.e. demographics, clinical exam, MRI and PET)
- For more information, from Windows Explorer, you can open/extract `ADNIMERGE_0.0.1.tar.gz` file using 7-zip. (7-zip is an open source file archiver designed for Windows.)
  - ✓ You see `data`, `inst`, `man`, `R` folders; `inst` folder contains useful examples.
  - ✓ `README` file contains instructions for how to use the package.

## ADNIMERGE: SAS users

Download ADNIMERGE\_SAS.zip

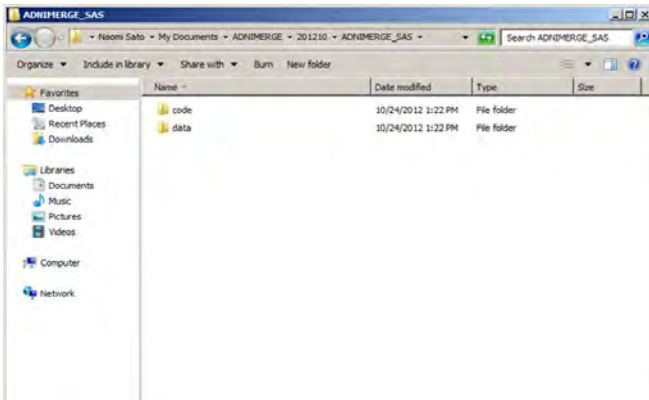




## ADNIMERGE: SAS users

Extract ADNIMERGE\_SAS.zip file.

Under ADNIMERGE\_SAS folder, you will find code folder and data folder.

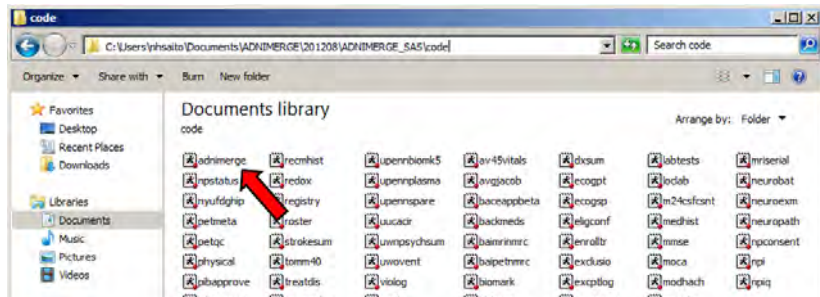


## ADNIMERGE: SAS users

In the code folder, there are more than 120 SAS programs.

For example, we can open `adnimerge.sas`.

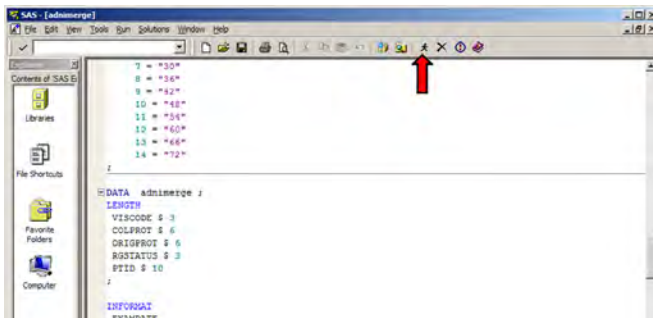
- The simplest method is double-click on `adnimerge.sas`.
- This initiates SAS and opens the programming file.
- This also sets the working directory under the code folder.



## ADNIMERGE: SAS users

You can Run the program.

- Because we set the working directory under the code folder, the program can call the data file correctly.
- SAS will create data called adnimerge under SAS's Work library.

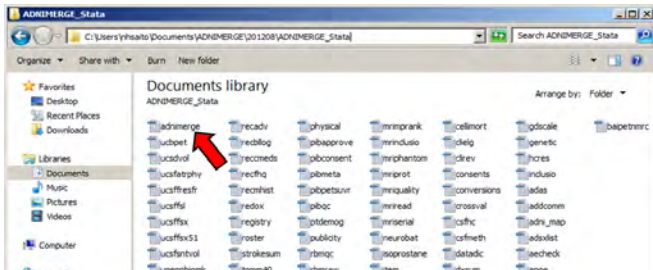


## ADNIMERGE: Other users

SPSS package is similar to SAS packages.

Stata users:

- After you extract zip file, you will see more than 120 Stata data(.dta).
- The simplest method: double click the data you want to open, and it initiates Stata and opens data.



## Useful Tips for Using ADNI Data

- Common variables for linking tables
  - ✓ RID
  - ✓ VISCODE (or VISCODE2)
  - ✓ EXAMDATE (date of assessment)
- VISCODE='f' means the subject failed screening (ADNI1).
- RID can tell which PHASE enrolled subject initially.
  - ✓  $RID < 2000$ : ADNI1 subjects
  - ✓  $2000 \leq RID < 4000$ : ADNIGO subjects
  - ✓  $RID \geq 4000$ : ADNI2 subjects
- About EXAMDATE
  - ✓ Clinical data in ADNIGO2 do not include EXAMDATE.
  - ✓ Use REGISTRY.csv to extract EXAMDATE for clinical data.

## Useful Tips for Using ADNI Data

Before analyzing data, taking following steps may be helpful.

1. DXSUM data: Since ADNI1 and ADNIGO2 use different variables for diagnosis, assign the diagnosis variable:DXCHANGE for ADNI1.
2. Merge DXSUM and ARM tables and assign baseline diagnosis (including EMCI/SMC).
3. Merge REGISTRY and DXSUM/ARM tables to have EXAMDATE for all visits.

Note: We can identify EMCI or SMC at baseline (or screening) time only. The variable: DXCHANGE is available for follow-up visits, and it tells us either Normal, MCI, or AD.

## Useful Tips for Using ADNI Data

1: Use ADNI1 diagnosis variables to assign DXCHANGE.  
(DXSUM\_PDXCONV\_ADNIALL)

- ADNI1 diagnosis variables are following:
  - ✓ DXCURRENT: 1=NL, 2=MCI, 3=AD.
  - ✓ DXCONV: 0=No, 1=Yes-Conversion, 2=Yes-Reversion.
  - ✓ DXREV: 1=MCI to Normal, 2=AD to MCI, 3=AD to Normal.
  - ✓ DXCONTYP: 1=Normal to MCI, 2=Normal to AD, 3=MCI to AD.
- ADNIGO 2 diagnosis variable:
  - ✓ DXCHANGE: 1=Stable:NL to NL, 2=Stable:MCI to MCI, 3=Stable:AD to AD, 4=Conv:NL to MCI, 5=Conv:MCI to AD, 6=Conv:NL to AD, 7=Rev:MCI to NL, 8=Rev:AD to MCI, 9=Rev:AD to NL.

## Example code

### R example code to assign DXCHANGE for ADNI1

```
dxsum = read.csv("DXSUM_PDXCONV_ADNIALALL.csv")
attach(dxsum)
dxsum$DXCHANGE[DXCONV==0 & DXCURREN==1] = 1
dxsum$DXCHANGE[DXCONV==0 & DXCURREN==2] = 2
dxsum$DXCHANGE[DXCONV==0 & DXCURREN==3] = 3
dxsum$DXCHANGE[DXCONV==1 & DXCONTYP==1] = 4
dxsum$DXCHANGE[DXCONV==1 & DXCONTYP==3] = 5
dxsum$DXCHANGE[DXCONV==1 & DXCONTYP==2] = 6
dxsum$DXCHANGE[DXCONV==2 & DXREV==1] = 7
dxsum$DXCHANGE[DXCONV==2 & DXREV==2] = 8
dxsum$DXCHANGE[DXCONV==2 & DXREV==3] = 9
detach(dxsum)
```



## Useful Tips for Using ADNI Data

2: Assign baseline diagnosis: including EMCI and SMC.

- Merge DXSUM\_PDXCONV\_ADNIALL and ARM tables using RID and PHASE.
- Keep key variables.
  - ✓ DXSUM: RID, PHASE, VISCODE, VISCODE2, DXCHANGE.
  - ✓ ARM: RID, PHASE, ARM, ENROLLED.
- Use baseline DXCHANGE and ARM to assign baselineDX variable.  
(see code in next slides)

## Example code

### SAS example code to merge ARM and DXSUM

```
* sort data first ;  
PROC SORT DATA=dxsum;  
  BY rid phase;  
PROC SORT DATA=arm;  
  BY rid phase;  
RUN;  
  
* merge data;  
DATA dxarm;  
  MERGE dxsum(KEEP=rid phase viscode viscode2 dxchange)  
        dxarm(KEEP=rid phase arm enrolled);  
  BY rid phase;  
RUN;
```

## Example code

### SAS example code to create baseline diagnosis

```
DATA baseData;  
  SET dxarm(WHERE= (viscode2='bl' and enrolled in(1,2,3)));  
  * pls format them as 1:Normal,2:SMC,3:EMCI,4:LMCI,5:AD,;  
  IF dxchange in(1,7,9) & arm NE 11 THEN baselineDx=1;  
  ELSE IF dxchange in(1,7,9) & arm=11 THEN baselineDx=2;  
  ELSE IF dxchange in(2,4,8) & arm=10 THEN baselineDx=3;  
  ELSE IF dxchange in(2,4,8) & arm NE 10 THEN baselineDx=4;  
  ELSE IF dxchange in(3,5,6) THEN baselineDx=5;  
RUN;  
  
* merge baseline diagnosis data and dxarm;  
DATA dxarm;  
  MERGE dxarm baseData(KEEP = rid baselineDx);  BY rid;  
RUN;
```

## Example code

### R example code to merge ARM and DXSUM

```
# readin csv files
arm <- read.csv("ARM.csv")

# identify variable to keep for merged data
armVars <- c("RID","Phase","ARM","ENROLLED")
dxsumVars <- c("RID","Phase","VISCODE", "VISCODE2",
"DXCHANGE")

# merge data
dxarm <- merge(subset(dxsum, select=dxsumVars), subset(arm,
select=armVars), by=c("RID", "Phase"))
# baseline data
baseData <- dxarm[dxarm$VISCODE2=='bl' & dxarm$ENROLLED
%in% c(1,2,3),]
```

## Example code

### R example code to assign baseline diagnosis

```
# assign baseline diagnosis

attach(baseData)
baseData$baselineDx[(DXCHANGE %in% c(1,7,9)) & ARM != 11 ] = 1
baseData$baselineDx[(DXCHANGE %in% c(1,7,9)) & ARM == 11 ] = 2
baseData$baselineDx[(DXCHANGE %in% c(2,4,8)) & ARM == 10 ] = 3
baseData$baselineDx[(DXCHANGE %in% c(2,4,8)) & ARM != 10 ] = 4
baseData$baselineDx[(DXCHANGE %in% c(3,5,6)) ] = 5
detach(baseData)

# merge baseline diagnosis
baseVars <- c("RID", "baselineDx")
dxarm <- merge( dxarm, subset(baseData, select=baseVars),
by=c("RID"))
```

## Useful Tips for Using ADNI Data

### 3: Keep EXAMDATE.

- Merge REGISTRY table and merged ARM/DXSUM table using RID, PHASE, and VISCODE.
- Keep key variables
  - ✓ REGISTRY: PHASE, RID, VISCODE, VISCODE2, EXAMDATE, PTSTATUS, RGCONDCT, RGSTATUS, VISTYPE.
- EXAMDATE in REGISTRY table is necessary when you merge with other clinical data for ADNIGO/2.

## Example code

### SAS example code to merge ARM/DXSUM and REGISTRY

```
* sort data first ;  
PROC SORT DATA=dxarm;  
  BY rid phase viscode;  
PROC SORT DATA=registry;  
  BY rid phase viscode;  
RUN;  
  
* merge data;  
DATA dxarm_reg;  
  MERGE registry(KEEP=rid phase viscode viscode2 examdate ptstatus  
    rgconduct rgstatus vistype) dxarm;  
  BY rid phase viscode;  
RUN;
```

## Example code

### R example code to merge ARM/DXSUM and REGISTRY

```
# readin csv files
registry <- read.csv("REGISTRY.csv")

# identify variable to keep for merged data
regVars <-c("RID", "Phase", "VISCODE", "VISCODE2",
"EXAMDATE", "PTSTATUS", "RGCONDUCT", "RGSTATUS",
"VISTYPE")

# merge data
dxarm_reg <- merge(dxarm, subset(registry, select=regVars),
by=c("RID", "Phase", "VISCODE"))
```



# Identify subjects in ADNI1

## ADNI1 Study

- 822 subjects passed screening but only 819 had baseline observation.
  - Identified by PHASE='ADNI1', VISCODE='bl', and RGCONDUCT=1 in merged REGISTRY/DXSUM/ARM table.
- Randomized to one of 3 arms and baseline diagnosis.

ARM	NL	MCI	AD	Total
1.5T Only	59	94	44	197
PET + 1.5T	107	210	102	419
3T + 1.5T	63	93	47	203
<b>Total</b>	229	397	193	819

## Identify subjects in ADNI1

### ADNI1 Study

- Lumbar puncture was not mandatory, and we have 415 subjects with baseline CSF in UPENNBBIOMK.csv

	NL	MCI	AD	Total
<b>Baseline CSF</b>	114	199	102	415

- All 819 subjects have ApoE Genotyping results (APOERES.csv)

## Identify subjects in ADNIGO

### ADNIGO Study

- New 128 subjects had baseline observation (Note: 127 EMCI, 1 subject reversion to Normal at baseline).
  - Identified by PHASE='ADNIGO', VISCODE='bl', and PTSTATUS=1(Active) in merged REGISTRY/DXSUM/ARM table(N=131). However, 3 subjects (RID:2071, 2314, 2351) were noted as early withdrawal at baseline (per TREATDIS.csv), and they don't have diagnosis at baseline.

## Identify subjects in ADNIGO

### ADNIGO Study

- 208 subjects from ADNI1 (originally enrolled as Normal or MCI) continued to ADNIGO.
  - 208 unique subjects after identified by PHASE='ADNIGO', PTSTATUS=1 (Active), RID<2000, and DXCHANGE is not missing in merged REGISTRY/DXSUM/ARM table (N=221 including repeated observations)
  - ADNI1 subjects moved to ADNIGO at month 36, month 48 or month 60.

## Identify subjects in ADNI2

### ADNI2 Study (As of July 1 2013)

- New 925 subjects had **screening** observation (Normal:N=262, SMC:N=49, EMCI:N=234, LMCI:N=217, AD:N=163), and N=655 had **baseline** (Normal:N=187, SMC:N=13, EMCI:N=175, LMCI:N=160, AD:N=120).
- Identified using merged REGISTRY/DXSUM/ARM by PHASE='ADNI2', VISCODE='v01'(screening) or 'v03'(baseline), RGSTATUS=1(Active), and DXCHANGE is not missing.

## Identify subjects in ADNI2

### ADNI2 Study (As of July 1 2013)

- ADNI1 subjects: N=258 continued to ADNI2.
- ADNIGO subjects: N=115 continued to ADNI2.
- Identified using merged REGISTRY/DXSUM/ARM by PHASE='ADNI2', VISCODE='v06'(ADNI2 Initial Visit-continuing Pt), RGSTATUS=1(Active), and DXCHANGE is not missing. (RID=751 has missing on DXCHANGE at v06; telephone visit only)

## Identify subjects: convert from NL to MCI

Create data contains NL to MCI converters using the variables:  
DXCHANGE(4:Conv:NL to MCI) and baselineDX=1(NL).

### SAS example code to identify NL to MCI converters

```
* sort data first ;  
PROC SORT DATA = dxarm_reg;  
  BY rid examdate;  
RUN;  
  
* output rid and visit time where first time dxchange=4 appeared;  
DATA conv_to_MCI(KEEP = rid dxchange phase viscode);  
  SET dxarm_reg(WHERE=( dxchange=4 and baselineDX=1));  
  BY rid;  
  IF FIRST.rid THEN OUTPUT;  
RUN;
```

## Identify subjects: having CSF results

Create data contains subjects who are in the newest data:  
UPENNBIOMK6.csv (contains ADNI1,GO,2 results) (Note: VISCODE in this data is VISCODE2)

### SAS example code to merge CSF and dxarm\_reg

```
PROC SORT DATA = upennbiomk6;  
  BY rid viscode;  
PROC SORT DATA = dxarm_reg;  
  BY rid viscode2; RUN;  
  
DATA upennbiomk6_dx;  
  MERGE dxarm_reg upennbiomk6(RENAME = (viscode = viscode2)) ;  
  BY rid viscode2;  
  IF abeta=. AND tau=. AND ptau=. THEN DELETE;  
RUN;
```



# Cross-validation

What is cross validation?

- Cross validation is a model evaluation method.
- Goal is to avoid over fitting; the model to be generalizable.
- Divide the data into training (to build the model) and test (to evaluate the model) set.
- There are several different ways to validate:
  - Hold-out validation (single train-and-test validation)
  - K-fold cross-validation (a common choice is  $K=10$ )
  - Leave-one-out cross-validation (leave one observation out at time; fit the model on the remaining training data)

## Cross-validation

### CROSSVAL.csv

- Currently, Cross validation file is under Imaging> PET Imaging Analysis.
- The file contains two variables (TRAINING, SET\_ID) to separate ADNI1 subjects into partitions.
- For assigning partitions, all ADNI1 subjects were stratified by:
  - Diagnosis: NC, MCI, AD.
  - Study Arm: 1.5T only, PET+ 1.5T, 1.5T and 3T.
  - Young (<76) vs old (>76).
- TRAINING: 40% of subjects are chosen for a training dataset (TRAINING=1), and 60% for a test dataset (TRAINING=0).
- SET\_ID: Subjects are divided into 10 parts. (a,b,c,...i,j)

# Cross-validation

Why do we need this file?

- Some imaging labs developed/identified an ROI using subjects in training set, so analysis should focus on subjects in the test set. (TBM.csv and BAINMRC.csv use this approach.)
- Some researchers may want to use these assignments in their own cross validation analysis.
- After enrollment closes for ADNI2, we will be posting similar assignment for ADNIGO2 participants.

# Cross-validation

Example: 10-fold Cross-validation

1. Merge ADNI1 data and CROSSVAL.csv using RID.
2. SET\_ID variable divides data into 10 parts
3. Set training(9/10) and test(1/10) datasets.
4. Fit the model using training data.
5. Apply the fitted model to the test data.
6. Repeat step 3,4&5 for all 10 sets of the data.
7. Calculate statistics of model accuracy/fit from the test data.

## Image Data Archive

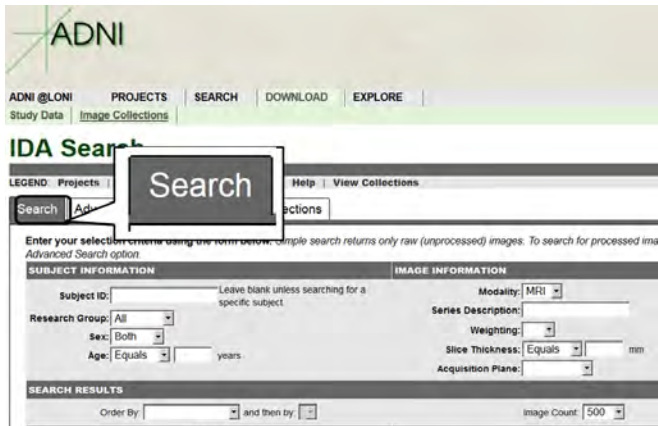
The Image Data Archive (IDA) system allows authorized users to download MRI/PET images.

From **Download Study Data** page click **Image Collections**.



## Image Data Archive

**Search** tab: Enables you to search the image database.  
This search returns a list of raw images.



The screenshot shows the ADNI IDA Search interface. At the top, the ADNI logo is displayed. Below it, a navigation bar includes links for ADNI @LONI, PROJECTS, SEARCH, DOWNLOAD, and EXPLORE. A secondary bar shows 'Study Data' and 'Image Collections'. The main heading is 'IDA Search'. A callout box with the word 'Search' points to the 'Search' button in the 'LEGEND Projects' section. Below this, a text box instructs users to enter selection criteria. The search form is divided into two columns: 'SUBJECT INFORMATION' and 'IMAGE INFORMATION'. The 'SUBJECT INFORMATION' column includes fields for Subject ID, Research Group (set to 'All'), Sex (set to 'Both'), and Age (set to 'Equals' with a blank space for years). The 'IMAGE INFORMATION' column includes fields for Modality (set to 'MRI'), Series Description, Weighting, Slice Thickness (set to 'Equals' with a blank space for mm), and Acquisition Plane. At the bottom, there is a 'SEARCH RESULTS' section with an 'Order By' dropdown and an 'Image Count' dropdown set to '500'.

ADNI

ADNI @LONI PROJECTS SEARCH DOWNLOAD EXPLORE

Study Data Image Collections

IDA Search

LEGEND Projects Search Advanced Search

Help View Collections

Enter your selection criteria using the form below. Simple search returns only raw (unprocessed) images. To search for processed images, use the Advanced Search option.

SUBJECT INFORMATION	IMAGE INFORMATION
Subject ID: <input type="text"/> Leave blank unless searching for a specific subject	Modality: <input type="text" value="MRI"/>
Research Group: <input type="text" value="All"/>	Series Description: <input type="text"/>
Sex: <input type="text" value="Both"/>	Weighting: <input type="text"/>
Age: <input type="text" value="Equals"/> years	Slice Thickness: <input type="text" value="Equals"/> mm
	Acquisition Plane: <input type="text"/>

SEARCH RESULTS

Order By:  and then by:

Image Count:

The screenshot shows the IDA Search interface. At the top, there's a navigation bar with 'LEGEND: Projects | Research Groups | Modalities | Help | View Collections'. Below this is a search bar with 'Search', 'Advanced Search (beta)', 'Search Results' (highlighted), and 'Data Collections' tabs. A large red arrow points down from the 'Search Results' tab to a table of results. A callout box with the text 'Search Results' is also present. The table has columns: Subject, Research Group, Sex, Scan Date, Age, Modality, Series Description, Field Strength, Slice Thickness, View, and Select All. The results show multiple entries for 'Resting State fMRI' with various subjects and scan dates.

Subject	Research Group	Sex	Scan Date	Age	Modality	Series Description	Field Strength	Slice Thickness	View	Select All
002_S_0295	Patient	M	6/02/2011	90	fMRI	Resting State fMRI	3.0	3.3	<a href="#">VIEW</a>	<input checked="" type="checkbox"/>
002_S_0295	Patient	M	5/10/2012	91	fMRI	Resting State fMRI	3.0	3.3	<a href="#">VIEW</a>	<input checked="" type="checkbox"/>
002_S_0413	Patient	F	6/16/2011	82	fMRI	Resting State fMRI	3.0	3.3	<a href="#">VIEW</a>	<input checked="" type="checkbox"/>
002_S_0413	Patient	F	5/15/2012	82	fMRI	Resting State fMRI	3.0	3.3	<a href="#">VIEW</a>	<input checked="" type="checkbox"/>
002_S_0413	Patient	F	5/10/2013	83	fMRI	Resting State fMRI	3.0	3.3	<a href="#">VIEW</a>	<input checked="" type="checkbox"/>
002_S_0685	Patient	F	7/08/2011	95	fMRI	Resting State fMRI	3.0	3.3	<a href="#">VIEW</a>	<input checked="" type="checkbox"/>
002_S_0685	Patient	F	7/27/2012	96	fMRI	Resting State fMRI	3.0	3.3	<a href="#">VIEW</a>	<input checked="" type="checkbox"/>
						Resting State fMRI	3.0	3.3	<a href="#">VIEW</a>	<input checked="" type="checkbox"/>
002_S_0729	Patient	F	8/16/2011	70	fMRI	Resting State fMRI	3.0	3.3	<a href="#">VIEW</a>	<input checked="" type="checkbox"/>
002_S_0729	Patient	F	8/07/2012	71	fMRI	Resting State fMRI	3.0	3.3	<a href="#">VIEW</a>	<input checked="" type="checkbox"/>

## Image Data Archive

**Data Collections** tab: Choose format and download images.

**CSV Download:** The file contains image info, age, gender, etc.

### IDA Search

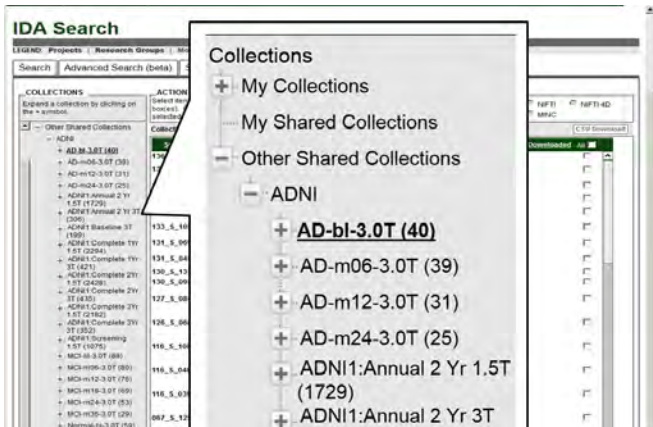
The screenshot shows the IDA Search web application interface. The 'Data Collections' tab is selected, and a red arrow points to the 'CSV Download' button. A table of image data is visible below the table.

Modality	Description	Time	Acq. Date	Format	Download	
Resting State fMRI	002_S_2010Patient	F	63	14	fMRI	<input checked="" type="checkbox"/>
Resting State fMRI	002_S_2010Patient	F	64	3	fMRI	<input checked="" type="checkbox"/>
Resting State fMRI	002_S_2010Patient	F	63	15	fMRI	<input checked="" type="checkbox"/>
Resting State fMRI	002_S_2010Patient	F	64	26	fMRI	<input checked="" type="checkbox"/>
Resting State fMRI	002_S_1280Patient	F	75	10	fMRI	<input checked="" type="checkbox"/>
Resting State fMRI	002_S_1280Patient	F	76	26	fMRI	<input checked="" type="checkbox"/>
Resting State fMRI	002_S_1280Patient	F	77	28	fMRI	<input checked="" type="checkbox"/>



## Image Data Archive

Under **COLLECTIONS** , you see **Other Shared Collections** where you can also download collection of images by diagnosis/visit.



## Image Data Archive

**Advanced Search(beta):** You can search for images by sex, diagnosis, clinical info(MMSE, CDR, NPI, etc), visit(baseline, month6, etc.), and image protocols.

**Advanced Search (beta)**

ADNI @ LONI PROJECTS SEARCH DOWNLOAD - EXPLORE LONI Home

Study Data Image Collections

**IDA Search**

LEGEND Projects Research Groups

Search Advanced Search (beta)

**Search 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

**Search Criteria**

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

**PROJECT/PHASE**

Projects ☒ ADNI

Phase ☐ ADNI 1 ☐ ADNI GO ☐ ADNI 2

**SUBJECT**

Subject ID \*  Separate multiple Subject ID's by commas ☐

Age (years)  Equals  ☐

Sex  Both ☐

Weight (kgs)  Equals  ☐

Research Group ☐ Patient ☐ Volunteer ☐ Phantom ☐

**SUBJECT SPECIFIC INFORMATION**

DX Group ☐ AD ☐ EMCI ☐ LMCI ☐ MCI ☐ Normal ☐

APOE A1 ☐ 2 ☐ 3 ☐ 4 ☐

APOE A2 ☐ 2 ☐ 3 ☐ 4 ☐

**ASSESSMENTS**

Functional Assessment Questionnaire Total Score  Equals  ☐

CDISCAT Total Score  Equals  ☐

## Image Data Archive

IDA manual can be downloaded from LONI Informatics Core page.

**Informatics Core**

The Informatics Core (IC), based at the Laboratory of Neuro Imaging (LONI) at UCLA, is responsible for de-identifying, archiving, and disseminating all clinical, biospecimen, genetic and imaging data including raw and processed MR and PET scans. All data are made available to approved ADNI investigators within days after the date of collection through the Image and Data Archive (IDA) website which provides search and data exploration interfaces for evaluating and obtaining data of interest. The IC also distributes methods and software tools created and/or used by the ADNI analysts.

[contact](#)

Click on the video thumbnail to see a demonstration of the ADNI Data Archive.

**Resources**

- Download the IDA Training Manual
- Go to the ADNI Data Archive
- Informatics Core News

**IDA Training Manual**

**ADNI Core Groups**

- Administrative
- Biomarker
- Biostatistics
- Clinical
- Genetics
- Informatics
- MRI
- Neuropathology
- PET

**ADNI Centers & Operations**

- Acquisition Sites
- Coordination Center
- Governance

## Having Question?

If you have questions, please check FAQ section first.



Still no answers?

## Having Question?

Search your question using **Experts Knowledge Base**.

The screenshot shows the ADNI (Alzheimer's Disease Neuroimaging) website's Experts Knowledge Base section. The header includes the ADNI logo and navigation links: ABOUT, STUDY DESIGN, DATA & SAMPLES, METHODS & TOOLS, SUPPORT, and NEWS & PUBLICATIONS. The main content area is titled "Experts Knowledge Base" and contains a welcome message, a search bar, and a list of core Q&As. The search bar is labeled "Type your term here." and has a magnifying glass icon. Below the search bar, there is a section for "Core Q&As" with links for "All Cores", "Clinical Core", and "MRI Core". The right sidebar features a section titled "All Core Q&As" with a link to "Testing the fixed links" dated 01/22/13. Below this, there is a question: "Is it possible to determine whether some of the early patients enrolled under ADNIGO-2 already converted stage of late MCI during the trial course. Are these changes documented somewhere in the ADNI data?" dated 01/22/13. Further down, there is a link to "What is ADNI?" dated 01/22/13, and a link to "Here is a final test question to answer" dated 01/17/13.

Still no answers?

# Having Question?

## Ask the Experts page

ABOUT STUDY DESIGN DATA & SAMPLES METHODS & TOOLS SUPPORT NEWS & PUBLICATIONS

Home > Support > Experts Knowledge Base > Ask the Experts

### Ask the Experts

Use this online form to submit an ADNI question to our experts. All fields are required. Please allow 3-5 business days for an email reply. Responses are made through the Experts Knowledge base and may be published to this site.

Name  Email

My question is for

Question

Enter the text you see in the captcha box on the right

**Vgc8q**

SUBMIT YOUR QUESTION

<b>Neuropathology Core</b> <ul style="list-style-type: none"> <li>Neuropathological examination</li> <li>Brain tissue archive</li> </ul>	<b>Data Sharing and Publications Committee (DPC)</b> <ul style="list-style-type: none"> <li>Your ADNI data application</li> <li>Manuscript submissions</li> <li>Data use policies</li> </ul>	<b>Genetics Core</b> <ul style="list-style-type: none"> <li>Genetic data and samples</li> <li>MRI and PET endophenotypes</li> </ul>	<b>Biomarker Core</b> <ul style="list-style-type: none"> <li>Biological fluids bank</li> <li>Biomarkers such as APOE genotyping, Plasma, CSF Aβ and tau, other promising biomarkers</li> </ul>
<b>MRI Core</b> <ul style="list-style-type: none"> <li>MRI protocols</li> <li>MRI data</li> </ul>	<b>Clinical Core</b> <ul style="list-style-type: none"> <li>Clinical data, CRFs</li> <li>Clinical Protocols</li> </ul>	<b>Informatics Core</b> <ul style="list-style-type: none"> <li>Data archive access &amp; usage</li> <li>Data archive technical issues</li> </ul>	<b>Coordinating Center</b> <ul style="list-style-type: none"> <li>Data collection</li> </ul>

## Having Question?

Or you may join ADNI Data User Google Group.  
<https://groups.google.com/d/forum/adni-data>

The screenshot shows the Google Groups interface for the 'Alzheimer's Disease Neuroimaging Initiative (ADNI) Data' group. The page has a blue header with the Google logo and a search bar. Below the header, there's a blue banner with the text 'Welcome to the new Google Groups! Learn about the new features you'll find.' The main content area is titled 'Groups' and features a red 'NEW TOPIC' button, a 'Mark all as read' button, and 'Actions' and 'Filters' dropdown menus. The group name 'Alzheimer's Disease Neuroimaging Initiative (ADNI) Data' is displayed, along with '0 of 0 topics' and 'Tags - Manage - M'. A yellow box on the right says 'There is one pending member to review.' On the left sidebar, there are links for 'My groups', 'Home', 'Starred', 'Announcements', 'Recently viewed', and 'Favorites'. A yellow box in the sidebar says 'Click on a group's star icon to add it to your favorites.' The main content area has a section titled 'ADNI Data User Group' with a description: 'This group is devoted to questions from users of the ADNI data. Please check the documentation available from Laboratory of Neuroimaging, University of California, San Diego, in particular <http://adni.loni.ucla.edu/data-samples/data-faq/>, before posting your question. To subscribe to list, send an email to [adni-data+subscribe@googlegroups.com](mailto:adni-data+subscribe@googlegroups.com).' Below this is a section titled 'ADNIMERGE data package for R' with a description: 'For users of R, we have developed a data package "ADNIMERGE" which contains coded data, documentation, and analysis vignettes. Documentation can be found at <http://adni.loni.ucla.edu> and more information about ADNI is available from <http://adni.loni.ucla.edu>. It depends on Frank Harrell's [Hmisc](#) package which can be installed from the R package repository (CRAN) by: 

```
R prompt> install.packages("Hmisc")
```

 To downloading the compressed ADNIMERGE\_0.0.1.tar.gz file, direct your browser to <http://adni.loni.ucla.edu> > Login > Download > Study Info > Merged ADNI 1/GO/2 Package for R. The package can be installed to your R system by entering the following at an R prompt: 

```
R prompt> install.packages("ADNIMERGE")
```

'

## Q & A

Any questions?



# Thank You

Thank you.