900 Subjects R820 Group-average rfMRI Connectivity data
released December 2015

A number of processing pipelines are currently being implemented and refined by the HCP that carry out further analyses at the group level. Using the improved analysis methods detailed on the HCP website for the S500 data: Correcting for the rfMRI Mound-and-Moat Effect, for the 900 Subjects Release we have updated the group-average functional connectivity dataset we are distributing to include a larger group of 820 subjects, including many subjects that are related (R820), with complete resting state fMRI data (all timepoints collected). The group-average data are available for download through the links on the WU-Minn HCP Project page in ConnectomeDB. One can view the subjects included in this analysis using the "Open group" function on the ConnectomeDB dashboard.

The group-average rfMRI data includes:

- Group-average functional connectivity matrix ("dense" functional connectome, the grayordinate × grayordinate full correlation matrix), for the R820 group in both MSMSulc and MSMAll registered versions, file names:

  HCP_S900_820_rfMRI_MSMSulc_groupPCA_d4500ROW_zcorr.dconn.nii

  HCP_S900_820_rfMRI_MSMAll_groupPCA_d4500ROW_zcorr.dconn.nii

  Because of their large sizes (33 GB each) these dense functional connectome files are released separately from the rest of the group average data.

- Group-PCA eigenmaps for the R820 group in both MSMSulc and MSMAll registered versions, file names:

  HCP_S900_820_rfMRI_MSMSulc_groupPCA_d4500_Eigenmaps.dtseries.nii

  HCP_S900_820_rfMRI_MSMAll_groupPCA_d4500_Eigenmaps.dtseries.nii

  These can be used as input to group-ICA. They can also be used to generate the dense connectome, but to do this optimally is not trivial, and requires following the procedures outlined in Section IV of the mound-and-moat document. The code for performing these steps is included in the S900 PTN release zip file.

If you prefer to view the dense connectome in the wb_view visualization software distributed as part of Connectome Workbench (recommended to avoid the large file size downloads), **you do not need to download it**, instead there are 2 other options (both require internet connection and ConnectomeDB login):

1. Download all the S900 Group Average data in the 900 Subjects Group Average Workbench dataset and open the included *.scene file to view in wb_view. The connectivity data is automatically loaded when you open the 4th scene entitled: **fcMRI, full correlation, R820 (MSM-Sulc vs. MSM-All Registered) on R881 inflated surfaces**. Further instructions are in the S900 Group Average Tutorial pdf included in the download.

2. Manually load the following URLs in wb_view using the **File>Open Location>Custom** option:

   https://db.humanconnectome.org/spring/cifti-average?resource=HCP_Resources:GroupAvg:HCP_S900_820_rfMRI_MSMSulc_groupPCA_d4500ROW_zcorr

   https://db.humanconnectome.org/spring/cifti-average?resource=HCP_Resources:GroupAvg:HCP_S900_820_rfMRI_MSMAll_groupPCA_d4500ROW_zcorr