

# Human Connectome Project (HCP) fMRI protocol at CFMRI

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## Introduction

The Human Connectome Project (HCP) is a 40 million dollar initiative under the NIH Blueprint for Neuroscience Research<sup>1</sup>. The project aims to characterize the structural and functional connectivity of the human brain in order to further our understanding of human brain networks and ultimately advance human health. One of the key components of the HCP is the acquisition of whole brain functional MRI data at high resolution and high speed. To enable this component, scientists have developed an HCP protocol that is capable of acquiring whole brain volume at 2x2x2mm resolution within a TR of 720 msec. The higher resolution and shorter TR greatly enhances our ability to capture the spatial and temporal variations of brain activity and connectivity. Figure 1 shows the default mode network estimated from an example HCP data set showing superb anatomical accuracy and specificity.

The CFMRI has recently implemented the HCP protocol on our GE 3T MR750 scanners, making UCSD one of the first GE sites in the nation to support the HCP protocol. Note that the HCP protocol requires the use of the Nova Medical 32 channel head coil.

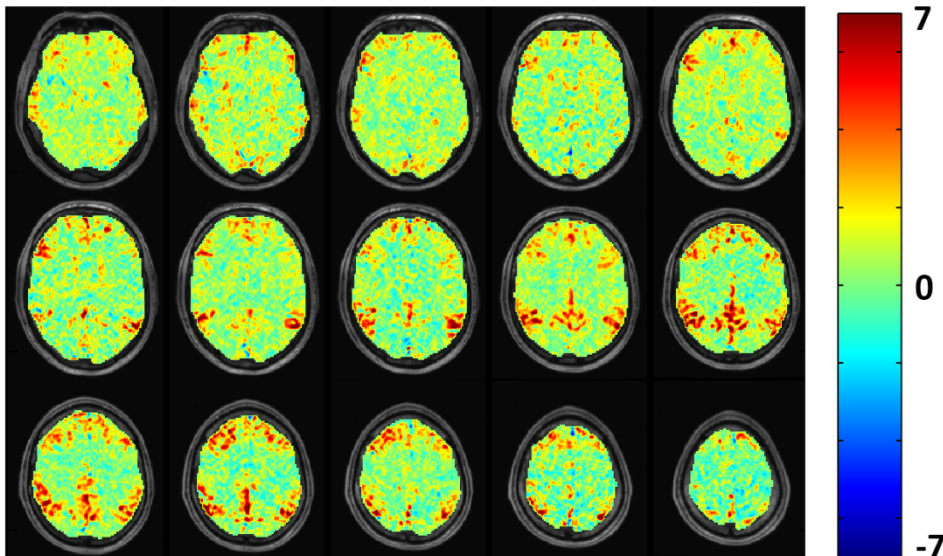


Figure 1: correlation map showing default mode network estimated from resting state fMRI data acquired with HCP protocol. The map shows superb anatomical accuracy and specificity (Figure credit: Alec Wong, PhD)

<sup>1</sup> <http://www.neuroscienceblueprint.nih.gov/connectome/index.htm>

## The CFMRI HCP Protocol

The CFMRI HCP protocol can be found on both the 3T West and 3T East scanners under ADULT->HEAD->HCP.

Table 1 compares some of the important fMRI parameters of the CFMRI HCP protocol and the Human Connectome Project protocol. The main difference between the two is the choice of the phase encoding direction. CFMRI uses Anterior-Posterior (A-P) phase encode direction to avoid peripheral nerve stimulation (PNS) on the GE scanners; whereas the Human Connectome Project uses Right-Left (R-L) phase encoding direction without the concern of PNS because they are using a special Siemens gradient insert that minimizes PNS. Using the R-L phase encoding direction has the advantage of saving time because the Right-Left dimension requires the least number of phase encoding lines; however, it also causes right-left distortions and leads to brain asymmetry. Therefore A-P is often the more desired phase encoding direction to use. **NOTE:** The technology underlying the HCP protocol can be used to develop customized protocols that achieve other spatial and temporal resolution targets. For example, some users may also be interested in the multi-echo simultaneous multi-slice (MEMS) protocol that is described in a separate manual.

Table 1. HCP fMRI parameters

	<b>CFMRI HCP Protocol</b>	<b>Human Connectome Protocol</b>
<b>Resolution</b>	2x2x2 mm <sup>3</sup>	2x2x2 mm <sup>3</sup>
<b>Slice orientation</b>	Axial or AC-PC aligned	AC-PC aligned
<b># slices</b> (must be multiple of 8)	72	72
<b>FOV</b>	20.8cm(A-P)x 18cm (R-L)	20.8cm(A-P) x18cm (R-L)
<b>Phase encoding direction</b>	Anterior-Posterior	Right-Left
<b>Matrix</b>	104x90	104x90
<b>Multi-slice Factor N</b>	N = 8	N = 8
<b>TR</b>	720 msec	720 msec
<b>TE</b>	34.6msec	33ms
<b>Flip angle</b>	52	52
<b>Scan time</b>	Adjustable (10 mins is recommended.)	15mins

The HCP protocol consists of the following scans:

1. **Localizer** (~ 15sec)
2. **ASSET calibration** (~6 sec)
3. **FSPGR** (~10mins, adjustable) : T1 weighted high resolution scan
4. **HOS**(~30 sec): High order shim
5. **HCP calibration fwd** (~18 sec): Calibration (forward phase encoding)
6. **HCP fMRI fwd**(10mins, adjustable): functional or resting fMRI scan (forward phase encoding)
7. **HCP calibration rvs** (~18 sec): Calibration (reversed phase encoding)
8. **HCP fMRI rvs**(10mins, adjustable): functional or resting fMRI scan (reversed phase encoding)
9. **HCP\_topup\_fwd**(~6 sec): TOPUP scan (forward phase encoding)
10. **HCP\_topup\_rvs**(~6 sec): TOPUP scan (reversed phase encoding)

The protocol as listed acquires fMRI data in both forward and reverse phase encoding directions (scans 6 and 8), as is done by the HCP. However, it is also possible to acquire the HCP data in just one phase-encoding direction (e.g. one could either omit the rvs calibration and fMRI scans (7 and 8) or omit the fwd calibration and fMRI scans (5 and 6)). Reversing the phase encoding direction causes the image distortions to flip. For example, forward phase encoding direction usually causes voxels to shift posteriorly, causing stretching of the back of the brain (e.g. occipital cortex) and compression in the front of the brain; whereas the reverse phase encoding direction shifts voxels anteriorly, causing bunching in the back and stretching in the front of the brain. Signal bunching is more difficult to correct than stretching using the existing field-mapping methods. Therefore users may choose the phase encoding direction accordingly to whether the focus is on the front or the back of the brain. If the preference is the whole brain, we have found that the reverse phase encoding direction is more beneficial in recovering the frontal lobe signal dropout after field map correction.

The duration of the fMRI scan can be adjusted. Typically we recommend 10 minutes for resting state scans, as longer scans make it increasingly difficult for subjects to stay still and focused (i.e. fall asleep). The Human Connectome Project acquires 15 minute long resting state scans.

A calibration scan with matching phase encoding direction is required for the fMRI scans. If there are multiple fMRI scans with the same phase encoding direction, only one calibration scan with matching phase encoding direction is needed.

The topup\_fwd and topup\_rvs scan pair are used to measure a fieldmap which can be applied to the fMRI images for correcting geometric distortions. They are typically scanned immediately before or after the fMRI scans. In cases of a scan session containing several fMRI scans in a row where there is concern about subject motion during the session, users may acquire one topup scan pair before the fMRI scans and another pair at the end of the session. The first pair can be used for correcting the fMRI data before the motion occurs, and the second pair for correcting the fMRI data after the motion.

## Run HCP protocol

### Set up and prepare for HCP scan

1. Place the 32channel coil on the scanner table and plug it in. Make sure the coil is recognized by the scanner by checking on the iROC monitor on top of the scanner.
2. Set up peripheral equipment such as the projector, screen, and stimulus laptop etc.
3. Set up the subject on the scanner patient table.
4. Setup physiological monitoring if needed.
5. On the console computer, click the downward arrow on the **Tools** icon. In the drop down menu, select **Command Window**. In the command window type 'RTctrl start' to start realtime. Drag this window to the lower right corner of the screen so it is easily accessible and not in the way. (**NOTE: this step must be done before Start Exam in step 6**)
6. Register the subject and **Start Exam**.

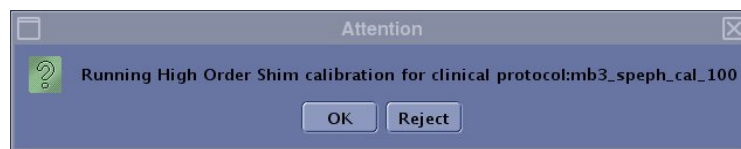
### Scan the HCP protocol

1. **Localizer**  
Save Rx and Scan
2. **Asset Cal**  
Setup, Prescribe Rx, Save Rx, and Scan
3. **FSPGR T1**  
Setup, Prescribe Rx, Save Rx, and Scan.

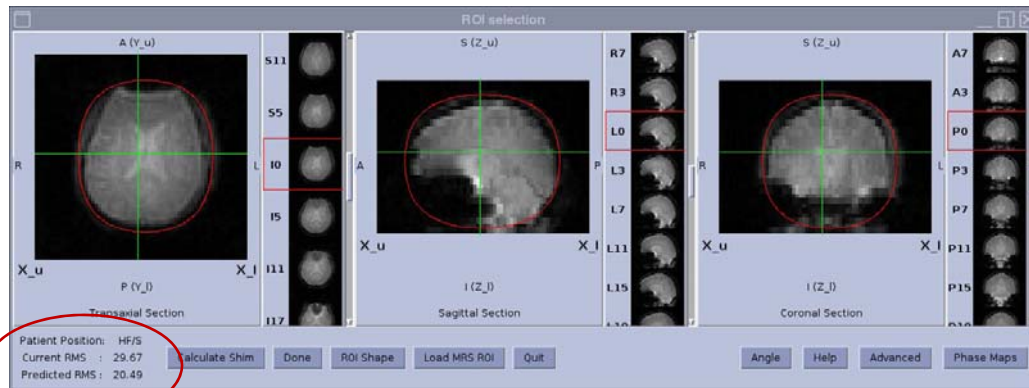
**NOTE: while waiting for the FSPGR to finish, prescribe and save the first hcp calibration scan immediately below the HOS scan. The slices could be either axial or AC-PC aligned (Human Connectome Project uses AC-PC). Please do not change number of slices (72 slices). This step must be done before running the HOS scan.**

4. **HOS** (high order shim)

Setup and Save Rx (no need to prescribe slices). Click **OK** in the popup window saying "Running high order shim for clinical Protocol: <the name of the scan that has been prescribed previously>" (see **NOTE** above). Then click **Scan**.



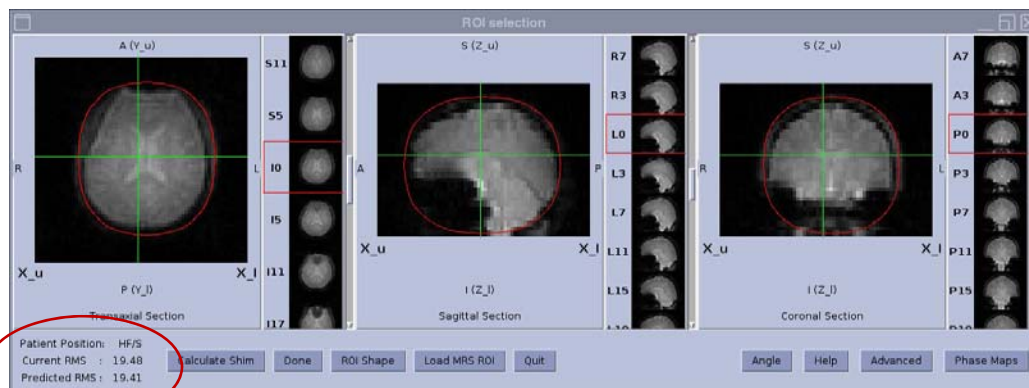
Once the scan finishes, an HOS window will appear. In the HOS window, adjust the size and location of the ROIs to enclose the whole brain (see figure below);



Click **Calculate Shim**, then **Done**. Make a note of the current RMS and predicted RMS values reported in the lower left of the window. The difference between the two values is indicative of HOS efficacy.

Run the HOS a second time by clicking **Scan** and choose **Same Series** in the popup window. Once the HOS window appears, click **Calculate Shim**. Do not modify the ROIs. Verify that the new current and predicted RMS values are converging and consistent with the previously predicted value (See figure below). If yes, click **Done** to finish.

The HOS scan can be repeated a third time if needed. We have typically seen RMS value convergence in two iterations. In case the RMS value does not converge in three iterations, please click **Quit** to skip HOS. Please alert the CFMRI staff of the HOS malfunction, or report the problem using the online web-schedule program at your earliest convenience.



5. **hcp\_cal\_fwd** (see NOTE below)  
download and scan.
6. **hcp\_rest\_fwd** (see NOTE below)  
Copy Rx, save Rx, download , and scan.
7. **hcp\_cal\_rvs** (see NOTE below)  
Copy Rx, , save Rx, download and scan.
8. **hcp\_rest\_rvs** (see NOTE below)  
Copy Rx, , save Rx, download, and scan.
9. **hcp\_topup\_fwd** (see NOTE below)  
Copy Rx, , save Rx, download and scan.
10. **hcp\_topup\_rvs** (see NOTE below)  
Copy Rx, , save Rx, download and scan.

**NOTE:**

- Each of the hcp scans (scan 5-10) needs to be downloaded prior to starting the respective scan. The download step ensures that the RDS client is started to receive the acquired MRI data. If the RDS client is not ON, no MRI data will be saved.

Below are some useful tools:

- Type **ck** in the command window to check if the RDS client is ON. If not ON, stop the hcp scan, copy & paste the scan, download. Type ck again to make sure RDS client is ON, then Scan.
- Type **memslist** in the command window to list the raw data files. Anytime during an hcp scan, use memslist to check if data is being saved.
- If an hcp scan has to be stopped before it finishes, for example when subject activates the emergency squeeze ball, please do the following:
  - Type **kk** in the command window to kill the RDS client then press **Stop Scan** button. After the emergency situation or errors are cleared, copy & paste the scan, download and Scan.
  - If the **Stop Scan** button is pressed before the RDS client is killed, a **TPS reset** must be performed before the scan can continue. A TPS reset usually takes 2-3 minutes. After the TPS reset, copy & paste the scan, download and Scan.
- Due to limitations with the RDS server software, after an hcp scan finishes, the status of the scan shows "Action Failed". You can ignore this status. Additionally, as soon as the next scan is downloaded, the previous hcp scan is pushed downward in the scan list. This tends to cause confusion. Please pay attention to which scan is the currently active scan.
- Appendix I lists all command-line tools available for use with the HCP protocol.

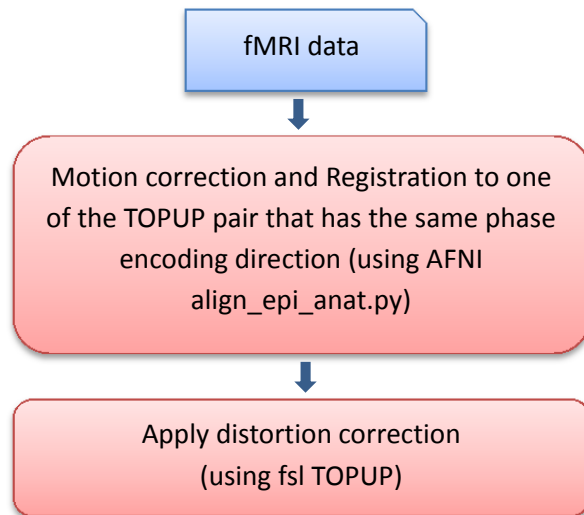
## End exam and transfer Data.

- On the computer console, click on **End -> End Exam**
- In the command window, type **RTctrl stop** to stop realtime.
- In the command window, type **memscopy** to transfer mems data (P files).  
*Usage:* `memscopy -s server -r raid# -d studyfolder login`  
*example:* `memscopy -s fmrimefs -r raid16 -d myhcpfolder mylogin`
- Transfer Dicom data using **gecopy**.  
*Usage:* `gecopy -s server -r raid# -d studyfolder login`  
*example:* `gecopy -s fmrimefs -r raid16 -d myhcpfolder mylogin`
- Transfer physio data using **physiocopy** as needed.  
*Usage:* `physiocopy -s server -d studyfolder starttime endtime login`  
*example:* `physiocopy -s fmrimefs -d myhcpfolder 14:00 15:00 mylogin`
- After data transfer completes, close all command windows and clean up the scanner suite.

## Reconstruct and pre-process HCP data

We provide a Pipeline for reconstructing the HCP data. The pipeline consists of four functional modules:

1. Data validation: checks if all required data files are present.
2. Data reconstruction: reconstructs the fMRI images.
3. Quality control: calculates temporal SNR maps.
4. Pre-processing: performs motion correction, registration and distortion correction (see the diagram below).



**NOTE:** The reconstruction may take a while (3-6 hours depending on the size of the data sets).



## System and Data Requirements

- Add the following path to your `~/matlab/startup.m` file. Create the file if the file does not exist.

```
path(path,'/apps/matlabcode/spiralfmap2');  
path(path,'/apps/matlabcode/domems');  
path(path,'/apps/afni_matlab/matlab');  
path(path,'/apps/matlabcode/fmritools');
```

- All Pfiles including data from one or more calibration/resting state fMRI scan sets, and the TOPUP scan pair, must be located in the same folder.

## Running the pipeline

1. Login into your assigned server (either `fmrimecs.ucsd.edu` or `fmrimecs2.ucsd.edu`).
2. Change to the directory where the data are located.
3. Type at the Linux prompt: **dohcp.py**

Your job will be queued. Type **qstat** to check queue status, or **qdel** followed by the job number to remove from the queue.

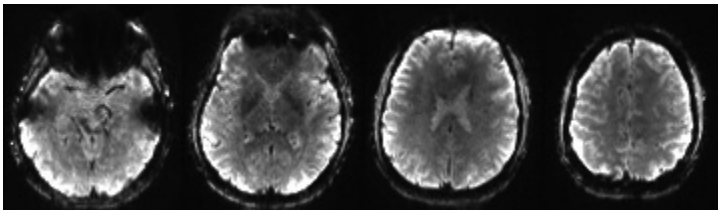
## Error Logging

A log file is automatically saved in the current data directory under the **log** folder. Automatic email notifications will also be sent upon job success or failure to the email address registered with the server account (usually the PI's email address).

## Output

All output is saved under the **processed** folder. The pre-processed fMRI data (motion and distortion corrected) can be found as: `myhifi<phase encoding direction pa/ap>_afni_al.nii.gz`

**Example:** `myhifipa_afni_al.nii.gz`



For a more complete description of the output files, please see Appendix II.

## Appendix I: Summary of Command-Line Tools

Command	Usage	Description
<b>RTctrl start</b>	RTctrl start	Start Realtime (Must be done before "Start Exam")
<b>RTctrl stop</b>	RTctrl stop	End Realtime (Must be done after "End Exam")
<b>ck</b>	Ck	Check if RDS client is ON
<b>kk</b>	kk	Kill all active RDS clients
<b>memslist</b>	memslist	List raw data files of the current MEMS scan session.
<b>memscopy</b>	memscopy -s server -d studyfolder login	Transfer HCP raw data files to server.
<b>gecopy</b>	gecopy -s server -r raid# -d studyfolder login	Transfer DICOM files to server.
<b>physiocracy</b>	physiocracy -s server -d studyfolder starttime endtime login <i>(*starttime and endtime format: hh:mm)</i>	Transfer physio files to fmrimeas server.
<b>cd tail</b>	cd /export/home/sdc/RTafni/var/log tail -f <last log file name>	Check realtime status and messages

## Appendix II: HCP Pipeline Output files

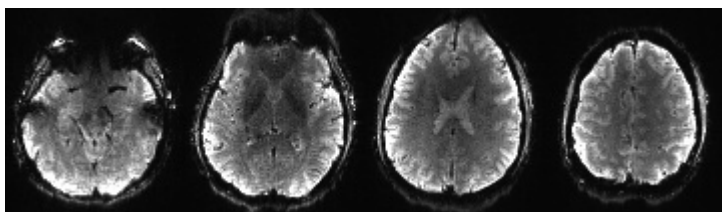
All outputs are saved under “processed” folder. Below is a list of selected outputs that users may examine for sanity check purpose or for trouble shooting when there are errors in the reconstruction process. Users should contact CFMRI ([cfmri@ucsd.edu](mailto:cfmri@ucsd.edu)) for questions regarding these files.

- `bcaipi_spep_hcp_rest_<phase encoding dir>brik+orig.BRIK`  
**Example:** `bcaipi_spep_hcp_rest_fwdbrik+orig.BRIK`

`rest<phase encoding dir>.nii.gz`

**Example:** `restpa.nii.gz, restap.nii.gz`

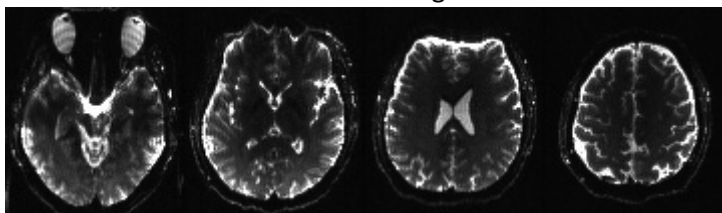
Reconstructed fMRI data in BRIK and NIFTI format before motion correction and distortion correction. These images have visible distortions, but should be free of obvious artifacts, and have typical T2\* BOLD contrast (the example below shows four brain slices acquired in reversed phase encoding direction).



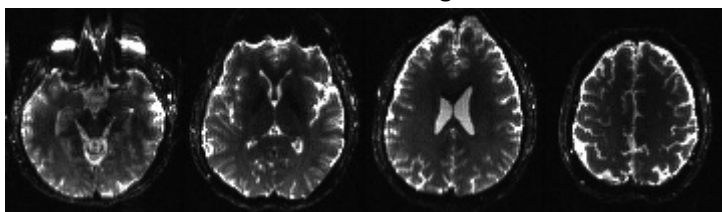
- `topup_epyneg0brik+orig.BRIK and topup_epyneg1brik+orig.BRIK`  
`PhaseOne.nii.gz and PhaseTwo.nii.gz`

Reconstructed images from the TOPUP scan pair in BRIK and NIFTI format. Verify that the distortions in these two datasets are opposite in direction to each other, and there are no obvious imaging artifacts.

PhaseOne.nii.gz

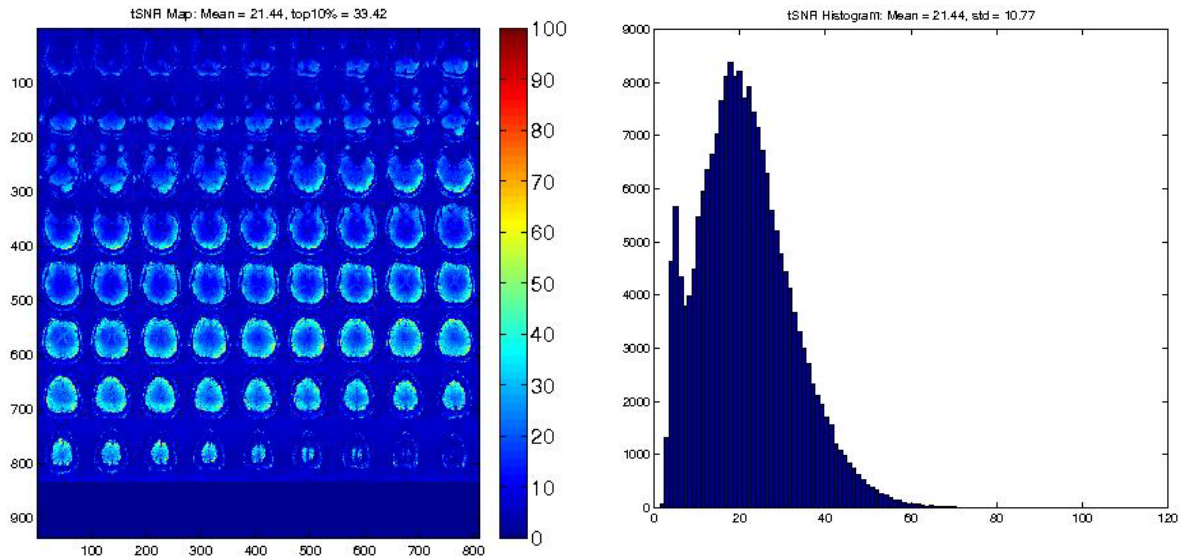


PhaseTwo.nii.gz



- *bcaipi\_spep\_hcp\_rest\_<phase encoding dir>brik\_tSNR.jpg*  
*bcaipi\_spep\_hcp\_rest\_<phase encoding dir>brik\_tSNR\_hist.jpg*

The temporal SNR (tSNR: mean divided by standard deviation over time) map and histograms generated for Quality Assurance. The mean tSNR for the HCP protocol is typically ~20.



- *b02b0.cnf*  
*acqparams5r.txt*  
*Coefficients\_fieldcoef.nii.gz*  
*Coefficients\_movpar.txt*  
*TopupField.nii.gz*

Topup configuration and intermediate files (for more information about the TOPUP distortion correction method please refer to the FSL web site).

- rest<phase encoding dir>\_afni\_al.nii.gz*  
*rest<phase encoding dir>.nii.gz\_vr\_motion.1D*  
*rest<phase encoding dir>\_afni\_al\_mat\_affi12.1D*  
*rest<phase encoding dir>\_afni\_al\_REG\_mat\_affi12.1D*

The fMRI dataset registered to one of the TOPUP scan pair that has the matching phase encoding direction. The 1D files are output motion parameters and transformation matrices from AFNI command `align_epi_anat.py`. Please see **Reconstruct and pre-process MEMS data** section for information on the registration steps.

- *script\_<timestamp>.sh*  
**Example:** *script\_2013-10-24-18:59:34.sh*

Pre-processing script containing motion correction, registration and distortion correction steps. User can look up the pre-processing steps carried out to fMRI dataset.