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Connectome Workbench v1.0 Tutorial

18 September 2014



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Introduction

*****This Tutorial is compatible with Workbench v1.0*****

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.

The Workbench platform includes `wb_view`, the visualization graphical user interface used in this tutorial, and `wb_command`, a set of command line tools for performing simple to complex operations using volume, surface, and grayordinate data. `wb_command` is a required program for running the [HCP pipelines](#) (released Sept 2014).

To get Workbench, users can download 64-bit Mac, Windows, and Linux versions from the HCP website (see [Downloading Connectome Workbench v1.0](#) below). Getting the HCP-generated data necessary to complete this tutorial requires a few more easy steps. To get the data, users must sign up for an account on [ConnectomeDB](#) and agree to the HCP Open Access data use terms before downloading (see [Downloading Tutorial Data](#) below).

This tutorial is written for users at all levels, from those new to brain mapping to regular users of FSL, FreeSurfer, Caret, and other brain-mapping platforms. Workbench has its roots in Caret software developed by the Van Essen laboratory, but it has been thoroughly re-designed and re-implemented. Novel features of Workbench include:

- Interactive viewing of functional connectivity
- Improved user interface for selecting data layers and maps
- Viewing fMRI time courses and other data series frame-by-frame, as movies, or as charts
- Options to display multiple surfaces and volumes as tabs, windows, or as a “montage” within a single window
- Parcellated connectivity matrix viewing with interactive parcel selection for viewing parcellated connectivity on surface and volumes
- Compatibility with [NIFTI](#), [GIFTI](#), and [CIFTI](#) (surface + volume) data formats (Note: the CIFTI-2 format was released in March 2014, see [this link](#) for details)
- Help information integrated into the `wb_view` interface
- Interactive viewing of structural connectivity and probabilistic fiber trajectories (coming soon!)

New to Workbench 1.0 is an improved border file format that requires borders to be on a single brain structure. Old border files can be read by `wb_view` and `wb_command` as long as the structures on which they were drawn are also loaded. In `wb_view`, old border files on a single brain structure will be automatically converted to the new format and just need to be saved using **Save/Manage Files** (see



[Scene 9](#) for more details) to complete the conversion to the new format. For old border files on multiple brain structures, the user must use the **Split Multi-Structure Border Files** option in the **Data Menu** to separate the borders by structure before editing or saving borders in the new format. Scenes created with old border files will also open, but if modifications to the border files are made, the scene will need to be replaced to reflect the changes.

You are encouraged to use this tutorial however it suits your experience level and learning style: You can run through the full tutorial as written or skip around to sections covering features of particular interest. We have streamlined this WB v1.0 tutorial to be a quick “get your feet wet” guide, touching on most features of the software while exploring HCP data released to date.

‘Scenes’ files, which provide a ready setup of data to show particular features, facilitate skipping between sections of interest (each scene has a separate section in the tutorial).

Those who have not previously used Caret software may find the topics in the `wb_view` **Help menu** an easy way to become familiar with Workbench functionality, including using Workbench tools such as drawing borders/foci and creating Regions of Interest (ROIs). Another option for getting a quick look at 500 Subjects HCP data released in June 2014, while learning Workbench basics, is to follow the **ConnectomeWorkbenchTutorial_HCP_Q1-Q6_GroupAvg_Related440_Unrelated100_v1.pdf** included in the Group Average Workbench Dataset available on the [WU-Minn HCP Data – 500 Subjects page](#) in [ConnectomeDB](#).

Information for running each command tool in `wb_command` is available at <http://humanconnectome.org/software/workbench-command.php>.

Basic information on setup and syntax for using `wb_command` and `wb_import`, a tool distributed with Workbench for converting Caret 5 files to Workbench format, is included as the last chapter of the **Workbench Beta v0.83 Tutorial and User Guide** available at <http://humanconnectome.org/documentation/tutorials/>. The Beta v0.83 Tutorial also includes much of the help information on `wb_view` features and functions that now appear within the software in **Help Menu ► Workbench Help...** in a printable document format that may be helpful to some users.

Connectome Workbench is under active development, with many new capabilities to be added in the coming years. We encourage user feedback to help identify and prioritize refinements and needed features (Feature requests can be directly submitted through the **Help Menu**). The HCP-users public discussion email list is an open forum for discussing such issues. You can join via <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 Connectome Workbench v1.0

*** Skip this section if you have already downloaded and installed **Workbench v1.0** (released September 2014). You are ready to get started!*

64-bit Mac, Windows, and Linux versions of Connectome Workbench v1.0 are available for download as zipped file archives from the [Workbench download page](#) on the HCP website (32-bit versions of Workbench are no longer being distributed because of multiple problems handling large data files).

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:** Windows XP SP3 or later

Download Instructions:

- Download Workbench for 64-bit MacOSX, 64-bit Linux, or 64-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 'workbench' folder to your Applications, Program Files folder, or other designated directory. Within the 'workbench' folder, is a 'bin' folder (named bin_[operating system]) that contains the executables for wb_view, wb_command and wb_import. If desired, make a short-cut icon to the program executable for your dock or desktop. For the mac64 version, the 'app' for wb_view is in workbench/macosx64_apps/wb_view.app

To run Workbench from a terminal window, you need to set your PATH environment variable to the appropriate executable 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 [directory you placed the unzipped Workbench folder]/bin_linux64 (or /bin_rh_linux64 for RHEL).

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

```
> echo 'export PATH=$PATH:/my/workbench/path/bin_linux64' >> ~/.bashrc
```

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

```
> echo 'set PATH = ($PATH /my/workbench/path/bin_linux64)' >> ~/.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.

Connectome Workbench is Open Source and the source code is available at:

<https://github.com/Washington-University/workbench>

Downloading Tutorial Data

Downloading the HCP-generated neuroimaging data necessary to complete this tutorial is easy, but requires a few more steps. Briefly, to get the data, users must have an account on [ConnectomeDB](#), have agreed to the HCP Open Access data use terms, and have installed the Aspera Connect plugin in their browser.


Because of the large size of the data, downloading is facilitated through an Aspera server that requires you to have the Aspera plugin installed in your browser (available free to end users). Before you start the download process, if you have not installed the plugin yet, a warning message will appear at the top of your browser when reminding you that you must [Install the Aspera plugin](#) before downloading.

Pre-download instructions:

- Follow [this link](#) to install the Aspera Connect plugin for your browser.

Download instructions:

- Click the Tutorial Data button on the [Workbench download page](#).
- Instructions outlining the steps for this download process will popup.
- Click on the “Go to ConnectomeDB” button. You will be taken to the ConnectomeDB login page.
 - If you have a ConnectomeDB account, enter your username/password and press Log In.
 - If you do not have an account, click the Register button to create one.
 - Click the link in the verification email that is sent to the email address you provided in registration.
 - Log in with your username/password.
- The ConnectomeDB multi-projects splash page will open.
 - If you have previously signed the WU-Minn HCP Data Use Terms, skip the next step.
 - If you have not yet signed the WU-Minn HCP Data Use Terms, the **WU-Minn HCP Data – 500 Subjects** section will show a button under the description containing the words “Data Use Terms Required”. Click the button.

 Data Use Terms Required

 - The Open Access Data Use Terms will popup.
 - Read the Data Use Terms and click the checkbox on the bottom left to agree to all terms.
 - Click the Accept Terms and Access Dataset button.
 - Click on “**WU-Minn HCP Data—500 Subjects**” or the “Resources” button in that section.
 - On the page that opens, scroll down to the **Connectome Workbench Data** section and click the **Download Tutorial Dataset** button.

- If you have the Aspera Connect plugin installed, the download will launch on your browser.
- If you do not have Aspera Connect installed, you will see a warning message at the top of your browser with the [link to the Aspera site](#).
- Unzip the **HCP_WB_Tutorial_1.0** zipped archive you just downloaded.

The **HCP_WB_Tutorial_1.0** folder contains a copy of these tutorial instructions and all the data files necessary to complete this tutorial, packaged in the same directory. You are ready to start the tutorial!

WB 1.0 Tutorial Dataset

As detailed above, the **HCP_WB_Tutorial_1.0** zipped archive is available for download from the [WU-Minn HCP Data -- 500 Subjects project page](#) in ConnectomeDB. The archive contains data Release notes, a copy of these tutorial instructions, and all the files necessary to complete this tutorial. The data contained in the archive includes individual subject (100307) and 440 subject (R440) group-average structural files (including surfaces at 32k and 164k mesh resolutions); maps of myelin, curvature, Freesurfer sulc and cortical thickness for 100307 and R440 (at 32k and 164k mesh resolutions); group-average tfMRI grayordinates analysis results for R440, 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 are remotely accessed in ConnectomeDB (shown below in Scenes [5](#) and [6](#)) 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 have internet access and login using their ConnectomeDB account credentials. For those that would like a local copy, these dense connectome files and the Group-PCA Eigenmaps that can be used to create them locally using `wb_command`, are also available for download from the [WU-Minn HCP Data -- 500 Subjects project page](#).

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**).
- Several technical terms are defined in the **Glossary** in the **Help Menu** within `wb_view`.
- All figures were made using the Mac OSX version of Workbench. The PC and Linux user interfaces appear slightly differently, but the functionality is the same.

Launching Connectome Workbench (`wb_view`)

- Windows: *double-click* the **wb_view icon** on the desktop or in your Program files folder.
- Mac OSX: *click* the **wb_view icon** in the dock or in your Applications folder.
- Linux (or Mac terminal): *change (cd)* to the **HCP_WB_Tutorial_1.0** directory in a terminal window, then *enter* **wb_view** and *press* **Return**.

Exploring HCP Data in wb_view

Workbench Orientation

This section provides a quick orientation to the Workbench GUI, `wb_view`, while exploring individual and group average data from the HCP. 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 (based on the NIFTI-2 format, hence the *.nii ending, with a unique header structure). 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 dataset also includes conventional hemisphere-specific GIFTI files (e.g. *.surf.gii).

Workbench Splash Screen

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

A spec file organizes a set of data files for loading into the program at one time.

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

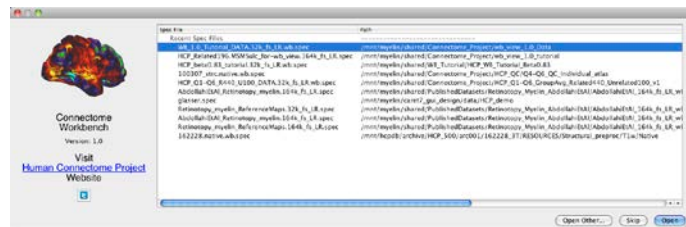



Figure 1 – Connectome Workbench Splash Screen

Menu Bar and Workbench Help

The Menu bar, located at the top of your screen (Mac) or top of the blank Workbench window that just opened (Linux/PC), contains several menus for program-wide functions like file loading, setting preferences, and view options.

The **Help Menu** ► **Workbench Help...** (**Figure 2**), accessible through the Help  button in the upper right corner of the Workbench Window, contains information about using `wb_view` and `wb_command` utilities, including a Glossary of terms that may be new to users and information on the options in the Menus, `wb_view` features, and `wb_command` tools. Most of the Workbench features/elements in **bold font** in the tutorial have Help entries. It may be useful to keep the Help window open as you explore the program.

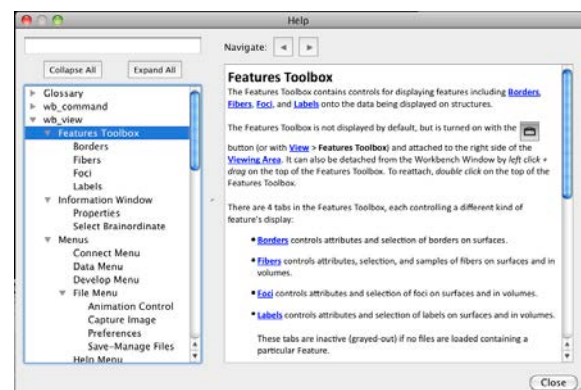


Figure 2 – Workbench Help Window

Opening a Spec File and Loading Scenes

- In the Menu bar, *select* **File** ► **Open File...** (shortcut cmd/ctrl + O) to display the **Open File Dialog**.
- In the **Open File Dialog** (**Figure 3**), Navigate to the folder or directory that contains the data, the **HCP_WB_Tutorial_1.0** folder.
 - The default file type filter is Specification Files (*.spec).
- *Select* the desired file:
WB_1.0_Tutorial_DATA.32k_fs_LR.wb.spec and *click* the **Open** button.

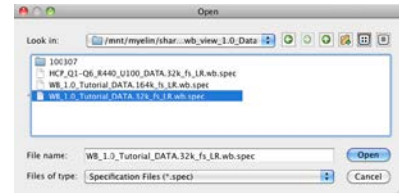


Figure 3 - The Open File Dialog

- *Select* the desired file:
WB_1.0_Tutorial_DATA.32k_fs_LR.wb.spec and *click* the **Open** button.

The **Open Spec File Dialog** (**Figure 4**) will appear, showing the files in this particular spec file, grouped into 8 types: Border, Dense Label, Dense Scalar, Dense Data Series, Foci, Scene, Surface and Volume.

- *Click* **Load Scenes** at the bottom left of the dialog to open the scene file necessary for the tutorial.

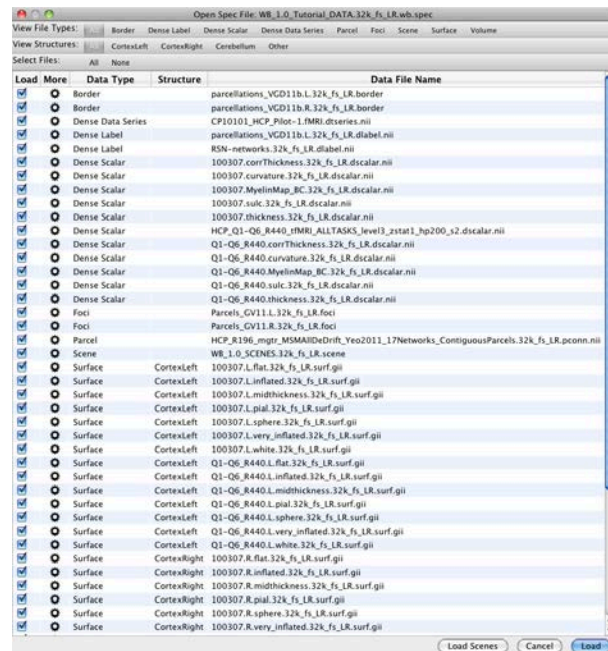


Figure 4 - The Open Spec File Dialog

Often views in Workbench require several steps to set up, so we have provided **scene files** that offer a quick way to load views that show off the HCP data provided and many features of Workbench.

- The **Scenes box** (**Figure 5**) will appear. In the Scenes field the first scene:

“1. Individual surfaces and volumes” should be highlighted, indicating that it is selected.

- *Click* **Show** to load the scene (Note: this might take several minutes if you are loading from a remote location).

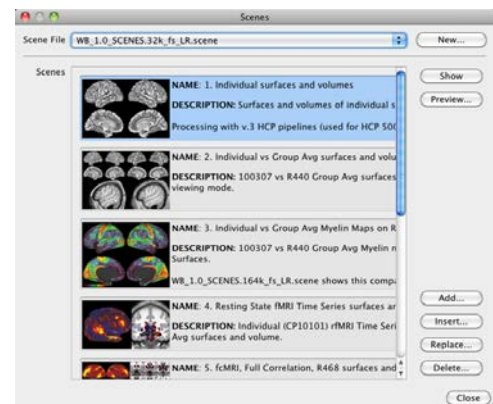


Figure 5 – The Scenes box

Scene 1: Individual surfaces and volumes

This scene is set up to show brain surfaces and volumes of an individual subject (100307) scanned in Q1 of the HCP to show the kind and quality of data generated at the single-subject level. It also provides a convenient backdrop to introduce the layout and some of the general features of Workbench.

Workbench Window Layout

The scene opens with the left hemisphere anatomical midthickness cortical surface (halfway between the pial and white matter surfaces) of the HCP subject 100307 in the **Viewing Area** of the **Workbench Window** (“Connectome Workbench 1”). Components of the Workbench Window are shown in **Figure 6**.

The Workbench Window contains five Viewing tabs: (1) Montage, (2) Volume, (3) All, (5) Cortex Left, and (6) Cortex Right.

The **Viewing Area** opens viewing **tab 1** (the **Active Tab**) showing a montage of lateral and medial views of both left and right cerebral cortex midthickness surfaces. We will browse all the tabs now and go through them in further detail below.

- Click on **Tab (2)**. This shows parasagittal, coronal and axial T1-weighted volume slices of this individual. The colored outlines demarcate the pial and white matter boundaries in this individual.
- Click on **Tab (3) All**. This view shows the midthickness surfaces of both hemispheres and all 3 volume planes (parasagittal, coronal, axial).
- Click on **Tab (5) CortexLeft**. This shows the left cerebral midthickness surface.
- Click on **Tab (6) CortexRight**. This shows the individual’s myelin map overlaid on the inflated

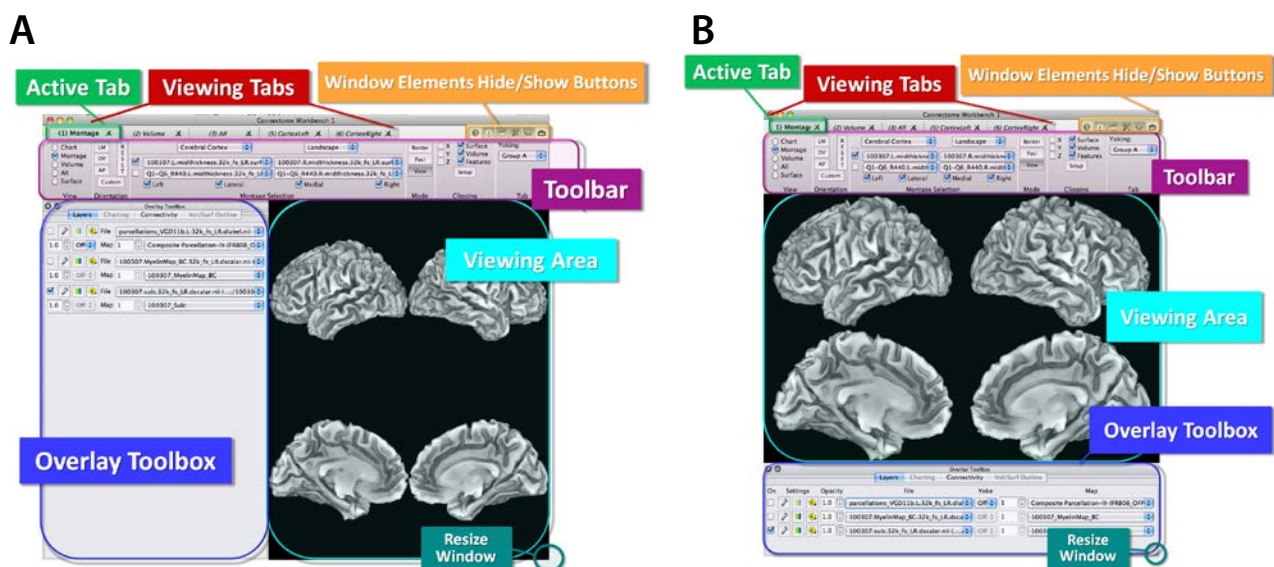


Figure 6 - The Workbench Viewing Window A) Vertical Orientation B) Horizontal Orientation

right cortical surface.

- *Click* through the tabs again and notice that the **Toolbar** changes when you switch tabs/views.

The **Overlay Toolbox** (where one sets data layers for viewing on structures) can be displayed in two locations/orientations: on the left or on the bottom of the Viewing Area, **Figure 6A 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 6B**), with the Overlay Toolbox attached to the bottom of the Viewing Area.

If you left click and drag the top of the **Overlay Toolbox**, it can be pulled off of its docking point in the **Workbench Window** to float any place on your desktop. As you do this, the images in the Viewing Area will resize to fill the Workbench Window. This is one convenient way to quickly get a larger view of the structures being displayed.

Double click on the top of the Overlay Toolbox to make it return to its docked position. The same functionality is also available for the [Features Toolbox](#) (described in the sections on Scenes [9](#) and [10](#)).

- *Click* back to **Tab (5) CortexLeft**.
- *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*.

If you accidentally *left clicked on the brain surface*, you have discovered the **Information Window**. Just *click* on Close at the bottom of the box to remove (the Information box is described in more detail below).

Toolbar

The **Toolbar** at the top of the Viewing Window contains display settings for the brain structures you are viewing.

- *Clicking* the **Orientation** buttons (right), you can display the surface in 6 standard views: **L** (Lateral), **M** (Medial), **D** (Dorsal), **V** (Ventral), **A** (Anterior), **P** (Posterior). *Click* the **Reset** button to reset to the lateral view at the original zoom setting.



The Brain Structure and Surface (**Selection**) section of the **Toolbar** lets you switch brain structures and also surface configurations.



- Click on the lower dropdown (currently showing 100307.L.**midthickness.32k_fs_LR**.surf.gii).
- The different left surface configurations available for subject 100307 are shown (flat, inflated, midthickness, pial, sphere, very inflated, white) along with the group average surfaces available for the HCP Q1-Q6 Related 440 (R440) subjects (more on the R440 data in [Scene 2: Individual vs. Group Avg surfaces](#)).
- Now, *right click* on the same lower dropdown and *press your up and down arrow keys* to browse through all the selections from both the individual and group surfaces.

Whenever you encounter any **dropdown menu** in Workbench, you can *right click* the menu and quickly browse through selections using your up and down arrow keys, or search through selections by name by typing the first letter of what you are looking for.

Surface Layers

- Click on tab **(6) CortexRight** at the top of the **Workbench Window** to switch the view to the **right hemisphere**. This tab is set to display the inflated right hemisphere surface of subject 100307 with the top layer displaying a map of myelin content.
- Rotate the surface (*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](#)).
- Move the cursor down to the **Overlay Toolbox** below the **Viewing Area**. There are 4 tabs in the **Overlay Toolbox**. 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.

In this case, a FreeSurfer generated parcellation dlabel file is listed on top (but is toggled off), the second layer is the Myelin Map file that you are viewing, and the third layer is a file representing cortical shape based on sulcal depth. These CIFTI scalars files contain scalar surface data for both left and right hemispheres (if data is available, CIFTI files can also contain surface data for cerebellar vertices and volume data for subcortical gray matter voxels).

- Click the checkbox to the left of the top layer to turn it on and show the **parcellations_VGD11b.L.32k_fs_LR.dlabel.nii** file. This is a composite cortical parcellation based on architectonic or retinotopic fMRI maps ([Van Essen et al. 2011b](#)) that covers only part of the cortical surface (that is why the myelin map “shows through” in areas).
- Now *toggle the top layer off* again to expose the myelin map fully.
- Click the **P** button for a posterior view in the **Orientation** section of the **Toolbar**, then *click* the **L** button for a lateral view.

- There is heavy myelination in much of the occipital lobe, including the orange-yellow patch around where area MT should be, near the occipito-temporal junction—lower left in lateral view.
- Click on the surface within this patch over area MT (see **Figure 7**).
- The **Information Window** will pop up.

You can move the placement of the **Information Window** by *dragging* the top of the box to the desired position on your desktop. This position is saved when you close the box and remains where you set it, even between WB sessions.

- In the Viewing Area, a white sphere has appeared at the brainordinate (i.e. surface vertex or volume voxel) you selected. Your viewing window should look like **Figure 7**.
- In the **Information Window**, information on the brainordinate that you clicked is listed. For example, the XYZ coordinates and the labels assigned to the identified vertex are shown.

Information (e.g. metric values, label names) on the vertex you selected is pulled from all currently loaded files that contain data for the structure being viewed (right hemisphere), whether or not they are currently being displayed.

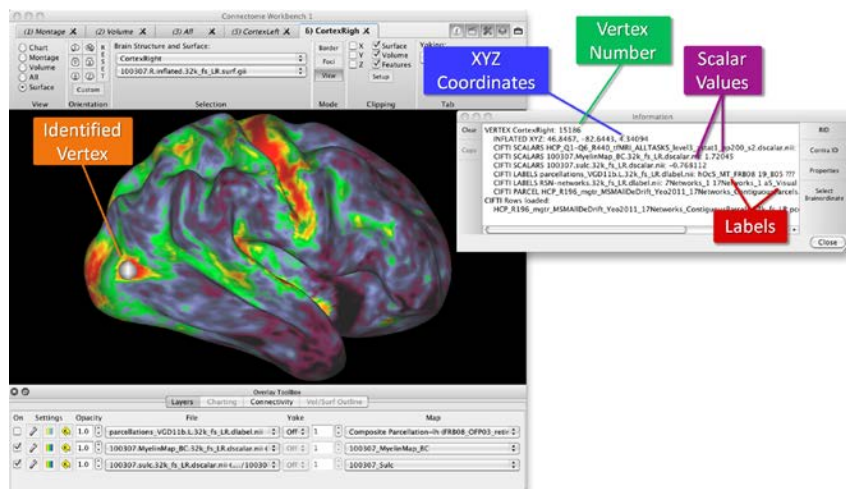



Figure 7 – Vertex Identification and the Information Window

- Toggle the top parcellation layer *back on*, and note that the vertex you identified in the myelin map is in the red patch defined by area MT in the VGD11b parcellation map.
- Click on several more places on the surface. Each time you click, information on the newly identified vertex appears at the bottom of the listed information in the Information Window.
- Notice that the last vertex you clicked appears larger than the ones you clicked earlier.
- Click the **Properties** button on the right side of the Information Window to open the **Symbol Properties** box to change the color or size of the earlier and most recently identified ID spheres.
- Change the ID symbol color to **Blue**. Click **Close**.



- Click the **Clear** button at the top left of the Information Window to clear all the information in the box, without removing the identified vertices from the surface.
- Click a few more places on the surface.
- Click the **RID** button (short for 'Remove ID') to remove all the identified nodes on the surface, without removing the ID information in the Information Window.
- Click the **Close** button at the bottom right of the Information Window. The Information box will stay closed until you identify another brainordinate. If you don't want the Information Box popping up every time you click a brainordinate, you can move it to the background (behind the Workbench Window) by clicking the **Information Window** button  in the upper right of the **Workbench Window**.

You can hide or show the **Help Window, Information Window, Scenes Window, Toolbar, Overlay Toolbox, or Features Toolbox** by clicking the buttons for each of these Window Elements, located in the upper right corner of the **Workbench Window**. As you do this for the **Toolbar, Overlay Toolbox, or Features Toolbox**, the images in the Viewing Area will resize to fill the Workbench Window.


Montage View

- Click on the first tab **(1) Montage** at the top of the **Workbench Window** to switch the view to display lateral and medial sides of both the left and the right hemisphere cortical surfaces. Here, we are looking at a Freesurfer sulc map on the midthickness surface of subject 100307. You can readily appreciate the differences in cortical folding between the hemispheres in this view.
- Click a few places on the left hemisphere lateral surface (upper left) to see highlighted brainordinates in blue (if you changed the ID symbol color to blue in the Surface Layers section above). The Information box should popup, if not, click the **Information box** button to bring it back to the foreground.
- In the right side of the **Information box** click the **Contra ID** button (short for 'Contralateral identification').
- Click again anywhere on the left hemisphere lateral surface. Now, a blue sphere will appear where you clicked and a green sphere will appear in the geographically corresponding location on the right hemisphere lateral surface (upper right).
- Click on the right hemisphere medial surface (bottom right) and note a green sphere appears on the corresponding location on the left hemisphere medial surface.
- Notice the checkboxes labeled "Left", "Lateral", "Medial" and "Right" at the top of the **Montage Selection** section of the **Toolbar** to toggle the surfaces on and off. When you do this, the surfaces resize to fill the available viewing space. You may need to resize your Workbench Window or zoom out if you don't want the montage surfaces to overlap.



- The checkboxes at the left side of **Montage Selection** allow you to toggle up to two selected surfaces on and off. *Click* the bottom checkbox to *toggle on* the group average midthickness surfaces.
- *Turn the surfaces* and see that they all move together in a yoked fashion.
- *Click RID* in the **Information Window**. *Click* the **Close** button.

Volume View

- *Click on* the second tab **(2) Volume** at the top of the **Workbench Window** to switch the view to display parasagittal, coronal, and axial (horizontal) volume views of subject 100307. In each slice, the pial surface is outlined in blue and the white matter/gray matter boundary is outlined in lime.
 - These are T1 weighted (T1w) volume slices at the slice indices indicated in the **Slice Indices/Coords** section of the **Toolbar**.
 - Notice also in the Slice Indices/Coords section, that the Move Volume Slice to Identified Location button  is gray, meaning that it is active. When this button is active, and a brainordinate is identified in this or any **Viewing Tab** that this tab is yoked to, the volume image slice plane shown will move to the plane of the identified brainordinate. Since you identified brainordinates in a yoked Viewing Tab in the previous (Montage View) section, the slice planes displayed will be at the last location you identified (likely close to the edge of the volume).
 - *Click* the vertical **ORIGIN** button at the right side of the **Slice Indices/Coords** section of the **Toolbar** to reset the slice planes.
 - *Click on* the “**P**” slice index field in **Toolbar: Slice Indices/Coords**.
 - *Scroll up and down* (or use the arrow keys) to move through the parasagittal slices. Notice that the vertical cross hair on the coronal and axial slices move as you scroll. Try this function on the coronal and axial slices.
- *Toggle* the **T1w** (first layer) *off* and the **T2w** (second layer) volume *on* in the **Overlay Toolbox Layers tab**. Now you are viewing the T2 weighted volume slices.
- *Click on* the **Vol/Surf Outline tab** at the top of the **Overlay Toolbox**.
- *Toggle off* the pial and white matter surface outlines. If you don't see these listed, *scroll down* on the right side of the tab.
- In the Viewing Area, zoom in on the slices to more clearly see the T2w data for this subject.
- *Click back* to the **Layers tab** of the **Overlay Toolbox**.
- *Toggle* the **T1w** top layer volume back *on*. *Toggle off/on* to compare with the **T2w** layer below.
 - In the T1 and T2 weighted volume data you see here, you can appreciate the exceptionally high quality and resolution we are achieving in HCP.

All (Whole Brain) View

- At the top right of the **Workbench Window**, click on tab (3) *All*.
- In the **Orientation** section of the toolbar, click the vertical **RESET** button.
- Click the vertical **ORIGIN** button at the right side of the **Slice Indices/Coords** section.
- Drag the surface up and to the right to rotate the surface and volume (whole brain) and see that surfaces of both hemispheres and all 3 volume planes (parasagittal, coronal, axial) are visible (**Figure 8**).
- Toggle the **VOLUME...** file (bottom 2 layers) off in **Overlay Toolbox:Layers**.
- In the **Toolbar: Surface Viewing** section, change the surface from Anatomical to **Inflated**.
- With your mouse cursor in the **Viewing Area**, zoom in.
- To pan, or move the surface vertically or horizontally within the Viewing Area, hold down the **shift key** while pressing the left mouse button and moving your mouse side to side or up and down.

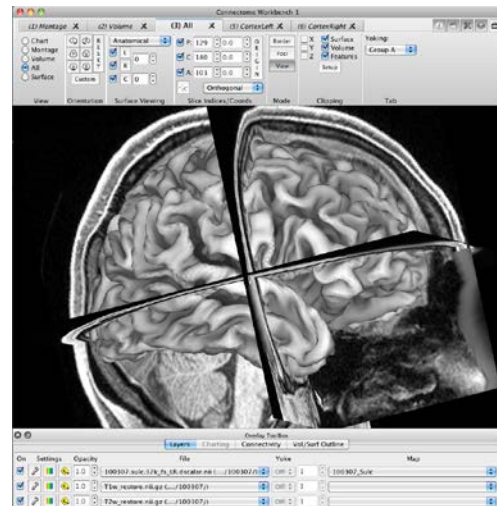



Figure 8 – All (Whole Brain) view

Scene 2: Individual vs. Group Avg surfaces and volumes



- Reopen the **Scenes Window** by clicking the **clapboard**  **button** in the upper right of the **Workbench Window**.
- Select “**Individual vs Group Avg surfaces and volumes**” and *click Show* to load the scene.

This scene compares the Individual surfaces and brain volume of HCP subject 100307 with the group averaged surfaces and volume of 440 subjects (some of whom are related, a.k.a. the R440 group) in the HCP 500 Subjects dataset (June 2014).

The scene opens with all tabs being displayed as tiled tabs: **(1) 100307 Montage** at the top left, showing both hemispheres of the individual anatomical midthickness cortical surface of subject 100307; **(2) R440 Montage** at the top right, showing the R440 group-average midthickness surface; **(3) 100307 Volume**, showing a parasagittal slice plane view of the 100307 individual T1 weighted volume; **(4) R440 Volume**, showing the R440 group-average T1w volume at the same parasagittal slice plane (117) as the individual.

As you can see, **Tile Tabs** view allows comparison between tabs within the same window. Enter and exit Tile Tabs view through the **View menu** and select **Enter/Exit Tile Tabs**, or shortcut *Cmd/Ctrl + M*. **Tile Tabs Configuration** (in the same menu) allows one to create custom configurations for viewing tabs that capitalize on the available display space.

The **Toolbar** and **Overlay Toolbox** show the controls for the **Active tab** (Tab 3). You can switch the controls to a different tab simply by clicking on the tab you want at the top of the Workbench Window—the “tile” in the Viewing Area that corresponds to that tab will be indicated by the brief appearance of a white box around it.

- Click on the  and  buttons to hide the Toolbar and Overlay Toolbox, respectively, allowing for a larger display (**Figure 9**).

You can see the marked difference between the midthickness surface of the individual 100307 and the averaged midthickness derived from 440 subjects, each of which was registered to FreeSurfer’s fsaverage atlas surface. The group-average has convolutions similar to those of the individual in regions of consistent folding and a very different pattern in regions of high inter-subject variability. Group-average surfaces are important to the HCP and other brain mapping projects as a substrate that reflects common characteristics and avoids the bias of any individual subject.

The group-average volume was generated using [FSL’s nonlinear FNIRT volume-based registration](#),

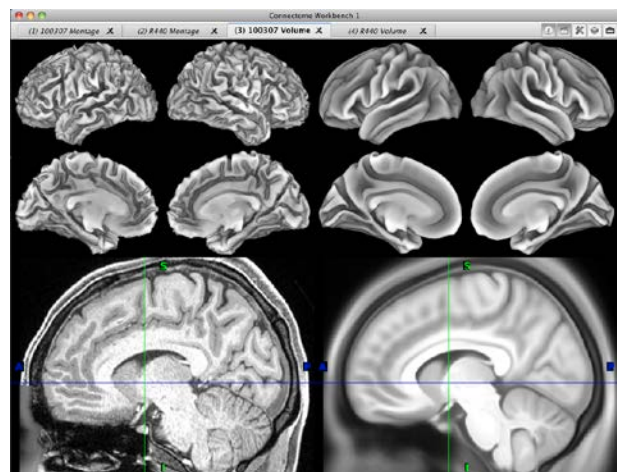


Figure 9 – Tile Tabs view comparing individual and group average surfaces and volumes


which aligns subcortical structures very accurately. For cortical gray matter, FNIRT registration does not invariably respect the topology of the cortical sheet (in contrast to the FreeSurfer surface-based registration discussed above).

Tiled tab view allows you to interact with the structures in each of the displayed tabs independently.



- *Move your mouse into the upper right quadrant, hold your left mouse button down and drag to rotate the group average surfaces.*

You can zoom, pan, and rotate any of the 3D structures separately (these functions, except rotation, also work for 2D structures, e.g. volume slices and flat surfaces).

Scene 3: Individual vs Group Avg Myelin Maps on R440 Surfaces

- In the **Scenes Window**, select “**3. Individual vs Group Avg Myelin Maps on R440 Surfaces**” and click **Show** to load the scene (if necessary, reopen the **Scenes Window** by clicking the  button). Leave the **Scenes Window** open.

This scene opens showing a map of subject 100307’s myelin content on R440 group-average surfaces overlaid on a (hidden) map of group-average myelin content averaged across the R440 subjects (layer 2).

- Click the *first layer off*. Now a map of group-average myelin content averaged across the R440 subjects (layer 2) is showing.
- Toggle *off and on* to compare with the individual myelin map (**Figure 10**). The R440 myelin map appears smoother since many 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](#)).
- Click the **Settings**  button next to the top layer. The **Overlay and Map Settings** box appears with the **Palette** tab selected (only type of Settings available for this dscalar file). Here, you can set palettes, thresholds, and view a histogram of the data.
- Click on the **Help**  button in the upper right of the **Workbench Window**. This opens the Help Window shown in [Figure 2](#).
- Scroll down on the left to:
 - ▼ Overlay Toolbox
 - ▼ Layers
 - Overlay and Map Settings
- Click on **Overlay and Map Settings** (resize the **Help Window** to see the full text). This opens Help information for the settings available in the different tabs of the Overlay and Map Settings box, including **Palette** settings. The image at the bottom of this Help entry shows the Palette tab with **Thresholds On**.

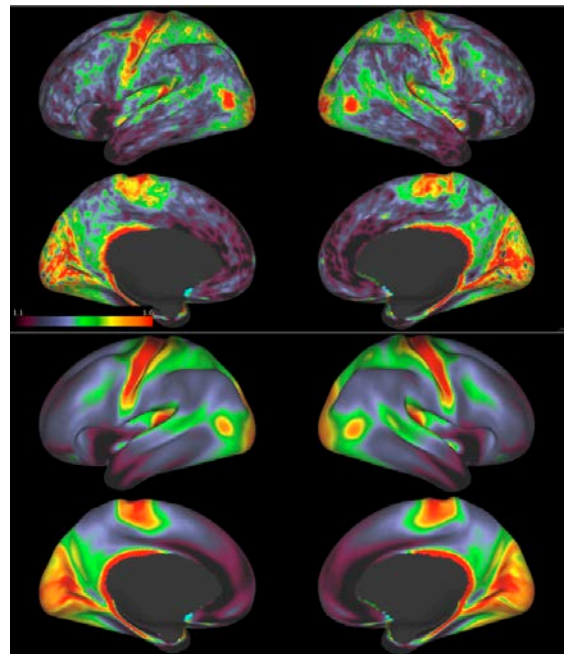



Figure 10 – Comparison of individual and R440 group average myelin maps.



- *Try changing* some of the **Palette** settings for this top layer. *Move* the **Help** and **Overlay and Map Settings** windows so that you can look at both and see the **Viewing Area** of the main **Workbench Window**.
- Maps of parcellation labels and resting state networks (RSN) mapped from other studies and thickness/corrected thickness maps are part of the tutorial dataset for comparison to the myelin maps. Use the Overlay Toolbox **Layers: File** dropdowns to display these loaded files on the surface and the **Map** pulldown to explore each file's maps.

We have provided borders and foci files in the dataset for comparison. These are loaded in this scene and can be shown using the controls in the **Features Toolbox** (open using the  button in the top right corner of the **Workbench Window**). See scenes [9](#) and [10](#) for more details.

Also, WB_1.0_SCENES.164k_fs_LR.scene (see [Exploring HCP data at 164k Vertex Resolution](#) below) shows this comparison and the others we have made in Scenes 1-3 at higher spatial resolution and the ability to browse individual maps for all R440 subjects. Note: Workbench can not load data at different mesh resolutions in the same session or scene.

Scene 4: Resting State fMRI Time Series surfaces and volumes

- In the **Scenes Window**, select “**Resting State fMRI Time Series surfaces and volumes**” and click **Show** to load the scene. Leave the **Scenes Window** open. (If necessary, reopen the **Scenes Window** by clicking the clipboard  button).

This scene opens showing the first frame of a resting state fMRI dense time series from an individual HCP pilot subject, CP10101.

On the left side of the **Viewing Area** (in **Tile Tabs** view), the CP10101 resting state time series is displayed on the R440 group averaged inflated left and right hemisphere surfaces (in All view). On the right side, the R440 group averaged volume with the same CP10101 resting state time series mapped for the subcortical volume voxels in a cortical slice and for the surface outline (of the R440 group averaged midthickness surface).

Note: Certain recent model Mac graphics cards show a blocky surface outline with small gaps—this is something we are working to fix.

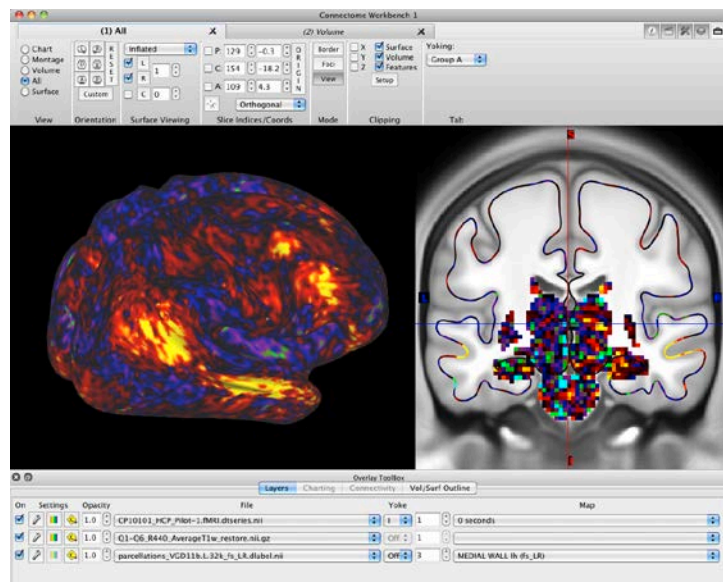


Figure 11 – BOLD Time-Series on surface and volume slice

This is the first (time 0 seconds) BOLD activation frame of the resting state time series. The default ROY-BIG palette (**Figure 11**)—shows high BOLD signal in yellow/orange/red and low BOLD signals in cyan/green/violet/blue (after regressing out the global mean signal).

- Click the *up arrow* in the frame number field, and watch the BOLD maps change for successive time frames.
- With the cursor in the frame number box, you can *hold down the up arrow button* on the keyboard (or *scroll* with your mouse scroll wheel) for an animation effect and watch the map change over time.
- Because the data in Tab 1 is yoked with the data in Tab 2, both the surface outline and the volume voxels will refresh with each new timepoint—pretty cool!
- Click on Tab **(2) Volume** to make it the **Active Tab**. Move your cursor to the “**C**” slice index field (coronal) of the **Slice Indices/Coords** section of the **Toolbar** and *scroll, toggle up and down* (or use the arrow keys) to look at the data for one timepoint as you move through the slice planes.

Charting dense timeseries

- **Select File ► New Tab** (shortcut Cmd/Ctrl + T). A new Viewing Tab will be created **(3) CortexLeft**.
- **Select View ► Tile Tabs Configuration ► All Tabs (Default)** to show the new tab in Tile Tabs.
- **Change the View** in the **Toolbar** to **Chart**. The **Charting tab** is automatically activated in the **Overlay Toolbox**.
- **Click the Select checkbox** in the **Overlay Toolbox:Charting>Loading** tab to turn on charting of the loaded CP10101 dense time series (*.dtseries) file when brainordinates are selected.
- **Click** on any yellow location on the surface in the first tiled tab. The chart will display a graph of the activation timecourse for the selected brainordinate. The graph is shown in the same color as the ID sphere shown on the surface.
- **Resize** the Workbench window to a greater width to better see the chart by *left click + dragging* the lower right corner of the window.
- **Click** again anywhere on the surface or on the colored subcortical voxels. The chart will update showing the second selected brainordinate's timecourse along with the first timecourse.
- **Click the History tab** in the **Overlay Toolbox**. Selected brainordinates with the associated plot color are listed in reverse order (most recent selected brainordinate on top). The checkboxes allow you to toggle off/on particular plots in the chart. The show last box sets how many selected brainordinates are shown in the history.
- **Click the Show Average** checkbox. The display is shown in **Figure 12**. This button computes the average of the plots currently displayed in the chart tab and shows the average in a different color on the chart. Toggle off the checkbox to turn off the average chart.

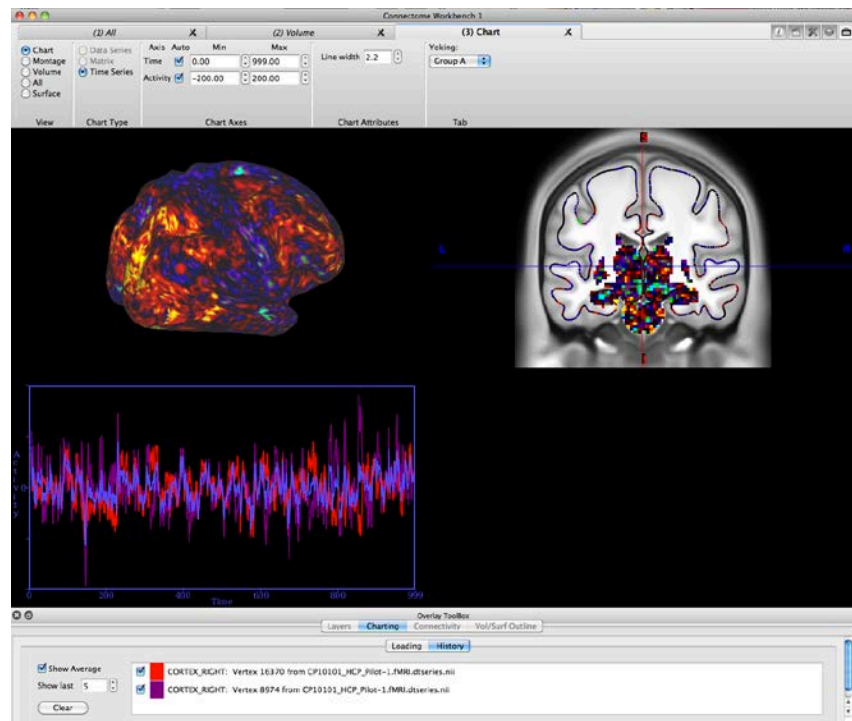


Figure 12 – Dense Time-Series display with Charting

Scene 5: fcMRI, Full Correlation, R468 surfaces and volume montage

****Note:** Scenes 5 and 6 use HCP R468 *group averaged* rfMRI data. To date (September 2014) HCP has not yet released the extensively processed resting state functional connectivity for *individuals* as we are still optimizing our pipelines for these analyses (but see <http://www.humanconnectome.org/data/> for descriptions of all HCP image and behavioral data released on [ConnectomeDB](#)).

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 surfaces and volume montage**” in the **Scenes Window** and click **Show** to load the scene. Leave the **Scenes Window** 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 (left) and coronal volume montage (right) of R468 group-average full correlation functional connectivity between the vertex on the left hemisphere surface (shown in white) and all other grayordinates, including subcortical voxels.

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.

- Click on the *left hemisphere surface* in the ventral part of the precentral gyrus, approximately the same place as the highlighted vertex in **Figure 13A** (upper left).

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

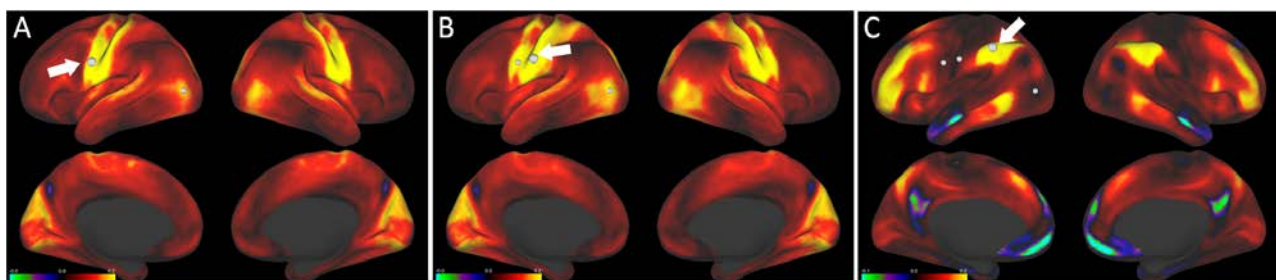


Figure 13 – Comparing group-average full correlation functional connectivity for three brain locations.

- *Click* on the location on the postcentral gyrus (shown in **Figure 13B**) 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 13C**). 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.
- *Click on a subcortical voxel* in the upper right panel of the volume montage (shown in **Figure 14A**) to view the R468 group-average full correlation and the other subcortical grayordinates shown.
- On the left side of the Workbench Window, we see the R468 full correlation connectivity between the subcortical voxel you identified in the volume slice and the surface grayordinates (**Figure 14B**).

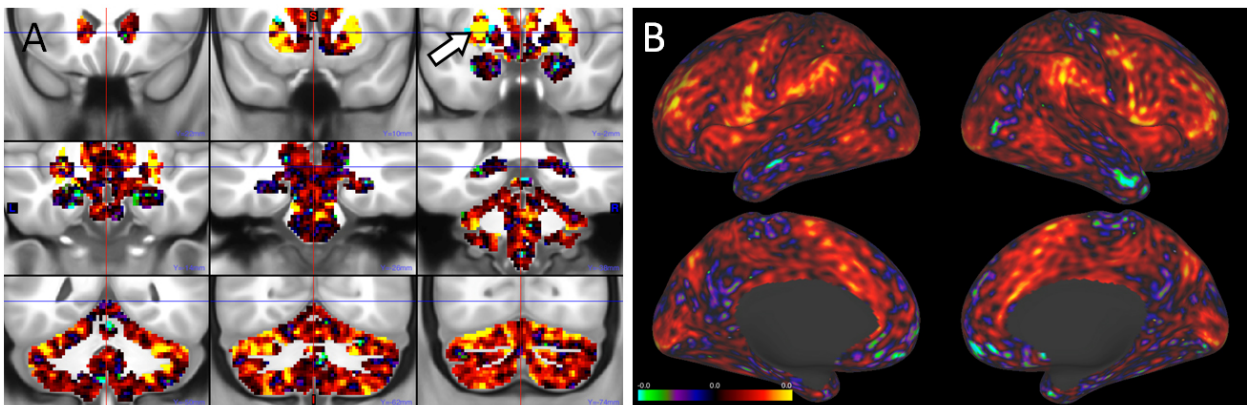


Figure 14 – Full correlation functional connectivity for a subcortical voxel seed. A) R468 group-average, subcortical volume view, B) R468 group-average, surface view.

Scene 6: fcMRI, MGT-regressed correlation, R468 surfaces and volume montage

Similar to Scene 5, 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 correlation, R468 surfaces and volume montage**” in the **Scenes Window** and *click Show* to load the scene. Leave the **Scenes Window** 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 (left) and coronal volume montage (right) 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.

- *Click on the left hemisphere surface* in the ventral part of the precentral gyrus, approximately the same place as the highlighted vertex in **Figure 15A** (upper left).

This shows R468 MGT-regressed functional connectivity associated with the face representation in motor cortex.

- *Click on the locations on the postcentral gyrus* (shown in **Figure 15B**) 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 15C**) to see a much different connectivity pattern than for either of the previous maps.

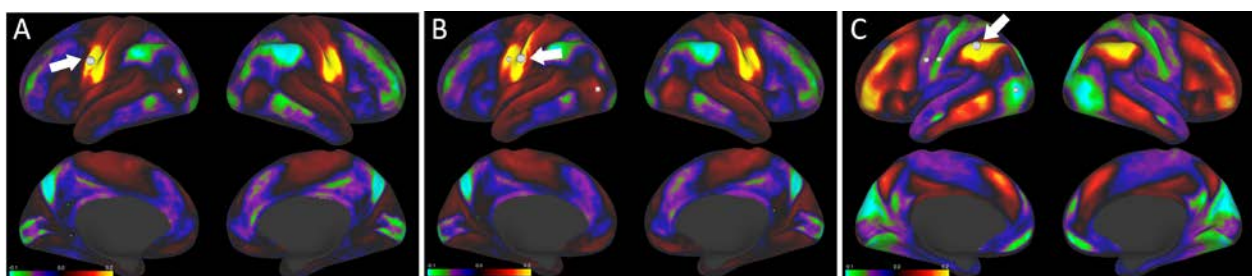


Figure 15 – Comparing R468 group-average functional connectivity correlation with mean grayordinate timecourse regression for three brain locations.

- As in Scene 5, you can *click* on the subcortical voxels in the volume slices to interactively view the MGT-regressed correlation functional connectivity maps seeded from subcortical gray matter.

Comparing functional connectivity maps: Correlation with regression of the mean gray timecourse vs. full correlation

- *Click* on the Overlay Toolbox: **Connectivity** tab.

The **On** checkboxes in the **Connectivity** tab allow one to control whether data is loaded for Connectivity files (or Fiber Orientation Files, if available) when brainordinates are identified.

- *Click* the **On** box for the ...: **HCP_Q1-Q6_R468_rfMRI_groupPCA_d4500** (Full correlation) group average Connectivity File.
- *Click back* to the **Layers** tab and click the **On** checkbox for the second layer (set to the **HCP_Q1-Q6_R468_rfMRI_groupPCA_d4500** Full correlation link).
- *Click* on a location on the surfaces. Note that the **Map** Row listed for both layers 1 and 2 update to match the newly identified vertex.
- *Toggle off/on* the first (MGT-correlation) layer to compare it with the Full correlation layer under it for the same brainordinate seed (**Figure 16** shows one such comparison).
- Repeat with other selected brainordinates.

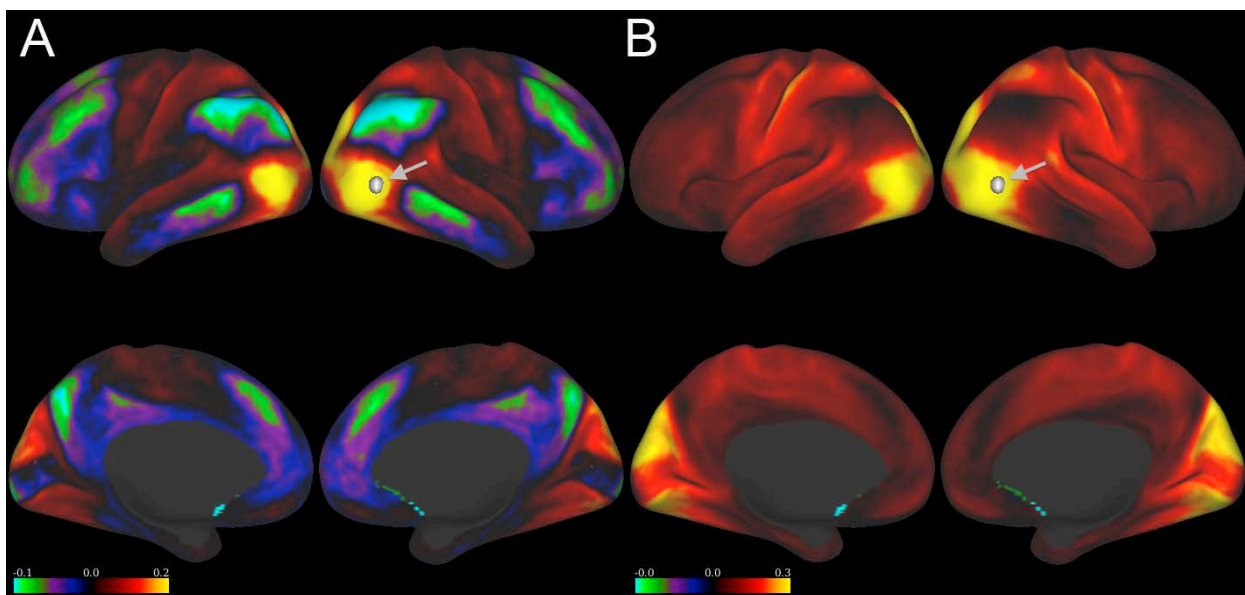


Figure 16 – Alternative representations of functional connectivity maps using an exemplar seed in the right MT+ area (gray arrows). A. Functional connectivity map after regression of the mean gray timecourse (MGT). B. Full correlation functional connectivity map for the same seed location.

- *Click* on the (2) *Volume Viewing* tab title to make it the **Active Tab**. Now the Overlay Toolbox shows the layers set for the Volume viewing tab.
- *Toggle off/on* the first (MGT-correlation) layer to compare it with the Full correlation layer under it in the volume slices.
- *Click* on a colored subcortical grayordinate voxel to seed the connectivity from that brainordinate.

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.

Scene 7: tfMRI (2BK-0BK WM), R440, on surfaces and volume montage

- Select “**tfMRI (2BK-0BK WM), R440, on surfaces and volume montage**” in the **Scenes Window** and click **Show** to load the scene. Leave the **Scenes Window** open.


****Note:** This scene shows HCP 500 Subjects *group averaged* data. Task fMRI data that has been analyzed across runs for *individual* HCP subjects at various smoothing levels on the surface and at 4mm smoothing across the volume has been released and is available from [ConnectomeDB](#).

This scene opens to show R440 group-average 2back-0back contrast of the HCP Working Memory task on the inflated R440 surfaces (left) and coronal volume montage (right) for subcortical graymatter.

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 [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 17 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:  button (see Help Menu ► Workbench Help... ► Overlay Toolbox ► Layers ► Overlay and Map Settings).

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

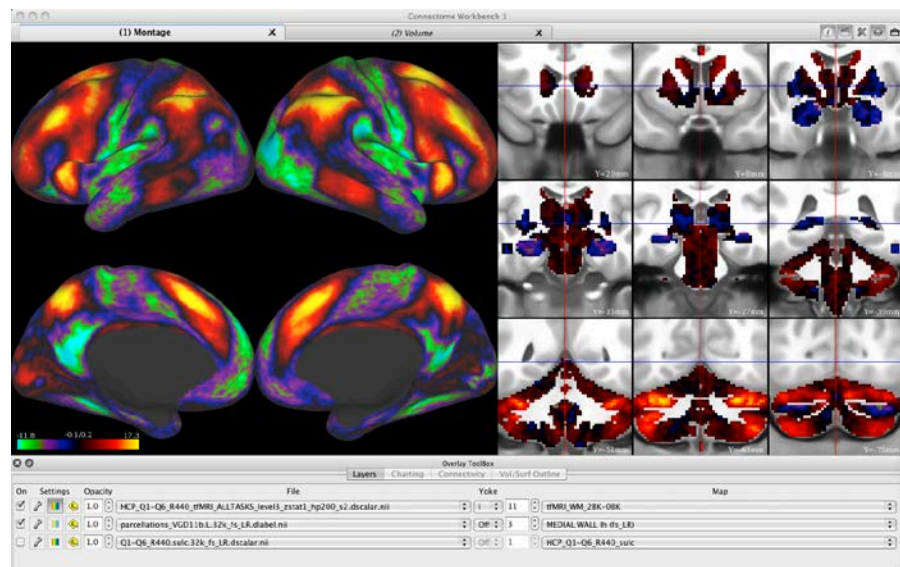


Figure 17 – R440 group-average task contrast for the 2-back vs 0-back working memory task.

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 the first layer. A listing of all the tfMRI contrasts from all of the tasks in the HCP protocol appears.
- Click on the names of other contrasts in this list to explore them as you wish.
- You may also *toggle the Frame number to the left up or down* to browse through the available contrasts .

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 8: Parcellated MGTR Connectivity, R196, RSN parcels: Surface and Matrix chart display

- Select “**Parcellated MGTR Connectivity, R196, RSN parcels: Surface and Matrix chart display**” in the **Scenes Window** and *click Show* to load the scene. Leave the **Scenes Window** open.

This scene opens to show group-average mean gray-time course-regressed connectivity between contiguous resting state network (RSN) parcels for a group of 196 related HCP subjects (R196) on cortical surfaces (left) and in a parcellated connectivity matrix chart (right).

The file HCP_R196_mgtr_MSMAIIDeDrift_Yeo2011_17Networks_ContiguousParcels.32k_fs_LR.pconn.nii being displayed as both the surface map and matrix chart was generated in `wb_command` as follows:

The ‘`cifti-parcellate`’ command was used on the R196 group average dense timeseries data to generate the average time series data within a set of resting-state network (RSN) parcels based on a study by [Yeo et al. \(2011\)](#), and further processed to subdivide each RSN into a set of topologically contiguous parcels. The ‘`cifti-correlation`’ command was used to determine the functional connectivity, based on the correlation between time-series data for each pair of parcels.

For details on `wb_command` tools, see the **Help Menu ► Workbench Help...** or the `wb_command` documentation available at: <http://humanconnectome.org/software/workbench-command.php>

The scene opens with a brainordinate already identified in the parietal cortex (**Figure 18**). Notice that the region around the selected brainordinate is colored yellow and outlined in white on the surface. The white outline indicates the selected parcel for which the connectivity with other parcels is shown. As with the previous functional connectivity scenes, the color spectrum is from yellow to cyan, with the highest correlation displayed in yellow. On the right, the selected parcel is indicated by a white outline around the matrix row showing the color-coded correlation values of that parcel with the others.

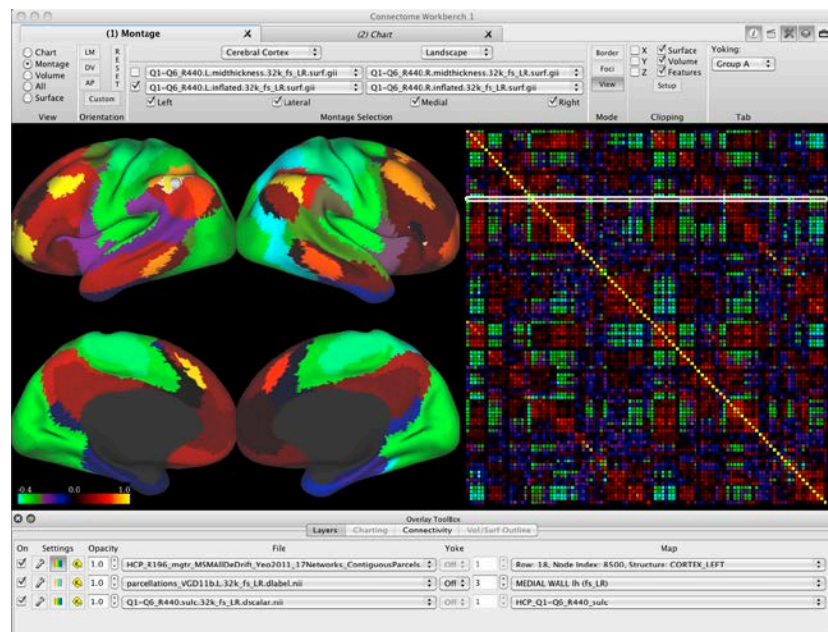




Figure 18 – R440 group-average task contrast for the 2-back vs 0-back working memory task.

- Select a brainordinate in a different parcel (the motor strip parcels surrounding the central sulcus provide a nice contrast).

- Notice that the white outlined row in the parcellated connectivity matrix has jumped to the row for the newly identified parcel.
- *Click* **RID** in in the **Information Box** to remove all the ID spheres.
- *Click* on a new row in the connectivity matrix.

Notice that the parcel selected in the matrix is outlined in white on the surface, but no ID spheres appear because an entire parcel was selected from the matrix (rather than a particular brainordinate within a parcel).

- In the **Montage** viewing tab (the currently active tab), *click* on the Settings  button next to the top layer's **On** checkbox.
- *Click* on the **Parcels** tab in the **Overlay and Map Settings** box that popped up. Here one may set the **Color Mode** of the selected parcel for a *.pconn file. **Outline** or **Fill** indicates the selected parcel by the **Color** selected below. The **Off** setting turns off the displayed indication of which parcel is selected.
- *Close* the **Overlay and Map Settings** box.
- *Click* on the **Chart** viewing tab at the top of the **Workbench Window**.
- In the **Overlay Toolbox**, the Charting and Connectivity tabs are active. In the **Charting** tab, The **Settings**  button opens the **Palette Color Mapping Editor** that controls the palette and thresholding for the displayed matrix file. The **Colorbar** button controls display of the matrix palette spectrum.
- *Click* on the **Connectivity** tab. The **On** checkbox in the Connectivity tab control whether data is loaded for the listed parcellated connectivity file as brainordinates are identified.
- *Toggle* the **On** checkbox off.
- *Click* the surface. Notice the connectivity map now does not change when you identify brainordinates.
- *Click* on a row in the parcellation connectivity matrix. Notice that the map does change because, rather than brainordinates, you are selecting parcels from the matrix for connectivity display.

Scene 9: Parcellation Borders displayed with parcellation labels on R440 surfaces

- Select Scene “**Parcellation Borders displayed with parcellation labels on R440 surfaces**” in the **Scenes Window** and click **Show** to load the scene.

This scene displays surface borders (contours demarcating boundaries between regions) and shows features of the Workbench **Features Toolbox**. The Features Toolbox currently enables you to display loaded borders, foci, and labels. With the changes to the border file format described in the [Introduction](#), we also show you the steps needed to convert older border files into the new format in the `wb_view` GUI.

The scene opens with a montage of R440 inflated cortex surfaces showing colored cortical areas depicting an architectonic and retinotopic parcellation map published by Van Essen, Glasser, Dierker *et al.* ([2011b](#)) (VGD11b) over the R440 sulc map.

The **Features Toolbox** is displayed on the right side of the Workbench Window and borders outlining the VGD11b parcels are set to display.

- Notice the borders that are being displayed match the parcellation map that is displayed as the top layer in the **Overlay Toolbox**.
- *Toggle the **Display Borders** checkbox off in the **Features Toolbox**.* This will turn off all the borders at once.
- *Toggle off the first layer and toggle on the second layer, the R440 group-average myelin map.*
- Rotate the surfaces (*press the left mouse button and drag your mouse*).
- *Toggle the **Display Borders** checkbox on and off in the **Features Toolbox**.* Notice how many of these outlines roughly line up with changes in myelin content (changes in the map color, recall myelin content is heaviest in the areas displayed in warmer colors) that suggest borders between cortical areas (**Figure 19**). Leave the Borders *on*.

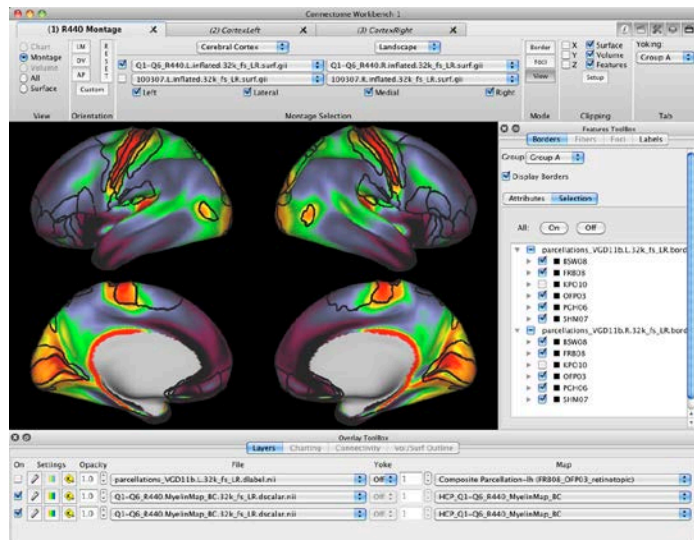


Figure 19 – Surface montage, showing group-average myelin map and parcellation borders.

As you can see, the borders are useful to mark just the edges of cortical areas when you are viewing various types of data on the cortical surface.

Notice in the **Features Toolbox** that we are currently in the **Borders tab**. We'll discuss the **Labels tab** later in this scene and the **Foci tab** in the next section. The **Fiber tab** is currently under development for use with diffusion MRI data and is greyed out unless WB-compatible fiber or trajectory files are loaded (not yet released).

In **Borders**, under the top level of tabs, there are two tabs for **Attributes** and **Selection**. We are currently in the **Selection tab**, which allows you to choose which of the loaded borders you want to display.

Borders are listed in a file tree grouped by hemisphere and border class. In this case, borders are classed by an abbreviation (e.g. BSW08) for the article in which the borders were defined.

- Note that the border KPO10 is currently toggled off in both the left hemisphere and right hemisphere lists. This was done to highlight area MT in the lateral side of the occipital lobe.
- *Click the checkbox* next to border **KPO10** in the left hemisphere list. *Toggle it on and off. Try this again* with KPO10 in the right hemisphere or some of the other sets of borders in the list.
- *Click on the grey triangle* ► next to border KPO10. This reveals the borders that make up this border class and allows you to turn them off and on one by one. *Try toggling* a few of these borders *off and on*.
- Above this border list there are two buttons for turning **All** the listed borders **Off** or **On**. *Click these buttons* and note that all the borders listed show checkboxes that match the Off or On status.
- Now *click* the **Attributes tab** above. The **Borders:Attributes tab** contains controls for adjusting the coloring, size, and symbol type for the borders displayed.
- *Toggle* the **contralateral checkbox**. This displays the corresponding borders from the contralateral hemisphere so that you can compare the differences between the cortical areas between hemispheres.
- *Click* the **contralateral checkbox** *again* to turn it off.
- *Click off* the **Display borders** checkbox.
- *Toggle* the top **parcellations...** layer *on again* in the **Overlay Toolbox**.

In Workbench, label files assign each surface vertex a specific 'categorical' name and an associated color (or paint). When labels are displayed, regions appear painted on the brain surface. The parcellation map in the top layer is made up of many of these labels that describe and color cortical areas.

- *Click* the **Labels tab** at the top right of the **Features Toolbox** and *click* on the **Selection tab**.

Here you see that the **Labels:Selection tab** has the same structure as we saw for Borders.

- *Click on the grey triangle* ► next to **Composite Parcellation-lh**. As we saw for borders, this reveals the labels that make up this label group and allows you to turn them off and on one by one.

- At the bottom of this long list is the red label **hOc5_MT** for area MT in the occipital lobe. Try *tooggling* this label *off and on* and notice how this label roughly lines up with an orange/yellow patch on the myelin map of the R440 subjects, indicating high myelin content.
- Scroll up to the top of the **Features Toolbox**. Click the **Attributes tab**.
- Move your mouse over the **Draw as: dropdown** and click and select **Outline Color** or **Outline Label Color**. Look at area MT again and see how you can now directly compare the outline of the label for MT and the myelin map in much the same way you did when we were looking at borders.

Converting old Border files to the new Format

Previously, border files could contain borders drawn on single or multiple brain surface structures. New to Workbench 1.0 is an improved border file format that requires borders in one file to be associated with a single structure. Old border files can still be read by `wb_view` and `wb_command` as long as the structures on which they were drawn are also loaded in the same session.

We recommend that users with border files created in previous versions of Workbench update their border files to the new format so that they may be edited in `wb_view`.

The border files that are provided in this dataset are in the old format drawn on single left and right hemisphere structures, respectively, so that we may demonstrate the conversion.

When the `parcellations_VGD11b.L.32k_fs_LR.border` and `parcellations_VGD11b.R.32k_fs_LR.border` files were loaded in this scene with their respective surface structures, `wb_view` automatically converted them to the new format for display/editing, but they need to be saved to make the changes permanent.

- To save the border files in the new format, click on **File ► Save/Manage Files...**
- Notice that the Border files listed have **YES** in the **Modified** column indicating that they have been changed since they were loaded.

When files are modified in a `wb_view` session, the **Save** checkbox is automatically checked to make it easy to save your changes. If you do not want to save your changes to particular files, you may uncheck these boxes before saving.

- Leave the **Save** checkboxes checked beside the Border files listed.
- Click the **Save Checked Files** button to complete the writing of the new border files (overwritten with the same name as the old format files).
- When this scene is reopened, the new format files will be read and the files will no longer be labeled as **Modified** in **Save/Manage Files**.

If you have old border files on multiple brain structures that you want to convert, you must use the **Split Multi-Structure Border Files** option in the **Data Menu** to separate the borders by structure before editing or saving borders in the new format (border editing and saving is blocked for multi-structure border files). Scenes created with old border files will also open, but if borders are edited or if the file name is changed, the scene will need to be replaced (or a new scene created) to reflect the changes, including updating the border file format.



For information on using tools in wb_view to draw or edit existing borders, see the **Help** sections under **▼Toolbar▼Mode▼Border Drawing**.

Scene 10: Foci displayed on R440 surfaces

- *Double click* on “**Foci displayed on R440 surfaces**” in the **Scenes Window**, to load the scene.

This scene displays identified foci (identified spatial coordinates of interest) that were generated by [Glasser and Van Essen \(2011\)](#) using the centers of gravity of the volumetrically analyzed probabilistic cytoarchitectonic areas delineated by the Zilles/Amunts group. Hence, the foci are given "Class Name" = ESM05 to reflect the [Eickhoff et al. \(2005\)](#) citation. These areas were used as an important comparison to the myelin maps in the Glasser and Van Essen paper.

The scene opens with the inflated group-average left hemisphere surface showing the identified foci. As with Borders and Labels, the **Foci tab** of the **Features Toolbox** has **Attributes** and **Selection** subtabs. Here, we begin in the **Attributes** tab.

- *Click* on the **Attributes** subtab in the Features Toolbox.
- *Toggle* the **Display Foci** checkbox to globally turn foci off and on.
- *Toggle* the **Contralateral** checkbox to display foci from the right hemisphere in their corresponding locations on the left hemisphere to compare foci positions between hemispheres. *Toggle* it back off.
- *Toggle* the **Paste to Surface** checkbox.

This option moves displayed foci to the nearest location on the surface being displayed. This is useful because identified foci are often slightly above or below the surface because of differences in anatomy between subjects, this option brings the foci back to the surface you are displaying them on so that you can see all of them clearly.

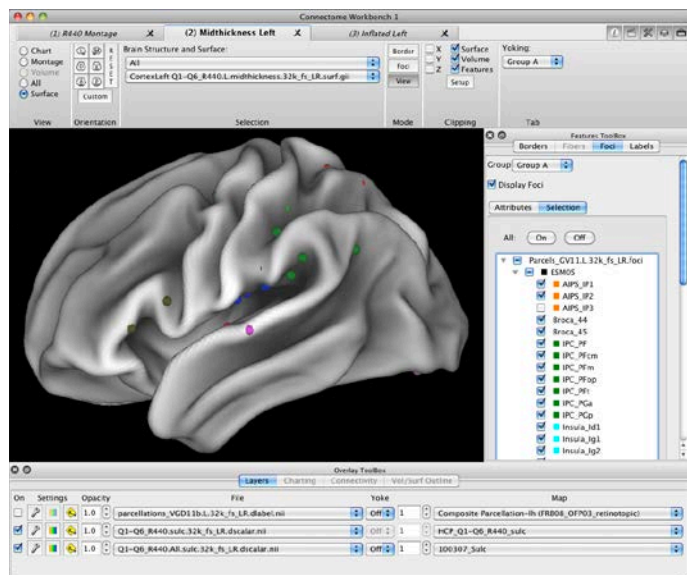


Figure 20 – Left midthickness group-average surface showing ESM05 foci. Focus AIPS_IP3 is deselected and therefore not displayed.

- *Click* on **Tab 2** at the top of the **Workbench Window**, showing the left group average midthickness surface (**Figure 20**).
- *Toggle* the **Paste to Surface** checkbox off and on again. This feature is especially useful when looking at foci in the sulci of anatomical surfaces.
- *Click on* the **Coloring dropdown**. You can set colors of foci based on individual name (the default) or by class (here all the foci have the same class, ESM05, which is set to black).

In order to *edit* individual foci name colors or class colors in Workbench, you must use the Edit Foci function described in **Help ▼ Toolbar ▼ Mode ▼ Foci Creation ▼ Foci Editing**.

- *Move your mouse over and scroll through or select the options in the **Draw As** and **Symbol Size** dropdowns.*
- *Click on the **Foci:Selection tab**, which allows you to choose which of the loaded foci you want to display.*
- *Try toggling a few of these foci *off and on*.*
- *Above this focus list there are two buttons for turning **All** the listed foci **Off** or **On**. *Click these buttons* and note that all the foci listed show checkboxes that match the Off or On status.*
- *Click on **Tab 1** at the top of the **Workbench Window**.*

This Montage view is displaying the Zilles/Amunts derived foci on both hemispheres.

- *Click the **On** checkbox for the top layer to show the combined architectonic and retinotopic parcellation labels that we explored in previous scenes. A subset of the identified foci represent the center of gravity of the parcels shown.*

The **Group setting** at the top of the **Features Toolbox** for **Borders**, **Foci**, or **Labels** allows you to set a display group for each Viewing Tab so that unique features settings (e.g. borders display on, foci displayed as squares, etc.) can be applied specifically to particular groups of Workbench Window display tabs and not others.

For information on using tools in `wb_view` to create or edit existing foci, see the **Help** sections under **▼ Toolbar ▼ Mode ▼ Foci Creation**.

Exploring HCP data at 164k Vertex Resolution

The following scenes explore the data provided on a higher resolution surface mesh. The higher resolution is useful for deciphering fine details of anatomical features such as curvature, cortical thickness and myelin maps. The scenes are setup very similarly to the first three scenes we explored on the 32k mesh to make it easy to compare the 164k data provided in the dataset.

Note: Since many of the files in these scenes are higher resolution, and several times larger than the 32k files, it will take a bit longer to load these scenes.

Scenes 1 and 2: Individual surfaces and volumes (164k) and Individual vs. Group Avg surfaces and volumes (164k)

- In the **Scenes Window**, *change* the **Scene File** dropdown to **WB_1.0_SCENES.164k_fs_LR.scene**.
- *Double click* on the scene names to load them. Roughly follow the instructions for Scenes [1](#) or [2](#) at 32k or explore the data loaded on your own.

Scene 3: Individual vs Group Avg Myelin Maps on R440 Surfaces (164k)

Scene 3 at 164k is setup similarly to Scene [3](#) at 32k, but we want to show another set of data files here that display maps from all R440 subjects. Because these files contain many maps at 164k, this scene takes a particularly longer time to load.

- *Double click* on “Individual vs Group Avg Myelin Maps on R440 Surfaces (164k)” to load the scene.

The scene opens with the myelin map for subject 100307 displayed on inflated R440 surfaces.

- *Click* on the **File** pull down for the top layer. *Select* the **Q1-Q6_R440.All.MyelinMap_BC.164k_fs_LR.dscalar.nii** file. *Note* that the myelin map displayed did not change.
- *Click* on the **Map** selection pulldown for the top layer. A long list of maps by subject number will appear with a checkbox next to the first subject listed, 100307 (**Figure 21**).

This file contains individual myelin maps for each of the R440 group that can be explored to see the individual differences in myelin content between subjects.

- *Select* subject 101915 near the top of the list. Notice that this subject displays high myelination in a well-defined, nearly circular area around MT+ in both hemispheres (**Figure 22**, left).

- Click the **Map** selection pulldown again and *select* subject 111413, near the middle of the list. Notice that this subject displays much less and diffuse myelination around MT+ in both hemispheres (**Figure 22**, center).
- Again, *click* the **Map** selection pulldown and *select* subject 131924, further down in the middle of the list. Notice that this subject displays diffuse myelination around MT+ in the left hemisphere, but high myelination in a well-defined area around MT+ in the right hemisphere (**Figure 22**, right).
- Click in the Map number box to the left of the Map selection pulldown to activate the box (should be outlined in a blue glow).

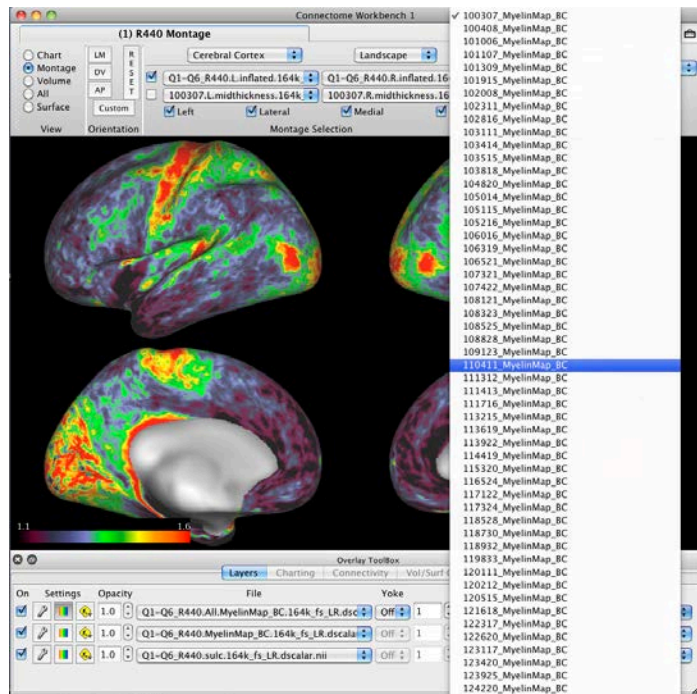


Figure 21 – Q1-Q6_R440.All.MyelinMap Map List.

- Use the mouse scroll wheel or arrow keys to *toggle quickly* through the myelin maps.
- Click on the *File* pulldown for the top layer and note the “All” files for corrected thickness, curvature, sulc, and thickness.
- Explore these data loaded and compare with the group average maps as you wish.

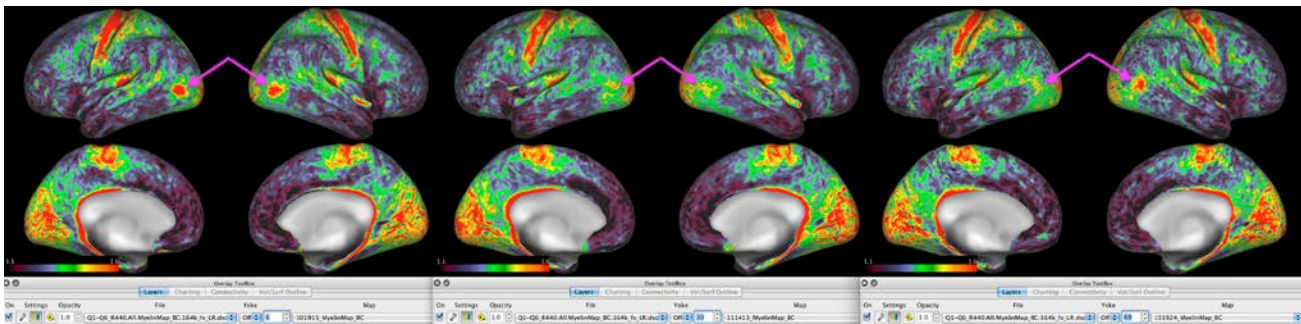


Figure 22 – Comparing individual Myelin maps for R440 subjects.

Thanks for sticking with the wb_view tutorial to the end! Check out the many topics in the **Help** menu as you explore other features of the platform. Remember to [join](#) and send bug reports or suggestions to the HCP-users list by emailing hcp-users@humanconnectome.org.

Enjoy using Connectome Workbench 1.0 !!

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** Further details on the data acquisition and analysis methods are available in eight papers 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](#), [Sotiropoulos 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.