### **GSP Open Access Documentation**



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# Part I Frequently Asked Questions

### What data are included within the GSP Open Access data release?

MRI data from 1570 unique subjects are included (ages 18-35). Each dataset has one high-resolution anatomical image (Dataverse, ANAT; LONI, T1\_MEMPRAGE\_RMS) and at least one eyes-open rest functional MRI run (BOLD). 1139 of the 1570 datasets include two BOLD runs. The imaging data are provided in NIfTI format.

Demographic data are included on all subjects (age, handedness, sex, etc) and cognitive/behavioral data are included for 926 subjects. A CSV file (GSP\_list\_140630.csv) contains the demographic and cognitive/behavioral data.

### What data are included within the extended GSP Open Access data release?

The extended data release includes one additional CSV file (GSP\_extended\_140630.csv) containing additional phenotypes (e.g., EstIQ\_Matrix\_Int\_Bin) for a subset of subjects.

The extended release is available for download through the LONI Image Data Archive following submission of the GSP Restricted Access Data Use Terms.

### How are the data organized on Dataverse?

The imaging data are provided in subject-specific folders (e.g., Sub0001\_Ses1). These unique subject folders are bundled into 10 separate tar files (each with 157 subjects). A single CSV file (GSP\_list\_140630.csv) contains the demographic and cognitive/behavioral data.

For help downloading the files, refer to the video tutorials on the Harvard Neuroinformatics Research Group website.

### How are the data organized within the LONI Image Data Archive?

The downloaded files are stored in a specific folder hierarchy e.g.,  $GSP > Sub0001\_S1 > BOLD1 > 2014-06-30\_00\_00\_00.0 > S237949 > GSP\_Sub0001\_S1\_MR\_BOLD1\_Br_20150406152938366\_S237949\_I482691.nii$ . The imaging data can be downloaded individually or in bulk.

A single CSV file (GSP\_list\_140630.csv) containing the demographic and cognitive/behavioral data can be downloaded from the Download Study Data page using the Demographic and Behavioral Data link.

A single extended CSV file (GSP\_extended\_140630.csv) containing additional phenotypes can be downloaded using the Demographic and Behavioral Data Extended link.

For help downloading the files, refer to the video tutorials on the Harvard Neuroinformatics Research Group website.

### Are there test-retest reliability data?

Yes. In addition to the 1570 unique subject datasets, there are 69 subjects who were scanned on two separate occasions. These MRI data are provided as a test-retest data set for development of methods. A separate CSV file (GSP\_retest\_140630.csv) contains metadata for these test-retest sessions.

On Dataverse, the test-retest data are contained within their own separate tar file (GSP\_retest\_140630.tar) and not within the 10 main tar files of unique subjects.

### What are the image file orientations?

The anatomical images (Dataverse, ANAT; LONI, T1\_MEMPRAGE\_RMS) are stored in Anterior-to-Posterior (x), Superior-to-Inferior (y), Right-to-Left (z) orientation. The BOLD images are stored in Right-to-Left (x), Anterior-to-Posterior (y), Inferior-to-Superior (z) orientation.

### What is the coverage and slice ordering for the BOLD runs?

The BOLD protocol has 47 interleaved slices covering the whole brain including the full cerebellum (TR = 3 sec, 3 mm isotropic voxels, no skip between slices). The slices are acquired ascending (foot - head). Odd numbered slices are acquired first, then even numbered slices so the order is: 1, 3, 5, .... 45, 47, 2, 4, 6 .... 44, 46. The exact slice timing can be found in the BOLD DICOM Header Reference element (0019, 1029).

### Should I discard any timepoints at the beginning of the BOLD runs?

Yes. There are 124 image volumes in each BOLD run. These include initial images before T1-stabilization is reached. We recommend discarding the first 4 image volumes and analyzing the remaining 120 timepoints.

### What are the anatomy (Dataverse, ANAT; LONI, T1\_MEMPRAGE\_RMS) images?

The structural images are T1-weighted Multi-Echo MPRAGE (ME-MPRAGE) images that are 1.2 mm isotropic resolution (see van der Kouwe et al., 2008 *NeuroImage*). The single image file contained in the release is the root mean square (RMS) average of the four echoes that were acquired and, for most purposes, can be analyzed as a standard structural T1-weighted image.

### Are the image files processed in anyway?

Yes. In addition to conversion to NIfTI format from DICOM, the face of each high-resolution file (Dataverse, ANAT; LONI, T1\_MEMPRAGE\_RMS) is blurred using the mask\_face software developed at Washington University in St. Louis (Milchenko and Marcus, 2013 *Neuroinformatics*).

We have observed that defacing has small effects on quantitative values such as output from morphometric analysis tools like FreeSurfer. To facilitate analysis, the CSV files (GSP\_list\_140630.csv and GSP\_retest\_140630.csv) include select morphometric values that were computed prior to defacing using FreeSurfer 4.5.0 (as used in Holmes et al., 2013 *J Neurosci*). Individuals computing such values on the defaced images provided in this release can expect highly correlated (but slightly different) values. It should also be noted that in our analysis we used a custom target, different from the default targets available in FreeSurfer, built from our ME-MPRAGE data. This ensured appropriate, matched contrast.

### Are all of the data acquired exactly the same?

Pretty close. All imaging datasets were captured on matched Siemens 3T MAGNETOM Tim Trio MRI systems (Erlangen, Germany) using the vendor-supplied 12-channel phase-array head coil. The exact same sequences, parameters, and instructions were used. But not all subjects were acquired on the same scanner. Five different scanners were used to acquire data. In addition, during the scanning period, the scanner console changed from B13 to B15 to B17.

The scanner (Scanner\_Bin) and console version (Console) for each imaging session are available within the CSV files (GSP list 140630.csv and GSP retest 140630.csv).

The test-retest data include individuals scanned twice on the different scanners and across different console versions. These data may be helpful in assessing any differences that are typically not detectable or minor. As a precaution we recommend regressing scanner and console from analyses.

### How are ages and IO estimates coded?

To protect identity, ages are reported to the nearest age bin. For example, the Age\_Bin 19 includes individuals age 18 and age 19 at the time of the scan.

Estimated IQ scores are binned to the nearest IQ bin. For example, EstIQ\_Shipley\_Int\_Bin 125 includes individuals with an estimated Shipley IQ of 124 and 125.

### I can't find all of the phenotypes listed in the Phenotypes Legend?

Several phenotypes, those listed in italics in the Phenotypes Legend list, are available in a separate extended CSV file (GSP\_extended\_140630.csv) on the LONI Image Data Archive. You must submit the GSP Restricted Access Data Use Terms application to request access to this file.

### Are there genetic data?

Yes. DNA via saliva was collected for almost all of the participants. The genetic data are planned for release in the future.

### How should I acknowledge the data in my papers?

No members of the GSP team nor the byline "GSP" should be included as an author on a paper solely because these data are used.

Papers that include results using GSP data should add the following section to the acknowledgements "Data were provided [in part] by the Brain Genomics Superstruct Project of Harvard University and the Massachusetts General Hospital, (Principal Investigators: Randy Buckner, Joshua Roffman, and Jordan Smoller), with support from the Center for Brain Science Neuroinformatics Research Group, the Athinoula A. Martinos Center for Biomedical Imaging, and

the Center for Human Genetic Research. 20 individual investigators at Harvard and MGH generously contributed data to the overall project."

A paper describing the data is in process. Once that paper is published, it would be appropriate to cite the paper in the methods section.

### How did the name GSP arise?

GSP is short for Brain Genomics Superstruct Project. The name comes from the fact that the project was conceived as an add-on to existing research studies already taking place on matched MRI scanners in the Boston area. The name comes from the word 'superstruct' which means "to erect upon a foundation."

### Who designed the GSP logo?

The GSP logo was designed by a talented local artist and designer, Julie Beck.

### Some useful references

Holmes AJ, Lee PH, Hollinshead M, Bakst L, Roffman JL, Smoller JW, Buckner RL (2012) Individual differences in amygdala-prefrontal anatomy link negative affect, impaired social functioning, and polygenetic depression risk. *J Neurosci*, 32: 18087-100.

Milchenko M, Marcus D (2013) Obscuring surface anatomy in volumetric imaging data. Neuroinformatics, 11:65-75.

van der Kouwe AJ, Benner T, Salat DH, Fischl B (2008) Brain morphometry with multiecho MPRAGE. *NeuroImage* 40: 559-69.

Yeo BT, Krienen FM, Sepulcre J, Sabuncu MR, Lashkari D, Hollinshead M, Roffman JL, Smoller JW, Zollei L, Polimeni JR, Fischl B, Liu H, Buckner RL (2011) The organization of the human cerebral cortex estimated by intrinsic functional connectivity. *J Neurophysiol*, 106: 1125-65.

# Part II Dataverse Release File List

The imaging data are stored in 10 separate tar files, each containing 157 subjects. There is a single description .csv file that contains the demographic and phenotype data for all 1570 unique subjects. All 10 tar files must be downloaded to obtain the full n=1570 dataset.

File Name	Size	Subject Range	Sample
GSP_list_140630.csv	<1 MB	Sub0001_Ses1 to Sub1570_Ses1	n=1570
GSP_part1_140630.tar	11 GB	Sub0001_Ses1 to Sub0157_Ses1	n=157
GSP_part2_140630.tar	11 GB	Sub0158_Ses1 to Sub0314_Ses1	n=157
GSP_part3_140630.tar	11 GB	Sub0315_Ses1 to Sub0471_Ses1	n=157
GSP_part4_140630.tar	10 GB	Sub0472_Ses1 to Sub0628_Ses1	n=157
GSP_part5_140630.tar	10 GB	Sub0629_Ses1 to Sub0785_Ses1	n=157
GSP_part6_140630.tar	11 GB	Sub0786_Ses1 to Sub0942_Ses1	n=157
GSP_part7_140630.tar	11 GB	Sub0943_Ses1 to Sub1099_Ses1	n=157
GSP_part8_140630.tar	10 GB	Sub1100_Ses1 to Sub1256_Ses1	n=157
GSP_part9_140630.tar	11 GB	Sub1257_Ses1 to Sub1413_Ses1	n=157
GSP_part10_140630.tar	10 GB	Sub1414_Ses1 to Sub1570_Ses1	n=157

The test-retest imaging data are stored in a single tar file that contains both sessions for each of the 69 test-retest subjects (the Ses1 image sets are the same as those included in the full dataset release above). There is a single description .csv file for the 69 test-retest subjects. Downloading the single retest tar file contains all of the data needed for analysis of reliability.

File Name	Size	Subject Range	Sample
GSP_retest_140630.csv	<1 MB	Sub0043_Ses1 to Sub1562_Ses1 Sub0043_Ses2 to Sub1562_Ses2	n=69
GSP_retest_140630.tar	9 GB	Sub0043_Ses1 to Sub1562_Ses1 Sub0043_Ses2 to Sub1562_Ses2	n=69

# Part III LONI Release File List

The imaging data for each subject are stored individually. There is a single description .csv file that contains the demographic and phenotype data for all 1570 unique subjects and a separate extended .csv file that contains additional phenotypes for a subset of subjects.

File Name	Size	Subject Range	Sample
GSP_list_140630.csv	<1 MB	Sub0001_S1 to Sub1570_S1	n=1570
GSP_extended_140630.csv	<1 MB	Sub0001_S1 to Sub1570_S1	n=1570
GSP_Sub*_S1_MR_BOLD1_*.nii	<60 MB	Sub0001_S1 to Sub1570_S1	n=1570
GSP_Sub*_S1_MR_BOLD2_*.nii	<60 MB	Sub0001_S1 to Sub1570_S1	n=1570
GSP_Sub*_S1_MR_T1_MEMPRAGE_RMS_*.nii	<11 MB	Sub0001_S1 to Sub1570_S1	n=1570

The retest (S2) imaging data are stored individually for each of the 69 test-retest subjects. There is a single description .csv file for the 69 test-retest subjects.

File Name	Size	Subject Range	Sample
GSP_retest_140630.csv	<1 MB	Sub0043_S1 to Sub1562_S1 Sub0043_S2 to Sub1562_S2	n=69
GSP_Sub*_S2_MR_BOLD1_*.nii	<60 MB	Sub0001_S2 to Sub1570_S2	n=69
GSP_Sub*_S2_MR_BOLD2_*.nii	<60 MB	Sub0001_S2 to Sub1570_S2	n=69
GSP_Sub*_S2_MR_T1_MEMPRAGE_RMS_*.nii	<11 MB	Sub0001_S2 to Sub1570_S2	n=69

# Part IV Phenotypes Legend

Phenotype	Description
Subject_ID	The anonymous data release ID.
Delay	The number of days between the test and retest scans.
Subject_Rescan_ID	The anonymous data release ID for subjects who were re-scanned within six months of their initial scan date.
MRI	Reflects the number of eyes open rest runs available $(1, 2)$ .
Behavior	Reflects the presence of behavioral data (Present, Absent).
Sex	Sex (M, F).
Age_Bin	The binned age (2 year bins) of each participant at the time of image acquisition. Participants who were from 18-19 years of age at the point of scan are coded as 19, participants who were 20-21 years of age are coded as 21, etc.
Hand	Participant handedness (RHT, LFT, AMB).
Educ	Years of education. Please note, due to the characteristics of the sample education is truncated by the age of the participant and should not be interpreted as an accurate reflection (nor a proxy) of SES.
Race_Ethn	Participant race/ethnicity (White not Hispanic = W_NOT_HL, all other race/ethnicities = Other).
Scanner_Bin	Site/Scanner bay where the data were acquired (A, B, C, D, E).
Console	Console software version on scanner at the time of image acquisition (B13, B15, B17).
Coil	Coil version (currently all 12-channel coils = Tim_12).
ANAT	The run number for the T1 MEMPRAGE anatomical scan (1).
BOLD1	The run number for the first eyes open rest run (2).
BOLD1_sSNR	Slice based SNR for first eyes open rest run.
BOLD1_MotMicro	Number of relative translations in 3D space $\geq 0.1$ mm.
BOLD1_MotAbsMax	Maximum absolute translation in 3D space (mm).
BOLD2	The run number for the second eyes open rest run when present (3).
BOLD2_sSNR	Slice based SNR for second eyes open rest run.
BOLD2_MotMicro	Number of relative translations in 3D space $\geq 0.1$ mm.
BOLD2_MotAbsMax	Maximum absolute translation in 3D space (mm).
Flank_S_CORRpc	The percentage of correct responses for the flanker task during switch blocks.
Flank_S_meanRTcorr	The mean reaction time (RT) for correct flanker task trials during switch blocks.
Flank_S_medRTcorr	The median RT for correct flanker task trials during switch blocks.
Flank_S_score	The number of correct trials minus the number of incorrect trials for the switch blocks.

Table 1 – continued from previous page

Phenotype	Description
Flank_NS_CORRpc	The percentage of correct responses for the flanker task during non-switch blocks.
Flank_NS_meanRTcorr	The mean RT for the correct flanker task trials during non-switch blocks.
Flank_NS_medRTcorr	The median RT for the correct flanker task trials during the non-switch blocks.
Flank_NS_score	The number of correct trials minus the number of incorrect trials for the non-switch blocks.
Flank_CORRpc	The percent of correct responses for the flanker task.
Flank_meanRTcorr	The mean flanker task RT for correct responses.
Flank_medRTcorr	The median flanker task RT for correct responses.
Flank_TOT_score	The number of correct trials minus the number of incorrect trials for the flanker task.
MenRot_0_CORRpc	Percent of correct responses for mental rotation 0-degree rotation trials.
MenRot_0_meanRTcorr	Mean RT of correct responses for mental rotation 0-degree rotation trials.
MenRot_0_medRTcorr	Median RT of correct responses for mental rotation 0-degree rotation trials.
MenRot_80_CORRpc	Percent of correct responses for mental rotation 80-degree rotation trials.
MenRot_80_meanRTcorr	Mean RT of correct responses for mental rotation 80-degree rotation trials.
MenRot_80_medRTcorr	Median RT of correct responses for mental rotation 80-degree rotation trials.
MenRot_120_CORRpc	Percent of correct responses for mental rotation 120-degree rotation trials.
MenRot_120_meanRTcorr	Mean RT of correct responses for mental rotation 120-degree rotation trials.
MenRot_120_medRTcorr	Median RT of correct responses for mental rotation 120-degree rotation trials.
MenRot_160_CORRpc	Mental rotation percent of correct responses for 160-degree rotation trials.
MenRot_160_meanRTcorr	Mean RT of correct responses for mental rotation 160-degree rotation trials.
MenRot_160_medRTcorr	Median RT of correct responses for mental rotation 160-degree rotation trials.
MenRot_TOT_CORRpc	Percent of correct responses for mental rotation task.
MenRot_TOT_meanRTcorr	Mean RT of correct responses for mental rotation task.
MenRot_TOT_medRTcorr	Median RT of correct responses for mental rotation task.
ICV	Estimated total intracranial volume (mm³; Buckner et al., 2004).
BrainSegVol	The volume of brain as the sum of the volumes of the segmentations that are in the brain.
BrainSegVolNonVent	The volume of brain as the sum of the volumes of the segmentations that are in the brain excluding the ventricles.

Table 1 – continued from previous page

Phenotype	Description
postCorCall_Vol	Posterior corpus callosum (mm <sup>3</sup> ).
midpostCorCall_Vol	Middle posterior corpus callosum (mm <sup>3</sup> ).
centCorCall_Vol	Central corpus callosum (mm <sup>3</sup> ).
midantCorCall_Vol	Middle anterior corpus callosum (mm <sup>3</sup> ).
antCorCall_Vol	Anterior corpus callosum (mm³).
R_AvgCortThick	Right hemisphere average cortical thickness (mm).
L_AvgCortThick	Left hemisphere average cortical thickness (mm).
R_TotCortSurfArea	Right hemisphere total cortical surface area (mm <sup>2</sup> ).
L_TotCortSurfArea	Left hemisphere total cortical surface area (mm <sup>2</sup> ).
R_Amy_Vol	Right hemisphere amygdala volume (mm³).
L_Amy_Vol	Left hemisphere amygdala volume (mm³).
R_Hipp_Vol	Right hemisphere hippocampal volume (mm <sup>3</sup> ).
L_Hipp_Vol	Left hemisphere hippocampal volume (mm <sup>3</sup> ).
R_rACC_Thick	Right hemisphere rostral anterior cingulate cortical thickness (mm).
L_rACC_Thick	Left hemisphere rostral anterior cingulate cortical thickness (mm).
R_cMF_Thick	Right hemisphere caudal middle frontal cortical thickness (mm).
L_cMF_Thick	Left hemisphere caudal middle frontal cortical thickness (mm).
R_lOcc_Thick	Right hemisphere lateral occipital thickness (mm).
L_lOcc_Thick	Left hemisphere lateral occipital thickness (mm).
R_lingual_Thick	Right hemisphere lingual thickness (mm).
L_lingual_Thick	Left hemisphere lingual thickness (mm).
R_cACC_Thick	Right caudal anterior cingulate thickness (mm).
L_cACC_Thick	Left caudal anterior cingulate thickness (mm).
R_PCC_Thick	Right posterior cingulate thickness (mm).
L_PCC_Thick	Left posterior cingulate thickness (mm).
R_isthmusACC_Thick	Right isthmus cingulate thickness (mm).
L_isthmusACC_Thick	Left isthmus cingulate thickness (mm).
R_Parahipp_Thick	Right parahippocampal thickness (mm).
L_Parahipp_Thick	Left parahippocampal thickness (mm).
R_Fform_Thick	Right fusiform thickness (mm).
L_Fform_Thick	Left fusiform thickness (mm).
R_supF_Thick	Right superiorfrontal thickness (mm).

Table 1 – continued from previous page

Phenotype	Description
L_supF_Thick	Left superiorfrontal thickness (mm).
R_iPar_Thick	Right inferiorparietal thickness (mm).
L_iPar_Thick	Left inferiorparietal thickness (mm).
R_Ins_Thick	Right insula thickness (mm).
L_Ins_Thick	Left insula thickness (mm).
Health_Rating	Compared to other people how would you rate your physical health? (1 – much worse than average; 2 – worse than average; 3 – average; 4 – better than average; 5 – much better than average).
Health_Satisfy	How satisfied are you with your present health? (1 – not at all satisfied; 2 – not very satisfied; 3 – neither satisfied nor dissatisfies; 4 – somewhat satisfied; 5 – extremely satisfied).
STAI_tAnxiety	State-trait anxiety inventory for adults; Measure of trait anxiety (Score range 20-80; Spielberger and Gorsuch, 1970).
STAI_sAnxiety	State-trait anxiety inventory for adults; Measure of state anxiety (Score range 20-80).
NEO_N	The NEO Five-factor model of personality; Neuroticism score (Score range 0-48; Costa and McCrae, 1992).
NEO_E	The NEO Five-factor model of personality; Extraversion score (Score range 0-48).
NEO_O	The NEO Five-factor model of personality; Openness score (Score range 0-48).
NEO_A	The NEO Five-factor model of personality; Agreeableness score (Score range 0-48).
NEO_C	The NEO Five-factor model of personality; Conscientiousness score (Score range 0-48).
BISBAS_BAS_Drive	Behavioral inhibition (BIS) and behavioral activation (BAS) scale; BAS drive score (Score range 4-16; Carver and White, 1994).
BISBAS_BAS_Fun	Behavioral inhibition (BIS) and behavioral activation (BAS) scale; BAS funseeking score (Score range 4-16).
BISBAS_BAS_Reward	Behavioral inhibition (BIS) and behavioral activation (BAS) scale; BAS reward score (Score range 5-20).
BISBAS_BIS	Behavioral inhibition (BIS) and behavioral activation (BAS) scale; BIS score (Score range 7-28).
MindWandering_Freq	Imaginal process inventory; 12-question mind wandering subscale (Score range 12-60; Singer and Antrobus, 1970)
Barratt_tot	Barratt Impulsivity Scale; Total score (Score range 30-120; Patton et al., 1995).

Table 1 – continued from previous page

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Phenotype	Description
Barratt_2atten	Barratt Impulsivity Scale; 2nd order attentional impulsiveness factor (Score range 8-32).
Barratt_2mot	Barratt Impulsivity Scale; 2nd order motor factor (Score range 11-44).
Barratt_2nonplan	Barratt Impulsivity Scale; 2nd order non-planning factor (Score range 11-44).
Barratt_1atten	Barratt Impulsivity Scale; 1st order attentional factor (Score range 5-20).
Barratt_1mot	Barratt Impulsivity Scale; 1st order motor factor (Score range 7-28).
Barratt_1selfcontrol	Barratt Impulsivity Scale; 1st order self-control factor (Score range 6-24).
Barratt_1complex	Barratt Impulsivity Scale; 1st order cognitive complexity factor (Score range 5-20).
Barratt_1persever	Barratt Impulsivity Scale; 1st order perseverance factor (Score range 4-16).
Barratt_linstability	Barratt Impulsivity Scale; 1st order cognitive instability factor (Score range 3-12).
DOSPERT_taking	Domain-specific risk-tasking scale; Risk taking (Score range 40-280; Weber et al., 2002).
DOSPERT_perception	Domain-specific risk-tasking scale; Risk perception (Score range 40-280).
POMS_TotMdDisturb	Profile of Mood States; Total Mood Disturbance score (Score range -20-100; McNair et al., 1971).
POMS_T_TensionAnxiety	Profile of Mood States; T-score Tension/Anxiety (Score range 30-67).
POMS_T_DepressionDejection	Profile of Mood States; T-score Depression/Dejection (Score range 32-69).
POMS_T_AngerHostility	Profile of Mood States; T-score Anger/Hostility (Score range 36-76).
POMS_T_VigorActivity	Profile of Mood States; T-score Vigor/Activity (Score range 36-80).
POMS_T_FatigueInertia	Profile of Mood States; T-score Fatigue/Inertia (Score range 30-76).
$POMS\_T\_Confusion Be wilder ment$	Profile of Mood States; T-score Confusion/Bewilderment (Score range 33-75).
TCI_Novelty	Temperament and Character Inventory (TCI-9); Novelty-seeking (Score range 20-100; Cloninger, 1987).
TCI_RewardDependence	Temperament and Character Inventory (TCI-9); Reward Dependence (Score range 20-100).
TCI_HarmAvoidance	Temperament and Character Inventory (TCI-9); Harm Avoidance (Score range 20-100).
Shipley_Vocab_Raw	Raw number correct for the Shipley vocabulary task (Score range 0-40).
EstIQ_Shipley_Int_Bin	Estimated IQ derived from Shipley-Hartford Age-Corrected T-Scores. Reported values are in integers and binned.

Table 1 – continued from previous page		
Phenotype	Description	
Matrix_WAIS	Matrix reasoning Wechsler Adult Intelligence Scale (WAIS) score. Scoring rules are as follows: 1. Examinee receives 1 point for each correct response. 2. If the examinee obtains perfect scores on items 4 and 5, give full credit for items 1-3. 3. Discontinue after 4 consecutive errors or 4 errors on five consecutive trials. 4. Count trials with RT < 300ms as errors.	
EstIQ_Matrix_Int_Bin	Estimated IQ derived through the OPIE3 formula (Schoenberg et al., 2002). Reported values are in integers and binned.	

# Part V MEMPRAGE Protocol Reference

### SIEMENS MAGNETOM TrioTim syngo MR B17

	JSER\Investigators\CAP_Ma		
TA: 2:12 PAT: 4	Voxel size: 1.2×1.2×1.2 mm	Rel. SNR: 1.00 USER: A	ndre\tfl_mgh_multiecho
Properties		Image Filter	Off
Prio Recon	Off	<ul><li>Distortion Corr.</li></ul>	Off
Before measurement	Oll	Unfiltered images	Off
After measurement		Prescan Normalize	On
Load to viewer	On	Normalize	Off
Inline movie	Off	B1 filter	Off
Auto store images	On	Raw filter	Off
Load to stamp segments	On	Elliptical filter	Off
Load images to graphic	Off	Geometry	
segments		Multi-slice mode	Single shot
Auto open inline display	Off	Series	Interleaved
Start measurement without	Off	Table position	Н
further preparation		Table position	0 mm
Wait for user to start	Off	Inline Composing	Off
Start measurements	single	, ,	
Routine		System  - Body	Off
Slab group 1		-   Body   HEP	On
Slabs	1	HEA	On
Dist. factor	50 %		
Position	R3.0 A12.0 F18.0	Positioning mode	REF
Orientation	Sagittal	MSMA	S - C - T
Phase enc. dir.	A >> P	Sagittal	R >> L
Rotation	12.50 deg	Coronal	A >> P
Phase oversampling Slice oversampling	0 % 0.0 %	Transversal	F >> H
Slices per slab	144	Save uncombined	Off
FoV read	230 mm	Coil Combine Mode AutoAlign	Adaptive Combine Head > Brain Atlas
FoV phase	100.0 %	Auto Coil Select	Off
Slice thickness	1.20 mm	Auto Con Select	
TR	2200 ms	Shim mode	Standard
TE 1	1.54 ms	Adjust with body coil	Off
TE 2	3.36 ms	Confirm freq. adjustment	Off
TE 3	5.18 ms	Assume Silicone	Off
TE 4	7 ms	? Ref. amplitude 1H	0.000 V
Averages	1	Adjustment Tolerance	Auto
Concatenations	1	Adjust volume ! Position	D0 0 40 0 H0 0
Filter	Prescan Normalize	! Orientation	R3.0 A3.0 H0.0 T > C-12.5
Coil elements	HEA;HEP	! Rotation	0.00 deg
Contrast		! R >> L	216 mm
Magn. preparation	Non-sel. IR	-   !N>> P	216 mm
TI	1100 ms	!F>> H	141 mm
Flip angle	7.0 deg	I	
Fat suppr.	None	Physio	Niere
Water suppr.	None	1st Signal/Mode	None
Averaging mode	Long term	Dark blood	Off
Reconstruction	Magn./Phase	Inline	
Measurements	1		Off
Multiple series	Each measurement	Subtract Std-Dev-Sag	Off Off
•		Std-Dev-Gor	Off
Resolution	100	- Std-Dev-Tra	Off
Base resolution	192	Std-Dev-Time	Off
Phase resolution Slice resolution	100 % 100 %	MIP-Sag	Off
Phase partial Fourier	100 % 6/8	MIP-Cor	Off
Slice partial Fourier	0/8 Off	MIP-Tra	Off
Interpolation	Off	MIP-Time	Off
		Save original images	On
PAT mode	GRAPPA	<del>-</del>	
Accel. factor PE	4	Sequence	
Ref. lines PE	32	Introduction	Off
Matrix Coil Mode	Auto (Triple)	Dimension	3D
Reference scan mode	Integrated	Elliptical scanning	

### SIEMENS MAGNETOM TrioTim syngo MR B17

Contrasts Bandwidth 1 Bandwidth 2 Bandwidth 3 Bandwidth 4 Flow comp. 1 Flow comp. 2 Flow comp. 3 Flow comp. 4 Echo spacing	4 651 Hz/Px 651 Hz/Px 651 Hz/Px 651 Hz/Px No No No No No 9.8 ms
RF pulse type Gradient mode Excitation RF spoiling	Fast Fast Non-sel. On
Readout polarity Readout trajectory Add. scale factor Gradient spoiling Gradient moment factor Siemens reconstruction Save raw k-space data Averaging	Positive Bipolar 4.0 Integral 3.0 On Off RMS

# Part VI BOLD Protocol Reference

### SIEMENS MAGNETOM TrioTim syngo MR B17

	\\USEF	${ m RINVestigators} \ { m CAP\_Matrix} \ { m CA$	CAP_Full\fMRI_re	sting_state	
TA: 6:12	PAT: Off	Voxel size: 3.0×3.0×3.0 mm	Rel. SNR: 1.00	USER: ep2d_bold_MGH	

Properties		Table position Inline Composing	0 mm Off
Prio Recon	Off	mille composing	Oil
Before measurement		System	
After measurement		Body	Off
Load to viewer	On	l HEP	On
Inline movie	Off	HEA	On
Auto store images	On		
Load to stamp segments	On	Positioning mode	REF
Load images to graphic	Off	MSMA	S - C - T
	Oli	Sagittal	R >> L
segments		Coronal	A >> P
Auto open inline display	On	Transversal	F >> H
Start measurement without	Off	Coil Combine Mode	Sum of Squares
further preparation		AutoAlign	Head > Brain Atlas
Wait for user to start	On		Off
Start measurements	single	Auto Coil Select	Off
Na	_	Shim mode	Standard
Routine		Adjust with body coil	Off
Slice group 1		Confirm freq. adjustment	Off
Slices	47	Assume Silicone	Off
Dist. factor	0 %	? Ref. amplitude 1H	0.000 V
Position	R3.0 A3.0 H0.0		
Orientation	T > C-12.5	Adjustment Tolerance	Auto
Phase enc. dir.	A >> P	Adjust volume	
Rotation	0.00 deg	Position	R3.0 A3.0 H0.0
Phase oversampling	0.00 deg	Orientation	T > C-12.5
FoV read	216 mm	Rotation	0.00 deg
		R >> L	216 mm
FoV phase	100.0 %	A >> P	216 mm
Slice thickness	3.00 mm	F >> H	141 mm
TR	3000 ms	I	
TE	30 ms	Physio	
Averages	1	1st Signal/Mode	None
Concatenations	1	DOLD.	
Filter	None	BOLD	
Coil elements	HEA;HEP	GLM Statistics	Off
		Dynamic t-maps	Off
Contrast		Starting ignore meas	0
MTC	Off	Ignore after transition	0
Flip angle	85 deg	Model transition states	Off
Fat suppr.	Fat sat.	Temp. highpass filter	Off
		Threshold	4.00
Averaging mode	Long term	Paradigm size	3
Reconstruction	Magnitude	Meas[1]	Baseline
Measurements	124		
Delay in TR	0 ms	Meas[2]	Baseline
Multiple series	Off	Meas[3]	Active
•		Motion correction	Off
Resolution		Spatial filter	Off
Base resolution	72	Sequence	
Phase resolution	100 %		Off
Phase partial Fourier	Off	Introduction	
Interpolation	Off	Bandwidth	2240 Hz/Px
		Free echo spacing	Off
PAT mode	None	Echo spacing	0.51 ms
Matrix Coil Mode	Auto (CP)	EPI factor	70
Distortion Cor-	Off		/2 Normal
Distortion Corr.	Off	RF pulse type	Normal
Prescan Normalize	Off	Gradient mode	Fast
Raw filter	On	Dummy Scans	0
Elliptical filter	Off	FFT Scale Factor	1.00
Hamming	Off	FFT Scale Factor	1.00
•			
Geometry			
Multi-slice mode	Interleaved		
Series	Interleaved		
Special sat.	None		
opeciai sat.	INUITE		
Table position	Н		
1		17/61	

# Part VII MEMPRAGE DICOM Header Reference

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(0008, 0070)
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               Manufacturer
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(0008, 1090)
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(0020, 000d)
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(0028, 0107)
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               WindowWidth
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(0040, 0245)
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                                                                    cs
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T:HEA;HEP
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TP 0
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                                                                                        4
                                                                    SH
                   unknown
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                                                                                             NORM
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(0051, 1019) unknown
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                                                                                             IR
                                                                                             PFP
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### Part VIII BOLD DICOM Header Reference

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(0008, 0021)
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(0008, 0022)
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(0008, 0030)
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306 þ√ø
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(0018, 0024)
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(0018, 1310)
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(0018, 1315)
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12 IMAGE NUM 4

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(0019, 1011)
(0019, 1012)
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(0019, 1014) unknown
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-736.79
(0019, 1015) unknown
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(0019, 1028)
(0019, 1029)
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27.233
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# Part IX GSP Data Use Terms



### GSP Open Access Data Use Terms

Last updated: Apr 22, 2014.

I request access to data collected as part of the Brain Genomics Superstruct Project (GSP) of Harvard University and the Massachusetts General Hospital, and I agree to the following:

- 1. I will not attempt to establish the identity of or attempt to contact any of the included human subjects.
- 2. I will not attempt to link any of the distributed data to any other data that might contain information about the included human subjects.
- 3. I understand that under no circumstances will the code that would link these data to Protected Health Information be given to me, nor will any additional information about individual human subjects be released to me under these Open Access Data Use Terms.
- 4. I will comply with all relevant rules and regulations imposed by my institution. This may mean that I need my research to be approved or declared exempt by a committee that oversees research on human subjects e.g., my Internal Review Board or Ethics Committee. Different committees operate under different national, state, and local laws and may interpret regulations differently, so it is important to ask about this.
- I may redistribute original GSP Open Access data and any derived data as long as the data are redistributed under these same Data Use Terms.
- 6. I will acknowledge the use of GSP data and data derived from GSP data when publicly presenting any results or algorithms that benefitted from their use.
  - a. Papers, book chapters, books, posters, oral presentations, and all other printed and digital presentations of results derived from GSP data should contain the following wording in the acknowledgments section: "Data were provided [in part] by the Brain Genomics Superstruct Project of Harvard University and the Massachusetts General Hospital, (Principal Investigators: Randy Buckner, Joshua Roffman, and Jordan Smoller), with support from the Center for Brain Science Neuroinformatics Research Group, the Athinoula A. Martinos Center for Biomedical Imaging, and the Center for Human Genetic Research. 20 individual investigators at Harvard and MGH generously contributed data to

GSP Open Access Data Use Terms Version: 2014-Apr-22

the overall project."

- b. Authors of publications or presentations using GSP data should cite relevant publications describing the methods used by the GSP to acquire and process the data. The specific publications that are appropriate to cite in any given study will depend on what GSP data were used and for what purposes. An annotated and appropriately up-to-date list of publications that may warrant consideration is available at http://neuroinformatics.harvard.edu/gsp/
- c. The GSP as a consortium should not be included as an author of publications or presentations if this authorship would be based solely on the use of GSP data.
- Failure to abide by these guidelines will result in termination of my privileges to access GSP data.

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