Imaging Overview

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General Information

An overview of the ABCD Study® can be found at abcdstudy.org and detailed descriptions of the assessment protocols are available at [ABCD Protocols](https://abcdstudy.org). This page describes the contents of various instruments available for download. To understand the context of this information, refer to the release note *Start Page*.

This document details how to to obtain information, metrics, and imaging files from the magnetic resonance imaging (MRI) components of the ABCD Study. An in-depth discussion and reference resource on the ABCD processing pipeline is available at https://doi.org/10.1016/j.neuroimage.2019.116091.

Please note the monthly download limit of 20TB. If you need to exceed this, you can request a temporary (one week) Download Threshold extension by emailing the NDA help desk at NDAHelp@mail.nih.gov with the name of the data you wish to download and the size of the data package.

Nomenclature

Within the ABCD Study, all data tables provided are referred to as instruments. As laid out in more detail in the *Start Page* release note, for release 5.0 all instruments for tabulated data were renamed to implement a consistent naming scheme. Furthermore, the grouping of variables into tables was reconsidered to create tables that are more cohesive. For the imaging domain in particular, the larger tables published in release 4.0 that grouped variables mainly based on imaging modality and table size limitations imposed by NDA were broken up into smaller tables that take into account different hierarchy levels.

Every table in the Imaging domain has the prefix `mri_y_` (`mri`: domain = "imaging"; `y`: source = "youth"), followed by abbreviations that represent

the different hierarchy levels a table belongs to:

Subdomain

- Administrative: `adm`
- Quality Control: `qc`
- Diffusion MRI (DTI): `dti`
- Diffusion MRI (RSI): `rsi`
- Resting State fMRI: `rsfmr`
- Structural MRI: `smr`
- Task fMRI: `tfmr`

Metric

- *Diffusion MRI (DTI)*
    - Fractional Anisotropy: `fa`
    - Longitudinal Diffusivity: `ld`
    - Mean Diffusivity: `md`
    - Transverse Diffusivity: `td`
    - Volume: `vol`
- *Diffusion MRI (RSI)*
    - Free Normalized Isotropic: `fni`
    - Hindered Normalized Directional: `hnd`
    - Hindered Normalized Isotropic: `hni`
    - Hindered Normalized Total: `hnt`
    - Restricted Normalized Directional: `rnd`
    - Restricted Normalized Isotropic: `rni`
    - Restricted Normalized Total: `rnt`
- *Resting State fMRI*
    - Correlation: `cor`
    - Temporal Variance: `var`
- *Structural MRI*
    - Cortical Thickness: `thk`
    - Sulcal Depth: `sulc`
    - Surface Area: `area`
    - T1 Intensity: `t1`
    - T2 Intensity: `t2`
    - Volume: `vol`
- *Task fMRI*
    - Emotional N-Back: `nback`
    - Monetary Incentive Delay: `mid`
    - Stop Signal Task: `sst`

Atlas

- *Diffusion MRI (DTI)*
  - AtlasTrack: `at`
  - Desikan: `dsk`
  - Destrieux: `dst`
  - Subcortical: `aseg`
- *Diffusion MRI (RSI)*
  - AtlasTrack: `at`
  - Desikan: `dsk`
  - Destrieux: `dst`
  - Subcortical: `aseg`
- *Resting State fMRI*
  - Desikan: `dsk`
  - Destrieux: `dst`
  - Gordon Parcellations: `gp`
  - Subcortical: `aseg`
- *Structural MRI*
  - Desikan: `dsk`
  - Destrieux: `dst`
  - Fuzzy Clustering: `fzy`
  - Subcortical: `aseg`
- *Task fMRI*
  - Behavior: `beh`
  - Desikan: `dsk`
  - Destrieux: `dst`
  - Subcortical: `aseg`

Within the different imaging modalities, variables are grouped into tables using additional criteria. The resulting tables are listed in more detail in the release notes for the specific imaging modalities. Users can use the accompanying [release 5.0 data dictionary application](#) to explore what variables a given instrument contains and how instruments are hierarchically organized within the ABCD ontology. For backward-compatibility, the application also allows users to look up the table names used in the 4.0 release as well as DEAP variable names. Abbreviations of anatomical locations for the ROI-based tabulated imaging tables are detailed in *[Supplementary Imaging Tables](#)*.

MRI Scanner Information

Name of Instrument	Table Name
MRI Info	mri_y_adm_info

This table provides information for each subject visit about the MRI scanner manufacturer, model, magnetic field strength, device software version, etc. used. <u>Note</u>: all scanners use 32 channel head coils with the exception of the Siemens scanners with the following device serial numbers (see variable `mri_info_deviceserialnumber`) that use 64 channel head coils:

```
HASH7911780b
HASH03db707f
HASH65b39280
HASHe4f6957a
HASH31ce566d
```

MRI Processed Data File Sharing

NDA Data Structure	Description
fmriresults01	Index of minimally processed data

Minimally processed MRI file sharing

The ABCD Data Release 5.0 contains minimally processed neuroimaging data for all the baseline ABCD Study participants, including:

- High-resolution structural data (3D T1w and T2w scans)
- Advanced diffusion MRI (multiple b-values and directions)
- Resting State fMRI
- Task fMRI (Monetary Incentive Delay, Stop-Signal, and Emotional N-Back) with event files for each fMRI run

These series have been run through standard modality-specific pre-processing stages including conversion from raw to compressed files, distortion correction, movement correction, alignment to standard space, and initial quality control (refer to the *MRI Quality Control* release notes). This is to enable researchers to use the ABCD neuroimaging data in their own processing pipelines more quickly and efficiently than starting with raw data. Note that minimal processing is identical for rs-fMRI and task-fMRI and does not include analysis-specific pre-processing steps (e.g. removal of initial TRs, normalization by mean, etc.).

The above listed NDA data structure allows data users to find the location of DICOMs and minimally processed MR data to download. Targets can be filtered for:

- ID (`subjectkey`)
- Date (`interview_date`)
- Age (`interview_age`)
- Gender (`sex at birth`)
- QC Score (`qc_outcome`: pass;fail;questionable)
- Series type (`scan_type`; sMRI, dMRI, fMRI, field maps)
- Raw DICOMs location (`file_source`)
- Minimally processed data location (`derived_files`)

Preprocessed imaging data are packaged in archive files (`.tgz`) for each image series containing BIDS formatted directory trees and NIfTI format data files (software to share preprocessed data: https://scicrunch.org/resolver/SCR_016016; consistent with BIDS specifications version 1.1.1: http://bids.neuroimaging.io/bids_spec.pdf). Imaging metadata derived from the original DICOM files are packaged along with each preprocessed data series as JSON files. The minimally processed T2w data are resampled into voxel-wise alignment with the T1w, which is rigid-body resampled into alignment with an atlas.

dMRI-specific information included diffusion gradients adjusted for head rotation (`bvecs.txt`), diffusion gradient strengths (`bvals.txt`), and a rigid-body transformation matrix specifying the registration between the dMRI image and the corresponding processed sMRI T1w image (stored in the JSON file). The dMRI minimally processed data are also kept in their original resolution, but reoriented into a standard alignment, based on registration to T1w, but not voxel-wise aligned with the T1w. A registration matrix is supplied with the minimally processed dMRI data.

fMRI-specific information includes estimated motion time courses and a rigid-body transformation matrix specifying the registration between the fMRI image and the T_1w image (stored in the JSON file). The fMRI minimally processed data are kept in their original space and resolution, but a registration matrix is supplied with the minimally processed fMRI data. For task-fMRI series, event timing information is included as tab-separated value (`.tsv`) files. The results of additional processing and ROI analysis are shared in tabulated form (see below).

Information about this is included in the release notes and in our recent publication, Hagler et al., 2019, NeuroImage. Image processing and analysis methods for the Adolescent Brain Cognitive Development Study

(doi: [10.1016/j.neuroimage.2019.116091](#)). They also describe what processing steps are included in the "minimally processed" data shared on NDA.

There is no script available to run the ABCD minimal processing. There is a Docker that runs the complete ABCD Release 2.0 processing and analysis pipeline available at https://www.nitrc.org/projects/mmps_docker/. Other useful software packages include https://github.com/ABCD-STUDY/abcd-dicom2bids and https://github.com/ABCD-STUDY/abcd-hcp-pipeline.

Expected File Sets

The number of expected files changes due to subject scheduling, scanner manufacturer requirements, and repeat acquisitions during scanning. Scanning sessions are typically performed in one session for ~2 hours. However, sometimes the family prefers to do this over two 1-hour sessions within a few days of each other. If the scanning is split over two sessions, an initial T1 is acquired for reference at the start of both sessions, leading to two available T1 images. Additionally, because the T1 is the first, short essential scan of the session, the operator will repeat the scan if there is a problem with the acquisition (e.g. excessive motion). Other series may also have a repeat acquisition if there is enough time. If there are multiple acquisitions beyond the expected number of files, please manually inspect the images for quality.

Below is a guide to the expected number of files per modality/scanner manufacturer:

Modality	GE	Philips	Siemens
sMRI	1 T1	1 T1	1 T1_NORM
	1 T2	1 T2	1 T2_NORM
dMRI	1 Field map	2 Field maps	2 Field maps
	1 DWI	2 DWIs	1 DWIs
rs-fMRI	2 Field maps	4 Field maps	4 Field maps
	4 BOLD	4 BOLD	4 BOLD
Task fMRI (MID)	1 Field map	2 Field maps	2 Field maps

	2 BOLD runs	2 BOLD runs	2 BOLD runs
Task fMRI (N-Back)	1 Field map	2 Field maps	2 Field maps
	2 BOLD runs	2 BOLD runs	2 BOLD runs
Task fMRI (SST)	1 Field map	2 Field maps	2 Field maps
	2 BOLD runs	2 BOLD runs	2 BOLD runs

Note that the order of the task fMRI series acquisition is randomized per subject.

MRI Raw Data File Sharing

NDA Data Structure	Description
`image03`	Index of Fast Track raw data
`fasttrackqc`	QC info for Fast Track data

Fast Track DICOM file sharing

If unprocessed raw imaging data is needed, DICOM files are also made publicly available via a Fast Track mechanism. These DICOM files are released on NDA on a continual basis within approximately one month of data collection using the ABCD fast-track image sharing scripts

(RRID: SCR_016021). DICOM files are arranged in BIDS-compliant directory trees and packaged in individual archive files (`.tgz`) for each series. Metadata are included in the form of JSON-format text files, and for task-fMRI series, also included are the files containing stimulus and behavioral response timing information exported from the stimulus program (E-Prime). A copy of the metadata is uploaded to NDA's image (version 03 – image03) database to link information to non-imaging-based assessments for the same participants. Raw DICOM Fast Track data have not undergone quality control or curation. The up-to-date index of Fast Track shared DICOM files can be downloaded in a separate `image03` instrument.

For more information regarding converting ABCD fasttrack data to BIDS format, refer to the [ABCC collection](#).

Notes:

- Some Siemens fMRI data have been reported to have negative values for the Siemens CSA slice timing parameter which can prevent the conversion of DICOMs files in some software. This issue has been overcome in some software (e.g. current version of `dcm2niix` available for download at https://github.com/rordenlab/dcm2niix).
- GE scanners are unable to correctly encode complex multi-shell EPI gradient table into the DICOM header (a generic default is applied instead). Raw diffusion gradient tables (b values and vectors) per scanner manufacturer have been provided as an accompanying compressed file (see below).

dMRI gradient tables for Fast Track dMRI DICOMs

Raw diffusion gradient tables (b values and vectors) per scanner manufacturer can be downloaded here:

⤓ ABCD_Diffusion_Tables.zip

This is primarily provided for ease of use. Additionally, this is to overcome the limitation of GE scanners which are unable to correctly encode complex multishell EPI gradient table into the DICOM header (a generic default is applied instead).

Notes:

- the gradient tables are only for raw Fast Track dMRI DICOM data. For minimally processed data, new vector tables are generated following motion correction and provided with the minimally processed data.
- For GE, there are two different versions of the bvecs/bvals files, labeled "DV25" and "DV26". The "DV25" version is specific to scans acquired with SoftwareVersion DV25. For all other software versions (DV26, DV28, DV29), the "DV26" files will work.
- For GE, prior to DV29, the diffusion values are not correct in the DICOM header and need to come from an external file (such as a bvec/bval file). As of DV29, the correct diffusion directions can be found in the DICOM header, so no external bvec/bval file is needed if you have the dcm files.
- For Siemens and Philips, the correct diffusion values can be found in the DICOM header.

High density, phased array head coils

The ABCD acquisition sites use either 32 channel head or 64 channel head/neck coils, depending on availability. Standard correction methods, such as those used by FreeSurfer, are limited when compensating for steep spatial intensity variation, leading to inaccurate brain segmentation or cortical surface reconstruction. For example, brain tissue farther from the coils, such as the temporal and frontal poles, typically have lower intensity values resulting in focal underestimation of the white matter surface or the elimination of large pieces of the cortical surface reconstruction. Furthermore, brain tissue close to coils with extremely high intensity values may be mistaken for non-brain tissue (e.g., scalp). To overcome this, the ABCD minimally processed structural MRI (sMRI) files include an improved intensity inhomogeneity correction, using a smoothly varying bias field optimized to standardize image intensities within all white matter voxels.

Siemens normalized sMRI DICOMs

Siemens scanners provide an intensity normalization procedure to correct for bias fields. As a result, Siemens scanners have two sets of DICOMs for each sMRI data series (i.e. T1, T2, T1_NORM, and T2_NORM). The non-normalized images with large intensity ranges (e.g. with a 64 channel head coil) may be clipped at 4095, impairing cortical reconstruction. The ABCD pipeline uses only the normalized sMRI (T1_NORM and T2_NORM).

Tabulated ROI-based Analysis

MR images are corrected for distortions and head motion, and cross-modality registrations are performed. Using the T1w sMRI scan, the cortical surface is reconstructed, and subcortical and white matter regions of the brain are segmented. From this, we carry out modality-specific analyses and extract imaging-derived measures using a variety of regions of interest (ROI).

Finally, ROI analysis results are compiled across participants and summarized in tabulated form. Information on the different tabulated imaging data instruments is detailed in modality-specific release notes:

- *Structural Magnetic Resonance Imaging*
- *Diffusion Magnetic Resonance Imaging*
- *Resting-State Functional Magnetic Resonance Imaging*
- *Task-Based Functional Magnetic Resonance Imaging (task-fMRI)*
- *Behavioral Performance During Task-Based fMRI*

Despite the convenience of ROI-based analyses and the advantages

related to reduced numbers of statistical comparisons, there are inherent limitations to this approach. Effects of interest (e.g., associations between cortical morphometry and cognitive variables, or task- related fMRI activation) could potentially straddle multiple ROIs, or occupy a small region of a large ROI, thereby reducing the sensitivity of an ROI-based analysis relative to mapping-based approaches. For this reason, users should be cautious about interpreting the results of ROI- based analyses, particularly for task fMRI.

Quality Control and Recommended Image Inclusion Criteria

QC procedures and image inclusion criteria are described in more detail in the *MRI Quality Control & Recommended Image Inclusion Criteria* release note.

Recommended Inclusion Criteria

The Recommended Imaging Inclusion instrument (`mri_y_qc_incl`) provides the simple option of include or exclude series (1 or 0) based on automated and manual QC review per MR measure - T1w, T2w, DTI/RSI, rsfMRI, SST, nBack and MID tfMRI.

Incidental Findings

T1w and T2w images, if available, were screened for incidental findings by a board-certified neuroradiologist. Any findings requiring clinical investigation were relayed to appropriate site personnel via the ABCD Coordinating Center (CC). These MR findings (see instrument `mri_y_qc_clfind`) are not included in our recommended inclusion criteria but are noted here because some investigators may find them to be relevant inclusion criteria for their analyses.

Protocol Compliance and Quality Control

All ABCD MRI exams have been systematically checked for MRI protocol compliance and completeness, and images have been manually rated for quality by trained MR analysts before and after processing. All MRI data are provided, but we highly recommend that researchers filter subjects by QC results based on the project aims and tolerance for MR artifacts/motion. Severe artifact in all T1w image in a given visit (MRI Quality Control: `iqc_t1_ok_ser = 0`) results in the inability to produce subsequent MR-metrics for all other modalities.

E-Prime errors in task fMRI

For task fMRI, series were also excluded due to E-Prime problems including missing, corrupted, duplicated or unsynchronized E-Prime files. The variety of E-Prime errors that would invalidate the series are generalized in the task-specific QC instruments as being "mismatched" (`iqc_mid_ep_t_series_match = 1`; `iqc_nback_ep_t_series_match = 1`; `iqc_sst_ep_t_series_match = 1`). In manual review, some errors can be corrected, so there is an additional override to this switch when needed (`eprime_mismatch_ok_mid = 1`; `eprime_mismatch_ok_mid = 1`, `eprime_mismatch_ok_mid = 1`).

Behavioral performance in task fMRI

Behavioral measures calculated from participant button presses during task fMRI acquisition are also included (see Behavioral Performance During Task-Based fMRI release note). Based on those measures, behavioral performance flags are provided, indicating whether a subject's performance for each task was within acceptable standards. It is suggested that users exclude subjects from group analysis based on sub-optimal performance and possibly additional criteria such as the number of degrees of freedom (reduced by motion censoring) in the individual subject task-fMRI analysis and/or based on outlier detection on the ROI-averages themselves. Users should choose inclusion/exclusion performance criteria that are appropriate for their analyses.

Methods

Image processing and analysis methods corresponding to ABCD Release 2.0.1 are described in Hagler et al., 2019, *Image processing and analysis methods for the Adolescent Brain Cognitive Development Study.* Neuroimage, 202:116091 (doi: 10.1016/j.neuroimage.2019.116091). Changes to image processing and analysis methods in Release 3.0 and Release 4.0 are documented in the relevant release notes below. No significant changes were made to the processing pipeline for Release 5.0.

- *Structural Magnetic Resonance Imaging*
- *Diffusion Magnetic Resonance Imaging*
- *Resting-State Functional Magnetic Resonance Imaging*
- *Task-Based Functional Magnetic Resonance Imaging (task-fMRI)*
- *Behavioral Performance During Task-Based fMRI*
- *MRI Quality Control & Recommended Image Inclusion Criteria*

Changes for ABCD 3.0

Various changes and bug fixes

During pre-release data review and curation, a number of small changes and bug fixes were made in an effort to recover missing imaging results where possible. Corrupted intermediate MATLAB data files—caused, for example, by abrupt job failure during file writing—occurred infrequently but led to missing results in our pre-release review. These corrupt files caused error on subsequent attempts to process that data, because existing data files are not overwritten by default. To recover such cases, changes in various parts of the processing pipelines were made to automatically remove corrupt MATLAB data files when encountered so that the processing would recreate those files and proceed on subsequent processing attempts. Miscellaneous coding changes slightly reduced the missingness of derived results by handling various data irregularities.

Changes for ABCD 4.0

Event labeling

Visit name variables (e.g., `mri_info_visitid` in 4.0 NDA data structure `abcd_mri01` or `smri_visitid` in 4.0 NDA data structure `abcd_smrip102`) were changed to use a shortened EventName instead of StudyDate. For example, the new visit name looks like `G031_INVXXX0000_baseline` instead of `G031_INVXX0000_20170601`.

Preventing missing results due to job failures

Changes were made to how image processing, analysis, and summary jobs were generated to allow for limiting the creation of jobs for only those participant-events for whom jobs had not been previously created or did not finish successfully. This allowed for the recovery of results which may have been missing previously due to essentially random job failures that occasionally occur with large-scale, parallel processing on computational clusters.