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ConnectomeDB—Sharing human brain connectivity data☆

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ABSTRACT

ConnectomeDB is a database for housing and disseminating data about human brain structure, function, and connectivity, along with associated behavioral and demographic data. It is the main archive and dissemination platform for data collected under the WU-Minn consortium Human Connectome Project. Additional connectome-style study data is and will be made available in the database under current and future projects, including the Connectome Coordination Facility. The database currently includes multiple modalities of magnetic resonance imaging (MRI) and magnetoencephalography (MEG) data along with associated behavioral data. MRI modalities include structural, task, resting state and diffusion. MEG modalities include resting state and task. Imaging data includes unprocessed, minimally preprocessed and analysis data. Imaging data and much of the behavioral data are publicly available, subject to acceptance of data use terms, while access to some sensitive behavioral data is restricted to qualified investigators under a more stringent set of terms. ConnectomeDB is the public side of the WU-Minn HCP database platform. As such, it is geared towards public distribution, with a web-based user interface designed to guide users to the optimal set of data for their needs and a robust backend mechanism based on the commercial Aspera *fasp* service to enable high speed downloads. HCP data is also available via direct shipment of hard drives and Amazon S3.

Introduction

ConnectomeDB (https://db.humanconnectome.org) is a database for housing and disseminating publicly available human brain connectivity data. It is a highly customized instance of the XNAT imaging informatics platform: an extensible, open source platform for managing and sharing imaging and related data (Marcus et al., 2007). ConnectomeDB is designed as the database and dissemination platform for the Human Connectome Project (HCP) consortium led by Washington University, University of Minnesota, and Oxford University (the WU-Minn HCP consortium), and it houses and distributes data collected under the WU-Minn HCP (Van Essen et al. 2013). In 2014, it expanded to include diffusion data collected by the USC-MGH HCP consortium (Setsompop et al., 2013; Toga et al., 2012) and multimodal data collected under the WU-Minn HCP consortium LifeSpan Pilot Project, which is designed to provide information on the sensitivity of HCP methods to age-related differences. Current WU-Minn HCP projects available in ConnectomeDB and details about their imaging data are found in Table 1. These projects have focused on providing normative data on healthy populations. However, ConnectomeDB will soon expand its portfolio to include data obtained through additional NIH-funded initiatives, including Connectomes of Human Diseases plus three Lifespan-HCP efforts. A Connectome Coordination Facility (CCF) centered at Washington University and also involving the University of Minnesota is being established to operate the expanded ConnectomeDB repository and provide support for the groups running these projects.

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Table 1
WU-Minn HCP imaging data currently available/planned for release in ConnectomeDB.

Project	Imaging Type/Scanner	Modality	Details	Processing Levels
WU-Minn HCP (currently 526 subjects with imaging data)	3T MRI	Structural	T1 weighted T2 weighted	Unprocessed, Preprocessed
		Resting state fMRI	Two sessions of 2 scans (1200 frames each per scan). Each session contains a pair of scans, acquired with opposing phase encoding directions (LR/RL)	Unprocessed, Preprocessed Group Analysis (functional connectivity maps/timeseries, ICA-based parcellation and network matrices)
		Task fMRI	Tasks: • Working Memory (405 frames/scan) • Gambling (253 frames/scan) • Motor (284 frames/scan) • Language (316 frames/scan) • Social Cognition (274 frames/scan) • Relational Processing (232 frames/scan) • Emotion Processing (176 frames/scan) One scan pair for each task with 1 scan in each phase encoding direction (LR/RL)	Unprocessed, Preprocessed, Analysis (individual subject and group analyses)
		Diffusion MRI	6 scans total (three gradient tables with 1 scan in each phase encoding direction per gradient table (LR/RL))	Unprocessed, Preprocessed, Analysis (to be released)
	7T MRI	Resting state fMRI	4 scans total. 900 frames/scan. Two scans in each phase encoding direction (AP/PA)	To be released
		Task fMRI	Tasks: • Retinotopy (6 scans for mapping retinotopy, using rotating wedges, expanding/contracting rings, and drifting bars. Three scans in each phase encoding direction (AP/PA)) • Movie (4 scans using 4 stimulus movies. Two scans in each phase encoding direction (AP/PA))	To be released
		Diffusion MRI	4 scans total (two gradient tables with 1 scan in each phase encoding direction per gradient table (AP/PA))	To be released
	MEG	Noise	Scans: • Empty room (One 5 min scan) • Patient noise (One or more 1 min scan)	Unprocessed
		Resting state	Three 6 minute scans	Unprocessed, Preprocessed, Source-level processed (time-series and connectivity data)
		Task	Tasks: • Working Memory (Two 10 minute scans) • Story Math (Two 7 minute scans) • Motor (Two 14 minute scans)	Unprocessed, Preprocessed, Source-level processed (averaged event-related and time-frequency responses)
WU-Minn Life Span Pilot (Currently 27 subjects with imaging data)	3T MRI	Structural	T1 weighted T2 weighted	Unprocessed
		Resting state fMRI	Four sessions of 2 scans (420 frames each per scan). Each session contains a pair of scans, acquired with opposing phase encoding directions (LR/RL)	Unprocessed
		Task fMRI	Tasks: • Working Memory (405 frames/scan) • Emotion Processing (199 frames/scan) • Social Cognition (274 frames/scan) • Gambling (253 frames/scan) One scan pair for each task with 1 scan in each phase encoding direction (LR/RL)	Unprocessed
		Diffusion fMRI	4 scans total (two gradient tables with 1 scan in each phase encoding direction per gradient table (LR/RL))	Unprocessed

What is available?

WU-Minn HCP data—overview

Data collected under the WU-Minn HCP project includes multiple modalities of imaging data, along with a large battery of behavioral data spanning numerous physical, behavioral, and personality dimensions. The final HCP dataset is expected to include data obtained from 1200 participants. The HCP population is a "healthy" population of twins and siblings aged 22–35, where "healthy" refers primarily to absence of conditions likely to affect brain structure and function or influence the ability to successfully complete study protocol. The HCP sample is described in further detail in Van Essen et al. (2013). As of January 2015, the consortium has shared data on over 500 subjects as part of its "500 Subjects + MEG2" release. This includes high resolution 3T MRI session data on 526 subjects, MEG data on 67 subjects, and demographic and behavioral data on 542 subjects. Imaging data and much of the behavioral data collected under the WU-Minn HCP project are freely and publicly available, subject to data use terms. Some sensitive behavioral data elements are restricted to qualified researchers under a more rigid set of data use terms.

WU-Minn HCP data—MRI

WU-Minn HCP MRI data released to date have been collected on a customized Siemens MAGNETOM Connectom 3T scanner at WU in multiple imaging sessions covering four modalities: structural (T1w and T2w), resting state fMRI (rfMRI), task fMRI (tfMRI, 7 tasks) and

diffusion MRI (dMRI). For a subset of 200 subjects, 3T imaging data is being supplemented by data collected on a 7T MRI scanner. The 7T data will include resting state, diffusion, and two additional tasks (retinotopy and movie clips).

MRI imaging data released under the WU-Minn HCP project includes unprocessed, minimally preprocessed, and analysis data. For MRI, the unprocessed data includes NIFTI files (with facial features anonymized; Milchenko and Marcus, 2013) from session scans along with scan-associated data (e.g. task timing and physiological monitoring files) in text format. Preprocessed data contains the output of the minimal preprocessing (MPP) pipelines, described in detail by Glasser et al. (2013). These pipelines minimize spatial distortions in the images, correct for subject motion, align data across modalities and bring the data into a common atlas space, thereby preparing the data for further processing. Preprocessed data also includes resting-state fMRI data denoised by the ICA-based "FIX" method, which greatly reduces spatially and temporally structured noise (Griffanti et al., 2014; Salimi-Khorshidi et al., 2014). Currently available individual subject analysis data includes results of the WU-Minn HCP task analysis pipeline. WU-Minn HCP pipeline scripts and documentation are available on GitHub at https://github.com/Washington-University/Pipelines/wiki. Additionally available are more extensively analyzed group-average rfMRI datasets: full correlation "dense" (grayordinate to grayordinate) functional connectomes, rfMRI independent component analysis (ICA)-derived parcellations, plus group-average and single-subject node time series and network functional connectivity matrices.

Many of the files HCP releases are quite large, due to the high spatial and temporal resolution attained using "multi-band" data acquisition (Ugurbil et al., 2013), which enables 2 mm isotropic voxels and a 0.72 s TR ('frame rate') for fMRI (compared to conventional scans that typically are ~3 mm voxel size and ~2 s TR) and 1.25 mm voxels for dMRI (vs conventional voxel size of ~2 mm). The HCP MPP pipelines are customized to handle such large datasets efficiently, for example, by generating 'grayordinate' representations of fMRI data that include only cortical surface vertices and subcortical gray-matter voxels (Glasser et al., 2013), using a standardized 'CIFTI' data format (http://www.nitrc.org/projects/cifti). The grayordinate-based files are much more compact than standard NIFTI volumes (but both formats are released in order to provide flexibility). Connectome Workbench software (http://www.humanconnectome.org/software/connectome-workbench.html) is customized for visualizing and analyzing HCP data and it capitalizes especially on the grayordinates/CIFTI data representations (see http://www.humanconnectome.org/documentation/tutorials).

WU-Minn HCP data—MEG

MEG data released under the WU-Minn HCP project includes unprocessed, anatomical and channel-level preprocessed, and source-level processed functional data. Unprocessed data consists of 16-bit raw binary c,rfDC files from the 4D scanner, supplemented by quality control (QC) figures and ascii text files. Stimulus-response files derived from E-Prime are included for task modalities. Anatomical preprocessed data includes individual anatomical models for volume conduction and source modeling. Coordinate transformation matrices are included for translating between MEG-system coordinates and MRI-based individual and normalized coordinate systems. Anatomical and channel-level preprocessed data are represented in MATLAB (Mathworks, Natick, MA) format. Source-level processed data are represented in CIFTI format and contain source-reconstructed output from multiple processing pipelines. All processed data are supplemented by QC figures and provenance details. The "megconnectome" processing software is implemented in MATLAB using the FieldTrip toolbox (Oostenveld et al., 2011) and is made available along with the data in each release. MEG task details, preprocessing and processing pipelines, and associated outputs are described in detail in Larson-Prior et al. (2013) and in HCP documentation.

WU-Minn HCP data—behavioral and other individual difference data

Along with imaging data, a wide array of behavioral and other non-imaging data is obtained under the HCP, with an emphasis on obtaining standardized measures that may covary with brain structure and function. These data are available in ConnectomeDB and can be downloaded as CSV files. The core components of these data are implementations of the NIH Toolbox (http://www.nihtoolbox.org/) and a modified web-based battery that includes components of the Penn Neurocognitive Battery (Gur et al., 2001,2010) as well as additional measures. These implementations assess many domains including cognition, emotion, motor, sensory, visual processing and personality. These core components are supplemented with additional instruments supplying information on other areas such as psychiatric history, substance use and family history. These non-imaging data are described in detail in Barch et al. (2013, Table 2) and Van Essen et al. (2013) and in project documentation. A list of categories of non-imaging data and associated instruments are provided in Table 2.

Quality control process

All imaging data collected under the WU-Minn consortium goes through an extensive automated validation process. In addition to this validation process, fMRI data goes through an automated QC process, while structural MRI and MEG data are submitted to additional manual QC processes. Furthermore, data collection staff follow detailed standard operating procedures (SOPs); they are trained to identify excessive movement and other issues that might affect data quality during scanning and to attempt rescans when appropriate. The HCP acquisition and QC process and pipelines are described in detail in Marcus et al. (2013).

Upon transfer of data from scanners to the internally-facing 'IntraDB' database (see below), data are sent through validation and QC pipelines. Validation pipelines perform initial checks, with MRI utilizing information from acquisition metadata embedded in the DICOM header (e.g., number of slices, resolution, TR, TE, flip angle), to ensure that data was acquired according to protocol. Structural scans are accepted for further processing if they receive at least a good rating in the manual QC four point rating scale (excellent, good, fair, poor; see Marcus et al., 2013). Following validation, a second round of pipelines are run, performing a more in-depth QC analyses on the fMRI data. These pipelines analyze signal to noise ratios, search for motion outliers and compute other measures affecting data quality, producing graphs and summary images to help in the evaluation of image quality. However, the HCP rarely excludes fMRI data from release solely due to motion (e.g., only in cases of *extremely* bad motion). Users should be diligent in dealing with the impact of motion in their analyses and are strongly encouraged to make use of the aforementioned FIX-denoised rfMRI datasets or to carry out other denoising strategies.

Data obtained under the WU-Minn LifeSpan pilot projects undergo nearly identical acquisition and QC processes as those for the young adult Human Connectome Project. The LifeSpan pilot projects involve similar scanning protocols as the young-adult HCP but are shorter in duration (~2 h total scan duration instead of ~4 hr). Owing to the pilot nature of these projects, the inclusion of both young and older subjects (often with concomitantly greater head movements), and a desire to maximize sample size for pilot analyses, structural scans are accepted for further processing if they receive at least a fair rating in the aforementioned manual QC four point rating scale.

The WU-Minn database platform and data processing

ConnectomeDB is the public-facing side of the WU-Minn consortium database platform. As such, it is designed for dissemination of the data and contains only released data or those data currently being processed for release. WU-Minn data acquisition and QC staff use a separate, internal database, IntraDB that (like ConnectomeDB) is a customized version of

Table 2
WU-Minn HCP non-imaging and behavioral data.

Category	Instrument
Subject information	Demographics (gender, age, twin status, zygosity, mother ID, father ID, race, ethnicity, handedness, employment status, household income, education, school status, relationship status)
Study completion	Study completion: 3T MR Image reconstruction version: 3T MR Study completion: MEG Study completion: behavioral
MR sessions	Session information
Health and family history	Physical health (height, weight, BMI, hematocrit, blood pressure, thyroid stimulating hormone levels, glucose levels, endocrine disorders) (self-report) Menstrual cycle information (in females) Parental history of psychiatric and neurologic disorders
Alertness	Cognitive status (mini mental status exam) Sleep: (Pittsburgh Sleep Quality Index)
Cognition	Episodic memory (picture sequence memory) Executive function/cognitive flexibility (dimensional change card sort) Executive function/inhibition (flanker task) Fluid intelligence (Penn progressive matrices) Language/reading decoding (oral reading recognition) Language/vocabulary comprehension (picture vocabulary) Processing speed (pattern completion processing speed) Self-regulation/impulsivity (delay discounting) Spatial orientation (variable short Penn line orientation test) Sustained attention (short Penn continuous performance test) Verbal episodic memory (Penn word memory test) Working memory (list sorting)
Emotion	Emotion recognition (Penn emotion recognition test) Negative affect (sadness, fear, anger) (self-report) Psychological well-being (positive affect, life satisfaction, meaning and purpose) (self-report) Social relationships (social support, companionship, social distress, positive social development) (self-report) Stress and self-efficacy (perceived stress, self-efficacy) (self-report)
FreeSurfer	FreeSurfer summary statistics Volume (subcortical) segmentation Surface area Surface thickness
In-scanner task performance (reaction time and accuracy)	Emotion processing task Gambling task Language processing task Relational processing task Social cognition task Working memory task
Motor	Endurance (2 minute walk test) Locomotion (4-meter walk test) Dexterity (9-hole pegboard) Strength (grip strength dynamometry)
Personality	Five factor model (NEO-FFI 60)
Psychiatric and life function	Life function (Achenbach adult self-report, syndrome scales and DSM-oriented scale) Psychiatric history
Sensory	Audition (words in noise) Olfaction (odor identification test) Pain (pain intensity and interference surveys) Taste (taste intensity test) Vision (EVA scores and Farnsworth test) Contrast sensitivity (Mars contrast sensitivity)
Substance use	Breathalyzer and drug test results Alcohol use 7-day retrospective Alcohol use and dependence Tobacco use 7-day retrospective Tobacco use and dependence Illicit drug use Marijuana use and dependence

XNAT. It is in IntraDB that quality determinations are made to inform what data will ultimately be transferred to ConnectomeDB for final processing and dissemination. Pipelines in IntraDB convert images from DICOM to NIFTI, while de-identifying subject data by masking facial structures in the image and removing data such as session dates. Identifying information like name, birthdate and address are never stored in either database.

Once a subject's data collection is completed and quality determinations are made, another set of programs are run to "sanity check" subject data, checking mainly for data completeness, incomplete processing, and corrupted files. Data must pass these checks before transfer from IntraDB to ConnectomeDB, where usable data from all scan sessions are joined into a single combined representation of the subject's imaging data. This process includes modifications of file names and/or directory structure from that which is optimized for the incoming data stream on the IntraDB side to that which is optimized for preprocessing and data sharing on the ConnectomeDB side. Separate session representations are built and customized for data obtained from different scanners (i.e., 3T MRI, 7T MRI and 4D MEG). Once data is in place in ConnectomeDB, processing pipelines are run and data are packaged and prepared for distribution.

Accessing the data

All imaging-related data and much of the non-imaging data in ConnectomeDB are freely and publicly available, subject to the user's agreement to open access data use terms via their ConnectomeDB user account. Accounts require validation by responding to a validation link e-mailed upon account registration. Acceptance of terms for publicly available data can be performed via the ConnectomeDB website immediately after account registration. Some non-imaging data are considered "restricted access", because they are either "sensitive" or have potential to reveal participant identity to family members or others. These data are made available only to qualified investigators under more stringent data use terms (Van Essen et al., 2013). Each project or dataset contained in ConnectomeDB may have its own sets of data use terms required for accessing public and restricted data. Before gaining access to restricted data, a signed form sent to the WU-Minn HCP consortium administration must be approved.

Upon login, users are directed to a unified page showing all publicly available datasets in ConnectomeDB along with current access level based on data use terms acceptance. From this page, users can initiate acceptance of data use terms, launch project pages (containing dataset resources and group average data), or launch a subject dashboard from which they can engage with and/or download project data.

Imaging data

Imaging and associated data (e.g., task timing files) are made available via data "packages" in ConnectomeDB. These packages organize data into meaningful groups of manageable size. For each subject, separate packages are created for each modality and processing level. Packages are further divided for task fMRI by task paradigm and for resting state fMRI by resting state scan pair. Packages are designed to contain all data files necessary to perform the expected types of additional processing and analyses that users might perform on those files while excluding unnecessary processing intermediates that would just increase package size. For example, unprocessed data packages contain the files necessary to run preprocessing pipelines, and preprocessed packages supply the files necessary to run additional HCP analysis pipelines. This approach does entail modest duplication of files in the supplied packages; for example, packages for different tasks may contain the same field map image files for distortion correction.

To facilitate robust, high speed downloads, ConnectomeDB uses a commercial UDP-based data transfer technology called Aspera *fasp*™ (http://asperasoft.com). This technology allows transfer rates much faster than those achievable by TCP-based technologies such as FTP and HTTP and enables reliable transfers with retry-and-resume capability. A downloadable plugin is required to enable Aspera-based transfers. This

client-side software allows for user controlled management of the download process and is available to users free of charge.

Non-imaging data

Non-imaging data can be searched and filtered in ConnectomeDB and is downloadable in CSV format. Links to download public non-imaging data are available in ConnectomeDB for all users who have registered and accepted the appropriate open access data use terms; links to download restricted CSV files are available only to users approved for restricted access. Users with restricted access permissions can switch between "Open Access", "Restricted", and "Sensitive" views in the ConnectomeDB user interface (UI). Once in the "Restricted" or "Sensitive" views, restricted data, associated fields, and download links become viewable in the UI.

In addition to the behavioral data collected, metadata about the imaging and non-imaging data are available in the DB. These data mainly provide information about the existence of and completeness of the various types and modalities of data available for individual subjects. These can be useful when filtering for subjects having complete data in the desired modality or domain (see next section).

Groups, filtering and the data dictionary

The HCP data stored within ConnectomeDB are immense and growing. The current "HCP S500" data release includes 17 terabytes of MRI data and approximately 3 terabytes of MEG data, including data from all processing levels. The size of these datasets will grow as additional subjects are added and additional processing and analysis output is made available.

Because of the size of the growing HCP database, it is important to provide users with tools to identify and obtain the minimum dataset required to meet their needs and conduct follow-up analyses. The organization of data into packages helps in this regard by facilitating selection of subsets of data within each subject, but it is also important to enable users to identify the optimal group of subjects for which to obtain data. To accomplish this, ConnectomeDB uses groups and filters. Groups are subsets of subjects, and ConnectomeDB supports both pre-defined and user-defined groups. ConnectomeDB has identified several meaningful subsets of subjects and has organized them into pre-defined groups. One example is the "Single Subject" group, which enables users to get a good feel for what the data contains by obtaining a representative subject with complete data. Another is the "100 Unrelated Subjects" group, which provides users with a practical amount of data for analysis without the need to correct for family structure.

In addition to preset groups, the UI supports filtering of subjects based on any project data field (e.g., gender, completeness of imaging, motor assessment results). These filtered sets of subjects may be saved as "user-defined groups" which the user can save and return to in later sessions. The filtering functionality is enabled and supported by the ConnectomeDB data dictionary (Herrick, et al., 2014).

The ConnectomeDB data dictionary contains metadata about all non-imaging data fields in ConnectomeDB as well as many fields that are derived by analysis of the imaging data (e.g., FreeSurfer results). These metadata, along with additional metadata used within the application, are assembled into the data dictionary used by the DB. Dictionary entries include information about data type, differing levels of description, expected values and other useful information about ConnectomeDB data.

Multiple methods of access

As noted above, HCP data is immense and growing. It is expected that many users of HCP data will be able to work with one of the predefined groups or a filtered subset of subjects. Furthermore, such users will likely be interested only in some subset of the packages (e.g., preprocessed diffusion data). ConnectomeDB and the Aspera UDP-based download mechanism serve these users well. Other users will prefer to have access to all of the available data. While it might be possible to eventually download all the data via ConnectomeDB, these users are generally better served by one of the alternative access methods, Connectome-In-A-Box and Amazon S3 cloud storage.

Connectome-In-A-Box (http://www.humanconnectome.org/data/connectome-in-a-box.html) is a process that sends a set of hard drives containing the entire HCP imaging database from a specific project or subproject to requesting users who have accepted data use terms. Currently available is a set of drives containing the 3T MRI data for the entire HCP 500 subject release, or a single drive option with all the 3T MRI data for the U100 group. Charges for this service recover only the costs of the physical hard drives and delivery.

In addition to local storage and availability via ConnectomeDB, a copy of the entire Human Connectome Project database has recently been made available via the cloud through Amazon S3. Users can access the data in Amazon S3 through ConnectomeDB in a process that links their ConnectomeDB credentials with their Amazon S3 account credentials. Users can then access HCP data directly from the cloud.

Documentation, mailing lists and feedback

All WU-Minn HCP data available in ConnectomeDB are extensively documented. Reference manuals are compiled for each major HCP data release and are available at http://humanconnectome.org/documentation. These manuals contain detailed information specific to each release about accessing the data, hardware and protocols, SOPs, directory structure and file information for downloaded data. They also contain detailed information about data collection procedures, task procedures, pipelines and more. In addition, an HCP wiki (https://wiki.humanconnectome.org/display/PublicData/Home) is maintained containing additional documentation and updates. Most notably, this site contains a "Known Issues and Planned Fixes" page that details recently discovered issues, including information regarding fixes and/or estimated timelines for fixes between data releases. For backwards compatibility of data, the HCP preserves an archive of previous data releases (including data with known issues) that are accessible upon request. (However, the user interface only provides access to the current version of the data). Similarly, previous versions of HCP software are available via GitHub

In addition to documentation, the HCP has established mechanisms for announcements and user feedback. The WU-Minn HCP consortium maintains a website portal (http://www.humanconnectome.org) where users and the public can find announcements, links to documentation, and general information about the project. Through the website and/or upon registration to ConnectomeDB, users are invited to subscribe to an announcement list and e-mail user forum. The announcement list is used to make announcements about data releases, software updates, events and issues. The forum is an open discussion group, actively monitored by project investigators and staff, where users can submit issues, requests and bug reports.

In addition to these groups, HCP administration has set up support and feedback e-mail addresses that are answered by HCP staff. Links to these are made available in "Contact" sections of ConnectomeDB and the HCP website. In addition, the software platform or scripts developed by HCP (ConnectomeDB, Connectome Workbench, FieldTrip, and the HCP Processing Pipelines), have user-friendly feedback mechanisms (bug report forms, user support email, wiki forums), built in for users to submit bug reports and feature requests. Submitted requests are transferred automatically or manually entered into issue tracking software to be managed by project staff and developers. This approach allows for user feedback from all sources of HCP information, data, and software to be organized and managed in one system.

Future directions

The neuroimaging community has expressed high interest in the HCP effort, and many investigators have started using HCP data in their work. As of April 2015, over a million package files totaling nearly 1.5 petabytes of data have been served to over 1900 users in 57 countries. Additionally, 168 users have requested data via Connectome-In-A-Box, and 431 drives have been shipped. Nearly 350 researchers have requested and been approved for access to restricted data. Over 50 publications using released HCP data and methods, including over 30 by investigators completely independent from the WU-Minn consortium, have been published since the initial HCP Q1 Data Release in March 2013.

Much has been learned during the course of the WU-Minn consortium HCP project and much remains to be done. The consortium will continue to release data as new subject data is acquired and processed. Further analysis outputs will be made available as they are made ready for release, including the release of diffusion tractography analyses and parcellated task fMRI data. Additional work on the ConnectomeDB application and platform is also planned, including the expansion of data mining tools, in order to provide a better within-DB platform for data exploration and analysis.

ConnectomeDB will become the foundation for the NIH-supported Connectome Coordination Facility (CCF) and the primary dissemination platform for NIH-funded HCP-style data acquisition and analysis supported by the Connectomes of Human Diseases (https://grants.nih.gov/grants/guide/pa-files/PAR-14-281.html) and Lifespan-HCP (http://grants.nih.gov/grants/guide/rfa-files/RFA-AG-16-004.html) funding mechanisms. An important function of the CCF will be to facilitate comparison and aggregation across datasets. Consequently, ConnectomeDB is being developed to provide an improved unified-yet-customized interface to support data from many sites and studies and to handle the corresponding increase in traffic these studies are expected to generate.

References

Barch, D.M., Burgess, G.C., Harms, M.P., Petersen, S.E., Schlaggar, B.L., Corbetta, M., Glasser, M.F., Curtiss, S., Dixit, S., Feldt, C., Nolan, D., Bryant, E., Hartley, T., Footer, O., Bjork, J.M., Poldrack, R., Smith, S., Johansen-Berg, H., Snyder, A.Z., Van Essen, D.C., for the WU-Minn HCP Consortium, 2013. Function in the human connectome: task-fMRI and individual differences in behavior. Neuroimage 80, 169–189.

Glasser, M.F., Sotiropoulos, S.N., Wilson, J.A., Coalson, T.S., Fischl, B., Andersson, J.L., et al., 2013. The minimal preprocessing pipelines for the Human Connectome Project. Neuroimage 80, 105–124.

Griffanti, L., Salimi-Khorshidi, G., Beckmann, C.F., Auerbach, E.J., Douaud, G., Sexton, C.E., Zsoldos, E., Ebmeier, K.P., Filippini, N., Mackay, C.E., Moeller, S., Xu, J., Yacoub, E., Baselli, G., Ugurbil, K., Miller, K.L., Smith, S.M., 2014. ICA-based artefact removal and accelerated fMRI acquisition for improved resting state network imaging. Neuroimage 95, 232–247.

Gur, R.C., Ragland, J.D., Moberg, P.J., Turner, T.H., Bilker, W.B., Kohler, C., Siegel, S.J., Gur, R.E., 2001. Computerized neurocognitive scanning: I. Methodology and validation in healthy people. Neuropsychopharmacology 25, 766–776.

Gur, R.C., Richard, J., Hughett, P., Calkins, M.E., Macy, L., Bilker, W.B., Brensinger, C., Gur, R.E., 2010. A cognitive neuroscience-based computerized battery for efficient measurement of individual differences: standardization and initial construct validation. J. Neurosci. Methods 187, 254–262.

Herrick, R., McKay, M., Olsen, T., Horton, W., Florida, M., Moore, C.J., Marcus, D.S., 2014. Data dictionary services in XNAT and the Human Connectome Project. Front. Neuroinform. 8, 65.

Larson-Prior, L.J., Oostenveld, R., Penna, S.D., Michalareas, G., Prior, F., Babajani-Feremi, A., Schoffelen, J.M., Marzetti, L., Pasquale, F., Pompeo, F.D., Stout, J., Woolrich, M., Luo, Q., Bucholz, R., Fries, P., Pizzella, V., Romani, G.L., Corbetta, M., Snyder, A.Z., 2013. Adding dynamics to the human connectome project with MEG. Neuroimage 80, 190–201.

Marcus, D.S., Olsen, T.R., Ramaratnam, M., Buckner, R.L., 2007. The Extensible Neuroimaging Archive Toolkit: an informatics platform for managing, exploring and sharing neuroimaging data. Neuroinformatics 5, 11–34.

Marcus, D.S., Harms, M.P., Snyder, A.Z., Jenkinson, M., Wilson, J.A., Glasser, M.F., Barch, D.M., Archie, K.A., Burgess, G.C., Ramaratnam, M., et al., 2013. Human connectome project informatics: quality control, database services, and data visualization. Neuroimage 80, 202–219.

Milchenko, M., Marcus, D.S., 2013. Obscuring surface anatomy in volumetric imaging data. Neuroinformatics 11, 65–75.

Oostenveld, R., Fries. P., Maris, E., and Schoffelen, J.M., FieldTrip: Open Source Software for Advanced Analysis of MEG, EEG, and Invasive Electrophysiological Data, Comput. Intell. Neurosci, vol. 2011, Article ID 156869, 9 pages.

Salimi-Khorshidi, G., Douaud, G., Beckmann, C.F., Glasser, M.F., Griffanti, L., Smith, S.M., 2014. Automatic denoising of functional MRI data: combining independent component analysis and hierarchical fusion of classifiers. Neuroimage 90, 449–468.

Setsompop, K., Kimmlingen, R., Eberlein, E., Witzel, T., Cohen-Adad, J., McNab, J.A., et al., 2013. Pushing the limits of in vivo diffusion MRI for the Human Connectome Project. Neuroimage 80, 220–233.

Toga, A., Clark, K., Thompson, P., Shattuck, D., Van Horn, J., 2012. Mapping the human connectome. Neurosurgery 71 (1), 1–5.

Ugurbil, K., Xu, J., Auerbach, E.J., Moeller, S., Vu, A., Duarte-Carvajalino, J.M., Lenglet, C., Wu, X., Schmitter, S., Van de Moortele, P.F., Strupp, J., Sapiro, G., De Martino, F., Wang, D., Harel, N., Garwood, M., Chen, L., Feinberg, D.A., Smith, S.M., Miller, K.L., Sotiropoulos, S.N., Jbabdi, S., Andersson, J.L., Behrens, T.E., Glasser, M.F., Van Essen, D., Yacoub, E., 2013. Pushing spatial and temporal resolution for functional and diffusion MRI in the Human Connectome Project. Neuroimage 80, 80–104.

Van Essen, D.C., Smith, S.M., Barch, D.M., Behrens, T.E., Yacoub, E., Ugurbil, K., et al., 2013. The WU-Minn Human Connectome Project: an overview. Neuroimage 80, 62–79.