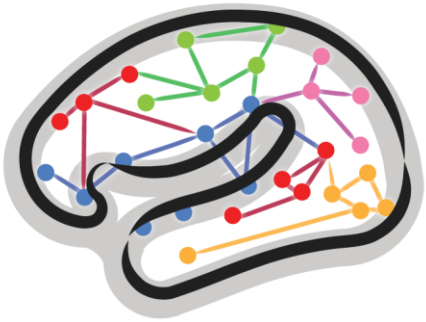


HUMAN
Connectome
PROJECT

WU-Minn HCP Open Access Initial Data Release: User Guide

Version 2 release: 21 December 2012.

Changes from Version 1:

- Diffusion imaging data are now included for all 12 subjects.
- FSL 5.0.1 was used for all processing.
- Gradient distortion correction was improved in structural images by not removing the oblique sform prior to correction. Also, gradient distortion code itself was updated to properly account for oblique sforms in all scans.
- EPI distortion correction was improved using the latest version (FSL 5.0.1+) of topup. Also, the EPI distortion correction pipeline module was rewritten to improve the alignment of the EPI distortion field estimated with topup to the fMRI data. This removes a LR/RL alignment bias that was present in Version 1.
    - There is a new file (all fMRI Runs): ${SubjectID}/MNINonLinear/Results/${fMRIName}/${fMRIName}_Jacobian.nii.gz -- Measure of the EPI distortion that was corrected by topup
- Intensity normalization is now global 4D mean=10000, rather than framewise mean=10000. This corrects an error in Version 1 where the global signal was being unintentionally removed by framewise intensity normalization.

Table of Contents

Introduction and overview

This document provides information and guidance on how to use the open access dataset released by the WU-Minn HCP consortium in October 2012, with Version 2 of the minimally pre-processed data released in December 2012. This initial data release includes data from 12 healthy adults scanned in August/September 2012, using MRI pulse sequences and protocols that were extensively optimized during the first two years of the HCP grant. The scanning modalities include structural images (T1w and T2w), resting-state fMRI (R-fMRI), task-fMRI (T-fMRI), and high angular resolution diffusion imaging (dMRI). Behavioral data from each subject is also available.

Why the initial HCP release?

The primary objective of this initial release is to enable neuroimaging-oriented investigators to become familiar with the imaging data types that have been acquired, the exceptionally high quality of the data, and the results from preprocessing pipelines that have been carried out for different modalities. **Investigators are cautioned against publishing results that are based solely on the data in this initial release**. For example, we are not yet releasing the information on family structure that would allow for control of bias due to the inclusion of twin data. Nevertheless, we anticipate that this initial release will allow investigators to prepare to do more substantive analyses beginning with our first full quarterly release in February 2013.

What comes next?

Over the next 3 years (2012-2015), a target number of 1,200 HCP subjects (twins and their non-twin siblings) will be scanned on the same scanner using the same protocol for every subject. Data will be released quarterly, starting with a Q1 release in February 2013 that will include data from ~80 subjects. The Q1 data release will be accompanied by capabilities for exploratory search queries and data mining using the ConnectomeDB database. In addition, it will offer interactive access to population-average functional connectivity maps viewed using Connectome Workbench visualization software.

Open access and controlled access databases

The initial HCP data release is fully open access, but it includes a registration process and an agreement to the Data Use Terms. For subsequent quarterly data releases, all of the imaging data and most of the behavioral data will remain open access. Demographic data (including family structure) and sensitive behavioral data will be accessed via a Controlled Access Database that includes a separate Data Use Agreement.

An important note about gradient nonlinearities. All HCP imaging data for this data release were acquired on a Siemens Skyra 3T scanner with a customized SC72 gradient insert that greatly improves the quality of diffusion imaging scans (the 'Connectome Skyra'). Higher performing gradients require compromises in bore diameter and gradient nonlinearities. Further, in custom-fitting the higher performing gradient set into a standard clinical system, technical limitations prevent centering of the subjects' heads in the bore isocenter. Consequently, the gradient nonlinearities associated with all Connectome Skyra scans exceed those of a conventional clinical 3T scanner. In the HCP processed datasets for all scan modalities (structural, fMRI, and dMRI), these distortions have been corrected for by spatially warping the images using gradient field information specific to the Connectome Skyra. The gradient unwarping code was provided by the Dale and Fischl Labs at Massachusetts General Hospital (MGH) and is available at https://github.com/ksubramz/gradunwarp/blob/master/Readme.md (Jovicich et al., 2006). The gradient field nonlinearity coefficients for the Connectome Skyra can be obtained from your Siemens collaboration manager or from Dingxin Wang at dingxin.wang@siemens.com; see Appendix 3).

Note: *If you are using the raw NIFTI datasets (Neuroimaging Informatics Technology Initiative format, see http://nifti.nimh.nih.gov), it is important to correct for the spatial distortions caused by these gradient nonlinearities, which are present in the raw images for ALL modalities.*

Version 2 of processed fMRI data

A recent improvement in preprocessing of fMRI volumes reduces distortions and yields significantly better alignment of fMRI scans to the structural MR volumes. All fMRI datasets (R-fMRI and T-fMRI) have been reprocessed and have replaced the original archives. The new 'fnca' and 'fncb' archives (see p.10; identified as version 2 in the release notes for each archive) have replaced the original archives on December 6, 2012. Be sure to keep track of the version number when carrying out further analyses of these datasets. For further details, see http://www.mail-archive.com/hcp-users@humanconnectome.org/msg00009.html (9 November 2012).

For diffusion MRI, the gradient nonlinearities also cause voxel-by-voxel changes in the strength and orientation of the diffusion encoding gradients. Consequently, the effective b-values and b-vectors in all the primary data that you can download will have variations from voxel to voxel. When analyzing the primary (raw) datasets or the preprocessed data (after distortion correction by 'TOPUP' and 'EDDY') you will need to use the code provided in Appendix 4 in your fitting routine in order to compute the correct gradient information at each voxel. In the future we will also provide an example of 4 correct 4D volumes that show the x,y,z, components of the effective gradient orientation, and the effective b-value separately at each voxel to allow the distortion correction code to be checked.

How to register and download HCP datasets?

Datasets can be downloaded by ftp (see below). The primary imaging datasets are all in NIFTI format (see http://nifti.nimh.nih.gov); DICOM versions are not currently available. To access the data, you must first

- Register at http://humanconnectome.org/data/
- Agree to the Data Use Terms
- Download using FTP, following the instructions in this document.

Data are organized by subject identifier and by scan session for each subject. See table of subject numbers and session structure (below) for details.

How do I download the data via FTP?

You can access the HCP datasets by using sftp in a terminal window or by using an FTP client, such as FileZilla.

Option 1: Downloading HCP data via the command-line.

Please see Appendix 6 for example scripts and instructions.

Option 2: Download the data using an FTP Client.

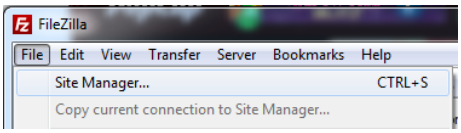
The Human Connectome Project FTP site will work with any major FTP client, as long as it supports SFTP connections (virtually all of them do). The following is a demo using FileZilla, which is a free and open-source FTP client that is available for Mac OS, Windows or Linux.

You can download FileZilla here: http://filezilla-project.org/

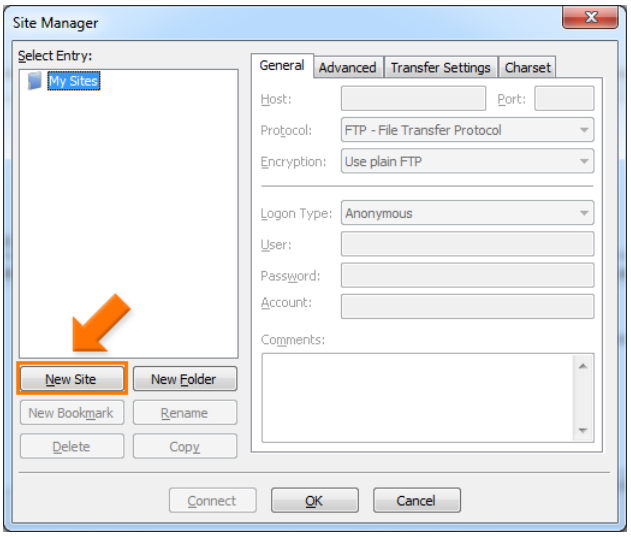
Quick connection tutorial using FileZilla

Step 1: Set up your connection

- Click on FILE > SITE MANAGER

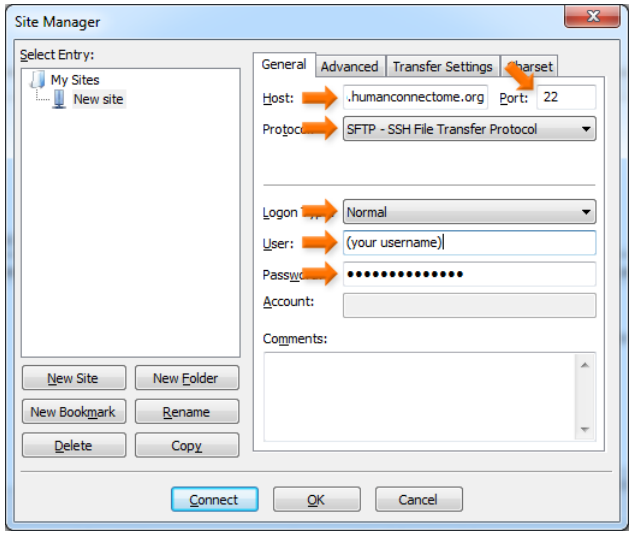


- Click on "New Site"



- Enter your FTP credentials as listed in the following table:

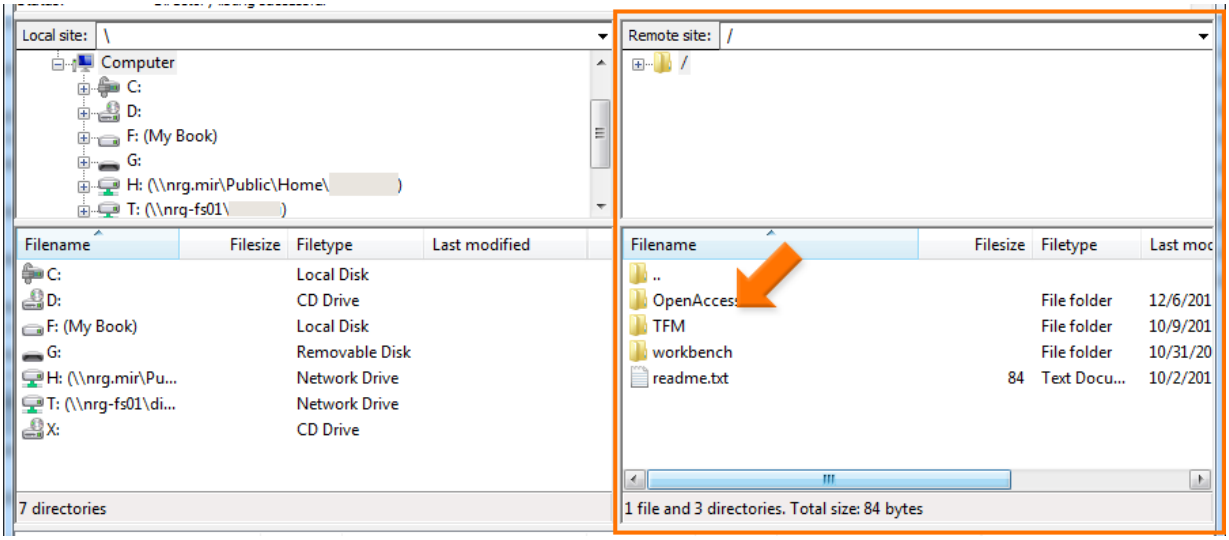
FTP Access:	**ftp.humanconnectome.org**
Login:	Your registered HCP Username
Password:	Your registered HCP Password
Directory:	/
Connection:	SFTP or FTP over SSL



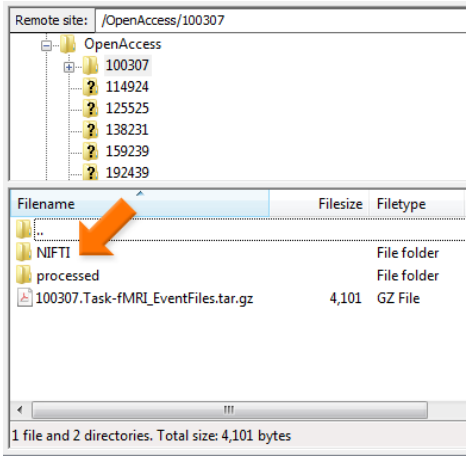
- Click "Connect" to connect and you will be logged in. You may be asked to confirm a security key on your first login. If so, click yes.

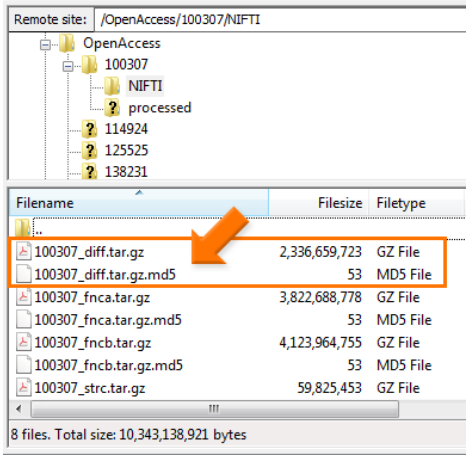
Step 2: Browse and download HCP data.

Once you are logged in, you will be able to browse data for each project that you have permission for. To get permission, you must accept the terms of use for that project via the ConnectomeDB website.



- Folders for each data set are visible on the right in FileZilla. Folders for your local file system are visible on the left.
- As you browse the data sets, you can transfer data from the FTP site to your local disk by dragging the contents of a folder from right to left.
  (Note: you cannot post non-HCP data to the public HCP FTP site.)
- Double-click on the 'OpenAccess' folder to open this project.
- Data is organized by subject, with NIFTI-formatted scan data located in the NIFTI folder.
- Inside each NIFTI folder are three sets of files, corresponding to the structural, functional, and diffusion MRI sessions that were performed on each subject.
- Each set of files consists of a tar.gz archive, and a md5 checksum. After you download the data you want, you can use the md5 file to verify the integrity of your downloaded file.





- To unzip a tar.gz file, you need an application that is compatible with gzip. For Windows users, we recommend 7-zip, which is a free utility. Linux has support for gzip built in, and Mac users can use the Mac Gzip utility.

- As noted above, the fnca and fncb data have been reprocessed, yielding better alignment to the structural MR data, and are identified as version 2 in the release notes and by a date of 12/06/2012 in the 'Last Modified' column.

- The processed datasets are also organized into Structural, fMRI, and Diffusion archives (<subject_id>_processed_structural.tar.gz, <subject_id>_processed_fMRI.tar.gz, and <subject_id>_processed_diffusion.tar.gz).

What about technical support, bug reports, and feature requests?

We anticipate a wide range of questions, suggestions, and discussion points as HCP data and software become freely available to the community. Users are strongly encouraged to join the HCP Data Users mailing list (hcp-users@humanconnectome.org) by signing up at http://www.humanconnectome.org/contact/ or by checking the appropriate box when registering to download HCP data.

Contributions to the hcp-users mailing list will be read by investigators and staff on the WU-Minn HCP consortium. Often this will entail prompt responses to answer questions or suggest solutions to technical problems. As with mailing lists for other brain-mapping platforms (e.g., FSL, FreeSurfer), investigators outside the HCP consortium are encouraged to respond as well. Bug reports and feature requests will be entered by trained HCP staff into the issue tracking system used by HCP software developers.

If you are not currently a member of the hcp-users mailing list, you can submit a feature request directly through this website at http://humanconnectome.org/contact/feature-request.php. Feature requests submitted this way will be posted to the hcp-users mailing list.

MR scanner and other hardware

Scanner hardware. All data in the initial open access release were acquired on a single Siemens Skyra 3T scanner housed at Washington University in St. Louis. The scanner has a customized SC72 gradient insert and a customized body transmitter coil with 56 cm bore size (*diffusion*: Gmax = 100 mT/m, max slew rate = 91 mT/m/ms; *readout/imaging*: Gmax = 42 mT/m, max slew rate = 200 mT/m/ms). The HCP Skyra has the standard set of Siemen's shim coils (up to 2nd order) and the HCP is using Siemens's standard 32 channel head coil.

Visual projection and E-Prime computer. Visual stimuli were presented and participant responses were collected using a Dell Optiplex 790 computer, running an Intel Core i3-2100 with 8GB of RAM and 64-bit Windows 7 Enterprise SP1. The E-Prime version was E-Prime 2.0 Professional Production Release (2.0.10.242). Visual stimuli were projected with a NEC V260X projector onto a lucite screen at 1024x768 resolution, and viewed by the participant using a mirror mounted on the top of the head coil. Participant responses were registered on a customized fiber-optic button box.

Summary of imaging protocols

Structural, fMRI, and dMRI acquisitions were collected over 4 total imaging sessions, each approximately 1 hour in duration. Resting-state and task fMRI data was collected in two sessions. Each session consisted of two resting-state acquisitions of approximately 15 minutes each, followed by two task-evoked acquisitions of approximately 15 minutes each.

Vitamin E capsule on right side. A capsule of vitamin E was taped to the subject's right temple in every scan session, to enable definitive determination of the right side in the image data.

The following provides basic parameters for the main scan types in each session, and pertinent details about each session. A more complete set of imaging parameters can be found in the protocol exports from the scanner, available in Appendix 1. FOV positioning in all runs was handled in an automated manner using Siemens AutoAlign feature.

Structural session

Type	Series Description	Description	TR (ms)	TE (ms)	TI (ms)	Flip Angle	FOV (mm)	Voxel Size	BW (Hz/Px)	iPAT	Acquisition Time (min:sec)
T1w	T1w_MPR1	3D MPRAGE	2400	2.14	1000	8 deg	224x224	0.7 mm isotropic	210	2	7:40
T2w	T2w_SPC1	3D T2-SPACE	3200	565		variable	224x224	0.7 mm isotropic	744	2	8:24

Resting-state fMRI (R-fMRI)

R-fMRI data were acquired in four runs of approximately 15 minutes each, two runs in one session and two in another session, with eyes open with relaxed fixation on a projected bright cross-hair on a dark background. Within each session, oblique axial acquisitions alternated between phase encoding in a right to left (RL) direction in one run and phase encoding in a left to right (LR) direction in the other run.

Resting state images were collected with the following parameters:

Parameter	Value
Sequence	Gradient-echo EPI
TR	720 ms
TE	33.1 ms
flip angle	52 deg
FOV	208x180 mm (RO x PE)

Parameter	Value
Matrix	104x90 (RO x PE)
Slice thickness	2.0 mm; 72 slices; 2.0 mm isotropic voxels
Multiband factor	8
Echo spacing	0.58 ms
BW	2290 Hz/Px

Condition	Runs	Frames per run	Run Duration (min:sec)
REST (Resting-state)	4	1200	14:33

Task-evoked fMRI (T-fMRI)

Following completion of R-fMRI in each of the two functional scanning sessions, subjects were asked to complete tasks that were designed to activate a variety of cortical and subcortical networks. The following table provides a listing of the fMRI scans collected. For each scan type, half the runs were acquired with right to left phase encoding, and the other half with left to right phase encoding (in-plane FOV [field of view] rotation obtained by inverting both the RO (readout) and PE [phase encoding] gradient polarity).

T-fMRI data were acquired with the same EPI pulse sequence parameters as R-fMRI, except for the timing information listed below. There are seven tasks (14 scan runs) totaling one hour of scan time, split into two scan sessions.

Task	Runs	Frames per run	Run Duration (min:sec)
Working Memory	2	405	5:01
Gambling	2	253	3:12
Motor	2	284	3:34
Language	2	316	3:57
Social Cognition	2	274	3:27
Relational Processing	2	232	2:56
Emotion Processing	2	176	2:16

A field map was also acquired in each of the fMRI scan sessions.

For additional information about Task-FMRI protocols, see Details of Task-fMRI protocol (Timing and Task Demands). To obtain the E-Prime files so that you have the option to run HCP

tasks in your own research project, contact Greg Burgess via email at burgessg@pcg.wustl.edu, please put "HCP E-Prime files" in the subject line of your message.

Diffusion imaging (dMRI)

Parameter	Value
Sequence	Spin-echo EPI
TR	5520 ms
TE	89.5 ms
flip angle	78 deg
refocusing flip angle	160 deg
FOV	210x180 (RO x PE)
matrix	168x144 (RO x PE)
slice thickness	1.25 mm, 111 slices, 1.25 mm isotropic voxels
Multiband factor	3
Echo spacing	0.78 ms
BW	1488 Hz/Px
Phase partial Fourier	6/8
b-values	1000, 2000, and 3000 s/mm^2

Other details: Monopolar diffusion gradients; Oblique axial acquisitions alternating between the right to left and left to right phase encoding directions in consecutive runs; SENSE1 multi-channel image reconstruction.

A full dMRI session consisted of 6 runs (each approximately 9 minutes and 50 seconds), representing 3 different gradient tables, with each table acquired once with right to left and left to right phase encoding polarities, respectively. Each gradient table consisted of approximately 90 diffusion weighting directions plus 6 b=0 acquisitions interspersed throughout each run. Diffusion weighting consisted of 3 shells of b=1000, 2000, and 3000 s/mm^2 interspersed with an approximately equal number of acquisitions on each shell within each run. The diffusion directions were obtained using a toolbox available from INRIA that returns uniformly distributed directions in multiple q-space shells. The directions are optimized so that every subset of the first M directions is also isotropic. References and the INRIA toolbox can be found at: http://www-sop.inria.fr/members/Emmanuel.Caruyer/q-space-sampling.php.

Quality Control measures

Each structural scan in the open access dataset has been visually evaluated and judged as being either good or excellent in quality (scans determined to be fair or poor in quality will not be included in HCP data releases). All structural and functional scans have been evaluated with a

variety of automated Quality Control (QC) algorithms, e.g. to verify that they include the expected number of frames and conformed to the protocol. In addition, QC evaluations of the minimally preprocessed datasets have been carried out for all structural scans (volumes and surfaces) and all fMRI scans. A complete description of Quality Control measures will be included with future releases. Many of these QC measures will be made available for each subject and each scan in future releases.

Full scanning protocols (PDF)

Complete scanning protocols for each imaging modality can be found in Appendix 1.

Summary of behavioral measures

NIH Toolbox behavioral measures will be included in future releases.

Non-Toolbox measures

The Non-Toolbox behavioral measures included in this release are:

- Visual processing – Farnsworth color vision test, Mars contrast sensitivity test
- Personality - Costa and McRae Neuroticism/Extroversion/Openness Five Factor Inventory
- Self-regulation (delay discounting)
- Sustained attention
- Verbal episodic memory.
- Emotion processing
- Spatial processing
- Fluid intelligence
- Self-reported function

Detailed descriptions of these measures can be found in the section entitled, "**Details of Behavioral Measures**".

Data in this release

Twelve healthy adult subjects in the age range 22 – 35 were tested. Subjects include both left- and right-handed individuals and both men and women.

Standard session structure

Each subject was scanned in four regular sessions (~4 hours total), with the following shorthand labels:

Day 1:

- strc: Structural scans (two T1w and two T2w scans)
- fnca: Two 15-min R-fMRI scans (RL and LR phase encoding) and three T-fMRI tasks (one RL and one LR scan for each task)

Day 2:

- diff: dMRI scan
- fncb: Two 15-min R-fMRI scans (RL and LR phase encoding) and the four remaining T-fMRI tasks (one RL and one LR scan for each task)
- Note: on scans acquired after Oct 1, counterbalancing of phase encoding directions was introduced by acquiring the R-fMRI fncb scans in the reverse order (LR then RL) relative to the fnca session. This counterbalancing was not done for any subjects in the initial data release.

In some cases, scans were acquired in an extra session (coded 'xtra' if it was a single extra session or 'xtrb' if it was a second extra session). This was done if the data quality was inadequate in the regular scan or if technical problems prevented a full set of acquisitions in the regular session.

DICOM to NIFTI conversion

Conversion of DICOM files to NIFTI format was carried out using the dcm2nii utility. This utility is a component of the MRIcron suite of tools developed by Chris Rorden: (http://www.nitrc.org/frs/?group_id=152).

File sizes of open access datasets

The compressed NIFTI tar.gz files total 10 – 14 GB per subject for the unprocessed data. The structural data ('strc') range from 60 – 100 MB; each of the BOLD sessions ('fnca' and 'fncb', each including R-fMRI and T-fMRI scans) are 4 – 6 GB in size; and the diffusion session is about 2.3 GB in size. Please be mindful of your internet bandwidth when downloading these data. After unpacking, the total file size changes little because most files are *.nii.gz.

The processed files are about 16 GB per subject for the tar.gz files (1.2 GB for the structural, 12 GB for the fMRI, and 3 GB for the diffusion.

Note: *Make sure you have sufficient disk space to handle whatever files you download and unpack.*

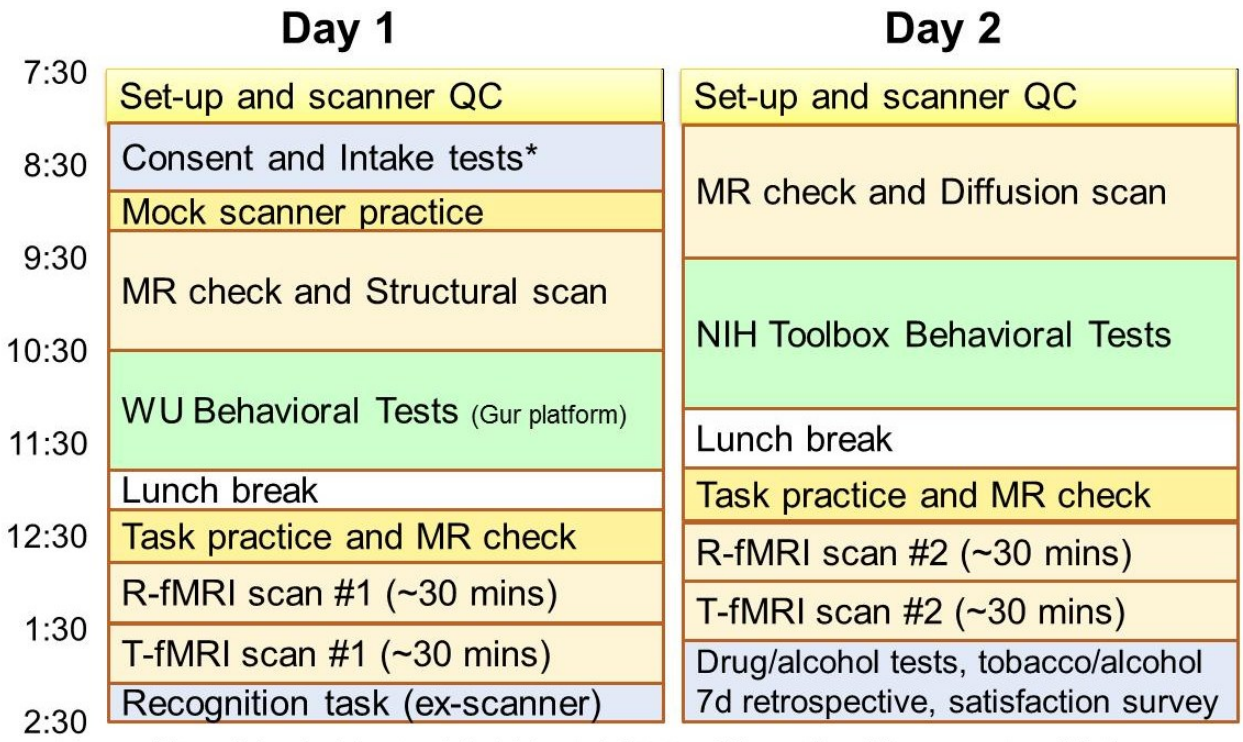
Sessions containing imaging data for each subject

Data for each imaging modality can be found in the following sessions:

Subject ID	Structurals	Diffusion	R-fMRI	T-fMRI
100307	strc	diff	fnca, fncb	fnca, fncb
114924	strc	diff	fnca, fncb	fnca, fncb
125525	strc	diff	fnca, fncb	fnca, fncb
138231	strc	**xtra**	fnca, fncb	fnca, fncb
159239	**xtra**	diff	fnca, fncb	fnca, fncb
192439	strc	diff	fnca, fncb	fnca, fncb
197550	strc	diff	fnca, fncb	fnca, fncb
249947	strc	diff	fnca, fncb	fnca, fncb
255639	strc	diff	fnca, fncb	fnca, fncb
499566	strc	diff	fnca, fncb	fnca, fncb
672756	strc	diff	fnca, fncb	fnca, **xtra**
792564	strc	diff	fnca, fncb	fnca, fncb

Standard two-day schedule for subject visits.

Most subjects complete the full HCP protocol during a two-day visit. A typical schedule is shown below. Scan sessions are always done in the order shown below, unless problems with a scan necessitate a rescan in an extra imaging session.



*Drug/alcohol tests, Mini Mental State, Sleep Quality, menstrual info, hematocrit, blood for genotyping. In Nov. will add HbA1c and TSH.

File naming conventions for primary datasets

The NIFTI file name consists of the experiment id, the scan type, and the series description: {ExperimentID}_{Modality}_{SeriesDesc(lowercase)}.nii.gz

Structurals (strc)

Scan Type	Series Description	NIFTI File Name
Localizer	Localizer	Not released
AAHScout	AAHScout	Not released
Localizer_aligned	Localizer_aligned	Not released
***Bias_Receive**	BIAS_BC	792564_strc_BIAS_BC.nii.gz*
***Bias_Receive**	BIAS_32CH	792564_strc_BIAS_32CH.nii.gz*
T1w	T1w_MPR1	792564_strc_T1w_MPR1.nii.gz
T2w	T2w_SPC1	792564_strc_T2w_SPC1.nii.gz
T1w	T1w_MPR2	792564_strc_T1w_ MPR2.nii.gz
T2w	T2w_SPC2	792564_strc_T2w_SPC2.nii.gz
***FieldMap**	FieldMap_Magnitude	792564_strc_FieldMap_Magnitude_1.nii.gz*
***FieldMap**	FieldMap_Phase	792564_strc_FieldMap_Phase_1.nii.gz*
***Bias_Transmit**	AFI	792564_strc_AFI.nii.gz*
*** To be included in a future release**		

Functional A (fnca)

Scan Type	Series Description	NIFTI File Name
Localizer	Localizer	Not released
AAHScout	AAHScout	Not released
Localizer_aligned	Localizer_aligned	Not released
***Bias_Receive**	BIAS_BC	792564_fnca_BIAS_BC.nii.gz*
***Bias_Receive**	BIAS_32CH	792564_fnca_BIAS_32CH.nii.gz*
FieldMap_SE_EPI	BOLD_RL_SB_SE	792564_fnca_BOLD_RL_SB_SE_1.nii.gz
FieldMap_SE_EPI	BOLD_LR_SB_SE	792564_fnca_BOLD_LR_SB_SE_1.nii.gz
rfMRI_SBRef**	BOLD_REST1_RL_SBRef	792564_fnca_BOLD_REST1_RL_SBRef.nii.gz
rfMRI	BOLD_REST1_RL	792564_fnca_BOLD_REST1_RL.nii.gz
rfMRI_SBRef	BOLD_REST2_LR_SBRef	792564_fnca_BOLD_REST2_LR_SBRef.nii.gz
rfMRI	BOLD_REST2_LR	792564_fnca_BOLD_REST2_LR.nii.gz

Scan Type	Series Description	NIFTI File Name
*FieldMap	FieldMap_Magnitude	792564_fnca_FieldMap_Magnitude_1.nii.gz*
*FieldMap	FieldMap_Phase	792564_fnca_FieldMap_Phase_1.nii.gz*
FieldMap_SE_EPI	BOLD_RL_SB_SE	792564_fnca_BOLD_RL_SB_SE_2.nii.gz
FieldMap_SE_EPI	BOLD_LR_SB_SE	792564_fnca_BOLD_LR_SB_SE_2.nii.gz
tfMRI_SBRef	BOLD_WM1_RL_SBRef	792564_fnca_BOLD_WM1_RL_SBRef .nii.gz
tfMRI	BOLD_WM1_RL	792564_fnca_BOLD_WM1.nii.gz
tfMRI_SBRef	BOLD_WM2_LR_SBRef	792564_fnca_BOLD_WM2_LR_SBRef.nii.gz
tfMRI	BOLD_WM2_LR	792564_fnca_BOLD_WM2_LR.nii.gz
tfMRI_SBRef	BOLD_GAMBLING1_RL_SBRef	792564_fnca_BOLD_GAMBLING1_RL_SBRef.nii.gz
tfMRI	BOLD_GAMBLING1_RL	792564_fnca_BOLD_GAMBLING1_RL.nii.gz
tfMRI_SBRef	BOLD_GAMBLING2_LR_SBRef	792564_fnca_BOLD_GAMBLING2_LR_SBRef.nii.gz
tfMRI	BOLD_GAMBLING2_LR	792564_fnca_BOLD_GAMBLING2_LR.nii.gz
tfMRI_SBRef	BOLD_MOTOR1_RL_SBRef	792564_fnca_BOLD_MOTOR1_RL_SBRef.nii.gz
tfMRI	BOLD_MOTOR1_RL	792564_fnca_ BOLD_MOTOR1_RL.nii.gz
tfMRI_SBRef	BOLD_MOTOR2_LR_SBRef	792564_fnca_BOLD_MOTOR2_LR_SBRef.nii.gz
tfMRI	BOLD_MOTOR2_LR	792564_fnca_BOLD_MOTOR2_LR.nii.gz
*FieldMap	FieldMap_Magnitude	792564_fnca_FieldMap_Magnitude_2.nii.gz*
*FieldMap	FieldMap_Phase	792564_fnca_FieldMap_Phase_2.nii.gz*

*** To be included in a future release**

**** The "SBRef" volumes are single-band reference images of high quality and increased contrast that are automatically generated as part of the multi-band imaging sequence. See section (D) of *Pre-Processing Pipelines* for a brief description of how they are used.**

Diffusion (diff)

Scan Type	Series Description	NIFTI File Name
Localizer	Localizer	Not released
AAHScout	AAHScout	Not released
Localizer_aligned	Localizer_aligned	Not released
Bias_Receive	BIAS_BC	792564_diff_BIAS_BC.nii.gz
Bias_Receive	BIAS_32CH	792564_diff_BIAS_32CH.nii.gz
dMRI_SBRef	DWI_RL_dir95_SBRef	792564_diff_DWI_RL_dir95_SBRef.nii.gz
dMRI	DWI_RL_dir95	792564_diff_DWI_RL_dir95.nii.gz
dMRI_SBRef	DWI_LR_dir95_SBRef	792564_diff_DWI_LR_dir95_SBRef.nii.gz
dMRI	DWI_LR_dir95	792564_diff_DWI_LR_dir95.nii.gz
dMRI_SBRef	DWI_RL_dir96_SBRef	792564_diff_DWI_RL_dir96_SBRef.nii.gz
dMRI	DWI_RL_dir96	792564_diff_DWI_RL_dir96.nii.gz

Scan Type	Series Description	NIFTI File Name
dMRI_SBRef	DWI_LR_dir96_SBRef	792564_diff_DWI_LR_dir96_SBRef.nii.gz
dMRI	DWI_LR_dir96	792564_diff_DWI_LR_dir96.nii.gz
dMRI_SBRef	DWI_RL_dir97_SBRef	792564_diff_DWI_RL_dir97_SBRef.nii.gz
dMRI	DWI_RL_dir97	792564_diff_DWI_RL_dir97.nii.gz
dMRI_SBRef	DWI_LR_dir97_SBRef	792564_diff_DWI_LR_dir97_SBRef.nii.gz
dMRI	DWI_LR_dir97	792564_diff_DWI_LR_dir97.nii.gz
FieldMap	FieldMap_Magnitude	792564_diff_FieldMap_Magnitude_1.nii.gz
FieldMap	FieldMap_Phase	792564_diff_FieldMap_Phase_1.nii.gz

Functional B (fncb)

Scan Type	Series Description	NIFTI File Name
Localizer	Localizer	Not released
AAHScout	AAHScout	Not released
Localizer_aligned	Localizer_aligned	Not released
***Bias_Receive**	BIAS_BC	792564_fncb_BIAS_BC.nii.gz*
***Bias_Receive**	BIAS_32CH	792564_fncb_BIAS_32CH.nii.gz*
FieldMap_SE_EPI	BOLD_RL_SB_SE	792564_fncb_BOLD_RL_SB_SE_1.nii.gz
FieldMap_SE_EPI	BOLD_LR_SB_SE	792564_fncb_BOLD_LR_SB_SE_1.nii.gz
rfMRI_SBRef	BOLD_REST3_RL_SBRef	792564_ fncb_BOLD_REST3_RL_SBRef.nii.gz
rfMRI	BOLD_REST3_RL	792564_ fncb_BOLD_REST3_RL.nii.gz
rfMRI_SBRef	BOLD_REST4_LR_SBRef	792564_ fncb_BOLD_REST4_LR_SBRef.nii.gz
rfMRI	BOLD_REST4_LR	792564_ fncb_BOLD_REST4_LR.nii.gz
***FieldMap**	FieldMap_Magnitude	792564_ fncb_FieldMap_Magnitude_1.nii.gz*
***FieldMap**	FieldMap_Phase	792564_ fncb_FieldMap_Phase_1.nii.gz*
FieldMap_SE_EPI	BOLD_RL_SB_SE	792564_ fncb_BOLD_RL_SB_SE_2.nii.gz
FieldMap_SE_EPI	BOLD_LR_SB_SE	792564_ fncb_BOLD_LR_SB_SE_2.nii.gz
tfMRI_SBRef	BOLD_LANGUAGE1_RL_SBRef	792564_ fncb_BOLD_LANGUAGE1_RL_SBRef.nii.gz
tfMRI	BOLD_LANGUAGE1_RL	792564_ fncb_BOLD_LANGUAGE1_RL.nii.gz
tfMRI_SBRef	BOLD_LANGUAGE2_LR_SBRef	792564_ fncb_BOLD_LANGUAGE2_LR_SBRef.nii.gz
tfMRI	BOLD_LANGUAGE2_LR	792564_ fncb_BOLD_LANGUAGE2_LR.nii.gz
tfMRI_SBRef	BOLD_SOCIAL1_RL_SBRef	792564_ fncb_BOLD_SOCIAL1_RL_SBRef.nii.gz
tfMRI	BOLD_SOCIAL1_RL	792564_ fncb_BOLD_SOCIAL1_RL.nii.gz
tfMRI_SBRef	BOLD_SOCIAL2_LR_SBRef	792564_ fncb_BOLD_SOCIAL2_LR_SBRef.nii.gz

Scan Type	Series Description	NIFTI File Name
tfMRI	BOLD_SOCIAL2_LR	792564_ fncb_BOLD_SOCIAL2_LR.nii.gz
tfMRI_SBRef	BOLD_RELATIONAL1_RL_SBRef	792564_ fncb_BOLD_RELATIONAL1_RL_SBRef.nii.gz
tfMRI	BOLD_RELATIONAL1_RL	792564_ fncb_BOLD_RELATIONAL1_RL.nii.gz
tfMRI_SBRef	BOLD_RELATIONAL2_LR_SBRef	792564_ fncb_BOLD_RELATIONAL2_LR_SBRef.nii.gz
tfMRI	BOLD_RELATIONAL2_LR	792564_fncb_BOLD_RELATIONAL2_LR.nii.gz
***FieldMap**	FieldMap_Magnitude	792564_ fncb_FieldMap_Magnitude_2.nii.gz*
***FieldMap**	FieldMap_Phase	792564_ fncb_FieldMap_Phase_2.nii.gz*
*** To be included in a future release**		

Structure of NIFTI subdirectory on the FTP site

"NIFTI" – Neuroimaging Informatics Technology Initiative (see http://nifti.nimh.nih.gov/)

- Inside each NIFTI folder are four sets of files, corresponding to the structural, functional, and diffusion MRI sessions that were performed on each subject.
- Each set of files consists of a tar.gz archive, and an md5 checksum. After you download the data you want, you can use the md5 file to verify the integrity of your downloaded file.
- For instructions on downloading from the FTP site, see How do I download the data via FTP? in this document.

Pre-processing pipelines

Structural MR and fMRI datasets were processed by a set of 6 pipelines aimed at providing high quality volume and surface data. These pipelines use freely available software from the FSL (Jenkinson M et al, 2012; http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/) and FreeSurfer (Dale AM et al, 1999; http://surfer.nmr.mgh.harvard.edu/) image analysis suites, and will be discussed in detail in a future publication (Glasser MG, Wilson, A, Coalson T, Fischl B, Andersson J, Xu J, Webster M, Polimeni J, Subramaniam K, Van Essen DC and Jenkinson M, in preparation). 'TOPUP' (Andersson JLR et al, 2003; http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/TOPUP) and 'EDDY' are tools distributed with FSL.

Diffusion data were preprocessed with a number of newly developed tools that are distributed as a part of FSL. The pipeline takes care of removing spatial distortions (some unique to HCP data) and cross-modal registration to the structural images. The pipeline will be described in the HCP Special Issue of Neuroimage to be published in 2013 (Glasser, Jenkinson, et al., in preparation).

A summary of the major processing steps for each pipeline is provided below.

A) Structural image processing pipeline

1. Gradient distortion correction
2. Coregistration and averaging of T1w and T2w runs
3. ACPC (i.e. 6 dof) registration for T1w and T2w (FLIRT plus a customized script). The acpc registered distortion corrected T1w image is in the "native" volume space.
4. Initial brain extraction for T1w and T2w (FNIRT-atlas-based-brain-mask)
5. Field map distortion correction and registration of T2w to T1w using a customized FLIRT BBR algorithm.
6. Bias field correction using sqrt(T1w X T2w) (Rilling et al, 2011)
7. Atlas registration (FLIRT linear + FNIRT nonlinear to MNI152)

B) FreeSurfer pipeline

1. Downsampling of 0.7mm T1w to 1mm using splines
2. Initial FreeSurfer steps (autorecon1 except -skullstrip)
3. Initialize FreeSurfer with skull registration using PreFreeSurfer brain mask for a more robust registration
4. FreeSurfer skullstripping
5. Further early FreeSurfer processing steps (-autorecon2 -nosmooth2 -noinflate2)
6. Adjustment of white matter surface placement using hires T1w (full 0.7mm data) with a customized mri_normalize, mris_make_surfaces, and fine tuning of T2w to T1w registration using bbregister

7. Middle FreeSurfer steps (-smooth2 -inflate2 -sphere -surfreg -jacobian_white -avgcurv -cortparc)
8. Creation of pial surface using hires T1w (full 0.7mm data) and adjustment of pial surface placement using hires T2w (full 0.7mm data) with a customized mris_make_surfaces to remove vessels and dura. Then grey matter intensity normalization of T1w, regeneration of pial surface and adjustment with T2w.
9. Final FreeSurfer steps (-surfvolume -parcstats -cortparc2 -parcstats2 -cortribbon -segstats -aparc2aseg -wmparc -balabels -label-exvivo-ec)

C) Post FreeSurfer processing pipeline

1. Creation of Caret5 and Connectome Workbench datafiles and spec files, creation of FreeSurfer segmentation brain mask, surface registration and downsampling, volume transformation of surfaces nonlinearly into MNI space
2. Creation of FreeSurfer ribbon files with full 0.7mm resolution data (masks of grey matter and white matter)
3. Myelin mapping and combination of all transforms for one step resampling of T1w and T2w images from original to MNI space (Glasser and Van Essen, 2011).

D) Volume generic fMRI processing pipeline (Volume-based analysis starts at the end of this pipeline)

1. Gradient distortion correction
2. FLIRT-based motion correction using the "SBRef" volume as the target (Smith SM *et al.*, in preparation).
3. TOPUP-based field map preprocessing using Spin echo field map (for each day of each BOLD run) [Note: An improved version of TOPUP was used for the version 2 release].
4. Distortion correction and EPI to T1w registration of the "SBRef" volume using a customized FLIRT BBR algorithm for distortion correction and bbregister to fine tune the registration.

Note: *This stage was modified for the version 2 release. Distortion correction and EPI to T1w registration now occur in separate steps. An improved TOPUP-based field map correction occurs first, followed by undistorted EPI to T1w registration using FLIRT BBR plus bbregister. Intensity inhomogeneities resulting from EPI distortion are corrected with Jacobian modulation.*

5. One step spline resampling from the original EPI frames to atlas space including all transforms (motion, EPI distortion, EPI to T1w from FLIRT BBR, fine tuning of EPI to T1w with bbregister, nonlinear T1w to MNI)
6. Intensity normalization to mean of 10000 (like in FEAT) and bias field removal. Brain mask based on FreeSurfer segmentation.

Note: *Version 1 normalization was inadvertently carried out separately on each time point ('-inm' instead of the desired '-ing' flag in a key FSL command). In all Version 2 data, normalization was carried out on the full (4D) timeseries volume.*

E) Surface generic fMRI processing pipeline (Surface-based analysis starts at the end of this pipeline)*

1. Cortical ribbon-based volume to surface mapping (from MNI space 2mm volume to MNI space native mesh surface).
    1. Voxels between white and pial surface are included in mapping. Voxels that are only partially between white and pial surface are weighted according to their partial volume that is between the two surfaces.
    2. Voxels with a temporal coefficient of variance greater than 0.5 standard deviations of their local neighborhood (sigma=5mm) are excluded from volume to surface mapping. The practical effect of this is to remove any small vessels and brain rim voxels remaining in the ribbon.
    3. Transformation of timeseries from native mesh to fs_LR registered 32k mesh (2mm average vertex spacing) in a single step
2. Surface-based smoothing (2mm FWHM)
3. Subcortical parcel-constrained smoothing and atlas resampling (2mm FWHM)
4. Creation of dense timeseries (on a standard set of brain ordinates).

Note: *Version 2 of the surface fMRI datasets makes use of the reduced distortion corrections achieved with version 2 of the volume fMRI pipeline, even though the surface processing steps were not modified.*

F) Diffusion processing pipeline

1. Basic preprocessing: Intensity normalization across runs, preparation for later modules
2. 'TOPUP' algorithm for EPI distortion correction
3. 'EDDY' algorithm for eddy current and motion correction
4. Gradient nonlinearity correction, calculation of gradient bvalue/bvector deviation
5. Registration of mean b0 to native volume T1w with FLIRT BBR+bbregister, and generation of diffusion to MNI transform

File names and directory structure for processed datasets.

Preprocessing generates thousands of files, many of which are of little or no use. The initial open access release provides a subset of files that are likely to be of general use to investigators. A list of file names in each directory and subdirectory is provided in Appendix 2, "File Names and Directory Structure of HCP Processed Data Oct 2012 (v2)".

Structural data:

- T1w/ contains T1w and T2w volume data
- T1w/Native/ contains FreeSurfer surfaces in their native mesh and original dimensions after rigid-body rotation to AC-PC alignment.
-
- MNINonLinear/ contains cortical surfaces and other data volumetrically registered to FNIRT NonLinear MNI space followed by surface registration to Conte69 '164k_fs_LR' mesh (via FreeSurfer fsaverage as an intermediate).
- MNINonLinear/Native/ replicates some of the files in T1w/Native/ but contains additional files used during surface-based registration.
- MNINonLinear/xfms/ contains files encoding the transformation between acpc and MNINonLinear volumetric space
- MNINonLinear/fsaverage_LR32k contains files spatially downsampled to a 32k mesh (average vertex spacing of ~2 mm), which is useful for analyses of R-fMRI and dMRI connectivity data.

BOLD data

- MNINonLinear/Results/ contains volumetric data for R-fMRI scans (15 min each) and motion parameters in four subdirectories
    - BOLD_REST1_RL
    - BOLD_REST2_LR
    - BOLD_REST3_RL
    - BOLD_REST4_LR

  plus volumetric data for 7 pairs of T-fMRI scans (each task run once with right-to-left and once with left-to-right phase encoding

    - BOLD_EMOTION1_RL
    - BOLD_EMOTION2_LR
    - BOLD_GAMBLING1_RL
    - BOLD_GAMBLING2_LR
    - BOLD_LANGUAGE1_RL
    - BOLD_LANGUAGE2_LR
    - BOLD_MOTOR1_RL

- BOLD_MOTOR2_LR
- BOLD_RELATIONAL1_RL
- BOLD_RELATIONAL2_LR
- BOLD_SOCIAL1_RL
- BOLD_SOCIAL2_LR
- BOLD_WM1_RL
- BOLD_WM2_LR

- **Motion parameters.** Estimates of motion parameters are saved into two different files - Movement_Regressors.txt and Movement_Regressors_dt.txt. The first file (Movement_Regressors.txt) contains 12 variables. The first six variables are the motion parameters estimates from a rigid-body transformation to the SBRef image acquired immediately prior to that scan.

  - trans_x (mm)
  - trans_y (mm)
  - trans_z (mm)
  - rot_x (deg)
  - rot_y (deg)
  - rot_z (deg)

  The second six variables are temporal derivatives of those motion parameters

  - trans_dx
  - trans_dy
  - trans_dz
  - rot_dx
  - rot_dy
  - rot_dz

  The second file (Movement_Regressors_dt.txt) contains 12 variables derived by removing the mean and linear trend from each variable in Movement_Regressors.txt

Diffusion Data

- Diffusion data includes diffusion weighting, direction, time series, brain mask, and gradient nonlinearity data, with the following files and directory structure:
  - Diffusion/data/bvals (contains the diffusion weighting (b value) for each timepoint)
  - Diffusion/data/bvecs (contains the diffusion direction (b vector) for each time point)
  - Diffusion/data/data.nii.gz (preprocessed diffusion time series file)
  - Diffusion/data/nodif_brain_mask.nii.gz (brain mask in diffusion space)
  - Diffusion/data/grad_dev.nii.gz (contains the effects of gradient nonlinearities on the bvals and bvecs for each voxel)

- Transforms for diffusion analysis are contained in the following files:
  - T1w/xfms/diff2str.mat (diffusion space to native [structural] volume space 6 degrees of freedom [dof] transform)
  - T1w/xfms/str2diff.mat (native [structural] volume space to diffusion space 6 dof transform)
  - MNINonLinear/xfms/diff2standard.nii.gz (diffusion space to MNI volume space nonlinear transform)
  - MNINonLinear/xfms/standard2diff.nii.gz (MNI volume space to diffusion space nonlinear transform)

Standard Operating Procedures (SOPs)

A major effort has been made to establish consistent procedures for all aspects of data acquisition and data processing. These are described in a set of Standard Operating Procedures (SOPs) that are included in Appendix 5. These SOPs provide a useful reference for investigators wanting to know more about exactly what was done. Any outdated versions of SOPs are retained and are available on request.

Details of Task-fMRI protocol (timing and task demands)

Task-Evoked Functional Brain Activity

We assessed seven major domains that we think sample the diversity of neural systems that will be of interest to a wide range of individuals in the field, including: 1) visual, motion, somatosensory, and motor systems; 2) category specific representations; 3) working memory/cognitive control systems; 4) language processing (semantic and phonological processing); 5) social cognition (Theory of Mind); 6) relational processing; and 7) emotion processing. These tasks are described in more detail below. Stimuli were projected onto a computer screen behind the subject's head within the imaging chamber. The screen was viewed by a mirror positioned approximately 8 cm above the subject's face.

Working Memory

The category specific representation task and the working memory task are combined into a single task paradigm. Participants were presented with blocks of trials that consisted of pictures of places, tools, faces and body parts (non-mutilated parts of bodies with no "nudity"). Within each run, the 4 different stimulus types were presented in separate blocks. Also, within each run, ½ of the blocks use a 2-back working memory task and ½ use a 0-back working memory task (as a working memory comparison). A 2.5 second cue indicates the task type (and target for 0-back) at the start of the block. Each of the two runs contains 8 task blocks (10 trials of 2.5 seconds each, for 25 seconds) and 4 fixation blocks (15 seconds). On each trial, the stimulus is presented for 2 seconds, followed by a 500 ms inter-task interval (ITI).

Conditions (Blocked)	
0-back faces	2-back faces
0-back places	2-back places
0-back tools	2-back tools
0-back body parts	2-back body parts

Conditions (Event-Related)	
0-back correct trials	2-back correct trials
0-back error trials	2-back error trials
0-back no response trials	2-back no response trials

Additional Contrasts. These event types can be combined to create two categories of contrasts.

Working Memory Contrasts
0-back contrast (activity combined across conditions 1-4)
2-back contrast (activity combined across conditions 5-8)
2-back versus 0-back contrast (2-back contrast minus 0-back contrast)

Category Contrasts	
Faces contrast	(0-back faces plus 2-back faces)
Places contrast	(0-back places plus 2-back places)
Tools contrast	(0-back tools plus 2-back tools)
Body contrast	(0-back body plus 2-back body)

Potential Additional Event Related Contrasts: Researchers can also use the EV output files to generate the following potential event-related contrasts:

1. Targets
    a. For 2-back tasks, targets are 2-back repeats
    b. For 0-back tasks, targets match the cue stimulus
2. Non-targets
    a. For 2-back tasks, non-targets are novel items
    b. For 0-back tasks, non-targets do not match the cue stimulus
3. Lures
    a. For 2-back tasks, lures are 1-back or 3-back repeats
    b. For 0-back tasks, lures are repeated stimuli that do not match the cue stimulus

Recognition Memory

After participants exit the scanner from the session that includes the working memory tasks, they are given a Remember, Know, New item recognition test for the faces and places that were presented during the working memory task. Responses to this recognition memory test can be used to create events to analyze the working memory trials as a function of whether the item

was subsequently recognized (remember or know) or not (new). This is referred to as a subsequent memory analysis.

References for Working Memory: Localizer (Drobyshevsky et al. 2006); Reliable across subjects (Drobyshevsky et al. 2006) and time (Caceres et al. 2009).

References for Category-Specific Representations: Faces, Places, Tools and Body Parts: Localizer (Downing et al. 2001; Peelen and Downing 2005; Taylor et al. 2007; Fox et al. 2009); Reliable across subjects (Downing et al. 2001; Fox et al. 2009) and time (Peelen and Downing 2005; Kung et al. 2007).

Gambling

This task was adapted from the one developed by Delgado and Fiez (Delgado et al. 2000). Participants play a card guessing game where they are asked to guess the number on a mystery card (represented by a "?") in order to win or lose money. Participants are told that potential card numbers range from 1-9 and to indicate if they think the mystery card number is more or less than 5 by pressing one of two buttons on the response box. Feedback is the number on the card (generated by the program as a function of whether the trial was a reward, loss or neutral trial) and either: 1) a green up arrow with "$1" for reward trials, 2) a red down arrow next to -$0.50 for loss trials; or 3) the number 5 and a gray double headed arrow for neutral trials. The "?" is presented for up to 1500 ms (if the participant responds before 1500 ms, a fixation cross is displayed for the remaining time), following by feedback for 1000 ms. There is a 1000 ms ITI with a "+" presented on the screen. The task is presented in blocks of 8 trials that are either mostly reward (6 reward trials pseudo randomly interleaved with either 1 neutral and 1 loss trial, 2 neutral trials, or 2 loss trials) or mostly loss (6 loss trials pseudo-randomly interleaved with either 1 neutral and 1 reward trial, 2 neutral trials, or 2 reward trials). In each of the two runs, there are 2 mostly reward and 2 mostly loss blocks, interleaved with 4 fixation blocks (15 seconds each).

Conditions (Blocked)
Mostly reward blocks
Mostly loss blocks

Conditions (Event-Related)
Reward trials
Loss trials
Neutral trials

References for Gambling Task: Reliable across subjects and robust activation in fMRI (Delgado et al. 2000; May et al. 2004; Tricomi et al. 2004; Forbes et al. 2009)

Motor

This task was adapted from the one developed by Buckner and colleagues (Buckner et al. 2011; Yeo et al. 2011). Participants are presented with visual cues that ask them to either tap their left or right fingers, or squeeze their left or right toes, or move their tongue to map motor areas. Each block of a movement type lasted 12 seconds (10 movements), and is preceded by a 3 second cue. In each of the two runs, there are 13 blocks, with 2 of tongue movements, 4 of hand movements (2 right and 2 left), and 4 of foot movements (2 right and 2 left). In addition, there are 3 15-second fixation blocks per run. This task contains the following events, each of which is computed against the fixation baseline.

Conditions (Blocked)
Left finger blocks
Right finger blocks
Left toe blocks
Right toe blocks
Tongue movement

References for Motor Task: Localizer (Morioka et al. 1995; Bizzi et al. 2008; Buckner et al. 2011; Yeo et al. 2011).

Language Processing

This task was developed by Binder and colleagues (Binder et al. 2011) and uses the E-prime scripts provided by these investigators. The task consists of two runs that each interleave 4 blocks of a story task and 4 blocks of a math task. The lengths of the blocks vary (average of approximately 30 seconds), but the task was designed so that the math task blocks match the length of the story task blocks, with some additional math trials at the end of the task to complete the 3.8 minute run as needed. The story blocks present participants with brief auditory stories (5-9 sentences) adapted from Aesop's fables, followed by a 2-alternative forced-choice question that asks participants about the topic of the story. The example provided in the original Binder paper (p. 1466) is "*For example, after a story about an eagle that saves a man who had done him a favor, participants were asked, "Was that about revenge or reciprocity?"* The math task also presents trials auditorially and requires subjects to complete addition and subtraction problems. The trials present subjects with a series of arithmetic operations (e.g., "fourteen plus twelve"), followed by "equals" and then two choices (e.g., "twenty-nine or twenty-six"). Participants push a button to select either the first or the second answer. The math task is adaptive to try to maintain a similar level of difficulty across participants. For more details on the task, please see (Binder *et al.* 2011).

Conditions (Blocked)
Story
Math

References for Language Task: Reliable across subjects and robust activation (Binder *et al.* 2011).

Social Cognition (Theory of Mind)

Participants were presented with short video clips (20 seconds) of objects (squares, circles, triangles) that either interacted in some way, or moved randomly on the screen. These videos were developed by either Castelli and colleagues (Castelli *et al.* 2000) or Martin and colleagues (Wheatley *et al.* 2007). After each video clip, participants judge whether the objects had a mental interaction (an interaction that appears as if the shapes are taking into account each other's feelings and thoughts), Not Sure, or No interaction (i.e., there is no obvious interaction between the shapes and the movement appears random). Each of the two task runs has 5 video blocks (2 Mental and 3 Random in one run, 3 Mental and 2 Random in the other run) and 5 fixation blocks (15 seconds each).

Conditions (Blocked)
Random interaction
Mental interaction

References for the Social Cognition Task: Reliable across subjects and robust activation (Castelli *et al*. 2000; Castelli *et al.* 2002; Wheatley *et al.* 2007; White *et al.* 2011).

Relational Processing

This task was adapted from the one developed by Christoff and colleagues (Smith *et al*. 2007). The stimuli are 6 different shapes filled with 1 of 6 different textures. In the relational processing condition, participants are presented with 2 pairs of objects, with one pair at the top of the screen and the other pair at the bottom of the screen. They are told that they should first decide what dimension differs across the top pair of objects (differed in shape or differed in texture) and then they should decide whether the bottom pair of objects also differ along that same dimension (e.g., if the top pair differs in shape, does the bottom pair also differ in shape). In the control matching condition, participants are shown two objects at the top of the screen and one object at the bottom of the screen, and a word in the middle of the screen (either "shape" or "texture"). They are told to decide whether the bottom object matches either of the top two objects on that dimension (e.g., if the word is "shape", is the bottom object the same shape as either of the top two objects. For both conditions, the subject responds yes or no using one button or another. For the relational condition, the stimuli are presented for 3500 ms, with a 500

ms ITI, and there are four trials per block. In the matching condition, stimuli are presented for 2800 ms, with a 400 ms ITI, and there are 5 trials per block. Each type of block (relational or matching) lasts a total of 18 seconds. In each of the two runs of this task, there are 3 relational blocks, 3 matching blocks and 3 16-second fixation blocks.

Conditions (Blocked)
Relational processing
Matching

References for the Relational Processing Task: Localizer (Smith *et al.* 2007).

Emotion Processing

This task was adapted from the one developed by Hariri and colleagues (Smith *et al.* 2007). Participants are presented with blocks of trials that either ask them to decide which of two faces presented on the bottom of the screen match the face at the top of the screen, or which of two shapes presented at the bottom of the screen match the shape at the top of the screen. The faces have either an angry or fearful expression. Trials are presented in blocks of 6 trials of the same task (face or shape), with the stimulus presented for 2000 ms and a 1000 ms ITI. Each block is preceded by a 3000 ms task cue ("shape" or "face"), so that each block is 21 seconds including the cue. Each of the two runs includes 3 face blocks and 3 shape blocks, with 8 seconds of fixation at the end of each run.

Conditions (Blocked)
Face
Shape

References for the Emotion Processing Task: Localizer (Hariri *et al.* 2002); Moderate reliability across time (Manuck *et al*. 2007).

T-fMRI scripts and data files

Script files in E-Prime are used to present stimuli and collect behavioral responses in the scanner. If you would like to run HCP tasks in your own research project, these files can be obtained by contacting Greg Burgess via email at burgessg@pcg.wustl.edu, please put "HCP E-Prime files" in the subject line of your message.

"EV" files are explanatory variables (predictors) in FSL format (3-columns: onset, duration, and amplitude). There is a separate EV directory for each task of the two runs, and the .txt files contained within those directories are named according to the task condition that they describe.

Here are examples for each task from one of the runs (the other run is named the same, but using “2”):

Working Memory

EV_WM1/0bk_body.txt	BLOCKED	onset of 0Back body block condition
EV_WM1/0bk_faces.txt	BLOCKED	onset of 0Back faces block condition
EV_WM1/0bk_places.txt	BLOCKED	onset of 0Back places block condition
EV_WM1/0bk_tools.txt	BLOCKED	onset of 0Back tools block condition
EV_WM1/2bk_body.txt	BLOCKED	onset of 2Back body block condition
EV_WM1/2bk_faces.txt	BLOCKED	onset of 2Back faces block condition
EV_WM1/2bk_places.txt	BLOCKED	onset of 2Back places block condition
EV_WM1/2bk_tools.txt	BLOCKED	onset of 2Back tools block condition
EV_WM1/0bk_cor.txt	EVENT	onset of correct trials in 0Back blocks
EV_WM1/0bk_err.txt	EVENT	onset of error trials in 0Back blocks
EV_WM1/0bk_nlr.txt	EVENT	onset of trials in 0Back blocks with no response
EV_WM1/2bk_cor.txt	EVENT	onset of correct trials in 2Back blocks
EV_WM1/2bk_err.txt	EVENT	onset of error trials in 2Back blocks
EV_WM1/2bk_nlr.txt	EVENT	onset of trials in 0Back blocks with no response
EV_WM1/all_bk_cor.txt	EVENT	onset of correct trials in 0- and 2Back blocks
EV_WM1/all_bk_err.txt	EVENT	onset of error trials in both 0- and 2Back blocks

Recognition Memory

EV_REC1/0bk_places_rem.txt	EVENT	onset of 0Back place trials that were subsequently rated as “remember”
EV_REC1/0bk_places_know.txt	EVENT	onset of 0Back place trials that were subsequently rated as “know”
EV_REC1/0bk_places_new.txt	EVENT	onset of 0Back place trials that were subsequently rated as “new”
EV_REC1/0bk_faces_rem.txt	EVENT	onset of 0Back face trials that were subsequently rated as “remember”
EV_REC1/0bk_faces_know.txt	EVENT	onset of 0Back face trials that were subsequently rated as “know”
EV_REC1/0bk_faces_new.txt	EVENT	onset of 0Back face trials that were subsequently rated as “new”
EV_REC1/2bk_places_rem.txt	EVENT	onset of 2Back place trials that were subsequently rated as “remember”

EV_REC1/2bk_places_know.txt	EVENT	onset of 2Back place trials that were subsequently rated as “know”
EV_REC1/2bk_places_new.txt	EVENT	onset of 2Back place trials that were subsequently rated as “new”
EV_REC1/2bk_faces_rem.txt	EVENT	onset of 2Back face trials that were subsequently rated as “remember”
EV_REC1/2bk_faces_know.txt	EVENT	onset of 2Back face trials that were subsequently rated as “know”
EV_REC1/2bk_faces_new.txt	EVENT	onset of 2Back face trials that were subsequently rated as “new”

Gambling

EV_GAMBLING1/win.txt	BLOCKED	Onset of mostly reward blocks
EV_GAMBLING1/loss.txt	BLOCKED	Onset of mostly loss blocks
EV_GAMBLING1/win_event.txt	EVENT	Onset of reward trials
EV_GAMBLING1/loss_event.txt	EVENT	Onset of loss trials
EV_GAMBLING1/neutral.txt	EVENT	Onset of neutral trials

Motor

EV_MOTOR1/cue.txt	BLOCKED	Onset of task cues
EV_MOTOR1/lf.txt	BLOCKED	Onset of left foot blocks
EV_MOTOR1/rf.txt	BLOCKED	Onset of right foot blocks
EV_MOTOR1/lh.txt	BLOCKED	Onset of left hand blocks
EV_MOTOR1/rh.txt	BLOCKED	Onset of right hand blocks
EV_MOTOR1/t.txt	BLOCKED	Onset of tongue blocks

Language

EV_LANGUAGE1/story.txt	BLOCKED	Onset of story blocks
EV_LANGUAGE1/math.txt	BLOCKED	Onset of math blocks

Social Cognition

EV_SOCIAL1/mental.txt	BLOCKED	Onset of mental interaction blocks
EV_SOCIAL1/rnd.txt	BLOCKED	Onset of random interaction blocks

EV_SOCIAL1/mental_resp.txt	EVENT	Onset of trials rated as mental interaction
EV_SOCIAL1/other_resp.txt	EVENT	Onset of trials not rated as mental interaction

Relational Processing

EV_RELATIONAL1/relation.txt	BLOCKED	Onset of relational blocks
EV_ RELATIONAL1/match.txt	BLOCKED	Onset of match blocks

Emotion Processing

EV_EMOTION1/fear.txt	BLOCKED	Onset of emotional face blocks
EV_EMOTION1/neut.txt	BLOCKED	Onset of shape blocks

Details of behavioral measures

Non-NIH Toolbox behavioral measures

We collect additional measures to assess several domains not covered by the NIH Toolbox. These tests are computerized.

Visual Processing

The NIH Toolbox does not measure color vision or contrast sensitivity. Thus, we are assessing color vision using the Farnsworth Test, a valid and reliable measure that provides more quantitative information than the commonly used Ishihara Test (Cole et al. 2007). In this task, participants order 15 colored blobs as a function of what they think are the closest matching colors. Based on the results, participants are classified as having Normal color vision, Protan (reduced sensitivity to red light), Deutan (reduced sensitivity to green light) or Tritian (reduced sensitivity to blue light) color vision problems. We are assessing contrast sensitivity using the Mars Contrast Sensitivity Test (Arditi et al. 2005), a brief, valid and reliable measure that improves upon the traditional Pelli-Robson measure (Dougherty *et al.* 2005; Haymes *et al.* 2006; Thayaparan *et al.* 2007).

Personality

There is consensus that a five factor model captures the major facets of human personality across cultures (Heine and Buchtel 2009): a) neuroticism; b) extroversion/introversion; c) agreeableness; d) openness; and e) conscientiousness (Goldberg 1993; McCrae and Costa 2008). We are administering the 60 item version of the Costa and McRae Neuroticism/Extroversion/Openness Five Factor Inventory (NEO-FFI), which has shown excellent reliability and validity (McCrae and Costa 2004). This measure was available as part of the Penn Computerized Cognitive Battery (Gur *et al*. 2001a; Gur *et al.* 2010).

Self-Regulation (Delay Discounting)

Delay discounting describes the undervaluing of rewards that are delayed in time. It is illustrated by the fact that humans (and other animals) will often choose a smaller immediate reward over an objectively larger, but delayed reward. We use a version of the discounting task that identifies 'indifference points' at which a person is equally likely to choose a smaller reward (e.g., $100) sooner versus a larger reward later (e.g., $200 in 3 years). Based on the work of Green and Myerson (Estle et al. 2006; Green et al. 2007), we use an adjusting-amount approach, in which delays are fixed and reward amounts are adjusted on a trial-by-trial basis based on participants' choices, to rapidly hone in on indifference points. This approach has been repeatedly validated to provide reliable estimates of delay discounting (Estle *et al.* 2006). As a summary measure, we use an area-under-the-curve discounting measure (AUC) that

provides a valid and reliable index of how steeply an individual discounts delayed rewards (Myerson *et al.* 2001). See below for exact details on the parameters of the Delay Discounting Task.

Sustained Attention

We measure continuous sustained attention using the Short Penn Continuous Performance Test (Number/Letter Version) (Gur *et al.* 2001; Gur *et al.* 2001; Gur *et al.* 2010). Participants see vertical and horizontal red lines flash on the computer screen. In one block, they must press the spacebar when the lines form a number and in the other block they press the spacebar when the lines form a letter. The lines are displayed for 300 ms followed by a 700 ms ITI. Each block contains 90 stimuli and lasts for 1.5 minutes.

Verbal Episodic Memory

The NIH Toolbox contains a measure of non-verbal episodic memory. Thus, we are assessing verbal episodic memory using Form A of the Penn Word Memory Test (Gur *et al.* 2001a; Gur *et al.* 2010). Participants are shown 20 words and asked to remember them for a subsequent memory test. They are then shown 40 words (the 20 previously presented words and 20 new words matched on memory related characteristics). They decide whether they have seen the word previously by choosing among “definitely yes,” “probably yes,” “probably no,” and “definitely no.”

Spatial Orientation

The NIH Toolbox does not contain any measures of visual-spatial processing. Thus, we are measuring spatial orientation processing using the Variable Short Penn Line Orientation Test (Gur *et al.* 2001a; Gur *et al.* 2010). Participants are shown two lines with different orientations. They have to rotate one of the lines (a moveable blue one) so that is parallel to the other line (a fixed red line). The rotation of the blue line is accomplished by clicking buttons on the keyboard that rotate the lines either clockwise or counterclockwise. Across trials, the lines vary in their relative location on the screen, though the distance between the centers of the two lines is always the same. The length of the red line is always the same, but the length of the blue line can be either short or long. There are a total of 24 trials.

Emotion Processing

The NIH Toolbox contains only self-report measures of emotional function. Thus, in order to obtain a behavioral measure of emotion processing, we are using the Penn Emotion Recognition Test (Gur *et al.* 2001a; Gur *et al.* 2010). Participants are presented with 40 faces, one at a time. They are asked to choose what emotion the face is showing from five choices: Happy, Sad, Angry, Scared and No Feeling. Half of the faces are males and half are females. There are 8 faces each that have a happy, sad, angry, scared or no feeling expression.

Fluid Intelligence

Although the Toolbox contains measures of crystallized IQ (e.g., vocabulary acquisition), an aspect of IQ strongly influenced by educational opportunities, and measures of executive function (which are both theoretically and empirically related to fluid intelligence), it does not contain a specific measure of fluid intelligence. This construct is strongly linked to specific functional outcomes and to variations in neuronal structure and function in humans (Duncan *et al.* 2000; Duncan 2003; Duncan 2005). The most commonly used measure of fluid intelligence is Raven's Progressive Matrices (Prabhakaran *et al.* 1997; Christoff *et al.* 2001; Gray *et al.* 2003; Conway *et al.* 2005; Gray *et al.* 2005; Wendelken *et al.* 2008). We use Form A of an abbreviated version of the Raven's developed by Gur and colleagues (Bilker *et al.* 2012). Participants are presented with patterns made up of 2x2, 3x3 or 1x5 arrangements of squares, with one of the squares missing. The participant must pick one of five response choices that best fits the missing square on the pattern. The task has 24 items and 3 bonus items, arranged in order of increasing difficulty. However, the task discontinues if the participant makes 5 incorrect responses in a row.

Self-Reported Function

The NIH toolbox contains self-report measures of a number of important domains of experience, including positive and negative affect, stress, anxiety, depression and social support. To obtain additional self-report information on an even broader variety of domains, we also administer the Achenbach Adult Self-Report for Ages 18-59 (Achenbach 2009). Specifically, we administer the 123 items from Section VIII. These can be used to generate the ASR Syndrome Scales and the ASR DSM-Oriented Scales.

Detailed Description of Delay Discounting Task

In this task, participants are presented with two choices on each trial – a smaller amount "today" or a larger amount at a later point in time. Participants make choices at each of 6 delays (1 month, 6 months, 1 year, 3 years, 5 years and 10 years) and for two delayed amounts ($200 and $40,000). For each combination of delay and amount of delayed reward (e.g., $200 in 1 month or $40,000 in 6 months), participants make 5 choices, and the value that would have been used for the immediate amount in a 6th choice is taken as the indifference point for that condition. The participants make all five choices for a particular combination of delay and amount before moving on to the next combination of delay and amount. The order is as follows:

Delayed amount of $200 dollars

- Today versus 6 months
- Today versus 3 years
- Today versus 1 month
- Today versus 5 years
- Today versus 10 years
- Today versus 1 year

Delayed amount of $40,000 dollars

- Today versus 6 months
- Today versus 3 years
- Today versus 1 month
- Today versus 5 years
- Today versus 10 years
- Today versus 1 year

The first choice at each delay is between the delayed amount ($200 or $40,000) and an immediate amount equal to ½ the delayed amount (e.g., $100 today or $200 in 1 month, $20,000 today or $40,000 in one month). The size of the adjustment after the first choice is always ½ the amount of the immediate value on the first choice (e.g., a change of $50 if the first immediate amount is $100). If the subject chooses the immediate amount, then the immediate amount is reduced on the next choice (e.g., $50 today versus $200 in 1 month). If the subject chooses the delayed amount, then the immediate amount is increased (e.g., $150 today versus $200 in 1 month). The amount of change on each subsequent choice is ½ the amount of the prior change (e.g., $25 on the 3rd trial), regardless of whether the subject chooses the immediate or the delayed amount. This procedure rapidly hones in on the amount of immediate gain that is close to the subjective value of the delayed gain.

This design means that for all the choices with $200 dollars as the delayed amount, the first choice will always be between $100 today, and $200 in the specified time period. The second

choice will always increment or decrement the immediate value by $50. The third choice will always increment or decrement the immediate value by $25. The fourth choice will always increment or decrement the immediate value by $12.50. The fifth choice will always increment or decrement the immediate value by $6.25. The "sixth" choice value, which is never presented to the subject, but is entered in the database, is always an increment or decrement of $3.125 from the immediate value on the 5th choice. Similarly, for all the choices with $40,000 dollars as the delayed amount, the first choice will always be between $20,000 today, and $40,000 in XX time period. The second choice will always increment or decrement the immediate value by $10,000. The third choice will always increment or decrement the immediate value by $5,000. The fourth choice will always increment or decrement the immediate value by $2,500. The fifth choice will always increment or decrement the immediate value by $1,250. The "sixth" choice value, which is never presented to the subject, but is entered in the database, will always be an increment or decrement of $625 from the immediate value on the 5th choice.

Thus, for the $200 amount, we will have 6 Subject Values:

- $SV_{1mo.2}$
- $SV_{6mo.2}$
- $SV_{1yr.2}$
- $SV_{3yr.2}$
- $SV_{5yr.2}$
- $SV_{10yr.2}$

Thus, for the $40,000 amount, we will have 6 Subject Values:

- $SV_{1mo.40}$
- $SV_{6mo.40}$
- $SV_{1yr.40}$
- $SV_{3yr.40}$
- $SV_{5yr.40}$
- $SV_{10yr.40}$

We compute an Area under the curve measure for each of the two amounts as described below.

Area under the Curve for $200 = $((1+SV_{1mo.2})/(120*200)) + ((SV_{1mo.2}+SV_{6mo.2})/(48*200)) + ((SV_{6mo.2}+SV_{1yr.2})/(40*200)) + ((SV_{1yr.2}+SV_{3yr.2})/(10*200)) + ((SV_{3yr.2}+SV_{5yr.2})/(10*200)) + ((SV_{5yr.2}+SV_{10yr.2})/(4*200))$

Area under the Curve for $40,000 = $((1+SV_{1mo.4})/(120*40,000)) + ((SV_{1mo.4}+SV_{6mo.4})/(48*40,000)) + ((SV_{6mo.4}+SV_{1yr.4})/(40*40,000)) + ((SV_{1yr.4}+SV_{3yr.4})/(10*40,000)) + ((SV_{3yr.4}+SV_{5yr.4})/(10*40,000)) + ((SV_{5yr.4}+SV_{10yr.4})/(4*40,000))$

Database of short names and descriptions for Non-NIH Toolbox behavioral measures

Variable Name	Description	Values
GUR_GURSCORINGDATA ID		
Subject	HCP Subject ID	
Date	Date of Testing	
Age	Age of Participant	
eye	Eye Used For Color Vision Test	"B" = Both eyes
correction	Participant reported level of eye glass correction	
ftest1	Results of first Farnsworth Test	
ftest2	Results of second Farnsworth Test (if needed)	
color_vision	Color Vision Category	Normal = normal; Protan = reduced red; Deutan = reduced green; Tritian = reduced blue
mars_log_score	Contrast Sensitivity Score	
mars_errs	Errors on Mars	
mars_final	Final Contrast Sensitivity Score	Higher scores indicate better contrast sensitivity
SV_1mo_200	Subjective Value for $200 at 1 month	
SV_6mo_200	Subjective Value for $200 at 6 months	
SV_3yr_200	Subjective Value for $200 at 3 years	
SV_1yr_200	Subjective Value for $200 at 1 year	
SV_5yr_200	Subjective Value for $200 at 5 years	
SV_10yr_200	Subjective Value for $200 at 10 years	
SV_1mo_40000	Subjective Value for $40,000 at 1 month	
SV_6mo_40000	Subjective Value for $40,000 at 6 months	
SV_1yr_40000	Subjective Value for $40,000 at 1 year	
SV_3yr_40000	Subjective Value for $40,000 at 3 years	
SV_5yr_40000	Subjective Value for $40,000 at 5 years	
SV_10yr_40000	Subjective Value for $40,000 at 10 years	
AUC_200	Area Under the Curve for Discounting of $200	See text above table
AUC_40000	Area Under the Curve for Discounting of $40,000	See text above table
NEOFAC_A	NEO-FFI Agreeableness	
NEOFAC_O	NEO-FFI Openness	

Variable Name	Description	Values
NEOFAC_C	NEO-FFI Conscientiousness	
NEOFAC_N	NEO-FFI Neuroticism	
NEOFAC_E	NEO-FFI Extroversion	
SCPT_TP	Short Penn CPT True Positives = Sum of CPN_TP and CPL_TP	0-60
SCPT_TN	Short Penn CPT True Negatives = Sum of CPN_TN and CPL_TPN	0-120
SCPT_FP	Short Penn CPT False Positives = Sum of CPN_FP and CPL_FP	0-120
SCPT_FN	Short Penn CPT False Negatives = Sum of CPN_FN and CPL_FN	0-60
SCPT_TPRT	Short Penn CPT Median Response Time for True Positive Responses	0-1000 ms
SCPT_SEN	Short Penn CPT Sensitivity = SCPT_TP/(SCPT_TP + SCPT_FN)	
SCPT_SPEC	Short Penn CPT Specificity = SCPT_TN/(SCPT_TN + SCPT_FP)	
SCPT_LRNR	Short Penn CPT Longest Run of Non-Responses)	
IWRD_TOT	Penn Word Memory: Total Number of Correct Responses	0-40
IWRD_RTC	Penn Word Memory: Median Reaction Time for Correct Responses	0-time variant
PMAT24_A_CR	Penn Matrix Test: Number of Correct Responses	0-24
PMAT24_A_SI	Penn Matrix Test: Total Skipped Items (items not presented because maximum errors allowed reached)	0-19
PMAT24_A_RTCR	Penn Matrix Test: Median Reaction Time for Correct Responses	0-time variant
VSPLOT_TC	Penn Line Orientation: Total Number Correct	0-24
VSPLOT_CRTE	Penn Line Orientation: Median Reaction Time Divided by Expected Number of Clicks for Correct Trials	0-time variant
VSPLOT_OFF	Penn Line Orientation: Total Positions Off for All Trials	0-165
ER40_CR	Penn Emotion Recognition: Number of Correct Responses	0-40
ER40_CRT	Penn Emotion Recognition: Correct Responses Median Response Time (ms)	0-time variant
ER40ANG	Penn Emotion Recognition: Number of Correct Anger Identifications	0-8
ER40FEAR	Penn Emotion Recognition: Number of Correct Fear Identifications	0-8
ER40HAP	Penn Emotion Recognition: Number of Correct Happy Identifications	0-8

Variable Name	Description	Values
ER40NOE	Penn Emotion Recognition: Number of Correct Neutral Identifications	0-8
ER40SAD	Penn Emotion Recognition: Number of Correct Sad Identifications	0-8
ASR_anxdp_raw	ASR Anxious/Depressed Raw Score	0-36
ASR_anxdp_t	ASR Anxious/Depressed Gender and Age Adjusted Percentile	50-100
ASR_wthdp_raw	ASR Withdrawn Raw Score	0-18
ASR_wthdp_t	ASR Withdrawn Gender and Age Adjusted Percentile	50-100
ASR_som_raw	ASR Somatic Complaints Raw Score	0-24
ASR_som_t	ASR Somatic Complaints Gender and Age Adjusted Percentile	50-100
ASR_tho_raw	ASR Thought Problems Raw Score	0-20
ASR_tho_t	ASR Thought Problems Gender and Age Adjusted Percentile	50-100
ASR_att_raw	ASR Attention Problems Raw Score	0-30
ASR_att_t	ASR Attention Problems Gender and Age Adjusted Percentile	50-100
ASR_agg_raw	ASR Aggressive Behavior Raw Score	0-30
ASR_agg_t	ASR Aggressive Behavior Gender and Age Adjusted Percentile	50-100
ASR_rule_raw	ASR Rule Breaking Behavior Raw Score	0-28
ASR_rule_t	ASR Rule Breaking Behavior Gender and Age Adjusted Percentile	50-100
ASR_int_raw	ASR Intrusive Raw Score	0-12
ASR_int_t	ASR Intrusive Gender and Age Adjusted Percentile	50-100
ASR_other_raw	ASR Other Raw Score	0-42
ASR_critical_raw	ASR Critical Items Raw Score	0-34
ASR_computed_internalizing_raw	ASR Internalizing Raw Score	0-78
ASR_computed_internalizing_t	ASR Internalizing Gender and Age Adjusted T-score	30-100
ASR_computed_externalizing_raw	ASR Externalizing Raw Score	0-70
ASR_computed_externalizing_t	ASR Externalizing Gender and Age Adjusted T-score	30-100
ASR_computed_other_raw	ASR Sum of IV, V and Other Raw Score	0-84
ASR_computed_total_raw	ASR Total Raw Score	0-240
ASR_computed_total_t	ASR Total Gender and Age Adjusted T-score	25-100
DSM_dep_raw	ASR DSM Depressive Problems Raw Score	0-28

Variable Name	Description	Values
DSM_dep_t	ASR DSM Depressive Problems Gender and Age Adjusted Percentile	50-100
DSM_anx_raw	ASR DSM Anxiety Problems Raw Score	0-14
DSM_anx_t	ASR DSM Anxiety Problems Gender and Age Adjusted Percentile	50-100
DSM_som_raw	ASR DSM Somatic Problems Raw Score	0-18
DSM_som_t	ASR DSM Somatic Problems Gender and Age Adjusted Percentile	50-100
DSM_avoid_raw	ASR DSM Avoidant Personality Problems Raw Score	0-14
DSM_avoid_t	ASR DSM Avoidant Personality Problems Gender and Age Adjusted Percentile	50-100
DSM_adh_raw	ASR DSM AD/H Problems Raw Score	0-26
DSM_adh_t	ASR DSM AD/H Problems Gender and Age Adjusted Percentile	50-100
DSM_inatt_raw	ASR DSM Inattention Problems Raw Score	0-14
DSM_hyp_raw	ASR DSM Hyperactivity Problems Raw Score	0-12
DSM_asoc_raw	ASR DSM Antisocial Personality Problems Raw Score	0-40
DSM_asoc_t	ASR DSM Antisocial Personality Problems Gender and Age Adjusted Percentile	50-100

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Appendices

Appendix 1. HCP scan protocols

Download Appendix 1 here: http://humanconnectome.org/documentation/data-release/October2012_Release_v2_Appendix1.pdf

Appendix 2. File names and directory structure of HCP processed data Oct 2012

Download Appendix 2 here: http://humanconnectome.org/documentation/data-release/October2012_Release_v2_Appendix2.pdf

Appendix 3. Skyra gradient field nonlinearity coefficients for the HCP Connectome Skyra

These coefficients are considered proprietary information by Siemens. To request access to these coefficients, please contact your Siemens collaboration manager or email Dingxin Wang at dingxin.wang@siemens.com.

Appendix 4. Matlab code for voxel-wise correction of dMRI gradients

Download Appendix 4 here: http://humanconnectome.org/documentation/data-release/October2012_Release_Appendix4.pdf

Appendix 5. Standard Operating Procedures (SOPs)

Download Appendix 5 here: http://humanconnectome.org/documentation/data-release/October2012_Release_Appendix5.pdf

Appendix 6. Command-line downloading from the HCP FTP site

Download Appendix 6 here: http://humanconnectome.org/documentation/data-release/October2012_Release_Appendix6.pdf