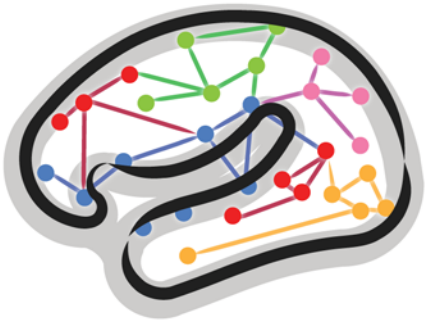

HUMAN Connectome PROJECT

Connectome Workbench Tutorial for HCP Q1-Q6 Group-Average Related 440 and Unrelated 100 Data v1

5 June 2014

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This Tutorial for Group-average functional data (Related 440 and Unrelated 100) is compatible with Workbench Beta v0.85*

Introduction

Connectome Workbench (herein called 'Workbench') is a freely available software platform for visualization and analysis of neuroimaging data. It is customized for handling data from the Human Connectome Project (HCP), including functional and structural connectivity and task-fMRI, using combined surface and volume visualization.

This tutorial is written specifically to aid in navigating HCP group-average functional MRI data on two groups of subjects that were scanned in quarters 1 through 6 (Q1-Q6) of HCP Phase II (production phase). Imaging and behavorial/demographic data for these subjects is released as part of the 500 Subjects Release (June 2014). The "Unrelated 100" (or U100) group is comprised of 100 subjects who are not related to each other. The "Related 440" and "Related 468" (R440, R468) groups contain 440 and 468 subjects, respectively, many of whom are siblings of one or more members of the group. One can view the subjects included in these analyses using the "Open group" function on the ConnectomeDB dashboard accessed through the "Explore" buttons on the ConnectomeDB splash page.

The task-fMRI and functional connectivity data that comprise the U100 and R440 datasets has been processed and additionally analyzed as described in the "Group-average functional data (Unrelated 100 and Related 400+)" section of the HCP 500 Subjects Release Reference Manual. Because it represents a larger group of subjects, we use surfaces and volumes generated from the R440 group-average as a structural atlas to display and compare the group average functional data for U100, R440, and R468 groups in Workbench.

For a more extensive introduction to using Workbench, download the Connectome Workbench Tutorial and User Guide and associated dataset from the ConnectomeDB splash page.

We encourage user feedback to help identify and prioritize refinements and needed features. The HCP-users public discussion email list is an open forum for discussing such issues. You can join at http://www.humanconnectome.org/contact/#subscribe. Once you have subscribed, you can set preferences to receive hcp-users postings to the list as individual messages or as a digest. Please send bug reports and suggestions to the list by emailing hcp-users@humanconnectome.org.

Downloading the Q1-Q6 Group-Average R440 U100 Dataset

The **HCP_Q1-Q6_GroupAvg_Related440_Unrelated100** zipped archive is available for download from the ConnectomeDB splash page. The archive contains Release notes, a copy of these tutorial instructions, and all the files necessary to complete this tutorial (the HCP_Q1-Q6_GroupAvg_Related440_Unrelated100 tutorial dataset). The data contained in the archive includes R440 group-average structural files, group-average myelin and cortical thickness maps for R440 and U100, group-average tfMRI analysis results for R440 and U100, and label, borders, and foci files

generated from other studies to use for reference. Because of their large size (33 GB each) the two group-average dense functional connectome files for R468 (shown below in Scenes 4 and 5) are released separately from the rest of the group average data. In this tutorial, we remotely access these files housed in ConnectomeDB (requires internet access) through the following links:

https://db.humanconnectome.org/spring/cifti-average?resource=HCP_Resources:GroupAvg:HCP_Q1-Q6_R468_rfMRI_groupPCA_d4500

https://db.humanconnectome.org/spring/cifti-average?resource=HCP_Resources:GroupAvg:HCP_Q1-Q6_R468_rfMRI_groupPCA_d4500_MGTR

to generate connectivity maps 'on the fly', requiring the user to log in with their ConnectomeDB account.

Downloading Connectome Workbench

*** Skip this section if you have already downloaded/installed **Workbench v0.85** (released March 2014).*

Operating system requirements for Workbench:

* **Mac 64-bit:** Snow Leopard (OS X 10.6.X or later)

* **Linux 64-bit:** Ubuntu 8.04 LTS or later, CentOS 6.2 or later and RHEL (Red Hat Enterprise Linux) version 6 or later (may run on earlier systems, but this is not supported)

* **Windows 64-bit (RECOMMENDED):** Windows XP SP3 or later

Download Instructions:

- Download Workbench for 64-bit MacOSX, 64-bit Linux, or 64 or 32-bit Windows operating systems (in a zipped folder containing all necessary libraries) from the Workbench download page.
- Unzip the folder. A subdirectory named 'workbench' will be created. Move the folder to your Applications, Program Files folder, or other designated directory. Within the 'workbench' folder you unzipped, is a 'bin' folder (named bin_[operating system]) that contains the executables for the workbench application and 'wb_command' and 'wb_import' command-line utilities. If desired, make a short-cut icon to the program executable for your dock or desktop. For the mac64 version, the 'app' for workbench is in workbench/macosx64_apps/workbench.app
- To run Workbench from a terminal window using the command line, you need to set your PATH environment variable to the appropriate directory.

  For Mac users: If you moved the unzipped Workbench folder to Applications, set your PATH to: /Applications/workbench/bin_macosx64

  For Linux users: Set your path to whatever directory you placed the unzipped Workbench folder.

  To set the PATH in Bash shell, enter this command in a terminal window:

  > echo 'export path=$path:/my/workbench/path' >> ~/.bashrc

To set the PATH in tcsh/csh shell, enter this command in a terminal window:

> echo 'set path = ($path /my/workbench/path)' >> ~/.cshrc

where "/my/workbench/path" is the directory that contains the Workbench folder.

Log out and log back in to make the change take effect.

Tutorial Conventions

Some conventions in this document:

- All tutorial steps are identified by bullets.
- Actions the user should take are in *italics*.
- *Click* refers to a left click with the mouse unless otherwise indicated.
- User-interface components and file names are in **bold**.
- Some instructions are streamlined using arrows (e.g. **Toolbar**►**L** means *press* the **L** button in the **Toolbar** or **File Menu**►**Open File** means *select* the item **Open File** from the **File Menu**).
- Technical terms highlighted in blue are defined in the online Workbench Glossary. The Workbench Glossary is also appended to this tutorial.
- All figures were made using the Mac OSX version of Workbench. The PC and Linux user interfaces appear slightly different, but the functionality is the same.

Launching Connectome Workbench

- Microsoft Windows: *double-click* the **Workbench icon** on the desktop or in your Program files folder.
- Mac OSX: *click* the **Workbench icon** in the dock or in your Applications folder.
- Linux (or Mac terminal): *change (cd)* to the **HCP_Q1-Q6_GroupAvg_Related440_Unrelated100_v1** directory in a terminal window, then *enter* `workbench` and *press* **Return**.

Workbench Orientation

This section is to provide a quick orientation to the Workbench GUI (a.k.a. wb_view) and its associated file types for the purposes of exploring the group average R440 and U100 data provided. For a more comprehensive introduction to Workbench, please download the Workbench Beta 0.83 tutorial and dataset from the Tutorials page on the HCP website.

One great feature of Workbench is the ability to utilize data files that include maps of both the left and right cerebral hemispheres in a single file using the CIFTI file format. For example, myelin maps for both hemispheres are contained in a single *.dscalar.nii file type; cortical parcellations for both hemispheres are contained in a single *.dlabel.nii file. The scenes illustrated herein make use of these cifti files, but

the downloaded datasets also include conventional hemisphere-specific GIFTI files (*.shape.gii; *.label.gii).

Workbench Splash Screen

When you launch Workbench, a splash screen opens (**Figure 1),** showing a list of Specification files (herein called "Spec Files") in the directory path you are currently opening Workbench from, plus Recently opened Spec Files, if you have launched Workbench before.

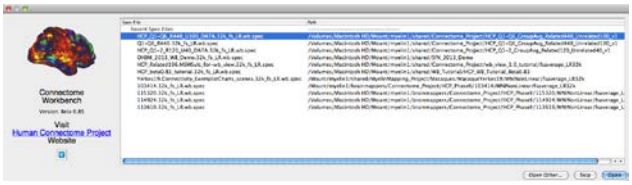

Figure 1 – Connectome Workbench Splash Screen

A Specification File contains an organized set of data files for loading into the program at once (e.g., surface, volume, 'label', and 'metric' files).

- For now, *click* the **Skip button** to launch Workbench without opening a file.

Opening a Spec File and Loading Scenes

- In the Workbench **Menu bar**, located at the top of your screen (Mac) or top of the Workbench window (Linux/PC), *select* **File►Open File…** (shortcut for Mac: command + O, Linux/PC: control + O) to display the **Open File Dialog**.

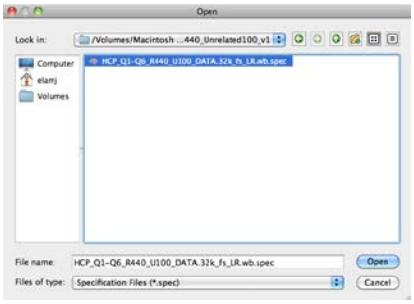

Figure 2 - The Open File Dialog

- In the **Open File Dialog** (**Figure 2**), navigate to the directory that contains the data, the **HCP_Q1-Q6_GroupAvg_Related440_Unrelated100_v1** folder.
    - The default file type filter is Specification Files (*.spec).
- *Select* the desired file:

  HCP_Q1-Q6_R440_U100_DATA.32k_fs_LR.wb.spec and *click* the **Open** button.

  The Spec File Dialog (**Figure 3**) will appear, showing the files in this particular spec file, grouped into 7 types: Border, Dense Label, Dense Scalar, Foci, Scene, Surface and Volume.

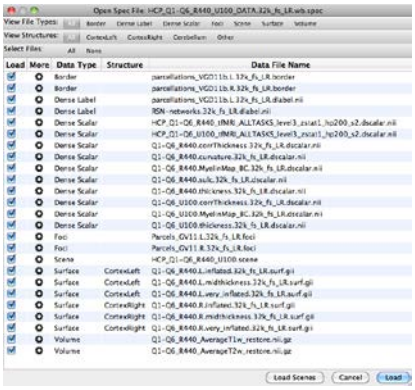

Figure 3 - The Spec File Dialog

- *Click* **Load Scenes** at the bottom left of the dialog to open the scene file necessary for the first section of this tutorial. The Specification File Dialog will automatically close once the scene file is loaded (a few seconds).

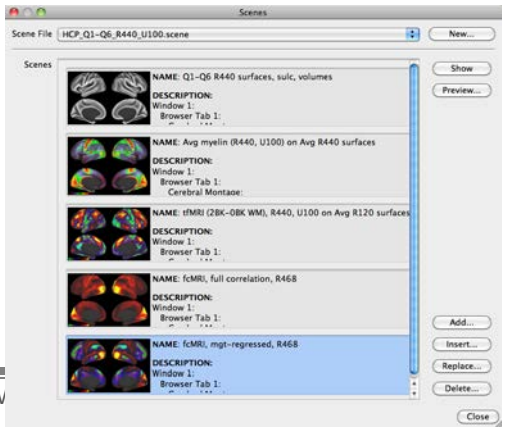

Figure 4 – The Scenes box

Often views in Workbench require several steps to set up, so we have provided a scene file that offers a quick way to load views that show off the group-average data and many features of Workbench.

- The **Scenes box** (**Figure 4**) will appear. In the Scenes field the first scene: "**Q1-Q6 R440 surfaces, sulc, volumes**" should be highlighted, indicating that it is selected.
- *Click* **Show** to load the scene.

Scene 1: Q1-Q6 R440 surfaces, sulc, volumes

This scene shows group average surfaces and volumes of the 440 "related" Q1-Q6 subjects in this dataset. It also provides a convenient backdrop to introduce you to the layout and some of the general features of Workbench.

Workbench Window Layout

The scene opens showing a group-average sulcal depth map on a montage of lateral and medial views of the R440 group average inflated cortical surfaces of both hemispheres in the **Viewing Area** of the **Workbench Window** ("Connectome Workbench 1").

The Workbench Window contains two **Viewing tabs**: (1) Montage and (2) Volume.

The **Viewing Area** defaults upon opening to view **tab 1** (the **Active Tab**). Components of the Workbench Window are shown in **Figure 5**.

The **Overlay Toolbox** (where one sets data layers for viewing on structures) can be displayed in two locations/orientations **Figure 5A and B**. On startup, the choice is automatically made based on the resolution of your monitor (if the vertical resolution is 800 or less, the overlay toolbox will be on the left).

For the purposes of this tutorial, all instructions and figures assume you are using the horizontal orientation layout (**Figure 5B**), with the Overlay Toolbox attached to the bottom of the Viewing Area.

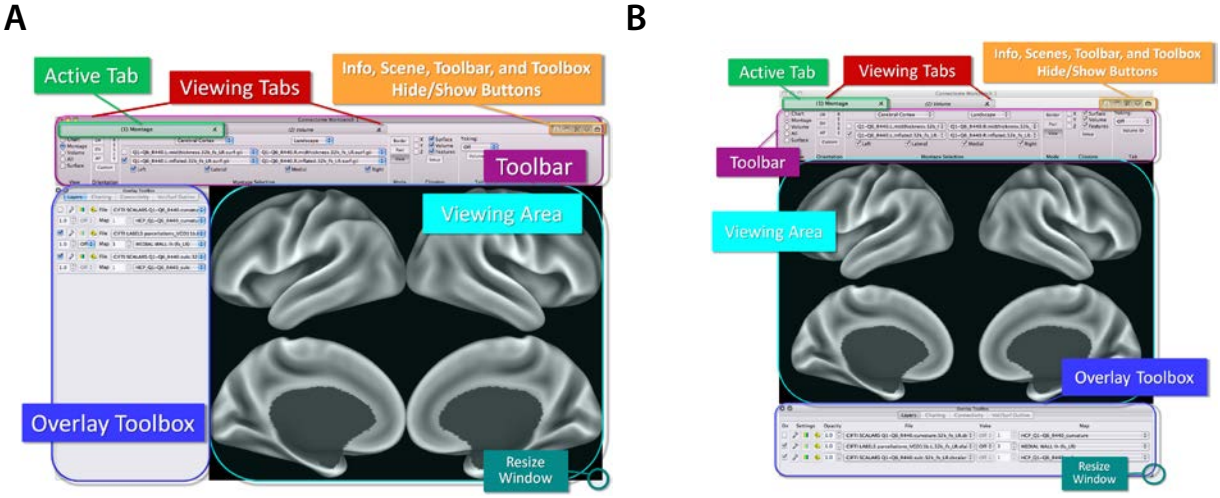

Figure 5 - The Workbench Viewing Window A) Vertical Orientation B) Horizontal Orientation

- *Move your cursor* to the **Montage Selection** section of the **Toolbar** at the top of the Workbench Window.

  Here, you can use the pulldowns to change the R440 group-average surfaces from inflated to midthickness or very inflated. The checkbox to the left indicates if the surfaces are displayed.

- *Move the cursor down* to the **Overlay Toolbox** below the **Viewing Area**. You are currently viewing the **Layers** tab.

Layers are arranged like a layer cake—the topmost layer to be displayed on the surface is listed first, the one below it second, etc. The 'On' toggle on the left controls whether a layer is currently displayed. Here, layer 1 is toggled off and layers 2-3 are toggled on, displaying the R440 group-average sulcal depth map on the bottom layer 3 and the black medial wall from the **CIFTI LABELS parcellations**… file in layer 2.

- *Click* the checkbox to the left of layer 1 to show the R440 group-average curvature map: **CIFTI SCALARS Q1-Q6_R440.curvature.32k_fs_LR.dlabel.nii**.
- Now *toggle the curvature layer off* again to expose the sulcal depth map for comparison.
- *Click on the file name in layer 1* to show a dropdown of all the files loaded that are available for display. Explore some of these other files, if desired, e.g. group-average cortical thickness maps (from FreeSurfer) and corrected thickness maps for R440 and U100 (thickness maps with the curvature regressed out as in Glasser & Van Essen, 2011).
- *Press the left mouse button and drag your mouse* anywhere in the **Viewing Area** to rotate the surfaces.
- To zoom, *scroll your mouse wheel up and down* anywhere in the **Viewing Area**. If you don't have a mouse wheel, *press* the command (Mac)/control (Linux/PC) key *while pressing the left mouse button and moving your mouse up and down*.
- *Click* on **Tab (2) Volume** at the top of the Workbench Window. This shows a montage of 4 R440 group average T1-weighted volume slices with the R440 group-average midthickness surface outlined in black. Note that even though this is a group average volume, there are clear boundaries between the gray and while matter regions reflecting the high quality of the HCP data.
- *Toggle* the first layer **VOLUME Q1-Q6_R440_AverageT1w_restore.nii.gz** *off and on* in the Overlay Toolbox to reveal and compare the R440 group-average T2-weighted volume below.
- If you would like to turn the midthickness surface outlines off, *click* on the **Vol/Surf Outline** tab and *toggle off* outlines 3 and 4.

Scene 2: Avg myelin (R440, U100) on Avg R440 surfaces

- In the **Scenes Dialog**, *select* "**Avg myelin (R440, U100) on Avg R440 surfaces**" and *click* **Show** to load the scene. Leave the **Scenes Dialog** open.

Note: If you had inadvertently closed the **Scenes Dialog,** you can reopen it by clicking the **clapboard**  **button** in the upper right of the **Workbench Window**.

This scene shows the same R440 group-average surfaces, but now overlaid with a map of group-average myelin content averaged across the unrelated 100 (U100) subjects (layer 2).

- *Click the first layer on*, the R440 group-average myelin map. *Toggle off and on* to compare with the U100 myelin map. The R440 myelin map appears smoother since many more subjects were averaged in this group.
- Rotate the surfaces (*press the left mouse button and drag your mouse*). Red and orange represent heavily myelinated regions, purple and black represent areas of low myelin content (Glasser & Van Essen, 2011).
    - There is heavy myelination in much of the occipital lobe, including the orange-yellow target-like patch around where area MT should be, near the occipito-temporal junction.
- *Click on the surface* within this patch over area MT (see **Figure 6**). The **Information box** will pop up.
- In the Viewing Area, a white sphere should be visible at the grayordinate (i.e. cortical surface vertex or gray-matter volume voxel) you selected. Your viewing window should look like **Figure 6**.
- Information on the grayordinate that you clicked is listed in the **Information box**. For example, the XYZ coordinates and the labels assigned to the identified vertex are shown. Information (e.g. label names, metric values) on the vertex you selected is pulled from all currently loaded files.

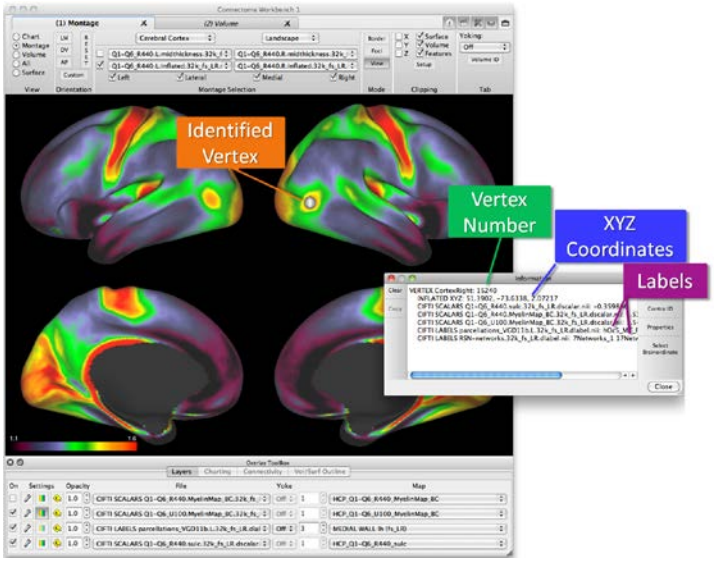

Figure 6 –U100 Myelin map showing Vertex Identification and the Information Box

- We have provided maps of parcellation labels and resting state networks mapped from other studies and corrected thickness maps as part of the group-average dataset for comparison to the myelin maps. Use the Layers: File dropdowns to display these loaded files on the surface and the map pulldown to explore each file's maps.
- We have also provided borders and foci files in the dataset for comparison. These can be shown using the controls in the Features Toolbox (open using the  icon). See the Connectome Workbench Tutorial and User Guide for beta v0.83, scenes 6-7, for further instructions).

Scene 3: tfMRI (2BK-0BK WM), R440, U100 on Avg R440

- *Select* "**tfMRI (2BK-0BK WM), R440, U100 on Avg R440**" in the **Scenes Dialog box** and *click* **Show** to load the scene. Leave the **Scenes Dialog** open.

This scene opens to show the U100 group-average 2back-0back contrast of the HCP Working Memory task on the inflated R440 surfaces.

- *Click the first layer on*, the R440 group-average tfMRI 2back-0back contrast map. *Toggle off and on* to compare with the U100 myelin map. Again, the R440 myelin map appears smoother since many more subjects were averaged in this group.

The fMRI data processing included grayordinate-constrained smoothing (2 mm FWHM, respecting cortical surface topology and subcortical parcel boundaries). This has advantages over the volume-based smoothing that is conventionally applied to fMRI data (see below and Glasser *et al.* 2013, Barch *et al.*, 2013). Additionally, the averaging across subjects occurs in the grayordinate space, in which the cerebral cortex is better aligned across subjects because of surface-based registration using MSM_{Sulc} (see HCP 500 Subjects Release Reference Manual for more details).

Figure 7 shows the unthresholded activation maps from the 2-back vs 0-back task contrast. Activations related to working memory are most prominent in lateral prefrontal cortex but also include anterior cingulate cortex and lateral parietal cortex.

The color bar in the lower left shows a maximum z-statistic value of 17.3 and minimum of -11.8. (In this and other figures, the color bars span the +/- 98% range of z-values; the actual ranges are higher. Options for setting z-statistic thresholds, adjusting the palette colors, etc. are available using the Layers: Settings: 'wrench' icon, as explained in the Workbench 0.83 tutorial.)

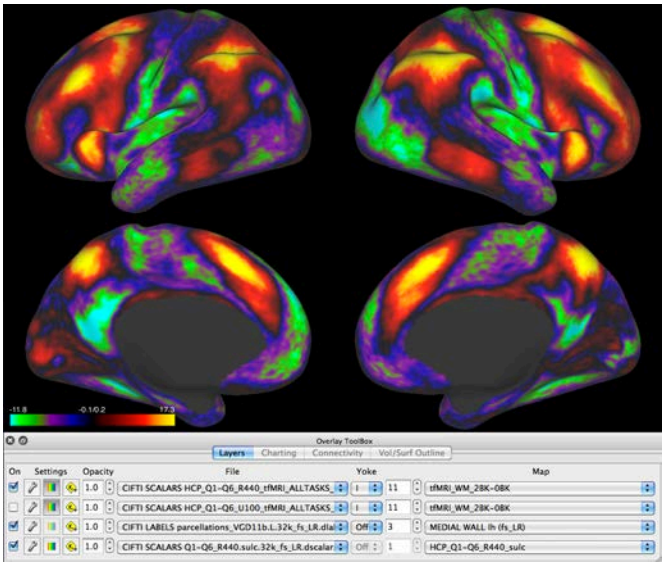

Figure 7 – R440 group-average task contrast for the 2-back vs 0-back working memory task.

In this task, participants were presented with blocks of trials that consisted of pictures of places, tools, faces and body parts (non-mutilated parts of bodies with no "nudity"). The participants are asked to perform a working memory task to remember the picture 2 pictures back (2 back condition) or remember the picture they just say (0 back condition).

- *Click* on the **Map** pulldown for either of the first 2 layers. A listing of all the tfMRI contrasts from all of the tasks in the HCP protocol appears. Explore the other contrasts as you wish.

A full description of the tasks in the HCP protocol is provided in the HCP 500 Subjects Reference Manual.

Important note about the Related 440 (R440) dataset. Many of the 440 subjects in the R440 dataset are related. However, family structure *was not* taken into account in the tfMRI group average analyses of R440. Therefore, the associated standard errors and p-values are optimistic. Since the p-values are not valid, any false discovery rate (FDR) inferences based on them will not be valid either. We plan for standard errors and p-values to be revised in future related datasets once family structure is incorporated into the analysis.

Scene 4: fcMRI, full correlation, R468

This scene displays full correlation group-average functional connectivity data from 468 'related' Q1-Q6 subjects (R468) with complete resting state fMRI interactively on the cortical surface and in subcortical volumes.

- *Select* "**fcMRI, full correlation, R468**" in the **Scenes Dialog box** and *click* **Show** to load the scene. Leave the **Scenes Dialog** open.
- A **Username and Password Dialog** will pop up.
- Enter your ConnectomeDB username and password (same information you used in the Workbench data download process). *Click* **OK**.
- Workbench is now accessing ConnectomeDB in order to retrieve functional connectivity data for a preselected surface vertex (this may take several seconds, if you get an error, make sure you are connected to the internet).

The scene opens displaying an inflated surface montage view of R468 group-average full correlation functional connectivity between the vertex on the left hemisphere surface (shown in white) and all other grayordinates.

With this color palette, brain regions that are positively correlated (by Pearson's r-value that has been Fisher transformed) to the identified grayordinate are yellow, orange, and red; those that are negatively correlated (very few places in the full correlation) are displayed in blue, green, and indigo.

- C*lick on the left hemisphere surface* in the ventral part of the precentral gyrus, approximately the same place as the highlighted vertex in **Figure 8A (upper left)**.

  This shows a map of R468 functional connectivity associated with the face representation in motor cortex.

- *Click* on the location on the postcentral gyrus (**shown in Figure 8B**) to view the similar functional connectivity map for the face representation of somatosensory cortex.

- *Now click* an area in the supramarginal gyrus (**shown in Figure 8C**). You will see a much different connectivity pattern than for either of the previous maps. This demonstrates how nearby brain regions can have very different resting state functional connectivity from each other.

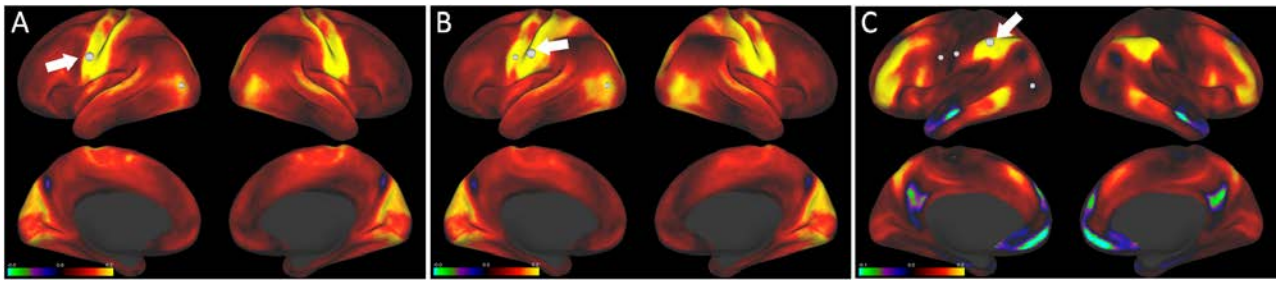

Figure 8 – Comparing group-average full correlation functional connectivity for three brain locations.

- Click on Workbench Window tab ***(2) Volume*** to view the same full correlation functional connectivity maps in the subcortical gray matter in 9 volume slices.
- *Click on a subcortical voxel* in the upper right panel (**shown in Figure 9A**) to view the R468 group-average full correlation and the other subcortical grayordinates shown.
- You can return to Window tab ***(1) Montage*** to view the R468 full correlation connectivity between the subcortical voxel you identified in the Volume tab and the surface grayordinates (**Figure 9B**).

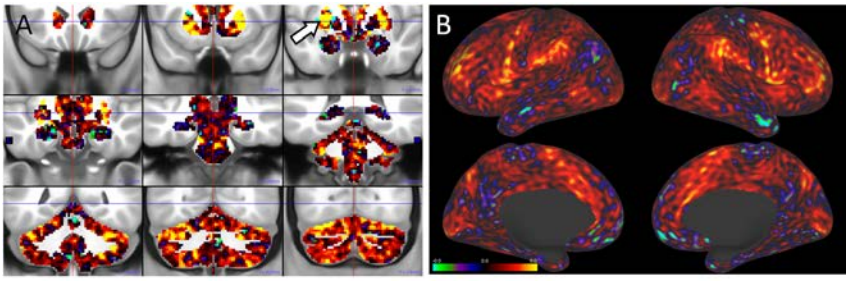

Figure 9 – Full correlation functional connectivity for a subcortical voxel seed. A) R468 group-average, subcortical volume view, B) R468 group-average, surface view.

Scene 5: fcMRI, mgt-regressed, R468

Similar to Scene 4, this scene displays group-average resting state correlation functional connectivity in which the mean grayordinate time series (MGT) has been regressed out of the data.

- *Select* "**fcMRI, mgt-regressed, R468**" in the **Scenes Dialog box** and *click* **Show** to load the scene. Leave the **Scenes Dialog** open.
- A **Username and Password Dialog** will pop up.
- Enter your ConnectomeDB username and password (same information you used in the Workbench data download process). *Click* **OK**.

- Workbench will retrieve R468 MGT-regressed functional connectivity data for a preselected surface vertex (again this may take several seconds, and requires an internet connection).

The scene opens displaying an inflated surface montage view of R468 group-average MGT-regressed correlation between the vertex on the left hemisphere surface (shown in white) and all other grayordinates.

With this color palette, brain regions that are positively correlated (by Pearson's r-value that has been Fisher transformed) to the identified grayordinate are yellow, orange, and red; those that are negatively correlated (after regression of the mean gray-matter timeseries) are displayed in blue, green, and indigo.

- C*lick on the left hemisphere surface* in the ventral part of the precentral gyrus, approximately the same place as the highlighted vertex in **Figure 10A (upper left)**, as you did for Scene 4.

This shows a map of R468 MGT-regressed functional connectivity associated with the face representation in motor cortex. **Figure 10** shows maps for the R468 group-average.

- *Click* on the locations on the postcentral gyrus (**shown in Figure 10B**) to view the similar functional connectivity map for the face representation of somatosensory cortex and on a green or blue area in the supramarginal gyrus (**shown in Figure 10C**) to see a much different connectivity pattern than for either of the previous maps.

- As in Scene 4, you can *click* on Workbench Window tab ***(2) Volume*** to interactively view the MGT-regressed correlation functional connectivity maps in the subcortical gray matter.

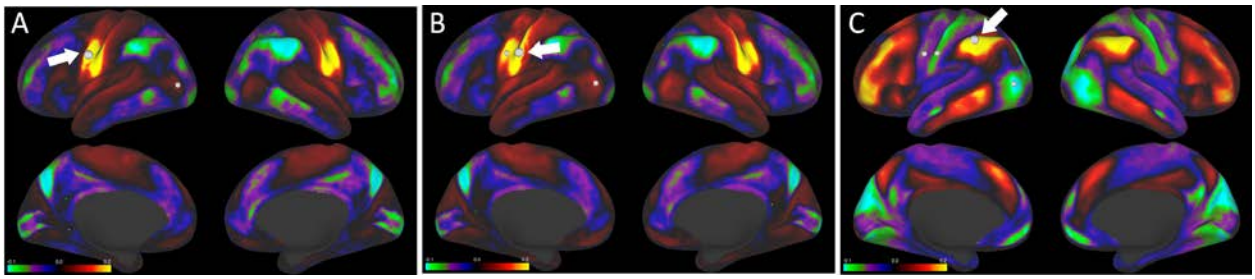

Figure 10 – Comparing R468 group-average functional connectivity correlation with mean grayordinate timecourse regression for three brain locations.

The interpretation of both types of functional connectivity map is complex. Neither the full connectivity map nor the MGT-regressed map represents 'ground truth' anatomical connectivity (see Smith *et al.*, 2013, Glasser *et al.* 2013, Van Essen *et al.*, 2013). Having both available for the same datasets should facilitate evaluation of the relative strengths and limitations of each way of representing functional connectivity. Alternative representations, such as partial correlation, can also be explored (see Smith *et al.*, 2013). It is likely that this will remain a topic of ongoing debate and discussion in the field.

References

Glasser M and Van Essen DC. 2011. Mapping human cortical areas in vivo based on myelin content as revealed by T1 and T2-weighted MRI. J Neuroscience. 31:11597-11616. Full Text

Nasr S, Liu N, Devaney KJ, Yue X, Rajimehr R, Ungerleider LG, Tootell RB. 2011. Scene-selective cortical regions in human and nonhuman primates.J Neuroscience. 31:13771-85. Full Text

** Further details on the data acquisition and analysis methods are available in eight manuscripts in a special Connectome issue of *NeuroImage* (Van Essen *et al.*, 2013, Ugurbil *et al.*, 2013, Glasser *et al.* 2013, Smith *et al.*, 2013, Barch *et al.*, 2013, Sotiropolous *et al.*, 2013, Marcus *et al.*, 2013, and Larson-Prior *et al.*, 2013). See http://www.humanconnectome.org/documentation/citations.html for updated lists of publications.

Glossary

Active tab is the currently selected viewing tab at the top of the Workbench Window. The Overlay and Features Toolboxes provide options for viewing that apply *only* to the Active tab.

Brainordinate is a brain location that can be specified by a surface vertex (node) or a volume voxel. Brainordinates include grayordinates (gray-matter vertices or voxels) and whiteordinates (white matter voxels). CIFTI files (see below) contain a list of brainordinates to handle combined surface/volume representations.

CIFTI file is a new file format that stores data from surfaces (vertices) and volumes (voxels) concurrently in a single file comprising a listed set of brainordinates. The volume component of a CIFTI file can be any selected list of voxels (e.g., only subcortical gray-matter voxels) that need not conform to cuboidal or 'N x M x O' volumetric dimensions. See http://www.nitrc.org/projects/cifti/ for a detailed exposition of the CIFTI file format. CIFTI files are consistent with the NIFTI-2 file format and by convention have the extension **.nii.** Workbench currently supports CIFTI files for dense time series (*.dtseries.nii) and dense connectomes (*.dconn.nii).

ConnectomeDB will be the web-accessible database that will handle all HCP data modalities (MR images, MEG/EEG, and behavioral data) and will be central to HCP data mining. Once operational, ConnectomeDB will be accessible from any web browser (see URL below) and also in an internal browser within Workbench using the **DB button** in the **Tools** section of the **Toolbar.** (See IntraDB for Phase I HCP data access.)

Deformation map file (*.deform_map) is a file type that allows transformation of data from one surface mesh (e.g., an individual subject's 'initial mesh') to another surface mesh (e.g., the fs_LR atlas mesh). The key step in creating a deformation map is to encode the relationship between each node in one sphere (the 'deformed source sphere') and the nearest surface tile in the 'target sphere'. A deformation map can also be used to resample a surface from one mesh density (e.g., a '164k' mesh) to another (e.g., a '32k' mesh), as done for this tutorial. (See Van Essen *et al.*, 2011a, 2011b for additional details on deformation maps and surface-based registration.)

Deformed data file is a file that has been operated on by a deformation map file, for instance when registering it from a source to a target surface. By default, the expression 'deformed_' is prepended to the file name and to the column name after applying a deformation map, but this can be modified as specified by the user or within the deformation map file.

Dense Time Series file is a type of dense data series file that contains BOLD activation maps for each timepoint in the resting state fMRI time series. A dense time series can be viewed as single maps at given timepoints or as a movie of sequential timepoint maps using the animate function in the Toolbox Connectivity tab. A **dense data series file** can also contain columnar brainordinate data of any kind (e.g. each column may contain an ICA component, a task activation map, etc.).

Dense Connectome refers to connectivity matrix files that contain correlations between every surface or volume brainordinate and every other surface or volume ordinate in our model of the brain. These files

are REALLY big (~30 GB for current resolution). Therefore, they are kept in the HCP database ConnectomeDB, which can access these large files as needed to view connectivity maps of interest. Dense connectomes can also be asymmetric, such as a structural connectivity matrix between grayordinates (all gray matter structures) and whiteordinates (all white matter structures).

Features Toolbox refers to the section of the Workbench Window that allows the user to select and set display attributes for Features such as Borders and Foci in the current Active Viewing tab.

GIFTI file is a file format for surface representations that is supported by many major brain mapping visualization platforms (http://www.nitrc.org/projects/gifti).

Grayordinate is a brain gray matter location that can be represented by a surface vertex (node) or a volume voxel.

ConnectomeDB is the web-accessible database for HCP data. To get an account for ConnectomeDB, go to: http://humanconnectome.org/data/and register for access.

Menu bar refers to the gray bar containing pulldowns (menus) of program-wide functions located at the very top of the screen (Mac) or at the top of the Workbench Window (PC and Linux). Menu items include File, View, Data, Surface, Volume, Window and Help.

NIFTI file (*.nii and *nii.gz) is a standard file format for volumetric data that is widely used in neuroimaging. The original NIFTI-1 file format was based on 16-bit signed integers and was limited to 32,767 in each dimension. The NIFTI-2 format (http://www.nitrc.org/forum/message.php?msg_id=3738) is based on 64-bit integers and can handle very large volumes and matrices.

Overlay Toolbox refers to the section of the Workbench Window that allows the user to set the data to be displayed on the structure in the active tab.

Parcellation refers to the division of the cerebral cortex and subcortical volume into regions that share functional or structural properties.

Scene refers to the current state (settings and files being visualized) within Workbench. You can save these settings globally in a scene file, which allows you to re-access your current Workbench session at a later time. By reopening a saved scene file, a user can “pick up where they left off” when they reopen Workbench.

Specification File (commonly called “Spec File”) is a file used to organize a set of data files (such as volume, label, and metric files) to be loaded into Workbench.

Splash Screen is the first window that opens upon launching Workbench that serves as a title page and shortcut for opening Spec files. It contains a list of Spec files in your current path and those that have been recently opened that can be selected and opened in one step. It also contains links to the HCP website and Twitter feed.

Montage is a viewing mode in which lateral and medial views of both left and right hemispheres are shown in a single viewing area and can be rotated in tandem for a full surface view of the brain.

Tab Montage is a setting that displays the images from all of the tabs you have open in the current Workbench Window in one Viewing Area. All the surfaces and/or volumes displayed in Tab Montage can still be manipulated with the mouse controls (rotate, zoom, pan). This option allows you to view and compare multiple structures and datasets at once. Access tab montage from the View►Screen menu, or through the keyboard shortcut: command + M (Mac) or control + M (PC/Linux).

Toolbar refers to the section at the top of the Workbench Window that contains viewing settings for the structure you are displaying in the current tab and access to Workbench functional modes (border drawing, region of interest definition, etc.).

A **Tooltip** is pop-up information on Workbench functions that appears when you hover your cursor over a button or pull-down menu. These are found throughout the entire Workbench for easy access to explanations of the functions of buttons and menus.

Viewing Area refers to the field of the Workbench Window where images of the surface, volume or whole brain are displayed. The default background is set to black, but this can be changed to any color in the Preferences.
(Menu bar►Workbench►Preferences►Colors►Set Background…)

Viewing Tabs refer to the set of viewing workspaces within a Workbench Window. Each tab contains an independent Toolbar, Viewing Area, and Toolbox. To navigate between Viewing Tabs, click on the tab name or press command-(Mac)/control-(PC/Linux) and the left and right arrow buttons. To remove a tab, click on the 'X' button to the right of the tab name. Further tab options are available in the Window menu.

Volume Montage is a setting available in Volume views that displays a series of slice images in the Viewing Area. Settings for the number of columns and rows, and the step number (stereotactic space between) of slices being viewed for this montage of images are located in the Toolbar.

Whiteordinate is a brain white matter location. It is generally represented by a list of white matter voxels, though in principle, it can also be represented surface vertices (nodes).

Workbench Window refers to the main interface of Workbench, containing the Viewing Tabs, Toolbar, Viewing Area and Toolbox. In PC/Linux, the Workbench Window also includes the Menu bar. More than one Workbench Window can be opened at one time, either by selecting New Window from the File menu or from selections made from the Window menu.