



# Developing Human Connectome Project (dHCP)

## Guidelines for downloading data from the NDA

**Warning!** We are aware that navigating the data in the NDA interface is challenging. The best way to access and download the data is by precisely following the steps outlined below.

If you need help, email the NDA Help Desk at [NDAHelp@mail.nih.gov](mailto:NDAHelp@mail.nih.gov) and quote collection 3955.

### Contents

Before you start you will need .....	2
Downloading data .....	2
Imaging modality look-up table .....	8
Brain Imaging Data Structure (BIDS) .....	8
Information about Data .....	8
Frequently asked questions .....	10



## Before you start you will need

1. NDA user account and login.gov account  
<https://nda.nih.gov/nda/creating-an-nda-account.html>
2. Data access permission <https://nda.nih.gov/nda/access-data-info.html>
3. Download the 'Download Manager Tool' <https://nda.nih.gov/nda/nda-tools.html#download-manager> (see FAQ for username and password)

## Downloading data

1. Click on the link [https://nda.nih.gov/edit\\_collection.html?id=3955](https://nda.nih.gov/edit_collection.html?id=3955)
2. Click "Add to cart"

The screenshot shows the NDA website interface for the 'Developing Human Connectome Project (dHCP) #3955'. The page includes a navigation bar with links like 'Contribute Data', 'Get Data', 'Data Dictionary', etc. The main content area displays collection details such as 'Collection Title', 'Collection Investigators', 'Collection Description', 'Data Repository', 'Permission Group', 'Collection Creation Date', 'Collection Phase', 'Blinded Clinical Trial', 'Subjects Shared', and 'Funding Sources'. A Venn diagram on the right shows the overlap of 'Imaging+', 'Omics', and 'Clinical' data. At the bottom, the 'Add to Cart' button is highlighted with a blue circle.

3. Click "Create Data package/Add data to study"

This screenshot shows the same NDA website page as the previous one, but with the 'Create Data Package/Add data to study' button circled in blue. The button is located in the top right corner of the main content area, next to the 'Filter Cart' button. The rest of the page content remains the same.



- Check that all options are selected in the left table (collections by Permission Group). Select the modality in the right table ('Data Structure by Category'). The [list below](#) describes the data available under each heading for the 'Data structure by Category'. More information on imaging modalities can be found in the '[imaging modality look-up table](#)' in page 8.

To access packages you have created, open the [Data Packages](#) page from your user profile.

Researchers who share data through NDA, or who conduct a secondary analysis on data shared through NDA, are expected to release, or publication directly to the underlying subject-level records for the data defined. Automatically, the NDA Study (DOI), which is expected to be referenced in the publication as a persistent link to the supporting dataset

**2. Select modality**

NOTE: This may not represent all available data for these subjects - click "Find All Subject Data" to return all data for these subjects.

**Collections by Permission Group**

[Collapse All](#) | [Deselect All](#)

☒ Developing Human Connectome Project (dHCP)  
You do not have access to this permission group. You can apply for access at [Developing Human Connectome Project \(dHCP\)](#)

☒ [13555] Developing Human Connectome Project (dHCP)  
Investigators: David Edwards, Jo Hajnal, Daniel Rueckert, Stephen Smith

as a precise global description of this connectome in detail will psychiatric diseases. Currently, the man Connectome Project (dHCP), led by King's College London, Imperial College London and Oxford University, aims to make major scientific progress by creating the first 4-dimensional connectome of early life. Our goal is to create a dynamic map of human brain connectivity from 20 to 44 weeks post-conceptual age, which will link together imaging, clinical, behavioural, and genetic information. This unique setting, with imaging and collateral data in an expandable open-source informatics structure, will permit wide use by the scientific community, and to undertake pioneer studies into normal and abnormal development by studying well-phenotyped and genotyped group of infants with specific genetic and environmental risks that could lead to Autistic Spectrum Disorder or Cerebral Palsy.

- ☒ Dataset - 52404 (85 subjects) - Shared pipeline\_BIDS\_files, 032500
- ☒ Dataset - 52405 (83 subjects) - Shared pipeline\_BIDS\_files, 032600
- ☒ Dataset - 52406 (85 subjects) - Shared pipeline\_BIDS\_files, 032700
- ☒ Dataset - 52407 (92 subjects) - Shared pipeline\_BIDS\_files, 032800
- ☒ Dataset - 52408 (95 subjects) - Shared pipeline\_BIDS\_files, 032900
- ☒ Dataset - 52409 (89 subjects) - Shared pipeline\_BIDS\_files, 033000
- ☒ Dataset - 52410 (92 subjects) - Shared pipeline\_BIDS\_files, 033100
- ☒ Dataset - 52411 (90 subjects) - Shared pipeline\_BIDS\_files, 033200
- ☒ Dataset - 52412 (82 subjects) - Shared pipeline\_BIDS\_files, 033300
- ☒ Dataset - 52413 (84 subjects) - Shared pipeline\_BIDS\_files, 033400

**Data Structure by Category**

[Collapse All](#) | [Deselect All](#)

- ☒ Adverse Events
  - ☒ NICU Episode Summary (190 of 190 subjects available) ⓘ
- ☒ Autism Spectrum Disorders
  - ☒ Quantitative Checklist for Autism in Toddlers (617 of 617 subjects available) ⓘ
- ☒ Checklist
  - ☒ Quantitative Checklist for Autism in Toddlers (617 of 617 subjects available) ⓘ
- ☒ DTI, MRI, fMRI
  - ☒ Image (782 of 782 subjects available) ⓘ
- ☒ Demographics
  - ☒ NICU Episode Summary (190 of 190 subjects available) ⓘ
  - ☒ Participant Enrollment (984 of 984 subjects available) ⓘ
- ☒ Depression
  - ☒ Edinburgh Postnatal Depression Scale (874 of 874 subjects available) ⓘ
- ☒ Diagnostic
  - ☒ NICU Episode Summary (190 of 190 subjects available) ⓘ
- ☒ Evaluated Data
  - ☒ Processed MRI Data (783 of 783 subjects available) ⓘ
- ☒ Eye Tracking
  - ☒ Eye Tracking Subject-Experiment (706 of 706 subjects available) ⓘ
- ☒ Family
  - ☒ Fetal Scan Information (273 of 273 subjects available) ⓘ
  - ☒ Neonatal Scan Information (805 of 805 subjects available) ⓘ

### **Adverse Events**

- **NICU Episode Summary:** Clinical information for babies that stayed in the NICU. Data in file nicu101.

### **Autism Spectrum Disorders**

- **Quantitative Checklist for Autism in Toddlers:** Q-CHAT scores (18 month follow-up) Scores in file qucht01.

### **Checklist**

- **Quantitative Checklist for Autism in Toddlers:** Q-CHAT scores (18 month follow-up) Scores in file qucht01.

### **DTI, MRI, fMRI**

- **Image:** Native data and motion corrected images including anatomical, dMRI, fMRI, calibrations maps and ancillary files related to the original examinations. Please also see the '[imaging modality look-up table](#)' in page 8.

### **Demographics**

- **NICU Episode Summary:** Clinical information for babies that stayed in the NICU. Data in file nicu101.
- **Participant Enrollment:** Parental clinical, demographic and socio-economic information. Data in file cpenr01.

### **Depression**

- **Edinburgh Postnatal Depression Scale:** EPDS scores. Data in file epds01.

### **Diagnostic**

- **NICU Episode Summary:** Clinical information for babies that stayed in the NICU. Data in file nicu101.

### **Evaluated Data**

- **Processed MRI Data.** Analysed metadata for each modality (anatomical, diffusion, functional), including brain segmentations and cortical surfaces. Please also see the '[imaging modality look-up table](#)' in page 8.



### Eye Tracking

- **Eye Tracking Subject-Experiment:** native and processed eye-tracking data. Data are in folder et\_subject\_experiment01. The data are organised in folders by participant. Documentation on eye-tracking task, acquisition and analysis are in folder et\_subject\_experiment01/experiments/experiment\_2018/block\_1/Block\_Design\_File/

### Family

- **Fetal Scan Information:** Information about the fetal scan, including the gestational age on the day of the scan. Data are in file fsi01.
- **Neonatal Scan Information:** Information about the neonatal scan, including age at scan, age at birth and sex. Data are in file nnsi01.
- **Parent's Questionnaire - Mother's and Father's Questionnaire Combined:** 18 month time point. Parenting Scale scores and parental demographics. Data are in file pqmf01.

### Health

- **Neonatal Scan Information:** Information about the neonatal scan, including the gestational age at birth, the baby's age on the day of the scan and the baby's sex. Data are in file nnsi01.

### Med History

- **Fetal Scan Information:** Information about the fetal scan, including the gestational age on the day of the scan. Data are in file fsi01.

### Omics

- **Genomics Sample:** Genomic data can be found in folder genomics\_sample03/Users/nickharper/cdb/dhcp\_plink\_files. Methylation data can be found in folder genomics\_sample03/Users/nickharper/cdb/Methylation.

### Parenting

- **Late Pregnancy and Birth:** clinical information about later stages of pregnancy and birth. Data are in file lpb01.
- **Parent's Questionnaire - Mother's and Father's Questionnaire Combined:** 18 month timepoint. Parenting Scale scores and parental demographics. Data are in file pqmf01.

### Phys Exam

- **Neonatal Scan Information:** Information about the neonatal scan, including the gestational age at birth, the baby's age on the day of the scan and the baby's sex. Data are in file nnsi01.

### Questionnaire

- **Bayley-III Scales of Infant Development:** 18 month timepoint, Bayley-III scores. Data are in file bsid\_iii01.
- **Child Behavior Checklist (CBCL) 1-5:** 18 month timepoint, CBCL scores. Data are in file cbcl1\_501.
- **Early Childhood Behavior Questionnaire:** 18 month timepoint, ECBQ scores. Data are in file ecbq01.
- **Parent's Questionnaire - Mother's and Father's Questionnaire Combined:** 18 month timepoint. Parenting Scale scores and parental demographics. Data are in file pqmf01.
- **Stimulating Parent Scale:** 18 month timepoint, SPS scores. Data are in file stps01.

### Resolve Identifiers

- **Genomics Subject:** List of every participant in the study for which we have genomics data. This is a subset of the Research Subject record below. Data are in file genomics\_subject02.
- **Research Subject:** List of every participant in study. Data are in file ndar\_subject01

### Other

- **Hammersmith Infant Neurological Examination (HINE):** A 26-item examination assessing different aspects of neurological examinations such as cranial nerves, posture, movements, tone, and reflexes. Data are in file hine01.
- **Fetal imaging QC:** Score of image quality.



- After selecting the modality (e.g. eye-tracking), click “Create Data Package”.

The screenshot shows the NDA interface with the 'Create Data Package' button highlighted. A yellow box labeled 'Example selection: eye-tracking' points to the 'Eye Tracking Subject-Experiment' option in the 'Data Structure by Category' list.

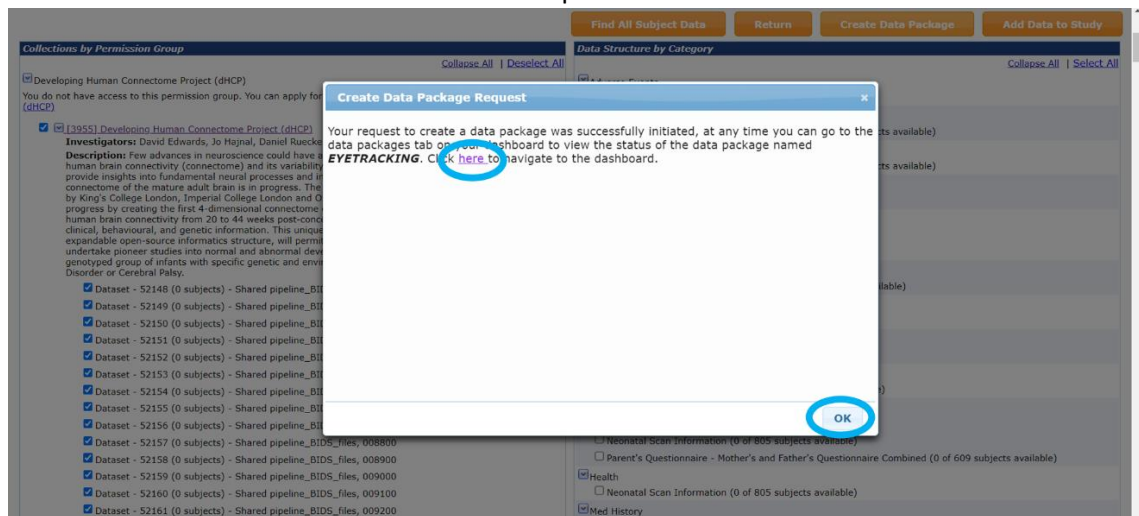
- Create a name for your selected data package and select option “include associated files”. Click “Create Data Package”.

The screenshot shows the 'Create Data Package' dialog box with three numbered steps: 1. Name your data package (with 'EYETRACKING' entered), 2. Select option (with 'Include associated data files' selected), and 3. Create Data Package (with the button highlighted).

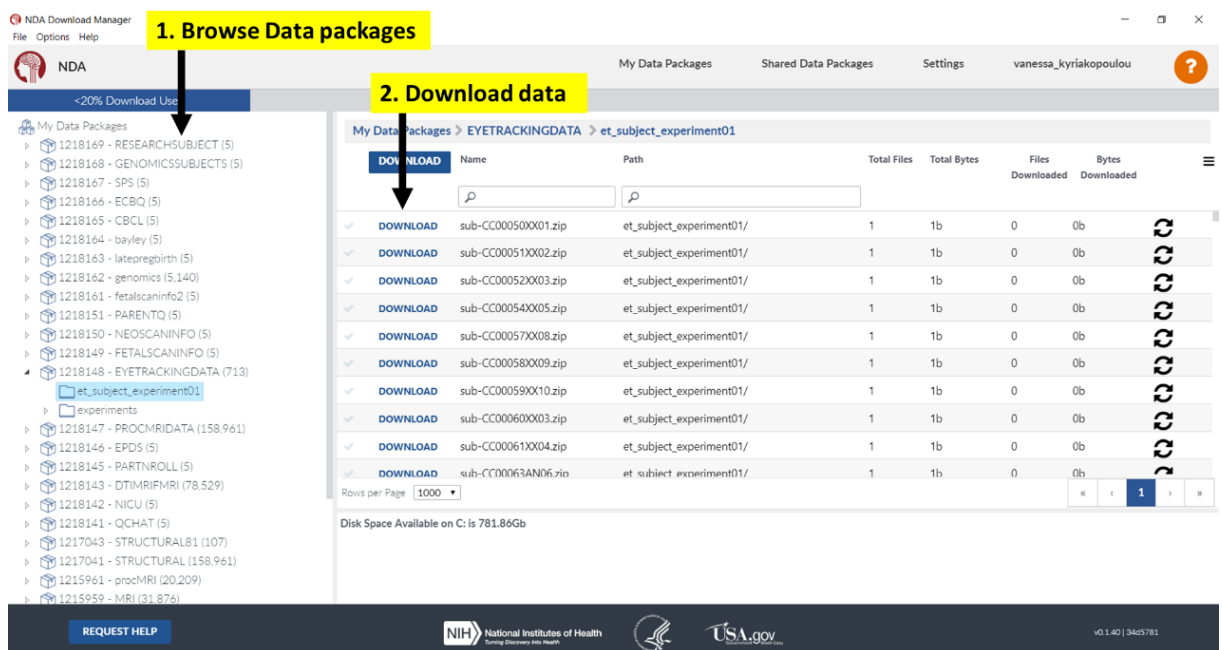




7. Popup window: Click 'here' to view the progress of the data package creation or 'ok' to stay on the package creation page. Once the data are ready to view, the status in the dashboard will change to "Ready to Download". You can now move to the next step.

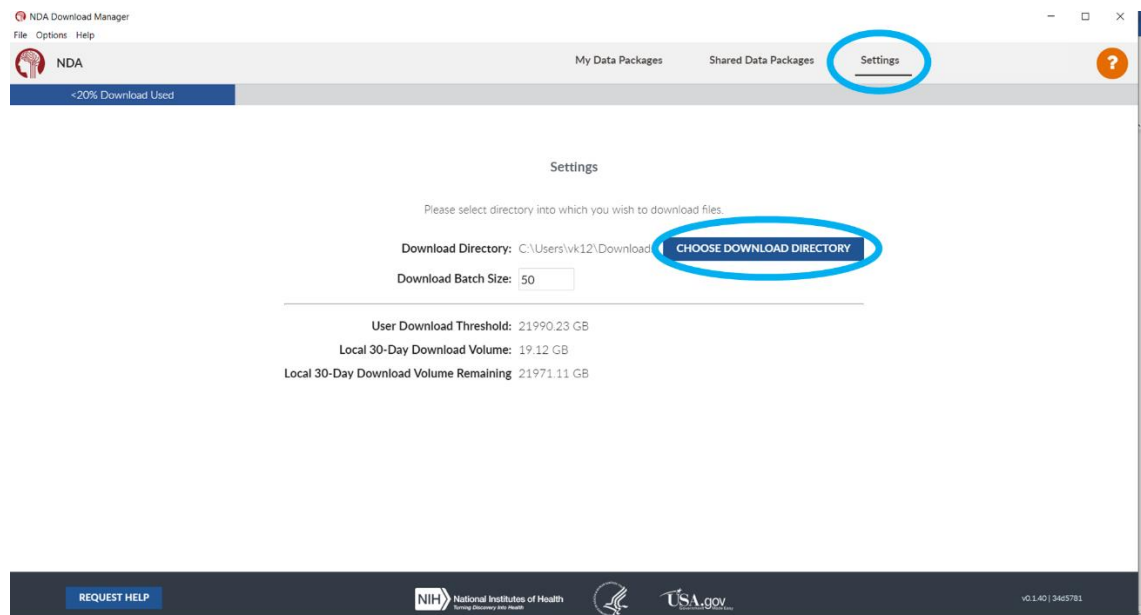


8. Open the 'Download Manager tool' and log in. The data packages are shown on the left. Navigate through the folders. The tool allows you to visualise the data available for download. Individual files can then be downloaded locally.





9. Check your download directory. Go to 'Setting' and 'choose your download directory'.



Data will be downloaded into a new folder within the download directory named “Package\_nnnnnn” where “nnnnn” is the package number assigned by the NIH download process. The folder will contain the following items:

- List of NIH data structures. These will be discussed further below but all consist of the structure name with the extension “.txt”, e.g. “image03.txt”. They are all tab delimited text files. These structures contain scalar variables and meta data for subjects. Note that the field “interview\_date” present in all structures has the North American date format “MM/DD/YYYY”.
- Supporting documentation including a README.pdf and a folder containing collection documents including this document. Supporting documentation may not be present if you did not tick “Include supporting documentation” when creating the package in step 6, above.
- Package metadata: package\_info.txt, dataset\_collection\_txt and md5\_values.txt.
- Folders containing the associated files. Present if you ticked “Include associated data files” in step 6 and if the selected structures include associated files. Structures with associated data files are image03, fmriresults01, et\_subject\_experiment01 and genetics\_sample01. Files within the folders are arranged as the on the servers from which the data was uploaded. For example, imaging data is arranged into separate sub-folders for anatomical, fmri and diffusion data.



## Imaging modality look-up table

	NDA website - Data Structure by category		Folder in Download manager
Neonatal Imaging	<b>Native data</b>		
	Anatomical	DTI, MRI, fMRI - Image	/image03/rel3_derivatives/rel3_rawdata_vol#/sub-CC#####XX###/ses-#####/anat/
	Functional	DTI, MRI, fMRI - Image	/image03/rel3_derivatives/rel3_rawdata_vol#/sub-CC#####XX###/ses-#####/func/
	Diffusion	DTI, MRI, fMRI - Image	/image03/rel3_derivatives/rel3_rawdata_vol#/sub-CC#####XX###/ses-#####/dwi/
	Calibration maps	DTI, MRI, fMRI - Image	/image03/rel3_derivatives/rel3_rawdata_vol#/sub-CC#####XX###/ses-#####/B1/
			/image03/rel3_derivatives/rel3_rawdata_vol#/sub-CC#####XX###/ses-#####/fmap/
	<b>Processed data</b>		
	Anatomical	Evaluated Data - Processed MRI Data	/fmriresults01/rel3_derivatives/rel3_dhcp_anat_pipeline/
	Functional	Evaluated Data - Processed MRI Data	/fmriresults01/rel3_derivatives/rel3_dhcp_fmri_pipeline/
	Diffusion	Evaluated Data - Processed MRI Data	/fmriresults01/rel3_derivatives/rel3_dhcp_dmri_eddy_pipeline/
Fetal Imaging	<b>Native data</b>		
	Anatomical	DTI, MRI, fMRI - Image	/image03/sub-CC#####XX###/ses-#####/anat/
	Functional	DTI, MRI, fMRI - Image	/image03/sub-CC#####XX###/ses-#####/func/
	Diffusion	DTI, MRI, fMRI - Image	/image03/sub-CC#####XX###/ses-#####/dwi/
	Calibration maps	DTI, MRI, fMRI - Image	/image03/sub-CC#####XX###/ses-#####/B1/
			/image03/sub-CC#####XX###/ses-#####/fmap/
	<b>Processed data</b>		
	Anatomical	Evaluated Data - Processed MRI Data	/fmriresults01/dhcp_anat_pipeline/
	Functional	Evaluated Data - Processed MRI Data	/fmriresults01/dhcp_fmri_pipeline/
	Diffusion	Evaluated Data - Processed MRI Data	/fmriresults01/dhcp_dmri_shard_pipeline/

## Brain Imaging Data Structure (BIDS)

We have taken every effort to follow the BIDS convention (<https://bids-standard.github.io/bids-starter-kit/>), however not all our data are BIDS-compliant. The main reason for this is that various types of imaging data could not easily fit in existing BIDS nomenclature. Consequently, when we were designing the format for the data naming, our prime goal was to ensure that users with some experience of working with BIDS-compliant datasets find it easy to navigate our dataset. For the data dictionary, please refer to our website documentation

## Information about Data

The layout of the various data structures can be found by selecting “Data Expected” on the ribbon after logging into the collection. This will show a list of all data structures together with statistics including number of subjects and number of subjects shared. There is an information button at the end of each Data Expected item. Clicking on this will generate a pop-up that lists the possible structures associated with that item. Usually there is only one possible structure that you can collect. Where options are given, select the structure with the name corresponding to the name of the structure in the download folder. After selection you will see a list of variable names, data type, description, limits on values and the meaning of categorical items. Because many of the structures are standard instruments used by NIG for multiple collections, not all the fields will be used in the dHCP project. These columns will be blank in all downloads. Ticking “Exclude null columns” when creating the package in step 6 above will allow you to ignore those fields entirely.

All data structures contain the following items:

- Subjectkey. This is the NDAR defined id that identifies the participant across all structures and across all collections.
- Src\_subject\_key. Alternative identifier that was used for data collection during the project. Has the form “sub-CCddddd[XX|AN|BN|CN|]ee where dddd and ee are





numbers. The XX, AN, BN, CN identifies singleton, twin and triplet participants. XX is used for singletons, AN for the first of twins or triplets, BN for the second of twins or triplets and CN for the third triplet. Twin and triplet participants will have the same values for dddddd and ee.

- Sex. Child's biological sex at birth: "M", "F" or "NR". There are only two participants with sex = NR. These were participants who were scanned in-utero and not seen subsequently so sex remained unknown.
- Interview\_date. The date that the data in the structure was collected. These dates are randomized by subtracting a random offset from the actual date. The same offset is used for all interview\_dates for each subject but different for different subjects. interview\_date can be used to determine the exact time difference between two events for the same participant. It cannot be used to determine seasonality of birth.
- Interview\_age and fetal\_age. Interview\_age is a common element in all data structures within the NIH archive. It is the age of the participant at time of data collection rounded to the nearest month. This is insufficiently precise for some analysis, e.g. image analysis; furthermore, age by this definition would be negative and possibly unknown for fetal participants scanned before birth. To address this limitation, data structures recording events that occur or could occur perinatally contain the field "fetal\_age". This is the postmenstrual age in days at the time of scan. For a given participant in a data structure, only one of interview\_age or fetal\_age can be meaningful. Use the following logic to determine which variable to use:
  - If fetal age does not exist in the structure or if fetal\_age is blank, interview\_age is valid. This will be the case for the data obtained at the 18 month follow up appointment and for the genomics\_sample03 structure.
  - If fetal age is present and has a non-blank value, this is the participant's post menstrual age at time of collection. Interview\_age will be 0 and has no meaning.



## Frequently asked questions

### 1. Where can I find information about the study and the data available?

You can visit the study website <http://www.developingconnectome.org/project/>. The neonatal data publication can be found <https://pubmed.ncbi.nlm.nih.gov/35677357/>.

### 2. Where can I find a list of all variables?

All variables can be found in the NDA website, under 'Expected data structure definitions'.

**Developing Human Connectome Project (dHCP) #3955**

General Experiments (5) Shared Data Publications (24) **Data Expected (19)** Submissions Associated Studies (0) Permissions

> Data Expected List: Mandatory Data Structures

▼ Data Expected List: Data Structures per Research Aims

These data structures are specific to your research aims and should list all data structures in which data will be collected and submitted for this NDA Collection. Please update the Targeted Enrollment number to accurately represent the number of subjects you expect to submit for the entire study.

+ New Data Expected ?

Data Expected	Targeted Enrollment	Initial Submission	Subjects Submitted	Initial Share	Subjects Shared	Status	Actions
Genomics/omics	1,000	06/15/2022	809	03/01/2023	0	Approved	[Icon] [Icon]
Eye Tracking	1,000	06/01/2022	706	09/01/2022	694	Approved	[Icon] [Icon]
Bayley Scales of Infant and Toddler Development, Third Edition (BSID)	1,000	11/01/2021	739	09/01/2022	0	Approved	[Icon] [Icon]
Child Behavior Checklist (CBCL)	1,000	06/01/2022	742	09/01/2022	0	Approved	[Icon] [Icon]
Processed MRI Data	1,000	06/15/2022	964	09/01/2022	783	Approved	[Icon] [Icon]
Early Childhood Behavioral Questionnaire (ECBQ)	1,000	06/01/2022	741	09/01/2022	0	Approved	[Icon] [Icon]
Imaging (Structural, fMRI, DTI, PET, microscopy)	1,000	06/15/2021	963	09/01/2022	782	Approved	[Icon] [Icon]
Edinburgh Postnatal Depression Scale	1,000	01/11/2021	874	09/01/2022	0	Approved	[Icon] [Icon]

Save Add to Cart

### 3. Where are the follow-up data/neurodevelopmental outcome data?

The follow-up data were collected at the 18 month time-point and can be found here:

- **Bayley-III Scales of Infant Development:** 18 month timepoint, Bayley-III scores. Data are in file bsid\_iii01.
- **Child Behavior Checklist (CBCL) 1-5:** 18 month timepoint, CBCL scores. Data are in file cbcl1\_501.
- **Early Childhood Behavior Questionnaire:** 18 month timepoint, ECBQ scores. Data are in file ecbq01.
- **Parent's Questionnaire - Mother's and Father's Questionnaire Combined:** 18 month timepoint. Parenting Scale scores and parental demographics. Data are in file pqmf01.
- **Stimulating Parent Scale:** 18 month timepoint, SPS scores. Data are in file stps01.
- **Parent's Questionnaire - Mother's and Father's Questionnaire Combined:** 18 month timepoint. Parenting Scale scores and parental demographics. Data are in file pqmf01.
- **Hammersmith Infant Neurological Examination (HINE):** A 26-item examination assessing different aspects of neurological examinations such as cranial nerves, posture, movements, tone, and reflexes. Data are in file hine01.
- **Eye Tracking Subject-Experiment:** native and processed eye-tracking data. Data are in folder et\_subject\_experiment01. The data are organised in folders by participant. Documentation on eye-tracking task, acquisition and analysis are in folder et\_subject\_experiment01/experiments/experiment\_2018/block\_1/Block\_Design\_File/



#### 4. Where can I find scalar variables for each participant?

Scalar variables are all found in the various data structures defined for the collection. The available structures are described in paragraph 4, above. Note that there isn't a one-to-one correspondence between the category of data shown on the download screen and the associated data structure, i.e. a given data structure may be included as part of the data for more than one category. The structure will not be duplicated in the download. When you download data as described in paragraph 5 you will find the various data structures in the downloaded folder "Package\_nnnnn" where nnnnn is assigned by the download manager. Scalar data is not large so it may be helpful to download the entire collection without selecting "Include Associated Data Files" as described in paragraph 6 above. This will create a package directory with all the study scalar variables and metadata. The individual data structures are tab downloaded as tab delimited files with the extension ".txt". Note that the "interview\_date" field, found in all structures, is in the North American "MM/DD/YYYY" format.

#### 5. How can I find an explanation of the meaning of the scalar variables?

Start by looking at the NIH data structure definitions on the "Data Expected" page. Further information about the specific meaning of data collected in this project can be found by visiting the study website <http://www.developingconnectome.org/project/>. The neonatal data publication can be found <https://pubmed.ncbi.nlm.nih.gov/35677357/>.

#### 6. Why are data incomplete?

Incomplete data may be due to various reasons such as incomplete image acquisitions because the participant was unable to complete the entire scanning protocol, the baby waking up during the scan, incomplete medical records or incomplete questionnaires, participating children refusing to complete tasks etc.

#### 7. Where are the clinical data about the perinatal period?

Clinical data about the perinatal period can here found here:

- **Late Pregnancy and Birth:** clinical information about later stages of pregnancy and birth. Data are in file lpb01.
- **Neonatal Scan Information:** Information about the neonatal scan, including the gestational age at birth, the baby's age on the day of the scan and the baby's sex. Data are in file nnsi01.
- **NICU Episode Summary:** Clinical information for babies that stayed in the NICU. Data in file nicu101.

#### 8. Where can I find the age at scan for my analysis?

For neonatal data analysis, age at scan and age at birth can be found in 'Neonatal scan information' (file nnsi01). Look at variables 'NSCAN\_GA\_AT\_BIRTH\_WEEKS' and 'NSCAN\_GA\_AT\_SCAN\_WEEKS'. The variable nscan\_age\_at\_scan\_days is the participant age in days at time of scan relative to the date of birth. For fetal data analysis, gestational age at scan can be found in 'Fetal scan information (file fsi01). Look at variable 'FSCAN\_GA\_AT\_SCAN'. These variables all report gestational (post menstrual)



age in weeks with the fractional component indicating days, e.g. 39.142857 is 39 weeks and 1 day.

## 9. Where can I find information about the parents?

Parental clinical, demographic and socio-economic information can be found in 'Participant enrollment' (file cpenr01). Note that the ethnicity categories are based on UK census categories. These are described in the data structure definition and do not correspond to ethnicity categories used in other countries.

## 10. What genomic data is there? What epigenomic data is there?

Genotyping: Saliva-derived DNA samples were genotyped by NIHR BioResource Centre Maudsley Genomics & Biomarker Core Facility on the Illumina Infinium Omni5-4 array v1.2, which comprises 4327108 single-nucleotide polymorphisms (SNPs). Genotype data are provided in binary PLINK format (see <https://www.cog-genomics.org/plink/1.9/formats> for details).

Methylation: Saliva-derived DNA from each sample was treated with sodium bisulfite (Zymo Research EZ-96 DNA Methylation Kit D5004). DNA methylation was quantified using the Illumina Infinium HumanMethylationEPIC BeadChip Kit. The raw files (.idat) are provided.

## 11. Where can I find the BIDS naming descriptions? Details can be found here <https://bids-standard.github.io/bids-starter-kit/>

## 12. Where can I find my username and password for the Download Manager?

Log into your NDA account and go to your profile page

<https://nda.nih.gov/user/dashboard/profile.html>

<https://nda.nih.gov/user/dashboard/profile.html>

**1. Username for Download manager tool**

**2. Reset password**

**Profile**

This page displays your personal account information. Use the menu to view your other dashboard pages. Collections and Studies allow you to manage your associated NDA Collections and Studies. Packages displays download packages you've created and allows management of mINDAR hosted databases. Data Permissions allows you to request access to shared data for research purposes.

Username:

Email Address:

First Name:

Last Name:

City:

State or Province:

Postal Code:

Country:

Work Phone Number:

My Institution: