

500 Subjects R468 Group-average rfMRI Connectivity data

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A number of processing pipelines are currently being implemented and refined by the HCP that carry out further analyses at the group level. As of April 2015, with improved analysis methods detailed on the HCP website: [Correcting for the rfMRI Mound-and-Moat Effect](#), we have updated the group-average functional connectivity dataset we are distributing on the 500 Subjects Release R468 group (468 subjects, including many subjects that are related, with complete resting state fMRI data). 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 R468 group (file name **HCP_S500_R468_rfMRI_MIGP_d4500ROW_zcorr.dconn.nii**). Because of its large size (33 GB) this dense functional connectome file is released separately from the rest of the group average data.
- Group-PCA eigenmaps for the R468 group (file name **HCP_S500_R468_rfMRI_groupPCA_d4500_Eigenmaps.dtseries.nii**). This file is identical to the previously released file named "HCP_Q1-Q6_R468_rfMRI_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 the mound-and-moat document.

If you prefer to view the dense connectome in [Connectome Workbench](#) (recommended), **you do not need to download it**. The data are accessible in Workbench by remote access (requires internet connection and ConnectomeDB login), using the following URL:

https://db.humanconnectome.org/spring/cifti-average?resource=HCP_Resources:GroupAvg:HCP_S500_R468_rfMRI_MIGP_d4500ROW_zcorr