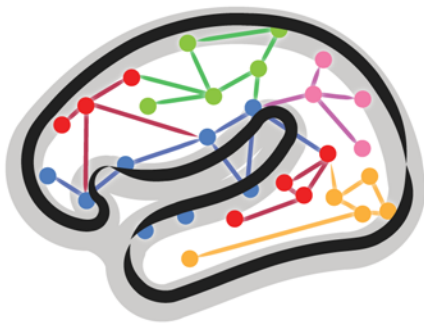




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WU-Minn HCP 500 Subjects + MEG2 Release: Reference Manual

Appendix I – Protocol Guidance and HCP Session Protocols

25 November 2014



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MR Protocol Guidance

What would be an “HCP-like” protocol on a Siemens Trio, Verio, or Skyra 3T magnet?

Many individuals/groups will probably have questions about how best to adapt the HCP scanning protocol to their magnet. It is difficult to suggest a specific “HCP-like” protocol since the majority of the protocol optimizations/investigations that informed the final HCP protocol were conducted on the Connectome Skyra, which is a customized Skyra platform with 100 mT/m gradients for diffusion encoding and ~ 42 mT/m gradients for imaging. Nonetheless, here we provide some general guidance for those seeking to adapt the HCP protocol to their scanner. After reading this guidance and familiarizing yourself with the rationale for the HCP protocols (detailed in [Ugurbil *et al.*, 2013](#), [Glasser *et al.*, 2013](#), [Smith *et al.*, 2013](#) and [Sotiropoulos *et al.*, 2013](#) in a Special Issue of *NeuroImage*), we highly recommend that you perform your own pilot studies on your specific system.

First, you’ll need a 32-channel head coil (12-channel head coil not recommended) and the multiband fMRI and dMRI sequences for your Siemens software version (<http://www.cmrr.umn.edu/multiband/>). Multiband sequences on other vendor platforms (i.e., GE and Philips) are currently being implemented at several research laboratories. Interested users should contact their vendors, but also watch for announcements and updates on the hcp-users mailing list.

Structural Imaging

For structural imaging, similar quality T1w and T2w acquisitions should be achievable on other Siemens 3T platforms using a 32-channel head coil and Siemens product (MPRAGE and SPACE) sequences. The HCP protocol uses 0.7 mm isotropic structural acquisitions. For users that want higher SNR structural scans, at the cost of some resolution, 0.8 mm isotropic acquisitions are also sufficient for deriving benefits from the HCP structural processing pipelines, and may confer some increased robustness against poor quality acquisitions in motion-prone subjects (although this was not specifically investigated by HCP). Slightly longer echo spacings (automatically adjusted in the T1w and T2w sequences) on conventional scanners are expected due to their reduced imaging gradient strength, which should not have a major effect on data quality. Note that the HCP carefully reviews every structural scan for quality, with fairly high standards for what constitutes a “good” or “excellent” scan (i.e., minimal motion-related blurring or ringing artifacts), and acquires a re-scan if necessary.

Functional Imaging

For functional imaging, key choice points relative to the HCP fMRI acquisitions involve the multiband (MB) factor, spatial resolution, TE, and phase encoding direction (the latter three of which all interact). While gradient strength is not as critical for fMRI (relative to dMRI), the Connectome Skyra gradients do allow it to operate at a lower echo spacing than a conventional 3T scanner (e.g., 0.58 ms vs. 0.69 ms at 2 mm, all other things being approximately equal). The limitations of maximal readout gradient [Siemens Trio (TQ) ~ 28mT/m, Verio (VQ) and Skyra (XQ) ~ 24 mT/m] and forbidden echo spacing (due to acoustic resonances) make 2 mm more of a “stretch” resolution on these 3T magnets. Note that considerable benefit as regards the accuracy of the mapping of activation to the cortical surface is already achieved by going to a 2.5 mm isotropic resolution, albeit with further incremental gains in accuracy in going down to 2.0 mm ([Glasser et al. 2013](#)). Overall then, we recommend that users of Trio, Verio, and Skyra systems test resolutions of 2.0 to 2.5 mm for fMRI and make a selection based on their requirements for temporal SNR, statistical power, and acceptable degree of susceptibility distortion, and signal dropout.

The good temporal stability of the Connectome Skyra and the low electronic noise of the Siemens Tim 4G[®] platform allow the HCP to robustly generate good quality BOLD data at an MB factor of 8 without in-plane acceleration. Users of other systems will want to look carefully at whether they are happy with the levels of residual aliasing and temporal SNR at MB=8. In general, we recommend a MB factor of MB=6 for robust image quality while retaining high temporal resolution for these systems.

We caution that performance may vary from system to system even within a single scanner platform. Individual scanners that require a lot of iron to shim will be much more susceptible to shift/drift because of gradient heating, and as such high gradient duty cycles will lead to temporal instability as data are collected. Therefore, for all systems, users should check the temporal stability of their acquisitions!

Many individuals may want to collect single resting-state or task-fMRI runs, or simply use the same phase encoding direction for all runs, in which case we recommend using either anterior-to-posterior (AP) or posterior-to-anterior (PA) phase encoding (rather than the RL and LR phase-encoded pairs used in the HCP acquisitions), so that there is not a right/left susceptibility asymmetry (bias) in the aggregate data. In pilot testing, we could not discern an overall preference for either AP or PA phase encoding, since each resulted in a different amount of signal dropout and local distortions in different brain areas with susceptibility artifact, and this dropout differs greatly depending on slice orientation (e.g., T>C vs C>T). Thus, we recommend that users make the choice between AP and PA phase encoding based on their own particular research aims and goals. Note that AP or PA phase encoding will require use of a full FOV in the phase direction (“FOV phase = 100%”), which will lengthen the total echo train, leading to some increase in T_2^* blurring, susceptibility distortion, and signal dropout (via increased

minimum TE) compared to the HCP acquisitions. In practice, this effect will be at least partially mitigated given the shorter minimum echo spacing achievable in the AP/PA phase encoding direction (due to lower peripheral nerve stimulation limitations with AP/PA than RL/LR). “Compensating” for these effects via use of partial Fourier and/or in-plane GRAPPA involve their own tradeoffs (e.g., for in-plane GRAPPA, reduced image SNR and a lower acceptable maximum multiband acceleration factor and thus longer minimum TR). The HCP investigated these tradeoffs to some degree during pilot testing, and ultimately settled on RL/LR phase encoding with no partial Fourier or in-plane GRAPPA as yielding the best overall quality on the Connectome Skyra. For users of other Siemens 3T systems desiring 2.3 – 2.5 mm isotropic spatial resolution with only a single phase encoding direction, we suggest trying AP or PA phase encoding without in-plane GRAPPA or partial Fourier (allows a minimum TE of ~ 33 ms), and a multiband factor of 6. For users desiring 2.0 mm resolution, 7/8 partial Fourier may be desirable (allows a minimum TE of ~ 36 ms). Note that even if you collect all your fMRI scans with a single phase encoding direction, we recommend collecting brief spin-echo EPI variants using opposing phase encoding directions for best distortion correction of the fMRI data (see “Functional Session A” below, and Glasser et al., submitted). TR can be set at the minimum allowed for the chosen slice coverage (assuming maximal temporal resolution is desired), and the flip angle set to the Ernst angle for that particular TR [i.e., $\cos(\theta_E) = \exp(-TR/T_1)$, where $T_1 \sim 1400$ ms for gray matter at 3T]. As multiband reconstruction is computationally intensive, individuals will also want to monitor the required reconstruction time for their chosen parameters and system. Note that there is a limit of 12 series in the Siemens reconstruction queue, at which point further scanning is not possible until under this limit.

Diffusion Imaging

It is harder to give advice for diffusion imaging, since for dMRI the higher gradient strength of the Connectome Skyra was a critical factor in setting the HCP diffusion protocol. However, our initial experience with other 3T magnets suggests that some of the insights from HCP piloting will be transferrable.

Phase encode directions and susceptibility distortions. Instead of averaging data, we strongly recommend that you acquire two phase encode directions with opposite polarities. Much of the SNR benefits associated with averaging are retained, and the benefit of being able to largely eliminate susceptibility distortions is a substantial one. We have found that it is most efficient for the two phase encode directions to be selected as RL and LR.

Multiband imaging. On the Connectome Skyra, MB=3 was substantially preferable to MB=2. We tested MB=4, but were not entirely comfortable with it for a large-scale study due to some increase in blurring and occasional artifacts. Thus we opted for MB=3, although future improvements in the design of RF pulses and reconstruction algorithms might render higher MB factors preferable. We do not yet have extensive experience with multiband diffusion imaging on other scanners, but the potential improvements are substantial as multiband allows for a much

denser covering of b-space for a given total imaging time (see next section). It was not our experience that the optimal MB factor depended substantially on voxel resolution within the ranges that we were considering (1.2 – 1.5 mm isotropic).

Sampling of b-space. Extensive testing of b-space sampling schemes suggested the following guidelines, at least when reconstructing with Bedpostx, q-ball or spherical harmonics. Note that the following guidelines refer to multiband data where extensive sampling of b-space is possible within a reasonable scan time (for us in the range of 300 datapoints acquired along each phase encode direction).

- 1) The sensitivity for detecting the presence and angular orientations of multiple fibers in a voxel benefit from having more than a single b-shell – various options were considered and several performed similarly well. We preferred $b=1,2,3k$ but this is clearly SNR dependent.
- 2) It is beneficial for sensitivity to remain entirely in the regime in which signal is easily visible in the raw data (i.e., we did not find it beneficial to go into the very high b-value regimes)
- 3) It is not necessarily beneficial for sensitivity to distribute more data points on higher b-shells. There is a clear trade off with time spent imaging at low SNR. We opted for distributing an equal number of data-points on each shell, but this can be piloted on individual scanners.
- 4) It is not beneficial to acquire the same orientations on each shell.
- 5) It is essential for later correction of eddy current distortions that orientations should be distributed on a whole sphere, and not on a hemisphere.

Monopolar vs bipolar gradients. The TE (and therefore SNR) benefits from using monopolar rather than bipolar diffusion encoding were found to be substantial on the Connectome Skyra. While there is an eddy current penalty for monopolar gradients, we found that the new eddy current correction tool of FSL performed excellently on our data, removing almost all eddy current effects that could be easily seen by eye. We have repeated this test on a Verio scanner with similar results. The alternative use of the bipolar gradient encoding lengthens the TE (decreasing SNR) but results in much less eddy current displacement artifacts if the TOPUP/EDDY tools are not used.

Voxel resolution. This clearly depends on the SNR performance of your scanner and sequence. However, the benefits for tractography of moving below 2 mm isotropic are substantial. We have recently acquired high quality 1.5 mm isotropic data with b-values up to $b=2000$ s/mm² on both Verio and Trio systems with standard gradient coils.

Reconstructing data acquired with multi-channel head coils. Sum-of-squares reconstruction should be avoided as it introduces artificial baselines into the data, which have a profound effect on diffusion reconstructions. This is particularly true for higher b-values or lower SNR data and the problem scales with the number of coil elements. A solution to this problem is to use SENSE (R=1) reconstruction, which eliminates the problem and returns the noise profile to Rician.

In-plane acceleration (iPAT/GRAPPA). The combination of in-plane GRAPPA (e.g., R=2) with multiband (e.g., MB=3) imaging leads to compromises in temporal stability due to the effect of physiological motion on multiband reconstruction. This issue is being actively investigated and may be satisfactorily addressed in a future version of the multiband sequence/reconstruction ([Ugurbil et al., 2013](#)).

What would be an “HCP-like” protocol on a Siemens Prisma 3T magnet?

The Siemens Prisma scanner has powerful gradients (80 mT/m gradients for diffusion encoding and ~ 42 mT/m gradients for imaging) similar to the customized HCP Connectome Skyra scanner. The HCP structural and fMRI protocols can be duplicated exactly on the Prisma scanner. The difference in the maximal gradient strength for diffusion encoding will necessitate small changes in TE, resolution, or b-values for a similar protocol on Prisma. The exact gradient table that HCP uses for dMRI is available for request via the HCP Data Users mailing list (see next paragraph).

Mailing List

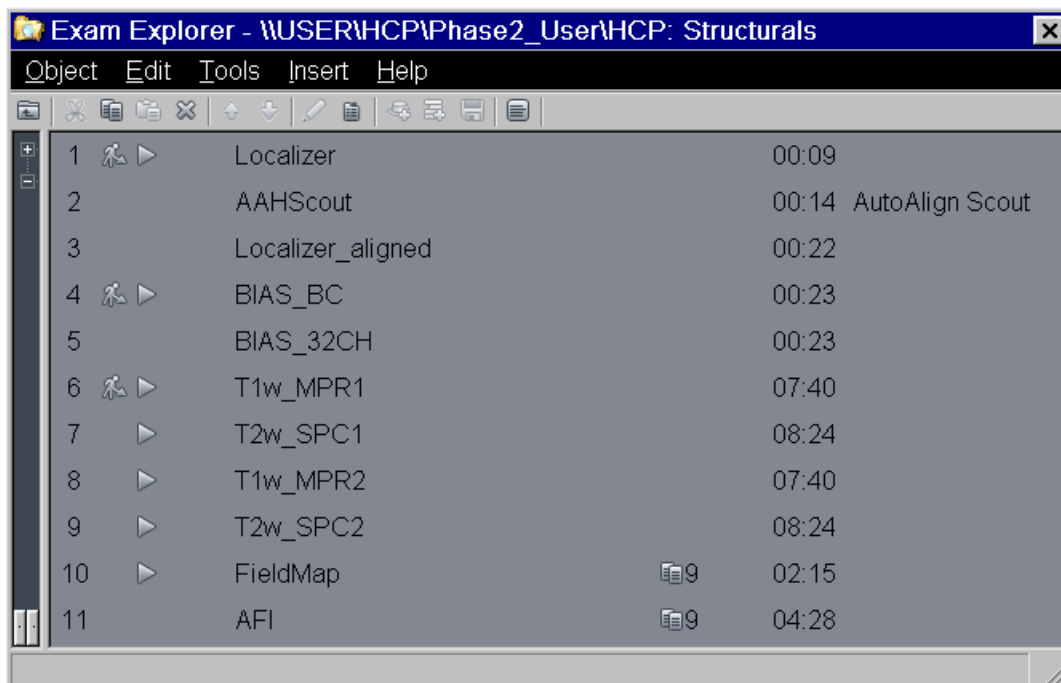
Individuals with further protocol-related questions are encouraged to use the HCP Data Users mailing list (hcp-users@humanconnectome.org) by signing up at <http://www.humanconnectome.org/contact/> or by checking the appropriate box when registering to download HCP data. We also encourage individuals to share their protocols of what they find works best (and what doesn't) via this forum!

MR Scan Protocols

HCP participants are scanned in the MR scanner for a possible total of five sessions: one structural session, two functional MRI sessions, and one diffusion session. If rescans are needed, they are performed in a fifth "extra" session. See [500 Subjects + MEG2 Release Appendix IV](#) for Standard Operating Procedures used by HCP research staff to ensure consistent data acquisition between subjects.

Here is a definition of each of the four defined sessions.

Structural Session



Object	Edit	Tools	Insert	Help
1	▶	Localizer	00:09	
2		AAHScout	00:14	AutoAlign Scout
3		Localizer_aligned	00:22	
4	▶	BIAS_BC	00:23	
5		BIAS_32CH	00:23	
6	▶	T1w_MPR1	07:40	
7		T2w_SPC1	08:24	
8		T1w_MPR2	07:40	
9		T2w_SPC2	08:24	
10		FieldMap	02:15	
11		AFI	04:28	

“AFI” stands for “actual flip-angle imaging” – a scan for three-dimensional mapping of the transmitted radiofrequency field (Yarnykh VL, MRM, 2007, 57:192-200). As of the Q1 Release, this scan is not being used in the structural preprocessing pipelines. The BIAS_BC and BIAS_32CH scans are collected as analogs of Siemen’s “Prescan Normalize” procedure, but these also are not being used. Rather, HCP is using the T1w and T2w scans for estimating the receive-coil bias field (see [Glasser et al. 2013](#)).

Note that the T1w scan is acquired with “Fat suppr. = Water excit. Fast” to reduce signal from bone marrow and scalp fat (which helps with non-linear registration in FSL’s FNIRT). Also, any vendor implemented receive-coil bias field corrections (e.g., Prescan Normalize) must be



matched between the T1w and T2w scans for use of these scans in the HCP preprocessing pipelines (either On for both or Off for both; the HCP has it Off for both).

The parameters for the second set of T1w and T2w scans are identical to the first. Consequently, those scans are deleted from the detailed list of parameters that follow.

Structural Session Scan Protocol

SIEMENS MAGNETOM ConnectomS syngo MR D11

```
-----
\\USER\HCP\Phase2_User\HCP: Structurals\Localizer
TA:9.2 s PAT:Off Voxel size:1.2x1.2x5.0 mm Rel. SNR:1.00 :f1
-----
```

Properties

Prio Recon	On
Before measurement	
After measurement	
Load to viewer	Off
Inline movie	Off
Auto store images	On
Load to stamp segments	On
Load images to graphic segments	On
Auto open inline display	Off
Wait for user to start	On
Start measurements	single

Routine

Nr. of slice groups	3
Slices	1
Dist. factor	20 %
Position	L0.0 A45.0 H0.0 mm
Orientation	Transversal
Phase enc. dir.	A >> P
AutoAlign	---
Phase oversampling	0 %
FoV read	300 mm
FoV phase	100.0 %
Slice thickness	5.0 mm
TR	40.0 ms
TE	3.00 ms
Averages	1
Concatenations	1
Filter	Prescan Normalize, Elliptical filter
Coil elements	HEA;HEP

Contrast

MTC	Off
Magn. preparation	None
Flip angle	15 deg
Fat suppr.	None
Water suppr.	None
SWI	Off
Averaging mode	Short term
Measurements	1



Reconstruction	Magnitude
Multiple series	Off
Resolution	
Base resolution	256
Phase resolution	75 %
Phase partial Fourier	Off
Interpolation	Off
PAT mode	None
Image Filter	Off
Distortion Corr.	Off
Unfiltered images	Off
Prescan Normalize	On
Normalize	Off
B1 filter	Off
Raw filter	Off
Elliptical filter	On
Mode	Inplane
Geometry	
Nr. of slice groups	3
Slices	1
Dist. factor	20 %
Position	L0.0 A45.0 H0.0 mm
Phase enc. dir.	A >> P
Phase oversampling	0 %
Multi-slice mode	Interleaved
Series	Interleaved
Saturation mode	Standard
Nr. of sat. regions	0
Position mode	L-P-H
Fat suppr.	None
Water suppr.	None
Special sat.	None
Special sat.	None
Table position	P
System	
Body	Off
HEP	On
HEA	On
Position mode	L-P-H
Positioning mode	REF
Table position	H
Table position	0 mm
MSMA	S - C - T
Sagittal	R >> L
Coronal	A >> P
Transversal	F >> H
Save uncombined	Off
Coil Combine Mode	Sum of Squares
AutoAlign	---
Auto Coil Select	Default
Shim mode	Tune up
Adjust with body coil	Off
Confirm freq. adjustment	Off
Assume Dominant Fat	Off
Assume Silicone	Off
Adjustment Tolerance	Auto
? Ref. amplitude 1H	0.000 V



Position	Isocenter
Rotation	0.00 deg
R >> L	350 mm
A >> P	263 mm
F >> H	350 mm
Frequency 1H	123.254038 MHz
Correction factor	1
SRFExcit 1H	19.146 V
Gain	High
Table position	0 mm
Img. Scale. Cor.	1.000
Physio	
1st Signal/Mode	None
Segments	1
Magn. preparation	None
Dark blood	Off
Resp. control	Off
Inline	
Distortion correction	Off
Sequence	
Introduction	On
Dimension	2D
Phase stabilisation	On
Averaging mode	Short term
Multi-slice mode	Interleaved
Asymmetric echo	Allowed
Contrasts	1
Bandwidth	260 Hz/Px
Flow comp.	No
Allowed delay	0 s
RF pulse type	Normal
Gradient mode	Fast
Excitation	Slice-sel.
RF spoiling	On
TX/RX delta frequency	0 Hz
TX Nucleus	None
TX delta frequency	0 Hz
Coil elements	HEA;HEP
Acquisition duration	0 ms
Mode	Off
BOLD	
Subtract	Off
Liver registration	Off
Save images	On
Autoscaling	Off
Scaling factor	1
Offset	0
Subtrahend	1
Subtraction indices	
StdDev	Off
Std-Dev-Sag	Off
Std-Dev-Cor	Off
Std-Dev-Tra	Off
Std-Dev-Time	Off
MIP-Sag	Off
MIP-Cor	Off
MIP-Tra	Off



MIP-Time	Off
Radial MIP	Off
Save original images	On
Distortion Corr.	Off
Contrasts	1
Save original images	On
Wash - In	Off
Wash - Out	Off
TTP	Off
PEI	Off
MIP - time	Off
Number of radial views	1
Axis of radial views	L-R
MPR Sag	Off
MPR Cor	Off
MPR Tra	Off

SIEMENS MAGNETOM ConnectomS syngo MR D11

 \\USER\HCP\Phase2_User\HCP: Structurals\AAHScout
 TA:0:14 PAT:3 Voxel size:1.6x1.6x1.6 mm Rel. SNR:1.00 :f1

Properties

Prio Recon	On
Before measurement	
After measurement	
Load to viewer	On
Inline movie	Off
Auto store images	On
Load to stamp segments	Off
Load images to graphic segments	Off
Auto open inline display	Off
Wait for user to start	Off
Start measurements	single

Routine

Nr. of slab groups	1
Slabs	1
Dist. factor	20 %
Position	L0.0 A45.0 H0.0 mm
Orientation	Sagittal
Phase enc. dir.	A >> P
Phase oversampling	0 %
Slice oversampling	0.0 %
FoV read	260 mm
FoV phase	100.0 %
Slice thickness	1.6 mm
TR	3.15 ms
TE	1.37 ms
Averages	1
Concatenations	1
Filter	Prescan Normalize
Coil elements	HEA;HEP
AutoAlign	Head

Contrast

Flip angle	8 deg
Averaging mode	Short term



Measurements	1
Reconstruction	Magnitude
Resolution	
Base resolution	160
Phase resolution	100 %
Phase partial Fourier	6/8
PAT mode	GRAPPA
Accel. factor PE	3
Ref. lines PE	24
Reference scan mode	Integrated
Image Filter	Off
Distortion Corr.	Off
Accel. factor 3D	1
Unfiltered images	Off
Prescan Normalize	On
Normalize	Off
B1 filter	Off
Raw filter	Off
Elliptical filter	Off
Slice resolution	69 %
Slice partial Fourier	6/8
Geometry	
Nr. of slab groups	1
Slabs	1
Dist. factor	20 %
Position	L0.0 A45.0 H0.0 mm
Phase enc. dir.	A >> P
Phase oversampling	0 %
Slice oversampling	0.0 %
Slices per slab	128
Multi-slice mode	Sequential
Series	Ascending
Nr. of sat. regions	0
Position mode	L-P-H
Special sat.	None
Table position	P
System	
Body	Off
HEP	On
HEA	On
Position mode	L-P-H
Positioning mode	REF
Table position	H
Table position	0 mm
MSMA	S - C - T
Sagittal	R >> L
Coronal	A >> P
Transversal	F >> H
Save uncombined	Off
Coil Combine Mode	Adaptive Combine
Auto Coil Select	Off
Shim mode	Tune up
Adjust with body coil	Off
Confirm freq. adjustment	Off
Assume Dominant Fat	Off
Assume Silicone	Off
Adjustment Tolerance	Auto



? Ref. amplitude 1H	0.000 V
Position	Isocenter
Rotation	0.00 deg
R >> L	350 mm
A >> P	263 mm
F >> H	350 mm
Frequency 1H	123.254038 MHz
Correction factor	1
SRFExcit 1H	23.852 V
Gain	Low
Table position	0 mm
Img. Scale. Cor.	1.000
Physio	
Inline	
Distortion correction	Off
Sequence	
Introduction	On
Dimension	3D
Averaging mode	Short term
Multi-slice mode	Sequential
Asymmetric echo	Weak
Contrasts	1
Bandwidth	540 Hz/Px
RF pulse type	Fast
Gradient mode	Normal
Excitation	Non-sel.
RF spoiling	On
TX/RX delta frequency	0 Hz
TX Nucleus	None
TX delta frequency	0 Hz
Coil elements	HEA;HEP
Acquisition duration	0 ms
Mode	Off
BOLD	
Time to center	6.2 s
Subtract	Off
Save images	On
Autoscaling	Off
Scaling factor	1
Offset	0
Subtrahend	1
Subtraction indices	
StdDev	Off
Std-Dev-Sag	Off
Std-Dev-Cor	Off
Std-Dev-Tra	Off
Std-Dev-Time	Off
MIP-Sag	Off
MIP-Cor	Off
MIP-Tra	Off
MIP-Time	Off
Radial MIP	Off
Save original images	On
Distortion Corr.	Off
Contrasts	1
Save original images	On
Number of radial views	1



Axis of radial views	L-R
MPR Sag	Off
MPR Cor	Off
MPR Tra	Off

SIEMENS MAGNETOM ConnectomS syngo MR D11

 \\USER\HCP\Phase2_User\HCP: Structurals\Localizer_aligned
 TA:0:22 PAT:Off Voxel size:1.2x1.2x5.0 mm Rel. SNR:1.00 :f1

Properties

Prio Recon	On
Before measurement	
After measurement	
Load to viewer	Off
Inline movie	Off
Auto store images	On
Load to stamp segments	On
Load images to graphic segments	On
Auto open inline display	Off
Wait for user to start	Off
Start measurements	single

Routine

Nr. of slice groups	3
Slices	1
Dist. factor	20 %
Position	Isocenter
Orientation	Transversal
Phase enc. dir.	A >> P
AutoAlign	Head > Brain
Phase oversampling	0 %
FoV read	300 mm
FoV phase	100.0 %
Slice thickness	5.0 mm
TR	104.0 ms
TE	3.00 ms
Averages	1
Concatenations	1
Filter	Prescan Normalize, Elliptical filter
Coil elements	HEA;HEP

Contrast

MTC	Off
Magn. preparation	None
Flip angle	15 deg
Fat suppr.	None
Water suppr.	None
SWI	Off
Averaging mode	Short term
Measurements	1
Reconstruction	Magnitude
Multiple series	Off

Resolution

Base resolution	256
Phase resolution	75 %
Phase partial Fourier	Off
Interpolation	Off



PAT mode	None
Image Filter	Off
Distortion Corr.	Off
Unfiltered images	Off
Prescan Normalize	On
Normalize	Off
B1 filter	Off
Raw filter	Off
Elliptical filter	On
Mode	Inplane
Geometry	
Nr. of slice groups	3
Slices	1
Dist. factor	20 %
Position	Isocenter
Phase enc. dir.	A >> P
Phase oversampling	0 %
Multi-slice mode	Interleaved
Series	Interleaved
Saturation mode	Standard
Nr. of sat. regions	0
Position mode	L-P-H
Fat suppr.	None
Water suppr.	None
Special sat.	None
Special sat.	None
Table position	P
System	
Body	Off
HEP	On
HEA	On
Position mode	L-P-H
Positioning mode	REF
Table position	H
Table position	0 mm
MSMA	S - C - T
Sagittal	R >> L
Coronal	A >> P
Transversal	F >> H
Save uncombined	Off
Coil Combine Mode	Sum of Squares
AutoAlign	Head > Brain
Auto Coil Select	Default
Shim mode	Tune up
Adjust with body coil	Off
Confirm freq. adjustment	Off
Assume Dominant Fat	Off
Assume Silicone	Off
Adjustment Tolerance	Auto
? Ref. amplitude 1H	0.000 V
Position	Isocenter
Rotation	0.00 deg
R >> L	350 mm
A >> P	263 mm
F >> H	350 mm
Frequency 1H	123.254038 MHz
Correction factor	1



SRFExcit 1H	19.146 V
Gain	High
Table position	0 mm
Img. Scale. Cor.	1.000
Physio	
1st Signal/Mode	None
Segments	1
Magn. preparation	None
Dark blood	Off
Resp. control	Off
Inline	
Distortion correction	Off
Sequence	
Introduction	On
Dimension	2D
Phase stabilisation	On
Averaging mode	Short term
Multi-slice mode	Interleaved
Asymmetric echo	Allowed
Contrasts	1
Bandwidth	260 Hz/Px
Flow comp.	No
Allowed delay	0 s
RF pulse type	Normal
Gradient mode	Fast
Excitation	Slice-sel.
RF spoiling	On
TX/RX delta frequency	0 Hz
TX Nucleus	None
TX delta frequency	0 Hz
Coil elements	HEA;HEP
Acquisition duration	0 ms
Mode	Off
BOLD	
Subtract	Off
Liver registration	Off
Save images	On
Autoscaling	Off
Scaling factor	1
Offset	0
Subtrahend	1
Subtraction indices	
StdDev	Off
Std-Dev-Sag	Off
Std-Dev-Cor	Off
Std-Dev-Tra	Off
Std-Dev-Time	Off
MIP-Sag	Off
MIP-Cor	Off
MIP-Tra	Off
MIP-Time	Off
Radial MIP	Off
Save original images	On
Distortion Corr.	Off
Contrasts	1
Save original images	On
Wash - In	Off



Wash - Out	Off
TTP	Off
PEI	Off
MIP - time	Off
Number of radial views	1
Axis of radial views	L-R
MPR Sag	Off
MPR Cor	Off
MPR Tra	Off

SIEMENS MAGNETOM ConnectomS syngo MR D11

\\USER\HCP\Phase2_User\HCP: Structurals\BIAS_BC
TA:0:23 PAT:Off Voxel size:2.0x2.0x2.0 mm Rel. SNR:1.00 :tfl

Properties

Prio Recon	On
Before measurement	
After measurement	
Load to viewer	On
Inline movie	Off
Auto store images	On
Load to stamp segments	Off
Load images to graphic segments	Off
Auto open inline display	Off
Wait for user to start	On
Start measurements	single

Routine

Nr. of slab groups	1
Slabs	1
Dist. factor	50 %
Position	Isocenter
Orientation	Sagittal
Phase enc. dir.	A >> P
AutoAlign	Head > Brain
Phase oversampling	0 %
Slice oversampling	18.2 %
FoV read	224 mm
FoV phase	100.0 %
Slice thickness	2.00 mm
TR	250.0 ms
TE	1.01 ms
Averages	1
Concatenations	1
Filter	None
Coil elements	BC

Contrast

Magn. preparation	None
Flip angle	3 deg
Fat suppr.	None
Water suppr.	None
Averaging mode	Long term
Measurements	1
Reconstruction	Magnitude
Multiple series	Each measurement

Resolution



Base resolution	112
Phase resolution	100 %
Phase partial Fourier	6/8
Interpolation	Off
PAT mode	None
Image Filter	Off
Distortion Corr.	Off
Prescan Normalize	Off
Normalize	Off
B1 filter	Off
Raw filter	Off
Elliptical filter	Off
Slice resolution	100 %
Slice partial Fourier	6/8
Geometry	
Nr. of slab groups	1
Slabs	1
Dist. factor	50 %
Position	Isocenter
Phase enc. dir.	A >> P
Phase oversampling	0 %
Slice oversampling	18.2 %
Slices per slab	88
Multi-slice mode	Single shot
Series	Interleaved
Nr. of sat. regions	0
Position mode	L-P-H
Fat suppr.	None
Water suppr.	None
Special sat.	None
Table position	P
System	
Body	On
HEP	Off
HEA	Off
Position mode	L-P-H
Positioning mode	FIX
Table position	H
Table position	0 mm
MSMA	S - C - T
Sagittal	R >> L
Coronal	A >> P
Transversal	F >> H
Save uncombined	Off
Coil Combine Mode	Sum of Squares
AutoAlign	Head > Brain
Auto Coil Select	Off
Shim mode	Tune up
Adjust with body coil	Off
Confirm freq. adjustment	Off
Assume Dominant Fat	Off
Assume Silicone	Off
Adjustment Tolerance	Auto
? Ref. amplitude 1H	0.000 V
Position	Isocenter
Rotation	0.00 deg
R >> L	350 mm



A >> P	263 mm
F >> H	350 mm
Frequency 1H	123.254038 MHz
Correction factor	1
SRFExcit 1H	26.833 V
Gain	Low
Table position	0 mm
Img. Scale. Cor.	1.000
Physio	
1st Signal/Mode	None
Magn. preparation	None
Dark blood	Off
Resp. control	Off
Inline	
Distortion correction	Off
Sequence	
Introduction	On
Dimension	3D
Elliptical scanning	Off
Averaging mode	Long term
Multi-slice mode	Single shot
Reordering	Linear
Asymmetric echo	Allowed
Bandwidth	540 Hz/Px
Flow comp.	No
Echo spacing	3 ms
Turbo factor	78
RF pulse type	Fast
Gradient mode	Fast*
Excitation	Non-sel.
RF spoiling	On
TX/RX delta frequency	0 Hz
TX Nucleus	None
TX delta frequency	0 Hz
Coil elements	BC
Acquisition duration	0 ms
Mode	Off
BOLD	
Subtract	Off
Save images	On
Autoscaling	Off
Scaling factor	1
Offset	0
Subtrahend	1
Subtraction indices	
StdDev	Off
Std-Dev-Sag	Off
Std-Dev-Cor	Off
Std-Dev-Tra	Off
Std-Dev-Time	Off
MIP-Sag	Off
MIP-Cor	Off
MIP-Tra	Off
MIP-Time	Off
Radial MIP	Off
Save original images	On
Distortion Corr.	Off



Save original images	On
Number of radial views	1
Axis of radial views	L-R
MPR Sag	Off
MPR Cor	Off
MPR Tra	Off

SIEMENS MAGNETOM ConnectomS syngo MR D11

 \\USER\HCP\Phase2_User\HCP: Structural\BIAS_32CH
 TA:0:23 PAT:Off Voxel size:2.0x2.0x2.0 mm Rel. SNR:1.00 :tfl

Properties

Prio Recon	On
Before measurement	
After measurement	
Load to viewer	On
Inline movie	Off
Auto store images	On
Load to stamp segments	Off
Load images to graphic segments	Off
Auto open inline display	Off
Wait for user to start	Off
Start measurements	single

Routine

Nr. of slab groups	1
Slabs	1
Dist. factor	50 %
Position	Isocenter
Orientation	Sagittal
Phase enc. dir.	A >> P
AutoAlign	Head > Brain
Phase oversampling	0 %
Slice oversampling	18.2 %
FoV read	224 mm
FoV phase	100.0 %
Slice thickness	2.00 mm
TR	250.0 ms
TE	1.01 ms
Averages	1
Concatenations	1
Filter	None
Coil elements	HEA;HEP

Contrast

Magn. preparation	None
Flip angle	3 deg
Fat suppr.	None
Water suppr.	None
Averaging mode	Long term
Measurements	1
Reconstruction	Magnitude
Multiple series	Each measurement

Resolution

Base resolution	112
Phase resolution	100 %
Phase partial Fourier	6/8



Interpolation	Off
PAT mode	None
Image Filter	Off
Distortion Corr.	Off
Prescan Normalize	Off
Normalize	Off
B1 filter	Off
Raw filter	Off
Elliptical filter	Off
Slice resolution	100 %
Slice partial Fourier	6/8
Geometry	
Nr. of slab groups	1
Slabs	1
Dist. factor	50 %
Position	Isocenter
Phase enc. dir.	A >> P
Phase oversampling	0 %
Slice oversampling	18.2 %
Slices per slab	88
Multi-slice mode	Single shot
Series	Interleaved
Nr. of sat. regions	0
Position mode	L-P-H
Fat suppr.	None
Water suppr.	None
Special sat.	None
Table position	P
System	
Body	Off
HEP	On
HEA	On
Position mode	L-P-H
Positioning mode	FIX
Table position	H
Table position	0 mm
MSMA	S - C - T
Sagittal	R >> L
Coronal	A >> P
Transversal	F >> H
Save uncombined	Off
Coil Combine Mode	Sum of Squares
AutoAlign	Head > Brain
Auto Coil Select	Default
Shim mode	Tune up
Adjust with body coil	Off
Confirm freq. adjustment	Off
Assume Dominant Fat	Off
Assume Silicone	Off
Adjustment Tolerance	Auto
? Ref. amplitude 1H	0.000 V
Position	Isocenter
Rotation	0.00 deg
R >> L	350 mm
A >> P	263 mm
F >> H	350 mm
Frequency 1H	123.254038 MHz



Correction factor	1
SRFExcit 1H	26.833 V
Gain	Low
Table position	0 mm
Img. Scale. Cor.	1.000
Physio	
1st Signal/Mode	None
Magn. preparation	None
Dark blood	Off
Resp. control	Off
Inline	
Distortion correction	Off
Sequence	
Introduction	On
Dimension	3D
Elliptical scanning	Off
Averaging mode	Long term
Multi-slice mode	Single shot
Reordering	Linear
Asymmetric echo	Allowed
Bandwidth	540 Hz/Px
Flow comp.	No
Echo spacing	3 ms
Turbo factor	78
RF pulse type	Fast
Gradient mode	Fast*
Excitation	Non-sel.
RF spoiling	On
TX/RX delta frequency	0 Hz
TX Nucleus	None
TX delta frequency	0 Hz
Coil elements	HEA;HEP
Acquisition duration	0 ms
Mode	Off
BOLD	
Subtract	Off
Save images	On
Autoscaling	Off
Scaling factor	1
Offset	0
Subtrahend	1
Subtraction indices	
StdDev	Off
Std-Dev-Sag	Off
Std-Dev-Cor	Off
Std-Dev-Tra	Off
Std-Dev-Time	Off
MIP-Sag	Off
MIP-Cor	Off
MIP-Tra	Off
MIP-Time	Off
Radial MIP	Off
Save original images	On
Distortion Corr.	Off
Save original images	On
Number of radial views	1
Axis of radial views	L-R



MPR Sag Off
MPR Cor Off
MPR Tra Off

SIEMENS MAGNETOM ConnectomS syngo MR D11

\\USER\HCP\Phase2_User\HCP: Structurals\T1w_MPR1
TA:7:40 PAT:2 Voxel size:0.7x0.7x0.7 mm Rel. SNR:1.00 :tfl

Properties

Prio Recon Off
Before measurement
After measurement
Load to viewer On
Inline movie Off
Auto store images On
Load to stamp segments Off
Load images to graphic segments Off
Auto open inline display Off
Wait for user to start On
Start measurements single

Routine

Nr. of slab groups 1
Slabs 1
Dist. factor 50 %
Position Isocenter
Orientation Sagittal
Phase enc. dir. A >> P
AutoAlign Head > Brain
Phase oversampling 10 %
Slice oversampling 0.0 %
FoV read 224 mm
FoV phase 100.0 %
Slice thickness 0.70 mm
TR 2400.0 ms
TE 2.14 ms
Averages 1
Concatenations 1
Filter None
Coil elements HEA;HEP

Contrast

Magn. preparation Non-sel. IR
TI 1000 ms
Flip angle 8 deg
Fat suppr. Water excit. fast
Water suppr. None
Averaging mode Long term
Measurements 1
Reconstruction Magnitude
Multiple series Each measurement

Resolution

Base resolution 320
Phase resolution 100 %
Phase partial Fourier Off
Interpolation Off
PAT mode GRAPPA



Accel. factor PE	2
Ref. lines PE	32
Reference scan mode	Integrated
Image Filter	Off
Distortion Corr.	Off
Accel. factor 3D	1
Prescan Normalize	Off
Normalize	Off
B1 filter	Off
Raw filter	Off
Elliptical filter	Off
Slice resolution	100 %
Slice partial Fourier	Off
Geometry	
Nr. of slab groups	1
Slabs	1
Dist. factor	50 %
Position	Isocenter
Phase enc. dir.	A >> P
Phase oversampling	10 %
Slice oversampling	0.0 %
Slices per slab	256
Multi-slice mode	Single shot
Series	Interleaved
Nr. of sat. regions	0
Position mode	L-P-H
Fat suppr.	Water excit. fast
Water suppr.	None
Special sat.	None
Table position	P
System	
Body	Off
HEP	On
HEA	On
Position mode	L-P-H
Positioning mode	FIX
Table position	H
Table position	0 mm
MSMA	S - C - T
Sagittal	R >> L
Coronal	A >> P
Transversal	F >> H
Save uncombined	Off
Coil Combine Mode	Adaptive Combine
AutoAlign	Head > Brain
Auto Coil Select	Default
Shim mode	Standard
Adjust with body coil	Off
Confirm freq. adjustment	Off
Assume Dominant Fat	Off
Assume Silicone	Off
Adjustment Tolerance	Auto
? Ref. amplitude 1H	0.000 V
Position	Isocenter
Rotation	0.00 deg
F >> H	224 mm
A >> P	224 mm



R >> L	180 mm
Frequency 1H	123.254038 MHz
Correction factor	1
ExcitWEns 0 1H	35.778 V
Gain	Low
Table position	0 mm
Img. Scale. Cor.	5.000
Physio	
1st Signal/Mode	None
Magn. preparation	Non-sel. IR
TI	1000 ms
Dark blood	Off
Resp. control	Off
Inline	
Distortion correction	Off
Sequence	
Introduction	On
Dimension	3D
Elliptical scanning	Off
Averaging mode	Long term
Multi-slice mode	Single shot
Reordering	Linear
Asymmetric echo	Allowed
Bandwidth	210 Hz/Px
Flow comp.	No
Echo spacing	7.6 ms
Turbo factor	256
RF pulse type	Normal
Gradient mode	Fast*
Excitation	Non-sel.
RF spoiling	On
TX/RX delta frequency	0 Hz
TX Nucleus	None
TX delta frequency	0 Hz
Coil elements	HEA;HEP
Acquisition duration	0 ms
Mode	Off
BOLD	
PostProcMoCo	Off
Spacial Filter	Off
Distortion Corr.	Off

SIEMENS MAGNETOM ConnectomS syngo MR D11

 \\USER\HCP\Phase2_User\HCP: Structurals\T2w_SPC1
 TA:8:24 PAT:2 Voxel size:0.7x0.7x0.7 mm Rel. SNR:1.00 :spc

Properties	
Prio Recon	Off
Before measurement	
After measurement	
Load to viewer	On
Inline movie	Off
Auto store images	On
Load to stamp segments	Off
Load images to graphic segments	Off



Auto open inline display	Off
Wait for user to start	On
Start measurements	single
Routine	
Nr. of slab groups	1
Slabs	1
Position	Isocenter
Orientation	Sagittal
Phase enc. dir.	A >> P
AutoAlign	Head > Brain
Phase oversampling	10 %
Slice oversampling	0.0 %
FoV read	224 mm
FoV phase	100.0 %
Slice thickness	0.70 mm
TR	3200 ms
TE	565.0 ms
Concatenations	1
Filter	None
Coil elements	HEA;HEP
Contrast	
MTC	Off
Magn. preparation	None
Fat suppr.	None
Water suppr.	None
Restore magn.	Off
Measurements	1
Reconstruction	Magnitude
Multiple series	Each measurement
Resolution	
Base resolution	320
Phase resolution	100 %
Phase partial Fourier	Allowed
Interpolation	Off
PAT mode	GRAPPA
Accel. factor PE	2
Ref. lines PE	32
Reference scan mode	Integrated
Image Filter	Off
Distortion Corr.	Off
Accel. factor 3D	1
Prescan Normalize	Off
Normalize	Off
B1 filter	Off
Raw filter	Off
Elliptical filter	Off
Slice resolution	100 %
Slice partial Fourier	Off
Geometry	
Nr. of slab groups	1
Slabs	1
Position	Isocenter
Phase enc. dir.	A >> P
Phase oversampling	10 %
Slice oversampling	0.0 %
Slices per slab	256
Series	Interleaved



Nr. of sat. regions	0
Position mode	L-P-H
Fat suppr.	None
Water suppr.	None
Special sat.	None
Special sat.	None
Table position	P
Restore magn.	Off
System	
Body	Off
HEP	On
HEA	On
Position mode	L-P-H
Positioning mode	FIX
Table position	H
Table position	0 mm
MSMA	S - C - T
Sagittal	R >> L
Coronal	A >> P
Transversal	F >> H
Save uncombined	Off
Coil Combine Mode	Adaptive Combine
AutoAlign	Head > Brain
Auto Coil Select	Default
Shim mode	Standard
Adjust with body coil	Off
Confirm freq. adjustment	Off
Assume Dominant Fat	Off
Assume Silicone	Off
Adjustment Tolerance	Auto
? Ref. amplitude 1H	0.000 V
Position	Isocenter
Rotation	0.00 deg
F >> H	224 mm
A >> P	224 mm
R >> L	180 mm
Frequency 1H	123.254038 MHz
Correction factor	1
SRFExcit 1H	134.167 V
! Gain	High
Table position	0 mm
Img. Scale. Cor.	5.000
Physio	
1st Signal/Mode	None
Trigger delay	0 ms
Magn. preparation	None
Dark blood	Off
Resp. control	Off
Inline	
Distortion correction	Off
Sequence	
Introduction	On
Dimension	3D
Elliptical scanning	Off
Reordering	Linear
Bandwidth	744 Hz/Px
Flow comp.	No



Allowed delay	0 s
Echo spacing	3.53 ms
Adiabatic-mode	Off
Turbo factor	314
Echo train duration	1105
RF pulse type	Fast
Gradient mode	Fast
Excitation	Non-sel.
Flip angle mode	T2 var
TX/RX delta frequency	0 Hz
TX Nucleus	None
TX delta frequency	0 Hz
Coil elements	HEA;HEP
Acquisition duration	0 ms
Organ under exam.	None
BOLD	
Subtract	Off
Save images	On
Autoscaling	Off
Scaling factor	1
Offset	0
Subtrahend	1
Subtraction indices	
StdDev	Off
Std-Dev-Sag	Off
Std-Dev-Cor	Off
Std-Dev-Tra	Off
Std-Dev-Time	Off
MIP-Sag	Off
MIP-Cor	Off
MIP-Tra	Off
MIP-Time	Off
Radial MIP	Off
Save original images	On
Distortion Corr.	Off
Save original images	On
Number of radial views	1
Axis of radial views	L-R
MPR Sag	Off
MPR Cor	Off
MPR Tra	Off

SIEMENS MAGNETOM ConnectomS syngo MR D11

 \\USER\HCP\Phase2_User\HCP: Structurals\FieldMap
 TA:2:15 Voxel size:2.0x2.0x2.0 mm Rel. SNR:1.00 :fm_r

Properties

Prio Recon	Off
Before measurement	
After measurement	
Load to viewer	On
Inline movie	Off
Auto store images	On
Load to stamp segments	Off
Load images to graphic segments	Off



Auto open inline display	Off
Wait for user to start	On
Start measurements	single
Routine	
Nr. of slice groups	1
Slices	72
Dist. factor	0 %
Position	Isocenter
Orientation	Transversal
Phase enc. dir.	R >> L
AutoAlign	Head > Brain
Phase oversampling	0 %
FoV read	208 mm
FoV phase	86.5 %
Slice thickness	2.0 mm
TR	731.0 ms
TE 1	4.92 ms
Averages	1
Concatenations	1
Filter	None
Coil elements	HEA;HEP
Contrast	
MTC	Off
Flip angle	50 deg
Fat suppr.	None
Averaging mode	Short term
Measurements	1
Reconstruction	Magn./Phase
Multiple series	Off
Resolution	
Base resolution	104
Phase resolution	100 %
Phase partial Fourier	Off
Interpolation	Off
Image Filter	Off
Distortion Corr.	Off
Prescan Normalize	Off
Normalize	Off
B1 filter	Off
Raw filter	Off
Elliptical filter	Off
Geometry	
Nr. of slice groups	1
Slices	72
Dist. factor	0 %
Position	Isocenter
Phase enc. dir.	R >> L
Phase oversampling	0 %
Multi-slice mode	Interleaved
Series	Interleaved
Nr. of sat. regions	0
Position mode	L-P-H
Fat suppr.	None
Special sat.	None
Special sat.	None
Table position	P
System	



Body	Off
HEP	On
HEA	On
Position mode	L-P-H
Positioning mode	FIX
Table position	H
Table position	0 mm
MSMA	S - C - T
Sagittal	R >> L
Coronal	A >> P
Transversal	F >> H
Save uncombined	Off
Coil Combine Mode	Sum of Squares
AutoAlign	Head > Brain
Auto Coil Select	Default
Shim mode	Standard
Adjust with body coil	Off
Confirm freq. adjustment	Off
Assume Dominant Fat	Off
Assume Silicone	Off
Adjustment Tolerance	Auto
? Ref. amplitude 1H	0.000 V
! Position	Isocenter
! Rotation	0.00 deg
! F >> H	224 mm
! A >> P	224 mm
! R >> L	180 mm
Frequency 1H	123.254038 MHz
Correction factor	1
Ø1GreFCE 1H	63.819 V
Gain	High
Table position	0 mm
Img. Scale. Cor.	1.000
Physio	
Inline	
Distortion correction	Off
Sequence	
Introduction	On
Dimension	2D
Averaging mode	Short term
Multi-slice mode	Interleaved
Asymmetric echo	Off
Contrasts	2
Bandwidth	433 Hz/Px
Flow comp.	Yes
RF pulse type	Normal
Gradient mode	Fast
RF spoiling	On
TX/RX delta frequency	0 Hz
TX Nucleus	None
TX delta frequency	0 Hz
Coil elements	HEA;HEP
Acquisition duration	0 ms
Mode	Off
BOLD	
Distortion Corr.	Off
Contrasts	2



SIEMENS MAGNETOM ConnectomS syngo MR D11

 \\USER\HCP\Phase2_User\HCP: Structurals\AFI
 TA:4:28 PAT:9 Voxel size:2.0x2.0x2.0 mm Rel. SNR:1.00 :f1

Properties

Prio Recon Off
 Before measurement
 After measurement
 Load to viewer On
 Inline movie Off
 Auto store images On
 Load to stamp segments Off
 Load images to graphic segments Off
 Auto open inline display Off
 Wait for user to start On
 Start measurements single

Routine

Nr. of slab groups 1
 Slabs 1
 Dist. factor 20 %
 Position Isocenter
 Orientation Sagittal
 Phase enc. dir. A >> P
 AutoAlign Head > Brain
 Phase oversampling 0 %
 Slice oversampling 9.1 %
 FoV read 256 mm
 FoV phase 100.0 %
 Slice thickness 2.00 mm
 TR 70.0 ms
 TE 1.90 ms
 Averages 1
 Concatenations 1
 Filter None
 Coil elements HEA;HEP

Contrast

MTC Off
 Magn. preparation None
 Flip angle 50 deg
 Fat suppr. None
 Water suppr. None
 SWI Off
 Averaging mode Short term
 Measurements 1
 Reconstruction Magnitude
 Multiple series Each measurement

Resolution

Base resolution 128
 Phase resolution 100 %
 Phase partial Fourier Off
 Interpolation Off
 PAT mode GRAPPA
 Accel. factor PE 3
 Ref. lines PE 24



Reference scan mode	Integrated
Image Filter	Off
Distortion Corr.	Off
Accel. factor 3D	3
Ref. lines 3D	24
Prescan Normalize	Off
Normalize	Off
B1 filter	Off
Raw filter	Off
Elliptical filter	Off
Slice resolution	100 %
Slice partial Fourier	Off
Geometry	
Nr. of slab groups	1
Slabs	1
Dist. factor	20 %
Position	Isocenter
Phase enc. dir.	A >> P
Phase oversampling	0 %
Slice oversampling	9.1 %
Slices per slab	88
Multi-slice mode	Interleaved
Series	Interleaved
Saturation mode	Standard
Nr. of sat. regions	0
Position mode	L-P-H
Fat suppr.	None
Water suppr.	None
Special sat.	None
Special sat.	None
Table position	P
System	
Body	Off
HEP	On
HEA	On
Position mode	L-P-H
Positioning mode	FIX
Table position	H
Table position	0 mm
MSMA	S - C - T
Sagittal	R >> L
Coronal	A >> P
Transversal	F >> H
Save uncombined	Off
Coil Combine Mode	Sum of Squares
AutoAlign	Head > Brain
Auto Coil Select	Default
Shim mode	Standard
Adjust with body coil	Off
Confirm freq. adjustment	Off
Assume Dominant Fat	Off
Assume Silicone	Off
Adjustment Tolerance	Auto
? Ref. amplitude 1H	0.000 V
! Position	Isocenter
! Rotation	0.00 deg
! F >> H	224 mm



! A >> P	224 mm
! R >> L	180 mm
Frequency 1H	123.254038 MHz
Correction factor	1
SRFExcit 1H	89.444 V
Gain	Low
Table position	0 mm
Img. Scale. Cor.	1.000
Physio	
1st Signal/Mode	None
Segments	1
Magn. preparation	None
Dark blood	Off
Resp. control	Off
Inline	
Distortion correction	Off
Sequence	
Introduction	On
Dimension	3D
Elliptical scanning	Off
Phase stabilisation	Off
Averaging mode	Short term
Multi-slice mode	Interleaved
Reordering	Linear
Asymmetric echo	Off
Contrasts	1
Bandwidth	450 Hz/Px
Flow comp.	No
Allowed delay	0 s
RF pulse type	Normal
Gradient mode	Fast
Excitation	Non-sel.
RF spoiling	On
Rel. R0 spoiler mom.	20.00
Rel. 3D spoiler mom.	40.00
Dual-TR B1 mapping	On
TR Offset	50000 us
Dual-TR spoiler ratio	0.170
Dummy scan duration	2000 ms
TX/RX delta frequency	0 Hz
TX Nucleus	None
TX delta frequency	0 Hz
Coil elements	HEA;HEP
Acquisition duration	0 ms
Mode	Off
BOLD	
Subtract	Off
Liver registration	Off
Save images	On
Autoscaling	Off
Scaling factor	1
Offset	0
Subtrahend	1
Subtraction indices	
StdDev	Off
Std-Dev-Sag	Off
Std-Dev-Cor	Off



Std-Dev-Tra	Off
Std-Dev-Time	Off
MIP-Sag	Off
MIP-Cor	Off
MIP-Tra	Off
MIP-Time	Off
Radial MIP	Off
Save original images	On
Distortion Corr.	Off
Contrasts	1
Save original images	On
Wash - In	Off
Wash - Out	Off
TTP	Off
PEI	Off
MIP - time	Off
Number of radial views	1
Axis of radial views	L-R
MPR Sag	Off
MPR Cor	Off
MPR Tra	Off

SIEMENS MAGNETOM ConnectomS syngo MR D11

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|BIAS_BC
|BIAS_32CH
|T1w_MPR1
|T2w_SPC1
|T1w_MPR2
|T2w_SPC2
|FieldMap
|AFI

```



Functional Session A

Object	Edit	Tools	Insert	Help
1	▶	Localizer	00:09	
2		AAHScout	00:14	AutoAlign Scout
3		Localizer_aligned	00:22	
4	▶	BIAS_BC	00:23	
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8	▶	BOLD_REST1_RL	14:33	
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12		BOLD_RL_SB_SE	00:28	
13		BOLD_LR_SB_SE	00:28	
14		BOLD_WM1_RL	05:01	
15		BOLD_WM2_LR	05:01	
16		BOLD_GAMBLING1_RL	03:12	
17		BOLD_GAMBLING2_LR	03:12	
18		BOLD_MOTOR1_RL	03:34	
19		BOLD_MOTOR2_LR	03:34	

The resting state and task-fMRI scans (REST, WM, GAMBLING, and MOTOR) are collected using an HCP-specific variant of the multiband BOLD sequence available at <http://www.cmrr.umn.edu/multiband>. The BOLD_{RL,LR}_SB_SE scans are single-band spin-echo EPI variants (available in the same multiband sequence package) that provide a mechanism for correcting for susceptibility distortion via FSL's 'TOPUP' tool. These scans are preferred to a traditional gradient-echo fieldmap approach because they allow matching (and subsequent correction) of z-gradient-blip-induced spatial distortions that are present in the multiband fMRI acquisitions (see Glasser et al., submitted). These scans were renamed to SpinEchoFieldMap_{RL,LR} in the ConnectomeDB.

Certain parameters that are not captured in the Siemens protocol listing are given next. Unless noted, these parameters all reside on the Sequence, Special tab.

For the SpinEchoFieldMap (BOLD_{RL,LR}_SB_SE) scans (sequence: cmrr_mbep2d_se):

Refocus flip angle (Contrast tab): 180 deg

*Fake MB factor for SB**: Set to same as the “Multi-band accel. Factor” used for fMRI scans.

Invert RO/PE polarity (select via arrows): Toggle “On” for one of the two scans to invert the PE polarity (e.g., HCP has this Off for the “RL” scan, and On for the “LR” scan).

* To expose “*Fake MB factor for SB*” in the Special tab, you will need to:

a) Create a configuration file called “MBAAdvancedSettings.ini” with the two lines:

```
[MultiBand]
SBFakeSliceBands = 1
```

b) Place that configuration file in C:\MedCom\MriCustomer\seq

You should then create a SE-EPI protocol matched in resolution, FOV, matrix size, bandwidth, and echo spacing to what you’ll use for your fMRI acquisitions (i.e., your gradient-echo EPI protocol). TR/TE doesn’t have to match.

For the fMRI scans (sequence: cmrr_mbep2d_bold):

Excite pulse duration: Set long enough to make sure that “MBExcRF 1H” in the System, Tx/Rx tab is not maxed out. The necessary value will be slice thickness dependent. (HCP protocol uses 7120 μ s).

Single-band images: Toggle “On” to save “SBRef” images for each acquisition (used in the HCP preprocessing pipelines).

Log physiology to file: Toggle “On” if you wish to save Siemens physiology data.

Invert RO/PE polarity: Toggle “On” to invert PE polarity as appropriate if that is part of your protocol (e.g., HCP has this Off for our “RL” fMRI scans, and On for the “LR” scans). Note that the “Phase enc. dir.” setting should remain the same for both scans when inverting the PE polarity using this mechanism.

Online multi-band recon: Set to “Remote” if using a remote reconstruction server.

For purposes of simplified presentation, in the detailed scan parameter listing that follows for “Functional Session A”, only the BOLD_RL_SB_SE (scan 6) and BOLD_REST1_RL (scan 8) acquisition parameters are listed, since:

- The Localizer, AAHScout, and BIAS field scans are identical to those in the structural session.



- The second set of “SpinEchoFieldMap” scans (scans 12, 13 above) are identical to the first set of such scans (scans 6, 7).
- The traditional gradient-echo fieldmap scan (“FieldMap”, scan 10 above) is not being released in the ConnectomeDB, because the approach of collecting two single-band spin-echo scans with inverted phase encoding polarity is needed for correcting all sources of distortion (see Glasser et al, submitted).
- The “LR” variants of each scan are identical to the “RL” variants, with the exception of the aforementioned method of inverting the phase encoding polarity via the “*Invert RO/PE polarity*” option on the Special tab.
- The task-fMRI scans are identical to the resting-state scans, with the exception of the number of frames (“Measurements”), which were 405, 253, and 284 for WM, GAMBLING, and MOTOR, respectively.



Functional Session A Scan Protocol

SIEMENS MAGNETOM ConnectomS syngo MR D11

 \\USER\HCP\Phase2_User\HCP: FNCA: rs-fMRI and T-fMRI\BOLD_RL_SB_SE
 TA:0:28 Voxel size:2.0x2.0x2.0 mm Rel. SNR:1.00 :epse

Properties

Prio Recon	Off
Before measurement	
After measurement	
Load to viewer	On
Inline movie	Off
Auto store images	On
Load to stamp segments	Off
Load images to graphic segments	Off
Auto open inline display	Off
Wait for user to start	Off
Start measurements	single

Routine

Nr. of slice groups	1
Slices	72
Dist. factor	0 %
Position	L0.0 P3.0 H6.0 mm
Orientation	T > C-20.0
Phase enc. dir.	R >> L
AutoAlign	Head > Brain
Phase oversampling	0 %
FoV read	208 mm
FoV phase	86.5 %
Slice thickness	2.0 mm
TR	7060 ms
TE	58.0 ms
Averages	1
Multi-band accel. factor	1
Filter	None
Coil elements	HEA;HEP

Contrast

MTC	Off
Magn. preparation	None
Flip angle	90 deg
Fat suppr.	Fat sat.
Fat sat. mode	Weak
Averaging mode	Long term
Measurements	3
Delay in TR	0 ms
Reconstruction	Magnitude
Multiple series	Off

Resolution

Base resolution	104
Phase resolution	100 %
Phase partial Fourier	Off
Interpolation	Off
Distortion Corr.	Off
Hamming	Off
Prescan Normalize	Off



Raw filter	Off
Elliptical filter	Off
Geometry	
Nr. of slice groups	1
Slices	72
Dist. factor	0 %
Position	L0.0 P3.0 H6.0 mm
Phase enc. dir.	R >> L
Phase oversampling	0 %
Multi-slice mode	Interleaved
Series	Interleaved
Nr. of sat. regions	0
Position mode	L-P-H
Fat suppr.	Fat sat.
Special sat.	None
Fat sat. mode	Weak
Special sat.	None
Table position	P
System	
Body	Off
HEP	On
HEA	On
Position mode	L-P-H
Positioning mode	REF
Table position	H
Table position	0 mm
MSMA	S - C - T
Sagittal	R >> L
Coronal	A >> P
Transversal	F >> H
Coil Combine Mode	Sum of Squares
AutoAlign	Head > Brain
Auto Coil Select	Default
Shim mode	Standard
Adjust with body coil	Off
Confirm freq. adjustment	Off
Assume Dominant Fat	Off
Assume Silicone	Off
Adjustment Tolerance	Auto
? Ref. amplitude 1H	0.000 V
Position	L0.0 P3.0 H6.0 mm
Rotation	90.00 deg
A >> P	208 mm
R >> L	180 mm
F >> H	144 mm
Frequency 1H	123.254038 MHz
Correction factor	1
AddCSaCSatNS 1H	39.688 V
Gain	High
Table position	0 mm
Img. Scale. Cor.	1.000
Physio	
1st Signal/Mode	None
Magn. preparation	None
Inline	
Distortion correction	Off
Sequence	



Introduction	Off
Averaging mode	Long term
Multi-slice mode	Interleaved
Bandwidth	2290 Hz/Px
Echo spacing	0.58 ms
EPI factor	90
RF pulse type	Normal
Gradient mode	Fast
Use triggering paradigm	Off
TX/RX delta frequency	0 Hz
TX Nucleus	None
TX delta frequency	0 Hz
Coil elements	HEA;HEP
Acquisition duration	0 ms
BOLD	
GLM Statistics	Off
Dynamic t-maps	Off
Starting ignore meas	0
Ignore after transition	0
Model transition states	Off
Temp. highpass filter	Off
Threshold	4.00
Paradigm size	3
Motion correction	Off
Spatial filter	Off
Delay in TR	0 ms
Distortion Corr.	Off

SIEMENS MAGNETOM ConnectomS syngo MR D11

 \\USER\HCP\Phase2_User\HCP: FNCA: rs-fMRI and T-fMRI\BOLD_REST1_RL
 TA:14:33 Voxel size:2.0x2.0x2.0 mm Rel. SNR:1.00 :epfid

Properties

Prio Recon	Off
Before measurement	
After measurement	
Load to viewer	On
Inline movie	Off
Auto store images	On
Load to stamp segments	Off
Load images to graphic segments	Off
Auto open inline display	Off
Wait for user to start	On
Start measurements	single

Routine

Nr. of slice groups	1
Slices	72
Dist. factor	0 %
Position	L0.0 P3.0 H6.0 mm
Orientation	T > C-20.0
Phase enc. dir.	R >> L
AutoAlign	Head > Brain
Phase oversampling	0 %
FoV read	208 mm
FoV phase	86.5 %



Slice thickness	2.0 mm
TR	720 ms
TE	33.10 ms
Averages	1
Multi-band accel. factor	8
Filter	None
Coil elements	HEA;HEP
Contrast	
MTC	Off
Flip angle	52 deg
Fat suppr.	Fat sat.
Averaging mode	Long term
Measurements	1200
Delay in TR	0 ms
Reconstruction	Magnitude
Multiple series	Off
Resolution	
Base resolution	104
Phase resolution	100 %
Phase partial Fourier	Off
Interpolation	Off
Distortion Corr.	Off
Hamming	Off
Prescan Normalize	Off
Raw filter	Off
Elliptical filter	Off
Geometry	
Nr. of slice groups	1
Slices	72
Dist. factor	0 %
Position	L0.0 P3.0 H6.0 mm
Phase enc. dir.	R >> L
Phase oversampling	0 %
Multi-slice mode	Interleaved
Series	Interleaved
Nr. of sat. regions	0
Position mode	L-P-H
Fat suppr.	Fat sat.
Special sat.	None
Special sat.	None
Table position	P
System	
Body	Off
HEP	On
HEA	On
Position mode	L-P-H
Positioning mode	REF
Table position	H
Table position	0 mm
MSMA	S - C - T
Sagittal	R >> L
Coronal	A >> P
Transversal	F >> H
Coil Combine Mode	Sum of Squares
AutoAlign	Head > Brain
Auto Coil Select	Default
Shim mode	Standard



Adjust with body coil	Off
Confirm freq. adjustment	Off
Assume Dominant Fat	Off
Assume Silicone	Off
Adjustment Tolerance	Auto
? Ref. amplitude 1H	0.000 V
Position	L0.0 P3.0 H6.0 mm
Rotation	90.00 deg
A >> P	208 mm
R >> L	180 mm
F >> H	144 mm
Frequency 1H	123.254038 MHz
Correction factor	1
MBExcRF 1H	271.671 V
Gain	High
Table position	0 mm
Img. Scale. Cor.	1.000
Physio	
1st Signal/Mode	None
Inline	
Distortion correction	Off
Sequence	
Introduction	Off
Averaging mode	Long term
Multi-slice mode	Interleaved
Bandwidth	2290 Hz/Px
Echo spacing	0.58 ms
EPI factor	90
RF pulse type	Normal
Gradient mode	Fast
Online multi-band recon.	Remote
Use triggering paradigm	Off
TX/RX delta frequency	0 Hz
TX Nucleus	None
TX delta frequency	0 Hz
Coil elements	HEA;HEP
Acquisition duration	0 ms
BOLD	
GLM Statistics	Off
Dynamic t-maps	Off
Starting ignore meas	0
Ignore after transition	0
Model transition states	On
Temp. highpass filter	On
Threshold	4.00
Paradigm size	3
Motion correction	Off
Spatial filter	Off
Delay in TR	0 ms
Distortion Corr.	Off



Table Of Contents

\\USER

HCP			
	Phase2_User		
		HCP: FNCA: rs-fMRI and T-fMRI	
		Localizer	
		AAHScout	
		Localizer_aligned	
		BIAS_BC	
		BIAS_32CH	
		BOLD_RL_SB_SE	
		BOLD_LR_SB_SE	
		BOLD_REST1_RL	
		BOLD_REST2_LR	
		FieldMap	
		BOLD_RL_SB_SE	
		BOLD_LR_SB_SE	
		BOLD_WM1_RL	
		BOLD_WM2_LR	
		BOLD_GAMBLING1_RL	
		BOLD_GAMBLING2_LR	
		BOLD_MOTOR1_RL	
		BOLD_MOTOR2_LR	



Functional Session B

The screenshot shows the 'Exam Explorer' window for a user named 'HCP: FNCB'. The window title is 'Exam Explorer - \\\USER\HCP\Phase2_User\HCP: FNCB: rs-fMRI and T-fMRI'. The menu bar includes 'Object', 'Edit', 'Tools', 'Insert', and 'Help'. The main area displays a list of 21 scan entries with their names and durations. The first entry, 'Localizer', is selected. The list includes various BOLD and FieldMap scans, with a separator line at entry 11 labeled '---- functionals ----'. The last entry is 'BOLD_EMOTION2_LR'.

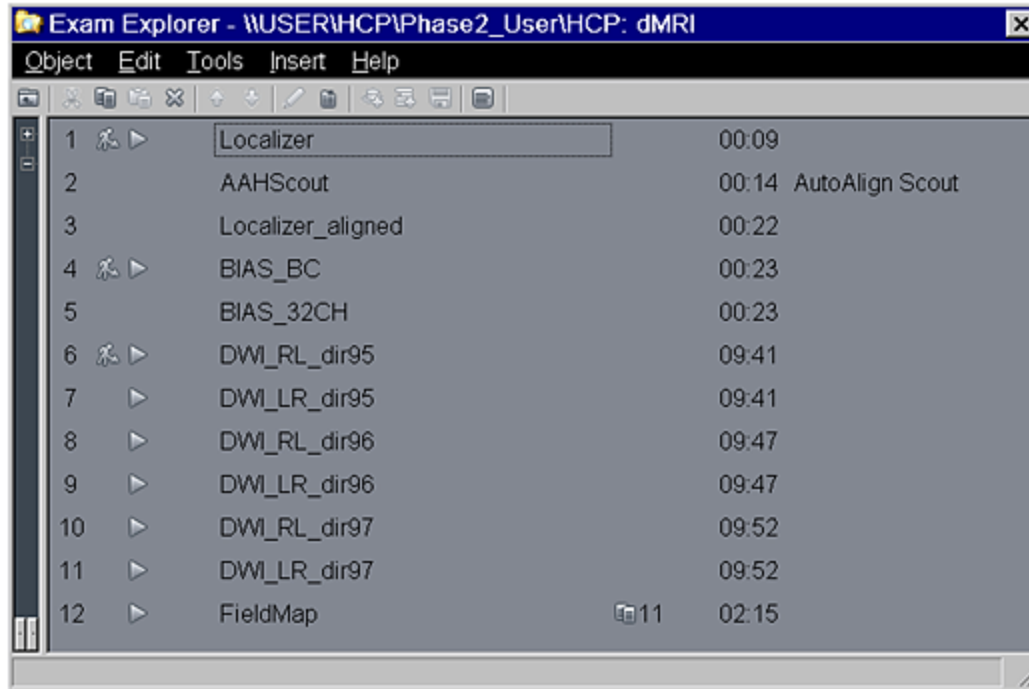
Object	Duration
1 Localizer	00:09
2 AAHScout	00:14 AutoAlign Scout
3 Localizer_aligned	00:22
4 BIAS_BC	00:23
5 BIAS_32CH	00:23
6 BOLD_RL_SB_SE	00:28
7 BOLD_LR_SB_SE	00:28
8 BOLD_REST3_LR	14:33
9 BOLD_REST4_RL	14:33
10 FieldMap	02:15
11 ---- functionals ----	
12 BOLD_RL_SB_SE	00:28
13 BOLD_LR_SB_SE	00:28
14 BOLD_LANGUAGE1_RL	03:57
15 BOLD_LANGUAGE2_LR	03:57
16 BOLD_SOCIAL1_RL	03:27
17 BOLD_SOCIAL2_LR	03:27
18 BOLD_RELATIONAL1_RL	02:56
19 BOLD_RELATIONAL2_LR	02:56
20 BOLD_EMOTION1_RL	02:16
21 BOLD_EMOTION2_LR	02:16

Functional Session B Scan Protocol

Number of frames (“Measurements”) were 316, 274, 232, and 176 for LANGUAGE, SOCIAL, RELATIONAL, and EMOTION, respectively. Otherwise, see “Functional Session A” for details.



Diffusion Session



The diffusion-weighted scans are collected using an HCP-specific variant of the multiband diffusion sequence available at <http://www.cmrr.umn.edu/multiband>. The dMRI data is collected with 3 different gradient tables (coded in Siemens “DiffusionVectors.txt” file in \MedCom\MriCustomer\seq), with each table acquired once with right-to-left and left-to-right phase encoding polarities. Each of the gradient tables includes 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>

Certain parameters that are not captured in the Siemens protocol listing are given next. Unless noted, these parameters all reside on the Sequence, Special tab.

DWI_{RL,LR}_dir{95,96,97} (sequence: cmrr_mbep2d_diff):

Refocus flip angle (Contrast tab): 160 deg

Diffusion Scheme (Diff tab): Monopolar

Excite pulse duration: Set long enough to make sure that “MBExcRF 1H” in the System,



Tx/Rx tab is not maxed out. The necessary value will be slice thickness dependent. (HCP protocol uses 3200 μ s).

Refocus pulse duration: Set long enough to make sure that “MBRefocRF 1H” in the System, Tx/Rx tab is not maxed out. The necessary value will be slice thickness dependent. (HCP protocol uses 7040 μ s).

Single-band images: Toggle “On” to save “SBRef” images for each acquisition. (The HCP is generating these, but not using them currently in its diffusion preprocessing pipeline).

SENSE1 coil combine: Toggle “On” for better noise-floor performance in the reconstructions.

Log physiology to file: Toggle “On” if you wish to save Siemens physiology data.

Invert RO/PE polarity: Toggle “On” to invert PE polarity as appropriate (e.g., HCP has this Off for our “RL” scans, and On for the “LR” scans). Note that the “Phase enc. dir.” setting should remain the same for both scans when inverting the PE polarity using this mechanism.

Online multi-band recon: Set to “Remote” if using a remote reconstruction server.

For purposes of simplified presentation, in the detailed scan parameter listing that follows, only the DWI_RL_dir95 (scan 6) acquisition parameters are listed, since:

- The Localizer, AAHScout, and BIAS field scans are identical to those in the structural session.
- The scans with 96 and 97 directions only differ in their selection of a different diffusion gradient table.
- The “LR” variants of each scan are identical to the “RL” variants, with the exception of the aforementioned method of inverting the phase encoding polarity via the “*Invert RO/PE polarity*” option on the Special tab.
- The traditional gradient-echo fieldmap scan (“FieldMap”, scan 12 above) is not being released in the ConnectomeDB because distortions are being corrected via FSL’s ‘TOPUP’ and ‘EDDY’.



Diffusion Session Scan Protocol

SIEMENS MAGNETOM ConnectomS syngo MR D11

 \\USER\HCP\Phase2_User\HCP: dMRI\DWI_RL_dir95
 TA:9:41 Voxel size:1.25x1.25x1.25 mm Rel. SNR:1.00 :epse

Properties

Prio Recon	Off
Before measurement	
After measurement	
Load to viewer	On
Inline movie	Off
Auto store images	On
Load to stamp segments	Off
Load images to graphic segments	Off
Auto open inline display	Off
Wait for user to start	On
Start measurements	single

Routine

Nr. of slice groups	1
Slices	111
Dist. factor	0 %
Position	L0.0 P3.0 H6.0 mm
Orientation	T > C-20.0
Phase enc. dir.	R >> L
AutoAlign	Head > Brain
Phase oversampling	0 %
FoV read	210 mm
FoV phase	85.7 %
Slice thickness	1.25 mm
TR	5520 ms
TE	89.50 ms
Averages	1
Multi-band accel. factor	3
Filter	None
Coil elements	HEA;HEP

Contrast

MTC	Off
Magn. preparation	None
Flip angle	78 deg
Fat suppr.	None
Averaging mode	Long term
Delay in TR	0 ms
Reconstruction	Magnitude
Multiple series	Off

Resolution

Base resolution	168
Phase resolution	100 %
Phase partial Fourier	6/8
Interpolation	Off
Distortion Corr.	Off
Prescan Normalize	Off
Normalize	Off
Raw filter	Off
Elliptical filter	Off



Dynamic Field Corr.	Off
Geometry	
Nr. of slice groups	1
Slices	111
Dist. factor	0 %
Position	L0.0 P3.0 H6.0 mm
Phase enc. dir.	R >> L
Phase oversampling	0 %
Multi-slice mode	Interleaved
Series	Interleaved
Nr. of sat. regions	0
Position mode	L-P-H
Fat suppr.	None
Special sat.	None
Special sat.	None
Table position	P
System	
Body	Off
HEP	On
HEA	On
Position mode	L-P-H
Positioning mode	FIX
Table position	H
Table position	0 mm
MSMA	S - C - T
Sagittal	R >> L
Coronal	A >> P
Transversal	F >> H
Coil Combine Mode	Sum of Squares
AutoAlign	Head > Brain
Auto Coil Select	Default
Shim mode	Standard
Adjust with body coil	Off
Confirm freq. adjustment	Off
Assume Dominant Fat	Off
Assume Silicone	Off
Adjustment Tolerance	Auto
? Ref. amplitude 1H	0.000 V
Position	L0.0 P3.0 H6.0 mm
Rotation	90.00 deg
A >> P	210 mm
R >> L	180 mm
F >> H	139 mm
Frequency 1H	123.254038 MHz
Correction factor	1
ExtExciteRF 1H	83.044 V
Gain	High
Table position	0 mm
Img. Scale. Cor.	1.000
Physio	
1st Signal/Mode	None
Magn. preparation	None
Resp. control	Off
Inline	
Distortion correction	Off
Sequence	
Introduction	On



Averaging mode	Long term
Multi-slice mode	Interleaved
Bandwidth	1488 Hz/Px
Optimization	None
Echo spacing	0.78 ms
EPI factor	144
RF pulse type	Normal
Gradient mode	Fast
Online multi-band recon.	Remote
TX/RX delta frequency	0 Hz
TX Nucleus	None
TX delta frequency	0 Hz
Coil elements	HEA;HEP
Acquisition duration	0 ms
BOLD	
Delay in TR	0 ms
Diffusion mode	Free
Diff. weightings	1
b-value	3000 s/mm ²
Diff. weighted images	On
Trace weighted images	Off
ADC maps	Off
FA maps	Off
Mosaic	On
Tensor	Off
Distortion Corr.	Off
b-Value >=	0 s/mm ²
Exponential ADC Maps	Off
Invert Gray Scale	Off
Calculated Image	Off
Calculated bValue	1400 s/mm ²

SIEMENS MAGNETOM ConnectomS syngo MR D11

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\\USER

```

|HCP
|
|Phase2_User
|HCP: dMRI
|Localizer
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|Localizer_aligned
|BIAS_BC
|BIAS_32CH
|DWI_RL_dir95
|DWI_LR_dir95
|DWI_RL_dir96
|DWI_LR_dir96
|DWI_RL_dir97
|DWI_LR_dir97
|FieldMap
  
```

HCP MEG Scan Protocol

HCP MEG data acquisition is performed on a whole head MAGNES 3600 (4D Neuroimaging, San Diego, CA) system housed in a magnetically shielded room, located at the Saint Louis University (SLU) medical campus. This document details the scan protocol and scanner parameters used for all HCP subjects selected for MEG scanning. See [500 Subjects Release Appendix IV](#) for Standard Operating Procedures used by HCP research staff to ensure consistent data acquisition between subjects.

When planning MEG experiments on your local system, we caution that performance may vary from system to system, even within a single scanner platform. For best performance, you may need to adjust your protocols.

Several key choices were made regarding the HCP MEG recordings. Sampling rate was selected to be as high as possible (2034.51 Hz) while collecting all channels (248 magnetometer channels together with 23 reference channels). Bandwidth was set (at DC, 400Hz) to capture physiological signals, and optimize file sizes and the signal-to-noise ratio. All our experiments were recorded in continuous mode to allow the greatest user flexibility in determining epoch widths in analyses. Since the bit noise on our system was higher than our sensor noise, Delta encoding is used to increase the bitrate.

The order of scans in the HCP MEG protocol is as follows for all subjects:

Scan	Description	Duration (min)
1-Rnoise	Empty Room scan establishes a baseline noise level	5:00
2-Pnoise	Patient scan, multiple if degaussing of the head is necessary.	1:00
	Participant Digitization	~ 20
3-Restin	First resting state scan, eyes open, fixated.	6:00
4-Restin	Second resting state scan, eyes open, fixated.	6:00
5-Restin	Third resting state scan, eyes open, fixated.	6:00
	Break for button box placement	~2
6-Wrkmem	First half, Working Memory scan	10:00
7-Wrkmem	Second half, Working Memory scan	10:00
	Break for otic placements	~2
8-StoryM	First Half, Language scan	7:00
9-StoryM	Second Half, Language scan	7:00
	Break for muscle sensor placement (EMG)	~10
10-Motort	First Half, Motor scan	14:00
11-Motort	Second Half, Motor scan	14:00

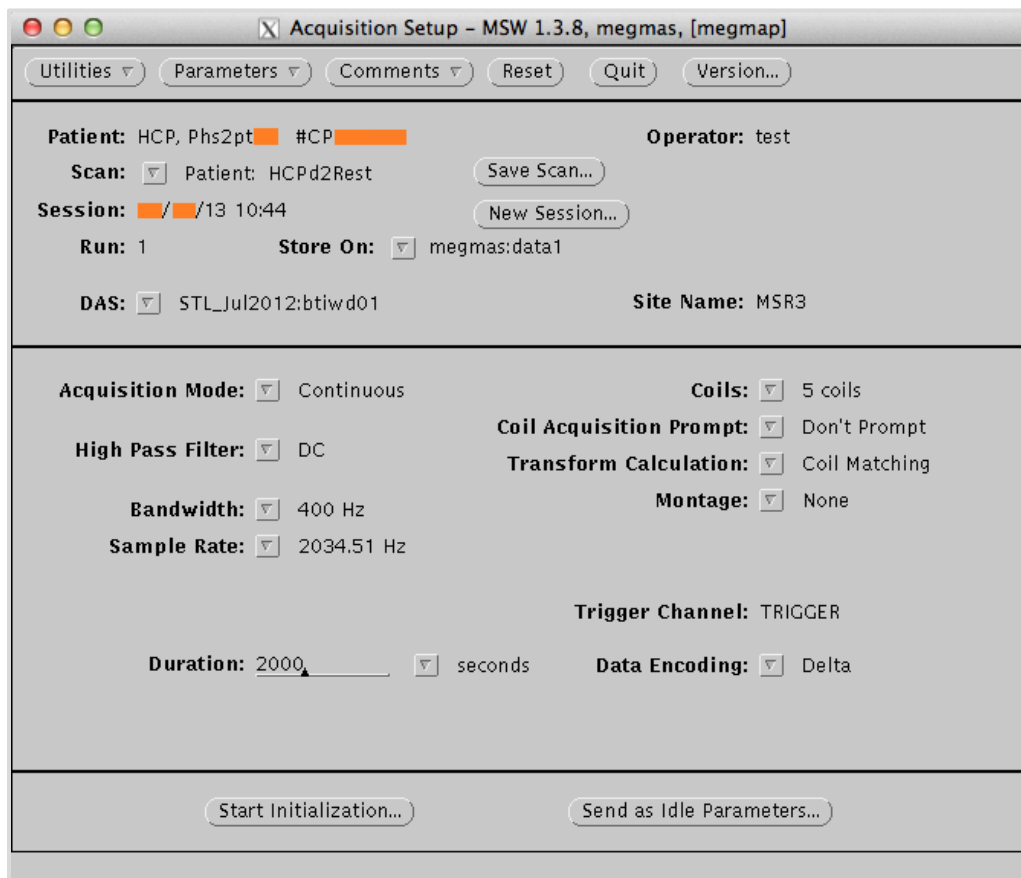
In a particular session, multiple PNoise scans may be performed if the first shows artifact, generally from missed metal on the head or body of the participant, or dental work with residual magnetic fields. We can degauss the participant, if necessary, and in such cases the PNoise will be repeated until a good artifact-free scan is reviewed. The final PNoise in a subfolder will represent the baseline noise-state of this participant for other scans in the session.

Particular scans may have been rejected from the data release for quality reasons in acquisition or preprocessing.

The exact duration of each scan in seconds is variable as the recording brackets the stimulus-presentation time with buffer at the start and end.

The screenshots below show the HCP acquisition setup and parameters set for the MAGNES 3600 magnetometer for an exemplar MEG session.

In the first shot, the general acquisition parameters are shown. Duration is set at 2000 seconds for most scans, and manually stopped after the E-Prime run is concluded, to ensure the data are not prematurely clipped.





In the Scan Information screenshot, whole head and the miscellaneous setup parameters are shown for a resting state scan. In all acquisitions 287 channels are acquired, always with a Gain of “x1”.

Patient ID: CP Patient Name: HCP, Phs2pt20
Scan: HCPd2Rest
Scan used by 1 process(es)

MAGNES 3600 WH (WHOLE HEAD) PARAMETERS:

SP_Version: 6
Acquisition Mode: Continuous
Duration: 2 ks
High Pass Filter: DC
Sample Rate: 2034.51 Hz
Bandwidth: 400 Hz

MISCELLANEOUS SETUP PARAMETERS:

Use Cardiac Mode: No
Transform Algorithm: Coil Matching
Coil Acquisition Prompt: None
Auto Artifact Reject Level: 0
Alternate Filter Card: 1
Alternate High Pass Filter: DC
Filter Name: 1p400
Notch Filter: None
Enable Delta: Yes
Use Coils on Head: Yes
Use Analog Weights: Yes
Use Digital Weights: Yes
Weight Table: "Supine"
EEG Montage File: None
External Data Tap Process: None
Default Video Setup: 1

CHANNELS ACQUIRED:

Name	Label	Type	Gain
"A1"	"	MEG	X1
"A2"	"	MEG	X1
"A3"	"	MEG	X1
"A4"	"	MEG	X1
"A5"	"	MEG	X1
"A6"	"	MEG	X1

Buttons: Display Data Size... Print

In the Data File Information screenshot, Channel reference information is given for the first few channels. A complete listing of this info is contained in the headers, which are accessible by reading the data into MATLAB. Because we record continuous data, “epoch information” will reflect the whole scan as a single epoch. Points (times) sample period = epoch duration.



Quit Version... Print

Patient Selection: Data File Information

Patient: CP
Scan: HCPd2Rest
Session: / /13 09:29
Run: 1
File: c,rfDC
pdf path:
/home/whsbti/data/megmas_data1/CP/HCPd2Rest/%13@09:29/1/c,rfDC

Version: 1
File Type: 'Bts'
Data Format: Float (32 bits)
Acquisition Mode: Continuous
Sample Period: 491.519 us(2.03451 kHz)
X Axis Label: 's'
Timestamp:
Total Channels: 287
Total Epochs: 1
Input Epochs: 0
Index of Longest Epoch: 0

Epoch information:
Points in Epoch: 745619
Epoch Duration: 366.486 s
Expected Intertrigger Interval: 0 s
Actual Intertrigger Interval: 0 s
Epoch Timestamp: 0 slices, 0.000 s
Number of Variable Events: 0

Fixed Event information:
Event Name: 'Trigger'
Start Latency: 0 s
End Latency: 10 ms
Fixed Event Flag: True

Channel Reference information:
Channel Name: 'TRIGGER'
Channel Label: 'TRIGGER'
Channel Number: 1
Attributes: Channel Triggered Acquisition
Scale: 1
Y Axis Label: 'bit'
Valid Min/Max Flag: True
Y Minimum: -32.767 kbit
Y Maximum: 32.767 kbit
Index: 0

Channel Name: 'RESPONSE'
Channel Label: 'RESPONSE'
Channel Number: 2
Attributes:
Scale: 1
Y Axis Label: 'bit'
Valid Min/Max Flag: True
Y Minimum: -32.767 kbit
Y Maximum: 32.767 kbit
Index: 1

Channel Name: 'MLzA'
Channel Label: 'MLzA'
Channel Number: 3
Attributes:
Scale: 1
Y Axis Label: 'T'
Valid Min/Max Flag: True
Y Minimum: -36.0437 nT
Y Maximum: 36.0437 nT
Index: 2



Mailing List

Individuals with further protocol-related questions are encouraged to use 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. We also encourage individuals to share their protocols of what they find works best (and what does not) via this forum!