



## Connectome Workbench Beta v0.83 Tutorial & User Guide

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*21 August 2013*

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## Introduction

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**\*\*This Tutorial and User Guide is compatible with Workbench Beta v0.83\*\***

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.

To get Workbench, users can download Mac, Windows, and Linux versions from the HCP website (see [Downloading Connectome Workbench beta v0.83](#) 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 or as movies
- Options to display multiple surfaces and volumes as tabs, windows, or as a “montage” within a single window
- Compatibility with [NIFTI](#), [GIFTI](#), and the new ‘[CIFTI](#)’ (surface + volume) data formats.
- Interactive viewing of structural connectivity and probabilistic fiber trajectories (coming soon!)

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. ‘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 it easier to begin with **Chapter 2**, which covers Workbench features more methodically and systematically. Another option for getting a quick look at HCP data released in Q1, while learning Workbench basics, is to follow the **Tutorial for Q1 Unrelated 20 Dataset (v1b)** included as an [Appendix](#) to this document.

[Chapter 1](#) (Exploring HCP Data in Workbench) is a tutorial designed to get you exploring the different types of data offered by HCP “get your feet wet” tutorial demonstrating major features of the user interface, including interactive viewing of functional connectivity maps. It uses extensively processed individual and group average data from the **HCP Quarter 1 (Q1) data release (March 2013)** (see ReleaseNotes\_HCP\_Q1\_GroupAvgUnrelated20\_v1b.txt included in the tutorial distribution). *Estimated time to complete: **40-60 minutes**.*

**Chapter 2** (Detailed Guide to the Workbench User Interface) is a more comprehensive feature-by-feature tour of major Workbench visualization tools and is a good starting point for capitalizing on the full range of Workbench capabilities. It is complemented by the [Workbench Help Guide](#), an online resource on the publically accessible HCP wiki.

*Estimated time to complete: approximately 1 hour*

**Chapter 3** (Using Workbench Tools) describes how to draw/edit borders and foci, display average connectivity within a border, and create Regions of Interest (ROIs).

**Chapter 4** (Using `wb_import` and `wb_command`) introduces some basic functions of these Workbench command line programs, including converting files to workbench format and creating spec files.

**Appendix** (Tutorial for Q1 Unrelated 20 Dataset (v1b)) introduces you to very basic functions in Workbench, while highlighting structural, resting state and task data made available as part of the HCP Q1 data release (see <http://humanconnectome.org/data/> for more information on HCP data releases).

*Estimated time to complete: 30 minutes*

**Future chapters** will describe additional tools in Workbench, including visualizing diffusion imaging data (fiber orientations, probabilistic fiber trajectories, and structural connectivity).

Connectome Workbench is under active development, with many new capabilities to be added in 2013. 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](mailto:hcp-users@humanconnectome.org).

## ConnectomeDB and Tutorial Data

In addition to handling locally stored data files (like those distributed with this Tutorial and User Guide), Workbench can access data files stored in [ConnectomeDB](#), the web-accessible database that houses all HCP data modalities available for download (MRI, MEG, and behavioral data). The interactivity between Workbench and ConnectomeDB will be increasingly critical, given the complexity of the datasets and the large file size for some data types (e.g., '[dense connectome](#)' files currently exceed 30 GB per subject). To circumvent downloading of these large files, connectivity maps for user-selected subjects and regions of interest can be extracted on the fly from ConnectomeDB and transmitted within seconds to Workbench through an internet connection.

For this tutorial, using Workbench Beta v0.83, the Workbench interaction with ConnectomeDB involves a single step: opening a dense connectome file from ConnectomeDB through the Open Location option in the File menu (see [Viewing Functional Connectivity](#) below).

- This tutorial uses dense functional connectome data that are for demonstration purposes only. (This restriction is necessary because the advanced methods used to analyze the connectivity

data have not been published or fully vetted). This restriction does not apply to the group-average task fMRI, myelin maps, and other surface and volume data that are part of the tutorial dataset.

- Unprocessed and minimally processed HCP image data and behavioral data is available for download and can be used freely by anyone who registers and accepts the Open Access Data Use Agreement at <http://humanconnectome.org/data/>.

## Downloading Connectome Workbench beta v0.83

*\*\* Skip this section if you have already downloaded and installed **Workbench v0.83** (released August 2013). You are ready to get started!*

Mac, Windows, and Linux versions of Connectome Workbench beta v0.83 are available for download as zipped file archives from the [Workbench download page](#) on the HCP website.

### 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 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.

## 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 login 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 splash page will open.
  - If you have not yet signed the HCP Data Use Terms, the page will show a button on the right side containing the words “Please sign Data Use Terms to access”. Click the button.
    - The Open Access Data Use Terms will popup.
    - Click each checkbox to agree to each Data Use Term. When you have accepted each term, the checkbox on the bottom left will be checked.
    - Click the Complete Registration button.

- Having signed the HCP Data Use Terms, now scroll down the page to the **Connectome Workbench Data** section of the ConnectomeDB splash page and *click* the **Download Tutorial Dataset** button.
  - If you have the Aspera Connect plugin installed, the download of the tutorial data 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\_Beta0.83** zipped archive you just downloaded.

The **HCP\_WB\_Tutorial\_Beta0.83** 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!

## 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\_WB\_Tutorial\_Beta0.83** directory in a terminal window, then *enter* workbench and *press Return*.

## Chapter 1: Exploring HCP Data in Workbench

### Workbench Orientation

This section provides a quick orientation to Workbench (and its associated file types) while exploring individual and group average data from the HCP that is currently available for download.

### Workbench Splash Screen

When you launch Workbench, a [splash screen](#) opens (**Figure 1.1**), 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.

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.

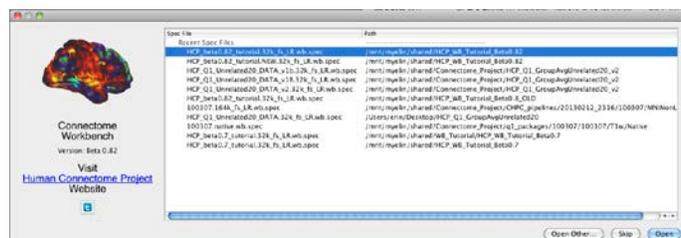


Figure 1.1 – Connectome Workbench Splash Screen

### Opening a Spec File and Loading Scenes

- In the Workbench [Menu bar](#), located at the top of your screen (Mac) or top of the blank Workbench window that just opened (Linux/PC), *select* **File ► Open File...** (shortcut for Mac: command + O, Linux/PC: control + O) to display the **Open File Dialog**.
- In the **Open File Dialog** (**Figure 1.2**), Navigate to the folder or directory that contains the data, the **HCP\_WB\_Tutorial\_Beta0.83** folder.

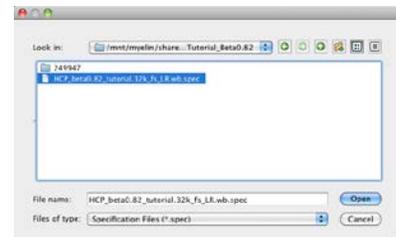


Figure 1.2 - The Open File Dialog

- The default file type filter is Specification Files (\*.spec).
  - Note: if you started from a terminal window in the directory containing the tutorial dataset, the tutorial spec file would already be available.
- *Select* the desired file: **HCP\_beta0.83\_tutorial.32k\_fs\_LR.wb.spec** and *click* the **Open** button. The **Open Spec File Dialog** (**Figure 1.3**) will appear, showing the 43 files in this particular spec file, grouped into 8 types: Border, Dense Data Series, Foci, Label, Metric, Scene, Surface, and Volume.

- At the very top of the Open Spec File Dialog, **click Border** next to View File Types: The list of files below will be filtered to only show Border files. The View Structures: row similarly filters the files by Structure.

*Note:* The data in this file includes surface and volume files from individual participant 249947 and from the population-average of data obtained from 20 healthy unrelated individuals in the HCP Q1 dataset.

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

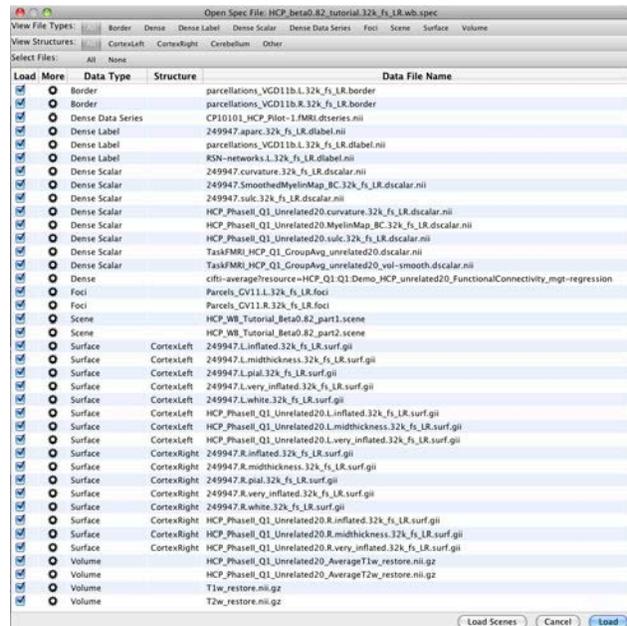


Figure 1.3 - The Open Spec File Dialog

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 1.4)** will appear with **HCP\_WB\_Tutorial\_Beta0.83\_part1.scene** file displayed. In the Scenes field our first scene: “**1. Individual surfaces and volumes**” should be highlighted, indicating that it is selected.
- Click Show** to load the scene (may take several seconds).
- Click Close** to close the Scenes box.

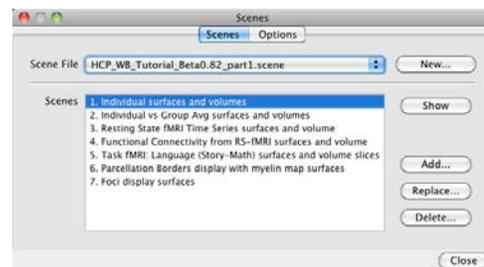


Figure 1.4 – The Scenes box

## Scene 1: Individual surfaces and volumes

This scene is set up to show brain surfaces and volumes of an individual subject (subject 249947) scanned as part of [Phase 2](#) (Final production phase) of the HCP. We are starting with an individual to give you a sense of the kind and quality of data generated at the single-subject level. It also provides a convenient backdrop to introduce you to the layout and some of the general features of Workbench.

### Workbench Window Layout

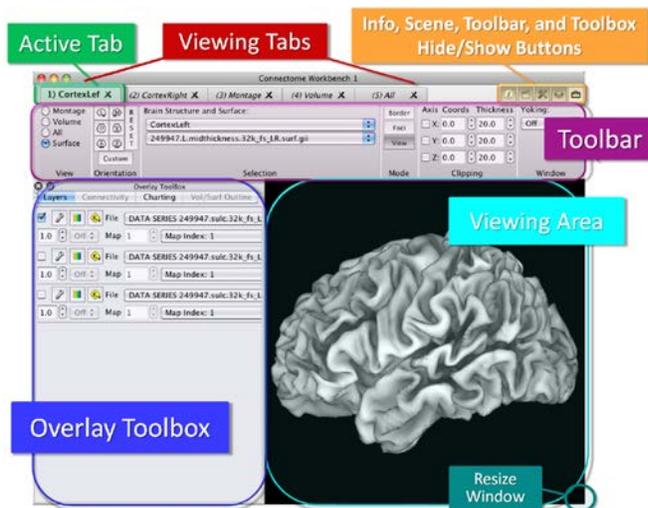
The scene opens with the left hemisphere anatomical midthickness cortical surface (halfway between the pial and white matter surfaces) of the HCP Phase 2 subject 249947 in the [Viewing Area](#) of the [Workbench Window](#) (“Connectome Workbench 1”). Components of the Workbench Window are shown in [Figure 1.5](#).

The Workbench Window contains five [Viewing tabs](#): (1) Cortex Left, (2) Cortex Right, (3) Montage, (4) Volume, and (5) All. (You may not see the 5<sup>th</sup> until the window is enlarged.)

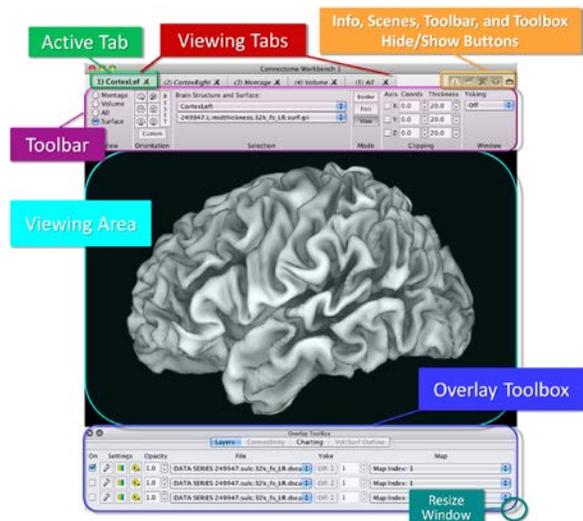
The [Viewing Area](#) opens viewing **tab 1** (the [Active Tab](#)) showing the left cerebral cortex surface. We will browse all the tabs now and go through them in further detail below.

- Click on **Tab (2)**, which shows a myelin map overlaid on the inflated right cortical surface.
- Click on **Tab (3)**. This shows a montage of lateral and medial views of both left and right hemispheres of individual 249947.
- Click on **Tab (4)**. This shows parasagittal, coronal and axial T1-weighted volume slices of this individual. The colored outlines demarcate the pial, midthickness, and white matter boundaries in this individual.

A



B



**Figure 1.5 - The Workbench Viewing Window A) Vertical Orientation B) Horizontal Orientation**

- Click on **Tab (5) All**. This view shows the midthickness surfaces of both hemispheres and all 3 volume planes (parasagittal, coronal, axial).
- 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 1.5A 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 1.5B**), 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 their docking points 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 6 and 7).

- Click back to **Tab (1) CortexLeft**.
- Press the left mouse button and drag your mouse anywhere in the **Viewing Area** to rotate the surface.
- 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 box](#). 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 249947.L.**midthickness.32k\_fs\_LR**.surf.gii).
- The different surface configurations available for subject 249947 are shown (midthickness, inflated, very inflated, pial, white) along with the group average surfaces (midthickness, inflated, very inflated) available for the HCP Q1 Unrelated 20 subjects (more on the Q1 Unrelated 20 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 the second tab **(2) 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 249947 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 5 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.

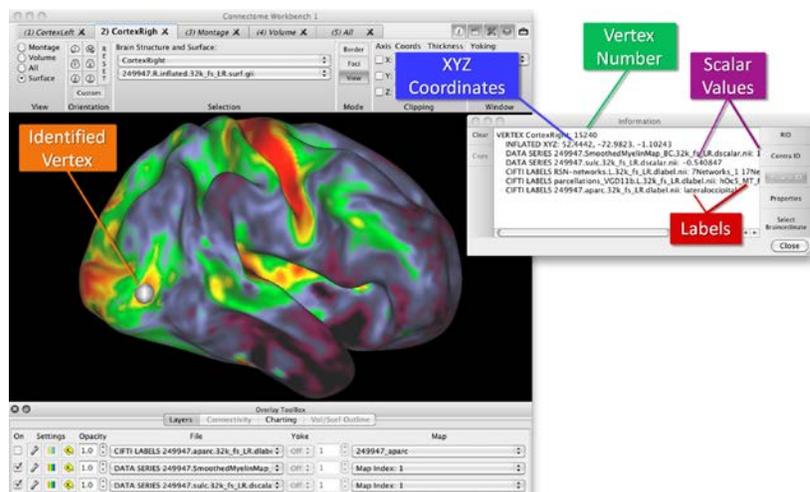
In this case, a FreeSurfer generated [parcellation](#) LABEL file is listed on top (but is toggled off), the second layer is the CIFTI SCALARS ‘myelin’ file that you are viewing, and the third layer is a CIFTI SCALARS file representing cortical shape based on sulcal depth. These CIFTI scalars files contain 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 FreeSurfer defined parcellation layer: **CIFTI LABELS 249947.aparc.32k\_fs\_LR.dlabel.nii**. Now change this top layer by *clicking the label file field and clicking the CIFTI LABELS 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](#)).
- Now *toggle the top layer off* again to expose the myelin map.

- 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 1.6**).
- The **Information box** will pop up.

You can move the placement of the **Information box** 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 1.6**.
- In the **Information box**, information on the brainordinate that you clicked is listed. For example, the XYZ coordinates and the labels assigned to the identified vertex are shown.



**Figure 1.6 – Vertex Identification and the Info Box**

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.

- *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 box**.
- 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 box 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 box 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 and all the ID information in the **Information box**.
- Click the **Close button** at the bottom right of the **Information box**. 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 box icon**  in the upper right of the Workbench Window.

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

## Montage View

- Click on the third tab **(3) 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 sulcal depth map on the midthickness surface of subject 249947. 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 icon** 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" and "Right" at the top of the **Montage Selection** section of the Toolbar. You can use these to toggle the left or right 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 very inflated surfaces.
- *Turn the surfaces* and see that they all move together in a yoked fashion.
- *Click RID* in the **Information box**. *Click* the **Close** button.

## Volume View

- *Click on* the fourth tab **(4) Volume** at the top of the **Workbench Window** to switch the view to display parasagittal, coronal, and axial (horizontal) volume views of subject 249947. In each slice, the pial surface is outlined in blue and the white matter/gray matter boundary is outlined in fuchsia (left hemisphere) and yellow (right hemisphere).
  - These are T1 weighted (T1w) volume slices at the slice indices indicated in the **Slice Indices/Coords** section of the **Toolbar**.
  - *Click* the vertical **ORIGIN button** at the right side of the **Slice Indices/Coords** section of the **Toolbar** to reset the slice planes (when you clicked on the surface in the previous section the volume planes moved to the planes containing the vertex you clicked).
  - *Click on* the “**P**” slice index field in **Toolbar: Slice Indices/Coords**.
  - *Scroll up and down* to move through the parasagittal slices. 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 it.
  - 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 Phase 2.

## All (Whole Brain) View

- At the top right of the **Workbench Window**, *click on* tab **(5) 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 left 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 1.7**).
- 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 out.
- 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.

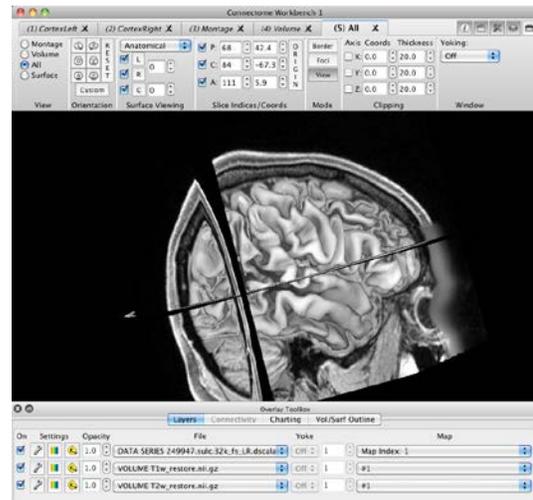


Figure 1.7 – All (Whole Brain) view

## Scene 2: Individual vs. Group Avg surfaces and volumes

- Reopen the **Scenes Dialog** by clicking the **clipboard**  **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 Q1 subject 249947 with the group averaged surfaces and volume of 20 unrelated subjects in the HCP Q1 Unrelated 20 dataset.

The scene opens with tab **(1) Indiv Montage** showing both hemispheres of the *individual* anatomical midthickness cortical surface of subject 249947.

- *Click* on tab **(2) Group Montage** at the top of the **Workbench Window**. This tab shows the *group-average* midthickness surface of 20 individuals.
- *Click between* tabs **(1)** and **(2)** to compare the surfaces.

You can see the marked difference between the midthickness surface of the individual 249947 and this averaged midthickness derived from 20 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.

- *Click* on tab **(3) Indiv Vol**. This tab is showing a parasagittal slice plane view of the 249947 *individual* T1 weighted volume.
- *Click* on tab **(4) Group Vol**. This tab shows the HCP Q1 Unrelated 20 *group average* T1w volume at the same parasagittal slice plane (168) as the individual.

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

- *Toggle back and forth* between tabs **(3)** and **(4)** and note the differences between the two.
- *Go to* the Workbench **View menu** at the top left of your screen (Mac/Linux)/window (PC) and *select* **Enter Tile Tabs**.

Now all 4 tabs are showing in a tiled view. This view allows comparison between tabs within the same window: here, the individual surface and volume are on the left and the group averaged surface and volume are on the right (**Figure 1.8**).

The Toolbar and Overlay Toolbox show the controls for the Workbench Window tab you were in when you entered Tile Tabs mode. You can switch the controls to a different tab simply by clicking on the tab

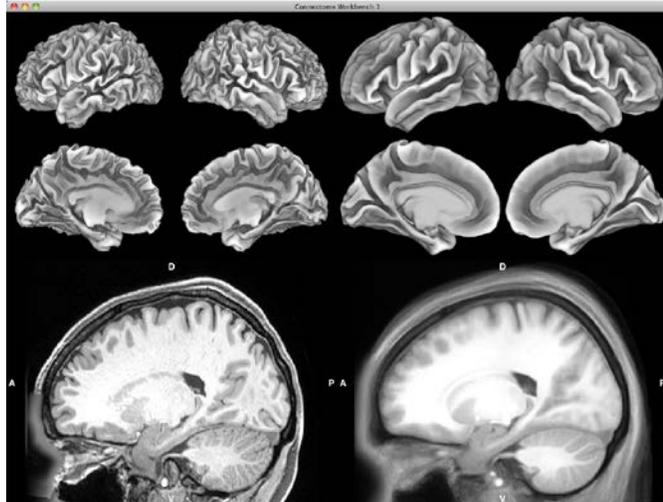
you want at the top of the Workbench Window—the “pane” in the Viewing Area that corresponds to that tab will be indicated by the brief appearance of a white box around it.

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).

- *Left click on either of the surfaces and note that the volume slices change to the parasagittal plane containing the identified grayordinate.*
- Use the shortcut **Command + M** (or **Control + M** in Windows/Linux) to exit **Tile Tabs View** and return to **Normal View**.



**Figure 1.8 – Tile Tabs view comparing individual and group average surfaces and volumes**

## Scene 3: Resting State fMRI Time Series surfaces and volumes

- In the **Scenes Dialog**, select “**Resting State fMRI Time Series surfaces and volumes**” 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 **clipboard**  button in the upper right of the **Workbench Window**.

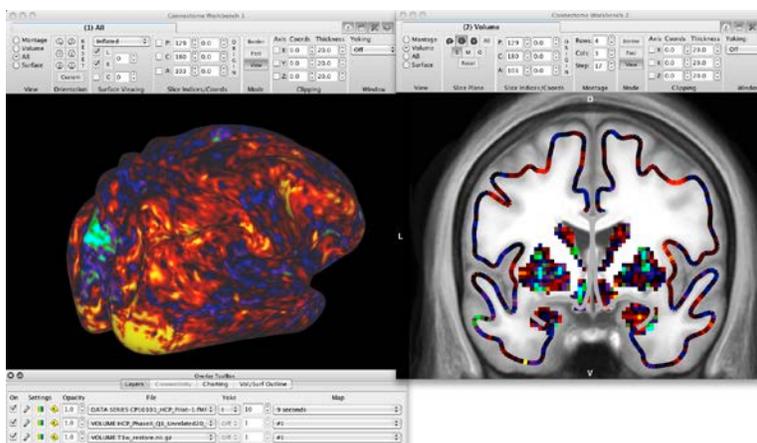
This scene opens with two windows showing the first frame of a resting state fMRI [dense time series](#) from an individual HCP pilot subject, CP10101.

The CP10101 resting state time series is displayed on the group averaged inflated left and right hemisphere surfaces (in All view) in the **Connectome Workbench 1 window**.

Also open is the **Connectome Workbench 2 window** showing the HCP Q1 Unrelated20 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 HCP Q1 Unrelated20 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.*

In both windows we are currently viewing the 10th (time 9 seconds) BOLD activation frame of the resting state time series. The default ROY-BIG palette (**Figure 1.9**)—shows high BOLD signal in yellow/orange/red and low BOLD signals in cyan/green/violet/blue (after regressing out the global mean signal).



**Figure 1.9 – BOLD Time-Series on surface and volume slice**

- 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 window 1 is yoked with the data in window 2, both the surface outline and the volume voxels will refresh with each new timepoint—pretty cool!
- Move your cursor to the “**C**” slice index field (coronal) of the **Slice Indices/Coords** section of the **Toolbar** in the **Connectome Workbench 2 window** and *scroll or toggle up and down* to look at the data for a one timepoint as you move through the slice planes.

## Scene 4: Functional Connectivity from RS-fMRI surfaces and volumes

**\*\*Note:** Scene 4 and the subsequent scenes in this tutorial use the HCP Q1 *group averaged* data exclusively. To date (August 2013) HCP has not yet released the extensively processed resting state functional connectivity or task data for *individuals* in Phase 2 as we are still optimizing our pipelines for these analyses (but see <http://www.humanconnectome.org/data/> for minimally preprocessed image and behavioral data from HCP Q1-Q3 participants).

### Viewing Functional Connectivity Data retrieved from ConnectomeDB (Correlations with Mean Gray Regression)

Functional connectivity data is derived from correlations between grayordinates in the resting state BOLD data (like viewed in [Scene 3: Resting State fMRI Time Series](#)). [Dense connectome](#) files that show functional connectivity are REALLY big (~30 GB for current resolution). Because of their size, these files are stored in [ConnectomeDB](#), which can tap into these large files as needed to view particular connectivity maps of interest.

This scene is set up for you to learn how access, display, and interact with group averaged functional connectivity data from the HCP Q1 Unrelated subjects on the cortical surface and in subcortical volumes.

- In the **Scenes Dialog**, select “**Functional Connectivity from RS-fMRI...**”, and click **Show**.
- 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).

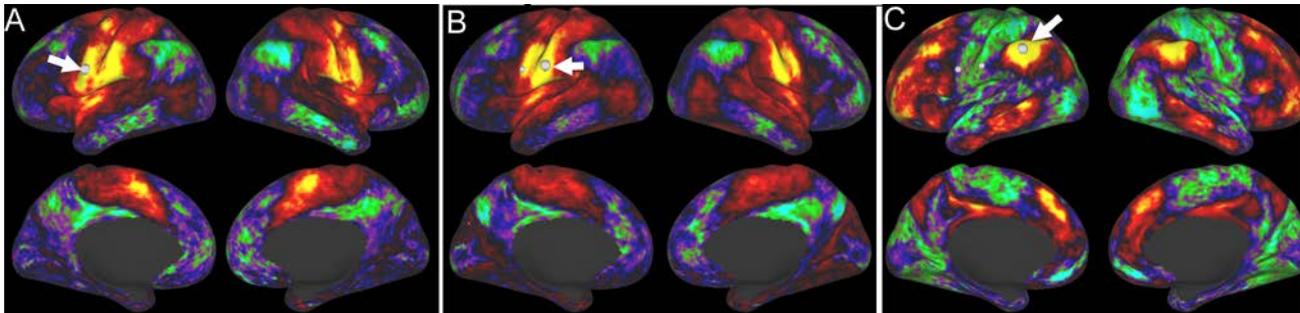
The scene opens displaying an inflated surface montage view (Window 1) of group average functional connectivity between the vertex on the left hemisphere surface (shown in white) and all other grayordinates. In Window 2, a coronal slice is displayed showing functional connectivity with the identified vertex in a surface outline and 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 (after regression of the mean gray-matter timeseries) are displayed in blue, green, and indigo.

The dataset is from 80 scan sessions (20 subjects, 15 min/scan, for a total of 20 hours of scan time). Data were averaged across subjects using surface based registration for cerebral cortex and nonlinear volume registration for subcortical and cerebellar voxels. Minimal spatial smoothing (2mm FWHM) was

done. Preprocessing and denoising were carried out as described in [Glasser et al. 2013](#), [Smith et al., 2013](#).

- Back in **Viewing Window 1**, *click on the left hemisphere surface* in the ventral part of the precentral gyrus, approximately the same place as the highlighted vertex in **Figure 1.10A** (**white arrow, upper left**).



**Figure 1.10 – Comparing functional connectivity for three brain locations.**

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

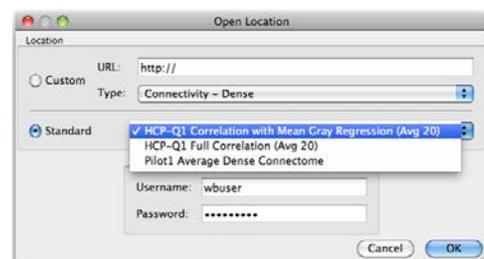
- *Click on the yellow location on the postcentral gyrus (white arrow in Figure 1.10B)* to view the similar functional connectivity map for the face representation of somatosensory cortex.
- *Now click a green or blue area in the supramarginal gyrus (white arrow in Figure 1.10C).* You will see a much different connectivity pattern than for either of the previous maps (**Figure 1.10C**). This demonstrates how nearby brain regions can have very different functional connectivity from each other in the resting state.

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

Now we will load another group average functional connectivity dataset from ConnectomeDB.

- In the **Menu bar**, select **File ► Open Location...** (shortcut for Mac: command + L, Linux/PC: control + L).
- A popup will appear as shown in **Figure 1.11**.
- Press the **Standard** radio button. Select “**HCP-Q1 Full Correlation (Avg 20)**” from the pull-down menu under “Standard”.

This dense connectome is from the same dataset as the preceding one, except that regression of the mean gray timeseries was not carried out.



**Figure 1.11 – Open Remote File Dialog**

- Your Username should be automatically filled in. Type in your Password if you haven't saved this to your preferences. **Click OK.**

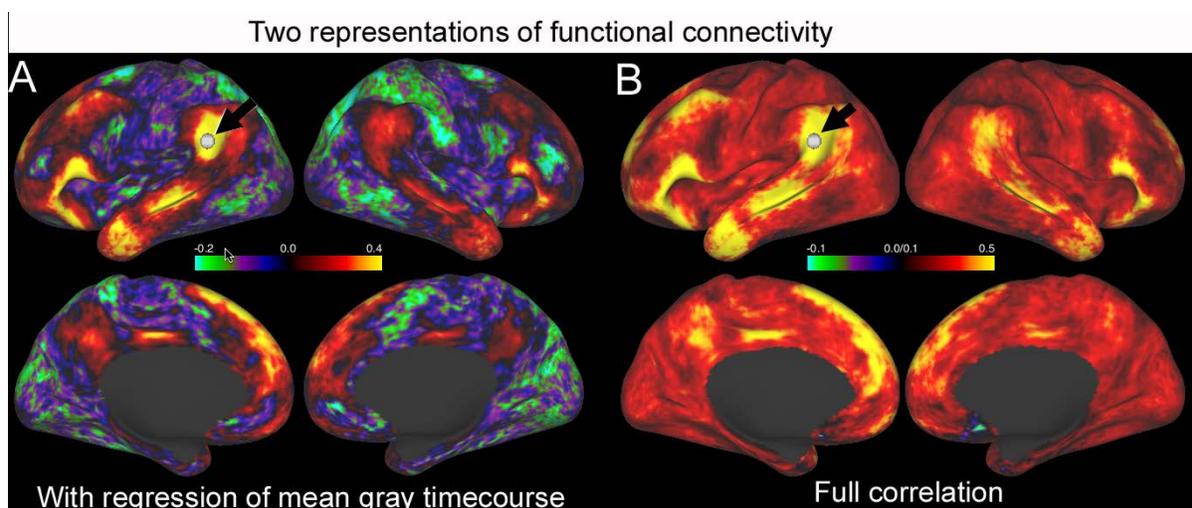
It will take a few seconds to access the file over the internet. This step makes the selected 30 GB dense connectome file accessible, but (fortunately!) does not attempt to load the file.

As a reminder, the dense connectome data are for demonstration purposes only. The [Q1 Open Access Data Use Agreement](#) you agreed to in order to access the tutorial data acknowledges this stipulation. (This restriction is necessary because the advanced methods used to analyze the functional connectivity data have not been published or fully vetted).

- In **Overlay Toolbox: Layers**, use the second layer's **File** dropdown and *select* **CONNECTIVITY** `cifti-average?resource=HCP-Q1:Q1:Demo_HCP_unrelated20_FunctionalConnectivity_FullCorrel`
- In **Overlay Toolbox: Layers**, turn the second layer **On**.
- In the **Information box**, *click* on **RID** to remove any previously selected vertices.
- *Click* on a vertex in the left supramarginal gyrus, close to that shown in **Figure 1.12A**.
- In **Overlay Toolbox: Layers**, turn the first layer **Off**.

The functional connectivity map should appear similar to that in **Figure 1.12B**. Most of the map will show positive correlations, but a few locations show negative values, indicating an anti-correlation even without regression of the mean gray timeseries (MGT).

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



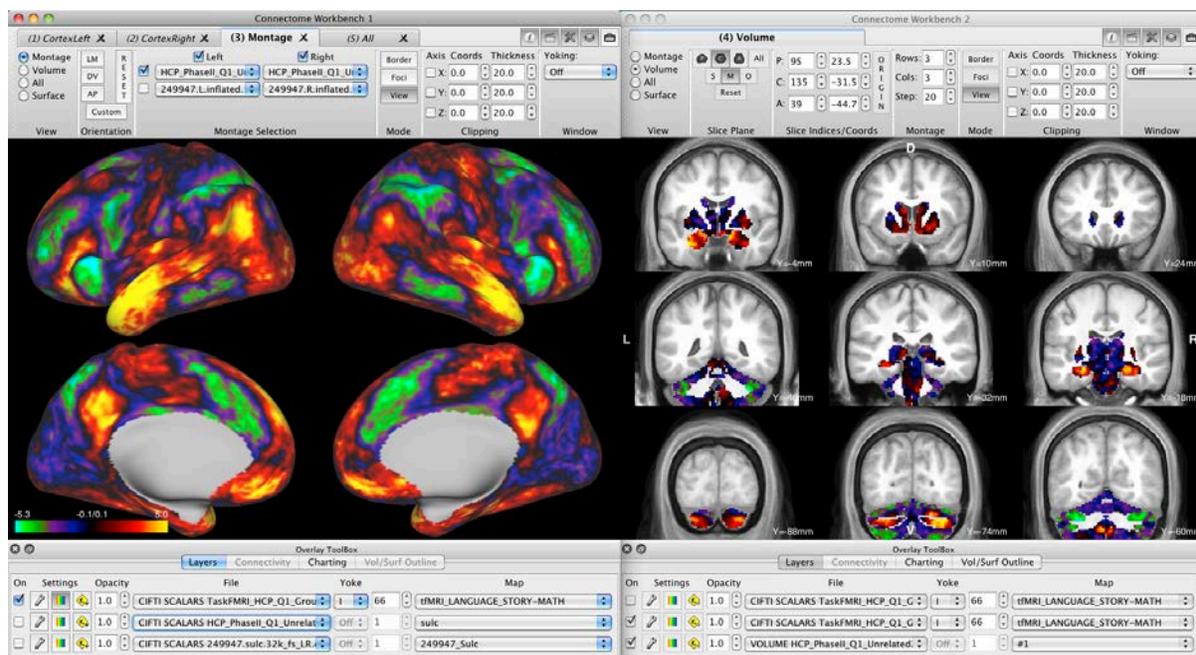
**Figure 1.12 – Alternative representations of functional connectivity maps using an exemplar seed in the left supramarginal gyrus (black arrows). A.** Functional connectivity map after regression of the mean gray timecourse (MGT). **B.** Full correlation functional connectivity map for the same seed location.

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 5: Task fMRI: Language (Story – Math) surfaces and volume slices

- Select “Task fMRI: Language (Story – Math) surfaces and volume slices” in the **Scenes Dialog box** and **click Show** to load the scene.

This scene (**Figure 1.13**) shows the group-average Story vs. Math contrast of the HCP Language Processing task, displayed on the inflated surfaces and in subcortical grayordinates on coronal volume slices.



**Figure 1.13 – Group-average map for the Story vs Math task contrast from the HCP Language task.**

The fMRI data processing included grayordinate-constrained smoothing (4 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.

Strong activations are evident in many regions, including anterior temporal cortex, posterior parietal cortex, posterior cingulate cortex, and cerebellar cortex. The color bar in the lower left shows a maximum z-statistic value of 5.0 and minimum of -5.3. (In this figure, the color bar spans 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 [Chapter 2](#)).

In this task, participants were presented a story task (brief auditory stories, followed by a 2-alternative forced-choice question that asks participants about the topic of the story) or a math task (aurally

presented addition and subtraction problems, followed by two choices for the correct arithmetic answer, e.g., “twenty-nine or twenty-six”).

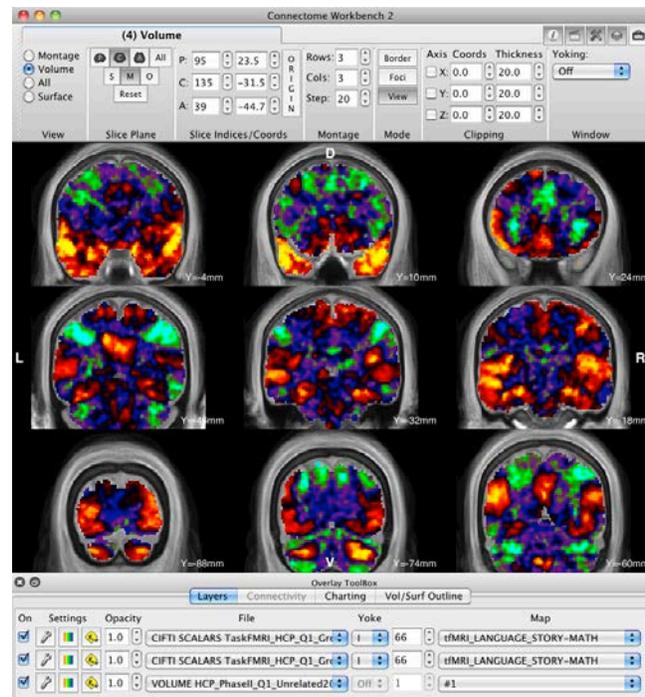
## Volume-smoothed contrasts of the Language (Story – Math) task

- In **Window 2: Overlay Toolbox: Layers**, toggle the first layer **On**.

This layer (**Figure 1.14**) shows the same Story vs. Math contrast of the HCP Language Processing task in conventional volume slices. For this analysis, smoothing (4 mm FWHM) was done in volume space, which increases spatial blurring across sulcal banks. Similarly, cortical activations across subjects in volume space induces greater blurring.

Activations are visible in anterior temporal cortex, posterior parietal cortex, posterior cingulate cortex, and cerebellar cortex, similar to those shown in the preceding figure. The peak z-statistic from the volume-average analysis is 4.8 (not shown here, but revealed by pressing the color bar icon in **Overlay Toolbox: Layers**), which is lower than that from the grayordinate-constrained analysis shown above. Various advantages of surface-based compared to volume-based analysis and visualization are discussed elsewhere ([Glasser et al. 2013](#)).

- In **Window 2: Overlay Toolbox: Layers**, toggle the first layer **Off**.



**Figure 1.14 – Volume slice montage, showing group-average task contrast for the Story-Math HCP working language task generated by a volumetric analysis (4mm FWHM volume smoothing).**

## Exploring other HCP Task fMRI contrasts

- In **Window 1: Overlay Toolbox: Layers: Map** pull-down menu, notice that all the tasks are listed.

The task data file (**TaskFMRI\_HCP\_Q1\_GroupAvg\_unrelated20.dscalar**) is listed. This file contains grayordinate-smoothed group average maps of all the tfMRI contrasts generated from the 7 tasks in the HCP protocol.

Currently, frame 66 with the map name **tfMRI\_LANGUAGE\_STORY-MATH** is being viewed. If you are having trouble seeing all the text in the File and Map fields, you can expand the Workbench Window horizontally and these will enlarge accordingly. You can also click on these fields to see the full names of all the Files and Maps loaded.

- *Toggle the Frame number up* and notice the Map name changes as you advance the frame. The TaskFMRI... files in Windows 1 and 2 are yoked so that the frames in the windows advance together. You can continue to toggle to explore the 86 frames available.

Specific scenes for each task in the HCP protocol are available in the HCP\_WB\_Tutorial\_Beta0.83\_part2.scene file included in the tutorial dataset. Detailed instructions and descriptions of these scenes and the contrasts highlighted were created for the WB Tutorial for the Q1 data release, which is included as an [Appendix](#) to this tutorial.

## Scene 6: Parcellation Borders display with myelin map surfaces

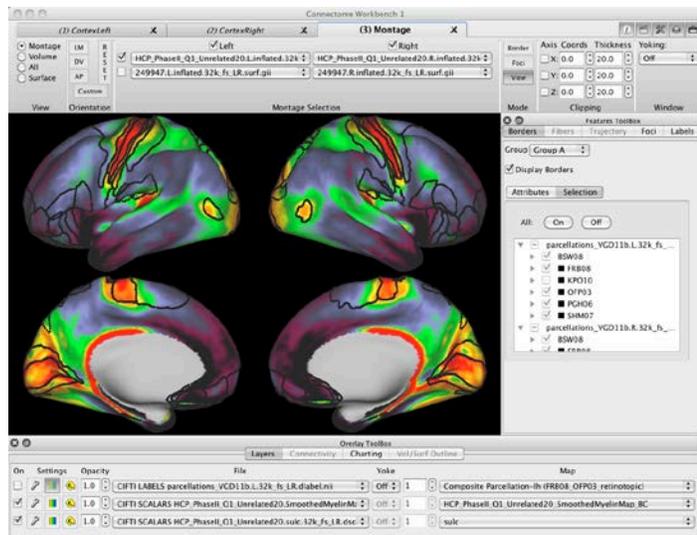
- Select Scene “**Parcellation Borders display with myelin map surfaces**” in the **Scenes Dialog box** and **click Show** to load the scene.

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.

The scene opens with a montage of the Q1 unrelated 20 group averaged inflated cortex surfaces showing colored cortical areas depicting an architectonic and retinotopic parcellation map published by Van Essen, Glasser, Dierker *et al.* (2011b) (VGD11b). The parcellation map layer is overlaid on the Q1 unrelated 20 group-average myelin 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.
- Rotate the surfaces (*press the left mouse button and drag your mouse*). As we saw above, red and orange represent heavily myelinated regions, purple and black represent areas of low myelin content (Glasser & Van Essen, 2011).
- **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) that indicate borders between cortical areas (Figure 1.15). Leave the Borders *on*.



**Figure 1.15 – 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 thus greyed out (inaccessible in WB beta v0.83).

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.

- Move your cursor into the field that lists borders, at the bottom of the Selection tab.
- *Scroll with your mouse wheel or use the up and down arrows of your keyboard to navigate through the list. Left hemisphere borders are listed in the first file tree, right hemisphere borders are in the second.*
- 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 one or more 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 group 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* the **Display borders** checkbox *off again*.
- *Toggle* the top **CIFTI LABELS parcellation** 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 Q1 unrelated 20 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**. 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.*

## Scene 7: Foci display surfaces

- Select “**Foci display surfaces**” in the **Scenes Dialog**, click **Show**, and click **Close**.

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.

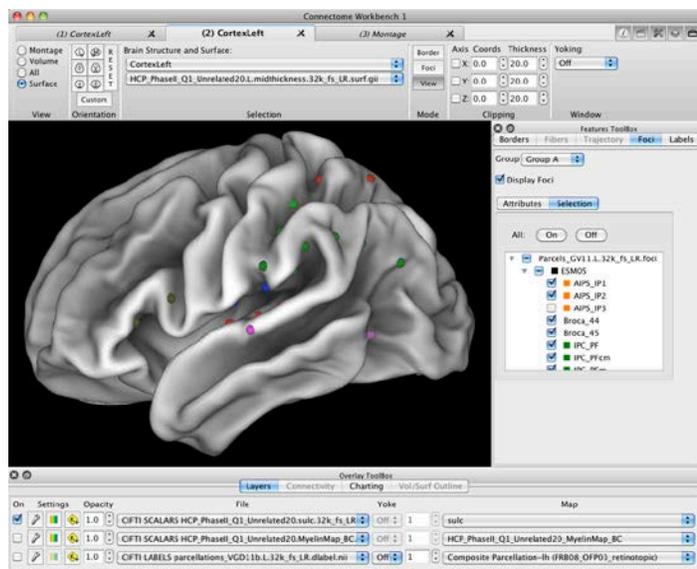
The scene opens with the inflated group-average left hemisphere surface showing the identified foci. As with Borders and Labels, the **Foci tab** of the **Features Toolbox** has **Attributes** and **Selection** subtabs. Here, we begin in the **Attributes** tab (if necessary, click on the **Attributes**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

- *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.

- *Click* on **Tab 2** at the top of the **Workbench Window**, showing the group average midthickness surface.
- *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



**Figure 1.16 – Left midthickness group-average surface showing ESM05 foci.** Focus AIPS\_IP3 is deselected and therefore not displayed.

must use the Edit Foci function described in [Chapter 3: Using Workbench Tools](#).

- *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.*
- *In the field that lists foci, **click on the grey triangle**  next to the foci class **ESM05**. This reveals the foci that make up this foci class and allows you to turn them off and on one by one (**Figure 1.16**).*
- *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 3** at the top of the **Workbench Window**.*

This Montage view is displaying the Zilles/Amunts derived foci and the combined architectonic and retinotopic parcellation labels that we explored in [Scene 6](#). Some 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 unique features settings (e.g. borders display on, foci displayed as squares, etc.) to be applied specifically to different set groups of Workbench Window display tabs.

## End Of Chapter 1: Exploring HCP Data in Workbench

Have fun exploring some of the buttons and options we didn't use in this first taste of Workbench. If you want more detail on how everything works, move on to **Chapter 2**. Check out the [Appendix](#) to explore more data from the HCP Q1 Unrelated 20 dataset.

## Chapter 2: A Detailed Tour of Workbench

If you have already completed [Chapter 1](#), you are familiar with some basics, but Workbench has many additional features that we will explore below.

*You need not have completed Chapter 1 in order to follow the feature-by-feature descriptions and instructions in Chapter 2. In fact, for all the features discussed in Chapter 2 to appear as written, it is best to start a new Workbench Session loading the WB beta v0.83 tutorial spec file as described below.*

### Workbench Splash Screen and Opening a Spec File

Typically, it is desirable to view many distinct files (surfaces, volumes, and data) concurrently in Workbench. To get started, it is convenient to load all such files at once. A [Specification File](#) (commonly called “Spec File”) is used by Workbench to organize a set of data files to be loaded into the program (such as volume, label, and metric files).

When Workbench is launched, a [Splash screen](#) opens ([Figure 1.1](#)), containing links to the Human Connectome Project (HCP) [website](#) and the HCP [Twitter account](#), and showing a list containing a) Spec files in the directory path you are currently opening Workbench from, if any, and b) Recently Opened Spec Files.

If you opened the Spec File in [Chapter 1](#), the `HCP_beta0.83_tutorial.32k_fs_LR.wb.spec` should be listed with its path under Recent Spec Files.

The Splash screen gives you three button options: **Open**, **Open Other...**, and **Skip**. Use the **Open** button, to open a highlighted spec file directly from the **Splash Screen**:

- *Click* on the spec file you want to open in the Recent Spec Files list, and *click* the **Open button**.

Use the **Open Other...** button to open a spec file not listed on the splash screen from the **Open file dialog** ([Figure 1.2](#)).

Use the **Skip** button, to go directly to the Workbench Window.

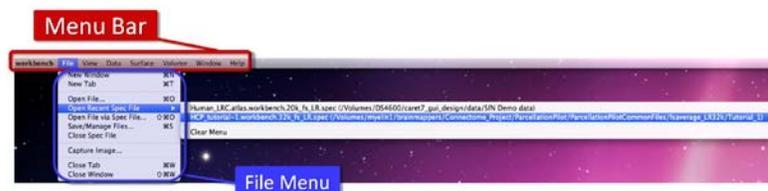


Figure 2.1 – File Menu (Open File... and Open Recent Spec File)

- From here, you can use the **File** menu in the **Menu bar** to open a spec file or any other Workbench readable file by *selecting* **File** ► **Open File...**
  - *Select* the desired file and *click* the **Open** button.
  - If you wish to re-open a previously opened spec file, *select* **File Menu** ► **Open Recent Spec File** and choose the file of interest ([Figure 2.1](#)).

In all three options, once you have *selected and opened* the desired file:

**HCP\_beta0.83\_tutorial.32k\_fs\_LR.wb.spec**, the Open Spec File Dialog will appear ([Figure 1.3](#)).

- The **Open Spec File Dialog** lists all the files contained in the spec file, organized by file type. The tabs in the **View File Types:** and **View Structures:** bars at the top of the dialog allow you to view a subset of the data files by *clicking* on a specific file or structure type.
- Checkboxes on the left indicate which files will be loaded once you press the **Load** button in the lower right. All files are selected by default. *Click* on the checkboxes to uncheck files that you do not want to load. If you want to check or uncheck all the files, click **All** or **None** in the **Select Files:** bar near the top of the dialog.
- The **Data Type**, **Structure**, and **Data File Name** headers can also be clicked to sort the list of files by these attributes.
- The **More** ⚙ gear buttons to the right of each checkbox will, once implemented, allow you to select options to set the structure for a file (e.g. Cerebellum, Cortex Left, etc.) or to view any metadata associated with the file. If you click on these buttons now, you will see these options greyed out indicating that this feature is not yet implemented.
- *Click Load* to open the checked files. It may take several seconds or so to load the data files after which the Open Spec File Dialog will automatically close.
- If a [scene](#) file is available in the spec file you opened, you can click **Load Scenes** to load just the scene file for now. When you load a particular scene from the [Scenes box](#), the files needed for that scene will be loaded into Workbench at that time.
- If you clicked **Load** above, proceed to the next section. If you clicked **Load Scenes**, double click the “Tutorial Chapter 2” scene in the **Scenes box**, and *click Close* before proceeding.

You can set a Preference to show/not show the Workbench Splash Screen when the program is launched. Once you have opened the main Workbench Window, *click*

**Menu bar ► Workbench ► Preferences** and *toggle off Show Splash Screen at Startup*.

## Elements of the Workbench Window

When you load a Spec file, a single [Workbench Window](#) (“Connectome Workbench 1”) will open containing [Viewing tabs](#). The number and type of tabs that open depends on the structures (brain volumes and surfaces) contained in the loaded spec file.

For the **HCP\_beta0.83\_tutorial.32k\_fs\_LR.wb.spec** file, 5 tabs will open: (1) Montage, (2) Volume, (3) All (Whole Brain), (4) Cortex Left, and (5) Cortex Right.

The [Viewing Area](#) defaults upon opening to view **tab (1) Montage** (the [Active Tab](#)) showing the left and right cerebral cortex surfaces, lateral and medial views. The top layer of data being shown on the surfaces is a map of seven resting state networks from Yeo *et al.* 2011.

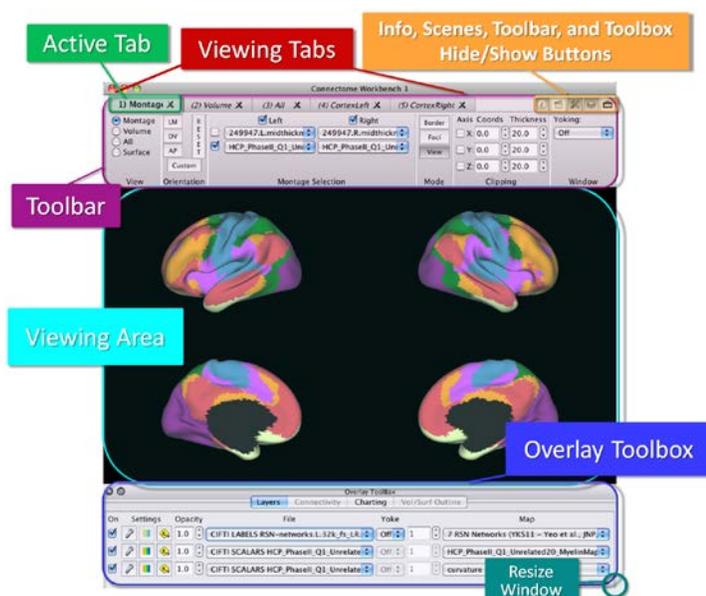
Components of the Workbench Window are shown in **Figure 2.2**. The [Overlay Toolbox](#) can be displayed in two locations/orientations (see [Figure 1.4](#)). On startup, the choice is based on the resolution of your monitor (if the vertical resolution is 800 or less, the Overlay Toolbox will be on the left).

- Selecting **View Menu ► Overlay Toolbox ► Attach to Bottom/Attach to Left** allows you to switch between the two layouts.

For the purposes of this tutorial, all instructions and figures assume you are using the layout shown in **Figure 2.2** with the [Overlay Toolbox](#) attached to the bottom of the [Viewing Area](#).

Workbench allows you to organize and view your data using windows and tabs analogous to those widely used in web browsers. Windows are stand-alone; tabs are “pages” within a window. In Workbench, all viewing settings of the viewed surface or volume in the current tab are set in the [Toolbar](#) (located at the top of the tab) and [Overlay Toolbox](#) within that tab.

With the spec file now loaded, let’s take a tour of the [Workbench Window](#) and [Viewing Tabs](#).



**Figure 2.2 – Elements of the Workbench Window**

- At the top of the window, you see the 5 tabs of loaded surfaces and volumes. Each tab is given a number and title such as *(1) Montage*. The title of the **Active tab** is in bold.
- Just under the tabs is the **Toolbar**, which contains basic controls for the structure being viewed in the current tab or window.
- The **Overlay Toolbox**, at the bottom of the window in **Figure 2.2**, contains settings for the data being viewed on the structure.
- The **Information box**, **Scenes box**, **Toolbar**, **Overlay Toolbox**, and **Features Toolbox** can be shown or hidden by *clicking* the icons in the upper right of the window.

Information box icon:  Scenes box icon: 

Toolbar icon:  Overlay Toolbox icon:  Features Toolbox icon: 

- To adjust the size of the **Workbench Window**, *click* and *drag* the grab tab in the lower right corner of the window.
- *Slowly move* the **mouse cursor** over the **Toolbar**. As the **mouse cursor** stops over a control, a yellow/gray highlighted [Tooltip](#) pops up describing the function of the control.
- The **Overlay Toolbox** and **Features Toolbox** can be pulled off their docking points in the **Workbench Window** to float any place on your desktop by *holding down the left mouse button as you drag* the top of the Toolbox away from the Viewing Area to the desired location. 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.

## Basic Navigation using Mouse Controls

Several basic surface and volume viewing and navigation functions are controlled with the mouse.

- In the first **Viewing tab** labeled *(1) Montage*, *move* your **mouse** into the viewing window depicting the brain surfaces. *Pressing* the **left mouse button**, *move* your **mouse** back and forth and up and down to change the orientation of the surfaces.
- To zoom, *press* the **command key** (Mac) or **control key** (PC, Linux), and *move* your **mouse** up and down. If you have a **mouse wheel**, you can also zoom by *moving* your mouse into the Viewing Area and *scroll up* to zoom out or *scroll down* to zoom in.
- To pan (move the brain surface to a different part of the [Viewing Area](#)), *press* the **shift key** on the keyboard, and *left click* and *move* your **mouse** left, right, up, or down.

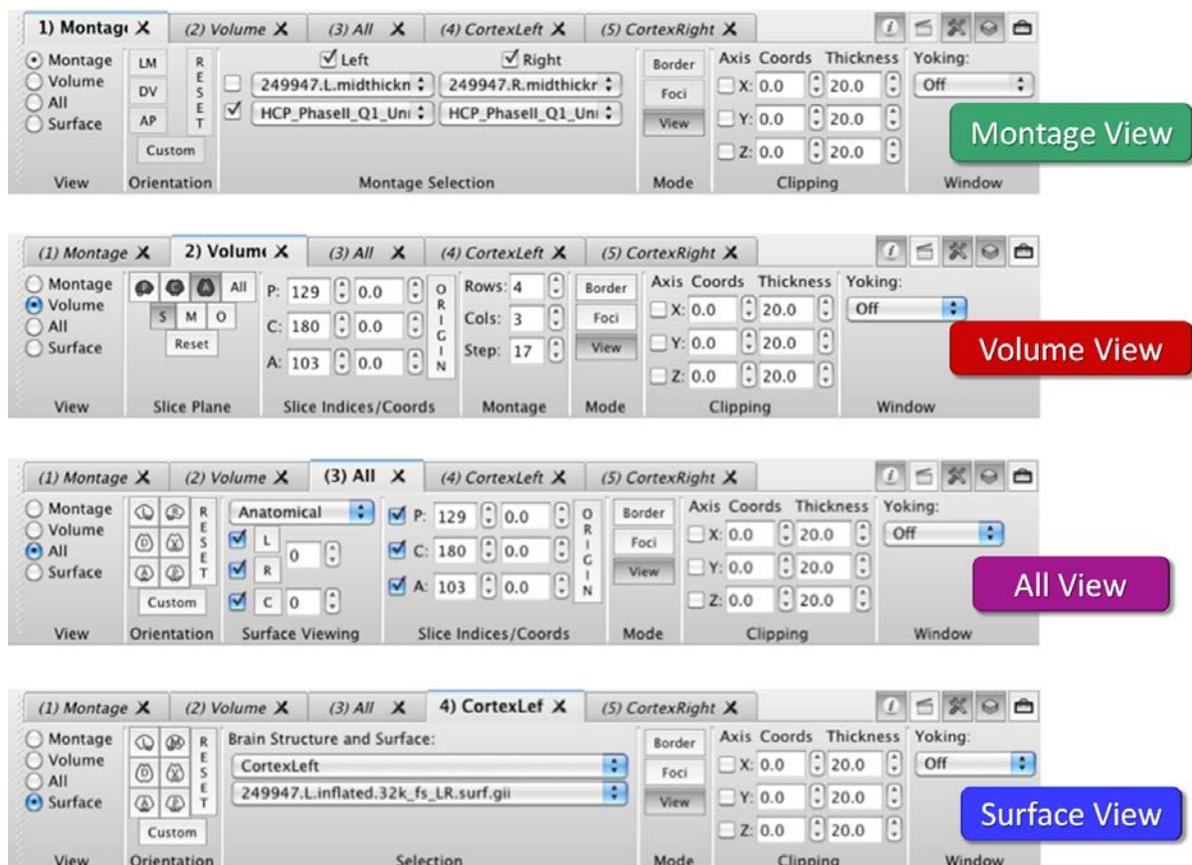
The default placement of the surface or volume is in the center of the **Viewing Area** and, in **Surface View**, rotation is about the surface's center of gravity. Use the **Reset button** in the **Toolbar** to return to the default zoom, pan, and orientation (see [Toolbar](#) below).

- To identify a [brainordinate](#), *click* on the brain surface. A sphere will appear where you clicked on the surface. Also, the **Information box** should pop up, showing information on the particular vertex that was clicked.
- The color and size of the ID sphere can be adjusted using the **Properties button** in the **Information Box** (more on the Information box below).
- By *reclicking* on the sphere that identifies the brainordinate, you can deselect that brainordinate and the sphere will disappear.
- *Click* on **Tab 2** at the top of the **Workbench Window**, labeled *(2) Volume*. *Move* your mouse cursor into the Viewing Area.
- *Zoom* on the displayed **Volume** slice as above, by *pressing* the **command (or control) key** and *moving* your **mouse** up and down, or *scrolling* up or down with your **mouse wheel**.

- *Pan* the **Volume** slice as above by *pressing* the **shift key** on the keyboard, and *moving* your **mouse** left, right, up, or down.
- *Note* that the mouse-controlled orientation function activated in **Surface or Whole Brain Views** by *pressing* the **left mouse button** and *moving* your **mouse** is *not active* in the **Volume View** mode. All other mouse controls are active in all views.
- *Click* anywhere on the Volume slice. As before, the **Toolbox Info tab** shows information of the particular brainordinate that was clicked.

## Toolbar

The **Toolbar** (**Figure 2.3**) contains settings for what brain surface(s) or volume slices you want to view from your loaded file (and how you want to view it/them) in the **Active Tab**. It is organized in sections from left to right across the toolbar according to the type of **View** selected. [Tooltips](#) are an easy way to find information on the buttons and functions on the Toolbar (or throughout Workbench).



**Figure 2.3 – The Toolbar for Montage, Volume, and All Brain and Surface Views**

- *Hover your mouse cursor over one of the **Orientation** buttons at the top left of the **Toolbar**. A yellow (Mac)/gray (PC/Linux) box of information describing the button your cursor is pointing to should popup (a [Tooltip](#)). If this doesn't work right away, make sure your mouse is *fully stopped* over the button.*
- In **View**, you can set the radio button to **Montage, Volume, All, or Surface** to view a brain surface montage, volume slice(s), any combination of the 3 orthogonal volume planes and all the surfaces loaded, or single brain surfaces respectively. When a new type of view is selected by *clicking* a radio button, the toolbar changes to accommodate selections useful to that view (compare in **Figure 2.3**).

## Montage View

**Montage View** allows you to simultaneously view lateral and medial views of both left (left column) and right (right column) hemisphere surfaces. When the **View** on the **Toolbar** is set to **Montage** (shown in the second panel of **Figure 2.3**), the Toolbar has 6 sections for the type of **View, Orientation, Montage Selection, Mode, Clipping**, and between **Window** viewing functions.

- *Click back to **Tab 1**, labeled (1) Montage.*
- **Orientation** contains buttons to set orthogonal and User-defined views of the brain surface displayed.
  - **Orthogonal view buttons** (right) are labeled: **LM** (lateral-medial), **DV** (dorsal-ventral), **AP** (anterior-posterior). 
  - *Move* the surfaces by *holding down* the **left mouse button** and *moving* the mouse left or right. *Click* the **orthogonal view buttons** to see how the view changes.
  - The **Reset button** reorients the surface, zooming, and panning to the original orientation, position, and zoom of the surface (orientation, etc. at file loading).
  - The **Custom button** allows the user to set and store the current brain orientation, zoom, and position being viewed as a particular view of interest.
    - *Move, zoom, and/or pan* the surfaces into a new orientation by using the [mouse controls](#) described above.
    - *Click* the **Custom button**, and select **Create and Edit...**
    - The **Custom Orientation box (Figure 2.4)** appears and shows the values for panning, rotation, and zoom for the surface you just reoriented in the active tab of Workbench Window 1.
    - *Click* the **New button** at the right and type **"Test"** in View Name field of the New Custom View dialog. You can also type notes in the Comment field to help you remember details about this orientation (e.g. "from Fig 2 of Van Essen et al. 2012").

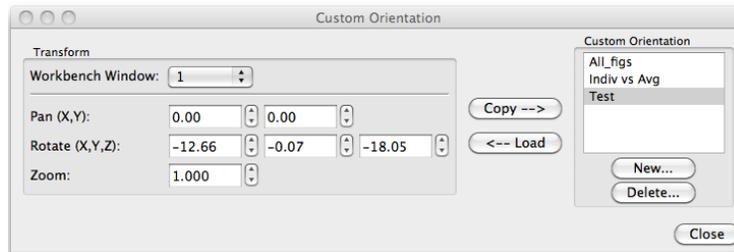


Figure 2.4 – Custom Orientation box

- *Move, zoom, or pan* the surface away from that orientation. Note that the values in the Custom Orientation Box change interactively.
- *Click the **Load** button* and the orientation of the surface will go back to the one you set as “Test”.
- *Again, move, zoom, or pan* the surface away from that orientation.
- *Click the **Copy** button* and the new orientation will now be saved as “Test”. Verify this by again, *moving, zooming, or panning* the surface away from that orientation and *clicking the **Load** button* again.
- *Click **Close**.*
- *Again, move, zoom, or pan* the surface away from the current orientation.
- *Click the **Custom** button* in the Toolbar again.
- *Select “Test”* from the listed Custom view(s) and the orientation will return to the modified “Test” orientation.

If you do not delete a Custom view you create, it will be available the next time you open Workbench. If you create a new view with the same name as a saved view, it will overwrite the original view.

- **Montage Selection** contains pull-downs to set the brain surface you want to view for each hemisphere from the list of loaded files.
  - *Click* on the lower **Left** Montage Selection **pull-down** to view the surfaces available for the left hemisphere, *click* on the HCP\_Phase1...midthickness surface to select it.
  - *Move your cursor* into the **Viewing Area**. *Zoom and turn* the surfaces as you would for a single surface (hold left mouse button and move mouse).

The surfaces rotate so that (i) you always have a full view of each hemisphere via the top and bottom rows, and (ii) the two hemispheres counter-rotate, so that the top panels show matched views (e.g., both frontal or both occipital) and the bottom panels show the opposite views.

- *Translate the surface* as you would a single surface (shift + mouse left/right). The upper left and lower right panels translate in one direction; the other two panels translate in

the opposite direction. This allows you to zoom in on a particular region of interest (e.g., the frontal pole) in all panels concurrently.

- Back in the Toolbar, the second row of **Montage Selection** pull-downs are used for Dual configuration mode.
- *Click* on the **checkbox** to the left of the top row of **Montage Selection**.
- *Zoom and turn* the surfaces to view how the surfaces move similarly in this mode.
- **Mode** contains buttons for performing actions including Border drawing (**Border**), Foci creation (**Foci**) and resetting the mouse controls to viewing mode (**View**). Mode/tool functions are covered further in [Chapter 3](#) in the tutorial.
- **Clipping** contains controls for clipping the view in the X, Y, and Z planes. You can set these at a specific coordinate plane or set the thickness of the slice of 3-D volume you want to view. The checkbox toggles to the left allow you to easily turn the clipping off or on in each plane, once it is set.
- **Window** contains controls for functions that apply between windows or tabs.
  - **Yoking** allows the user to define groups of tabs or windows that will have linked rotation, panning, and zooming. Surfaces are yoked so that the corresponding lateral or medial contralateral hemispheres can be viewed at the same time (e.g. superior temporal gyrus on the lateral surface can be viewed on the right and left hemisphere simultaneously).

## Volume View

- *Click* on **Tab 2** at the top of the **Workbench Window**, labeled (2) *Volume*.

When the **View** on the **Toolbar** is set to **Volume** (shown in the third panel of **Figure 2.3**), the Toolbar has 7 sections for the type of **View**, **Slice Plane**, **Slice Indices/Coordinates**, **Montage**, **Mode**, **Clipping**, and between **Window** viewing functions.

- **Slice Plane** contains buttons to set the orthogonal volume slice(s) you want to view, whether you want to view a single slice, a montage, or oblique angle slices (not yet functional), and a reset button.
  - **Orthogonal Slice plane buttons** are labeled **P** (parasagittal), **C** (coronal), **A** (axial, i.e. horizontal) superimposed on simple drawings of the appropriate slice view. The **All** button allows you to look at all three orthogonal slice planes simultaneously.
 
    - *Move* your mouse cursor into the Toolbar. *Click* on the **P**, **C**, **A**, and **All** buttons to see their functions
  - The **S** (Single Slice), **M** (Montage), and **O** (Oblique) buttons set what type of volume view you are interested in viewing.



- **Single Slice (S) volume view** shows a single parasagittal, coronal, or axial volume slice (or all three orientations) at a single set of slice indices, depending on which Orthogonal Slice plane button is depressed.
- The **Montage (M) volume view** shows a [volume montage](#), a series of volume slices in one orientation at regular intervals that are set in the **Montage** controls in the **Volume View Toolbar** (see below).
- The **Oblique (O) volume view** shows a single slice that is rotatable about an oblique axis. You can rotate the axis by holding down the left mouse button and moving the mouse over the viewing area. The **Oblique volume view** is not yet functional in Workbench.
- The **Reset** button in **Slice Plane** resets the zooming and panning of the volume slice(s) you are viewing.
  - *Click* on the **M** button to view a montage of one of the slice planes.
  - *Move* your mouse into the viewing area and *scroll* your **mouse wheel** (or *press* command/control and *move* your **mouse up**) to zoom in on the slices.
  - *Click* the **Reset** button to return to the default view.
- **Slice Indices/Coordinates** contains settings for the slice index and stereotaxic (Talairach) coordinate for each orthogonal axis for the currently viewed slice.
- **Montage** contains settings for the number of **Rows** and **Columns** of slices you would like to view when montage volume view is active (activated by clicking the **M** button, see above). **Step** settings control the size of the gap between slices (in slice index units) that you view in the montage.

The montage slices by default are set to have equal numbers above and below the origin, which is typically the anterior commissure (AC), and to approximately span the full extent of the brain.

  - The **Origin** button in **Slice Indices/Coords** resets all indices/coordinates to the default position centered at the anterior commissure (AC) along the AC-PC (posterior commissure) line.
- [Mode, Clipping, and Window](#) **Toolbar** sections are described above in **Montage View**.

## All (Whole Brain) View

- *Click* on **Tab 3** at the top of the **Viewing Window**, labeled (3) *All*.

**All (Whole Brain)** view allows you to view one or more brain surfaces and volumes in the 3 orthogonal slice planes at one time. When the **View** on the **Toolbar** is set to **All** (shown in the lower panel of **Figure 2.3**), the **Toolbar** has 7 sections for the type of **View**, **Orientation**, **Surface Viewing**, **Slice Indices/Coordinates**, **Mode**, **Clipping**, and between **Window** viewing functions.

- [Orientation](#) is described in Montage View above, except the orthogonal view buttons are replaced with **L** (left perspective) and **R** (right perspective), **D** (dorsal), **V** (ventral), **A** (anterior), and **P** (posterior) superimposed on simple drawings of the appropriate brain view.
 
- **Surface Viewing** allows you to set the type of surfaces and select the structures you want to view.
  - Click on the **pull-down** at the top of the **Surface Viewing** section. Click and select the surface you prefer to view.
  - *Uncheck* and *recheck* the checkboxes next to **L** (left hemisphere), **R** (right hemisphere), and **C** (cerebellum).
  - Click on the **L**, **R**, or **C** square buttons to set which of the loaded left and right hemisphere surfaces you want to view
  - The **settings box** to the right of the **L** and **R** checkboxes controls the separation between the left and right hemisphere surfaces.

The box to the right of the “**C**” checkbox controls the vertical separation between the cerebellum surface and the cerebral cortex surfaces. A cerebellar surface is not included in this tutorial but is available in the Conte69 atlas dataset:  
[http://sumsdb.wustl.edu/sums/directory.do?id=8291494&dir\\_name=CONTE69](http://sumsdb.wustl.edu/sums/directory.do?id=8291494&dir_name=CONTE69)

  - Click the up or down arrows to the right of the **settings boxes** (or mouse over and scroll with the **mouse wheel**) to move the surfaces relative to each other.
- [Slice Indices/Coordinates](#) **Toolbar** sections are described above in **Volume View**.
- [Mode, Clipping, and Window](#) **Toolbar** sections are described above in **Montage View**.

## Surface View

- Click on **Tab 4** at the top of the **Viewing Window**, labeled (4) *Cortex Left*.

When the **View** on the **Toolbar** is set to **Surface** (shown in the top panel of **Figure 2.3**), the **Toolbar** has 6 sections for the type of **View**, **Orientation**, structure **Selection**, **Mode**, **Clipping**, and between **Window** viewing functions.

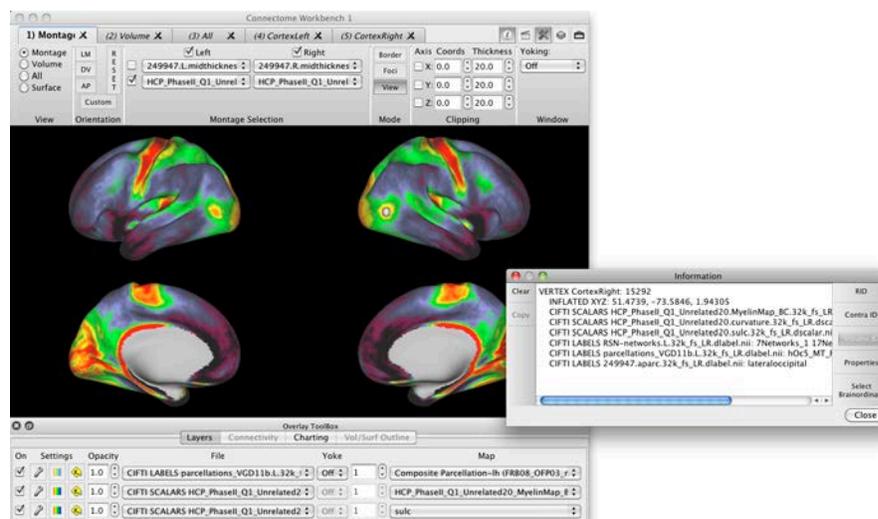
- [Orientation](#) is described in All View above, except the L and R orthogonal view buttons are replaced with **L** (lateral) and **M** (medial) buttons.
 
- **Selection** contains pull-downs to set the brain structure and surface you want to view from the list of loaded files.
  - Click on the lower **Surface Selection pull-down** to view and select the 249947.L.very\_inflated... surface for Cortex Left.

- [Mode, Clipping, and Window](#) **Toolbar** sections are described above in **Montage View**.

## Information Box

The **Information box** shows you data on brainordinates selected interactively by clicking your mouse on a surface or volume.

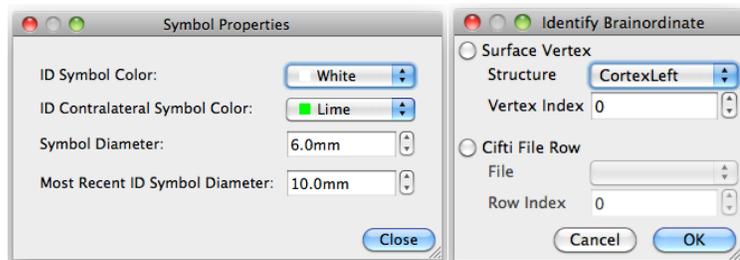
- Click back to **Tab 1**, labeled (1) *Montage*.
- Click anywhere on the brain surface in the Viewing Area.
- Upon making a selection, a sphere will appear where you clicked and the **Information box** will appear (**Figure 2.5**).



**Figure 2.5 – Information box**

- Move the **Information box** wherever you prefer by *dragging* the top of the box.
- Information provided for surface ordinates includes the vertex number, surface name, x, y, z coordinates on the surface being displayed, and the values for scalars and labels (plus any other data that is being displayed) at that ordinate available from files loaded in the current Workbench session (**Figure 2.5** and [Figure 1.5](#)).
- For volume ordinates, voxel coordinates in stereotactic space and slice indices for the loaded volume are given, along with values for connectivity or metric data loaded that displays in volumes.
- Click on **RID (Remove Identification)** in the right side of the **Information box**. The identified brainordinates will clear on the displayed surface and in the Information box.
- Click *again* on the brain surface in the **Viewing Area**.
- Clicking on the **Clear button** will clear all text in the **Information box**. Note this does not clear the identification of brainordinates in the **Viewing Area**.

- The **Copy button** copies all manually highlighted text in the Information box for pasting information you want to keep into an external text editor.
- *Click* the **Contra ID** button.
- *Click* a few places on one hemisphere of the surface montage. As before, a sphere appears at the brainordinate you selected. However, you will see lime spheres have appeared at brainordinates contralateral to those you selected (i.e. on the corresponding ordinate in the opposite hemisphere).
- *Click* on the **Properties** button. A **Symbol Properties** box will pop up (**Figure 2.6**, left).
- *Change* the **ID symbol color** to Fuchsia, the **ID Contralateral Symbol Color** to Teal, and the **Symbol Diameter** to 9 and the **Most Recent ID Symbol Diameter** to 12.
- *Click* **OK** to enter your changes. Notice that the ID symbols change on the surfaces.



**Figure 2.6 – Symbol Properties (left) and Identify Brainordinate (right) boxes**

- *Click* **OK** to enter your changes. Notice that the ID symbols change on the surfaces.
- *Click again* on the **Contra ID button** to deactivate it.
- *Click* on the Select Brainordinate button.
- An **Identify Brainordinate box** will pop up (**Figure 2.6**, right) where for any loaded surface you can select a vertex by index number or, if one or more dense connectome CIFTI files are loaded, you can select a File and File Row index to identify. *Click* **Cancel**.
- *Click* the **Close button** to close the **Information box**.
- *Click* on the **Information box**  icon in the upper right corner of the Workbench Window. The icon should appear unselected. This means that when you click on a surface or volume to identify a brainordinate, the Information box will NOT pop up.
- *Click again* on the **Information box icon** anytime to show the information box.

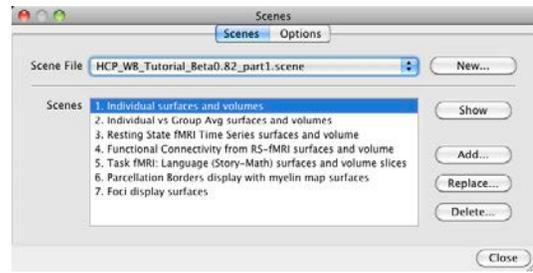
Even when the **Information box** is inactivated, information on identified brainordinates is still stored and can be seen by showing the Information box (clicking on the icon to reactivate it).

## Scenes Box

The **Scenes box** allows you to save your current Workbench session (loaded files and settings) in a file as a “[Scene](#)”. Often views in Workbench require several steps to set up. Scenes allow the user to save a snapshot of a Workbench session that contains a record of all of the files loaded and view settings for that session.

We have provided a **scene file** in the tutorial dataset with several scenes that offers a quick way to load views that show off the HCP data provided and many features of Workbench. By reopening a saved scene file, a user can “pick up where they left off” when they reopen Workbench.

- Open the **Scenes box** by clicking the **clapboard**  **button** in the upper right of the **Workbench Window**.
- The **Scenes box (Figure 2.7)** will appear.
- To load a scene, *click* any of the Scene names in the **Scenes field** to select it and click the **Show** **button**. (Alternatively, double click on any of the Scene names to load it).



**Figure 2.7 – Scenes box**

For now, you don’t need to open one of the preset tutorial scenes (they are explored scene-by-scene in Chapter 1). We will create a new scene in the next section (Screen Views).

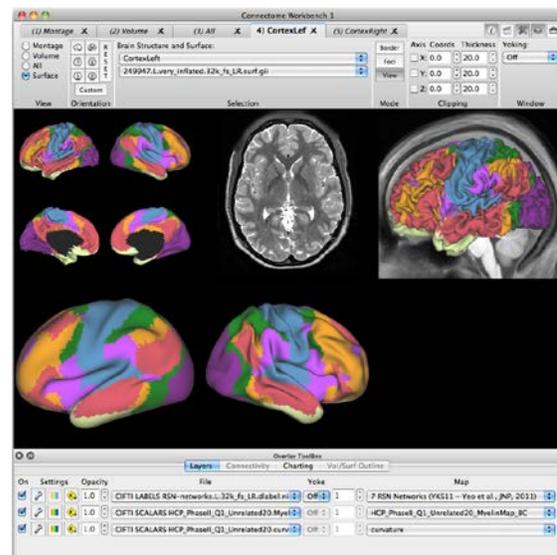
- To create a new scene of your current Workbench session to be stored within the current scene file, *click* the **Add... button**.
- The **New Scene popup** will appear in which you need to name your scene and add a description of the scene (optional).
- If you have modified an existing scene and want to save your changes, make sure that the correct scene is highlighted and *click* the **Replace... button**.
- To create a new scene file (file that can contain several scenes), click the **New... button** next to the Scene File field. The new scene file you create will have no scenes within it to begin with, so you will need to add scenes to it.
- If you did load one of the other scenes above, double click on the “**Tutorial Chapter 2**” scene to continue with the tutorial.
- When done, *click* **Close** at the bottom of the **Scenes box**.

## Screen Views and the Window Menu

In addition to the normal tab-by-tab window-based viewing mode we have been using so far in this tutorial, Workbench also has **Full Screen** and **Tile Tabs** views.

- In order to change between views, *click* on **View** in the **Menu bar** at the top of your screen (Mac) or at the top of your **Workbench Window** (PC/Linux). *Select* **Enter Full Screen** or use the keyboard shortcut **Cmd/Ctrl+F**.

- **Full screen** view shows your Normal Viewing Area without Toolbar or Toolboxes over your entire screen. Press **Esc** or **Cmd/Ctrl+F** to go back to Normal view.
- **Tile Tabs** view allows you to view and interact with all of the brain surfaces and volumes you have open in the tabs of a Workbench Window as “panes” in one Viewing Area.
- **Select View ► Enter Tile Tabs** (or use the keyboard shortcut **Cmd/Ctrl+M**). The views for each tab in the active window are tiled in order and your view should resemble **Figure 2.8**.
- **Click** on any of the surfaces. Notice that the brainordinate you identified is shown in all “panes” of the montage.
- Rotate one of the surfaces. Each surface/volume rotates, pans, and zooms independently of each other unless they are **yoked**.

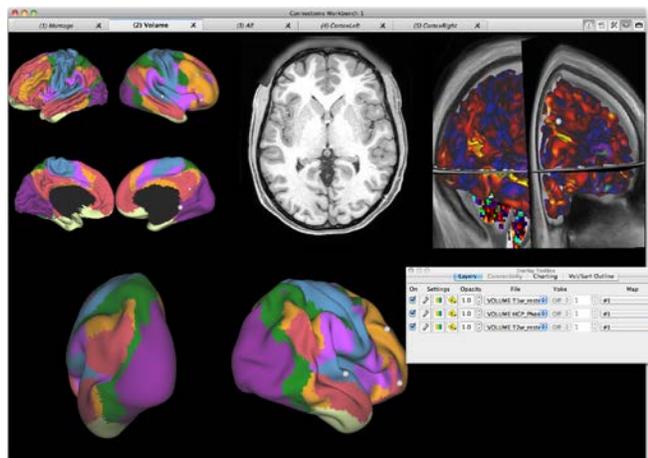


**Figure 2.8 – Tile Tabs view**

In Tile Tabs view, even though you are viewing multiple tabs at once, the Toolbar and Toolboxes control the structures and data for the selected tab only.

You can switch the controls to a different tab simply by clicking on the tab you want at the top of the Workbench Window (or using the shortcuts **Cmd/Ctrl+right/left** arrow keys)—the “pane” in the Viewing Area that corresponds to that tab will be indicated by the brief appearance of a white box around it.

- **Click** on Tab (3) *All* and note the white box indicating your controls have shifted to that tab.
- **Change** the top layer to **DATASERIES CP10101...dtseries.nii**.
- **Click** the **Toolbar icon**  to hide the Toolbar.
- **Drag** the top of the **Overlay Toolbox** to detach it from its anchorpoint at the bottom of the Viewing Area.
- **Change** the width of the now floating Overlay Toolbox by left clicking + dragging the resize button on the lower right.
- **Click** on Tab (2) *Volume*.
- **Change** the top layer to **VOLUME T1w...nii**. Your workspace should now look similar to **Figure 2.9**.

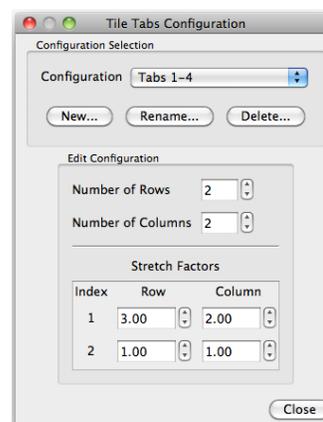


**Figure 2.9 – Tile Tabs view without Toolbar and floating Overlay Toolbox**

This is a convenient setup for your workspace that maximizes your ability to do side-by-side comparisons of different structures and data while also allowing you to easily make changes to what you are viewing in each tiled tab.

Using the Tile Tabs configuration option in the View menu, you can also control the number and size of the panes in your Tile Tabs view window and save these settings.

- Select **View ► Tile Tabs Configuration**, then select **Create and Edit....** (shortcut shift+Cmd/Ctrl +M).
- The **Tile Tabs Configuration box (Figure 2.10)** will appear.
- Click the **New** button.
- Type **“Tabs 1-4”** as the View Name.
- Set the number of rows to **“2”** and set the number of columns to **“2”**.



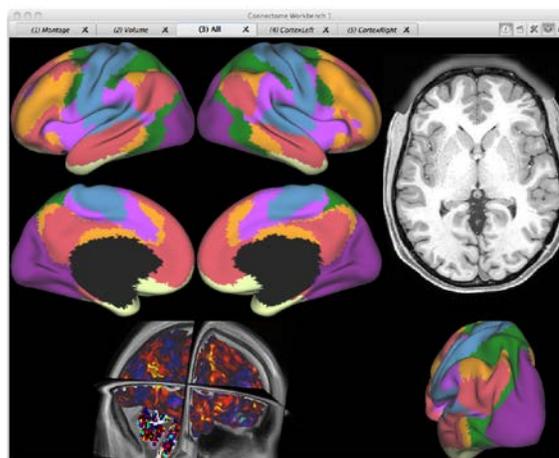
**Figure 2.10 – Tile Tabs Configuration box**

The Stretch factors allow you to adjust the relative size of the Tile Tabs “panes”. With 2 rows and 2 columns, the Index refers to the first (1) and second (2) row and column.

- Click on the **Index 1 Row field** and use the toggles, your mouse scroll wheel, or up arrow button to set the stretch factor to **2.00**. Notice how the first row expands accordingly, while the second row shrinks.
- Click on the **Index 1 Column field** and also set this stretch factor to **2.00**. Notice how the first column also expands, while the second column shrinks. Click the **Close** button.
- Move the Overlay Toolbox off to the side of the Viewing Area.
- Move your cursor into the Viewing Area and zoom in on each structure until it fills its “pane”. Your Viewing Window should now look like **Figure 2.11**.

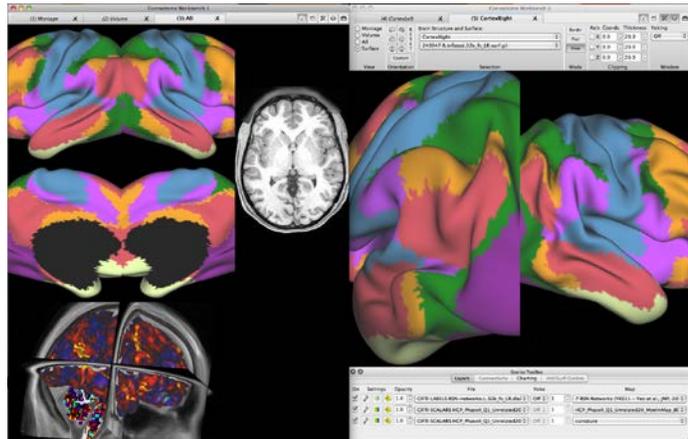
In any screen view, you can control the number of tabs you are showing by controlling which tabs you have open in a particular window using options in the **Window Menu**. As an example, let’s move tabs 4 and 5, Cortex Left and Cortex Right to a new Window.

- Click on Tab (4) *CortexLeft*.
- Click on the **Window Menu** at the top of your Desktop or Workbench Window.



**Figure 2.11 – Four “pane” zoomed Tile Tabs configuration**

- **Select Move Selected Tab to Window ► New Window.** A second Workbench Window will appear with Tab (4) in it. Notice that Tab (5) replaced Tab (4) in the Tile Tabs configuration of Window 1.
- *Click on Tab (5) CortexRight.*
- Similarly move this tab to the **Connectome Workbench Window 2** that you just created. Now Tabs (4) and (5) are in a window together in the normal screen view.



**Figure 2.12 –Tile Windows view**

- *Click* anywhere on this new Workbench Window 2 to select it. Now that it is selected, use the shortcut **Cmd/Ctrl +M** to invoke Tile Tab view for this window.
- *Click* on the Window Menu again and **select Tile Windows.** This will resize both windows to fill your Desktop as in **Figure 2.12.**
- Resize the windows, and move or turn on/off the Overlay Toolbox and Toolbar as desired.

Once you find a workspace configuration and particular view for a set of data that you like, you can save a scene with those settings so that you can easily come back to that view of the data.

- Open the **Scenes box** by *clicking* the **clipboard**  button in the upper right of the **Workbench Window.**
- *Click Add* and name the scene as desired, e.g. “My Tutorial Screen View”.
- *Click OK.* You should see you new scene added to the scenes list.
- Double click on any of the other scenes listed to load them.
- Double click on the scene you just created and notice that all your settings were saved.
- Double click on the “**Tutorial Chapter 2**” scene to continue with the tutorial.

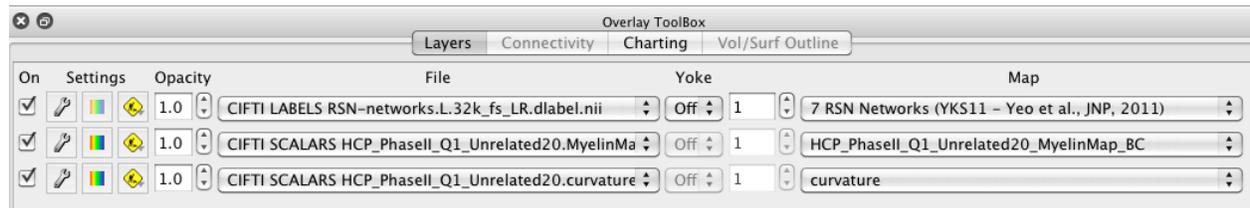
## Overlay Toolbox

The **Overlay Toolbox**, located below the **Viewing Area**, contains settings for what loaded data you want to view on the brain structure you are viewing in the currently **Active Tab**. When you change a setting in the **Overlay Toolbox**, the changes only apply to the tab you are currently viewing. The **Overlay Toolbox** is organized in tabbed menus: **Layers**, **Connectivity**, **Data Series**, and **Vol/Surf Outline**.

- *Click back* to **Tab 1** labeled (1) *Montage* at the top of the Viewing Window.
- *Click* on the Overlay Toolbox **Layers Tab**.

## Layers Tab

The **Layers Tab** (Figure 2.13) allows you to set the files and maps you want to visualize on the brain surface or volume currently displayed in the **Viewing Area** of the **Active Workbench Window Tab**.



**Figure 2.13 – Overlay Toolbox: Layers Tab**

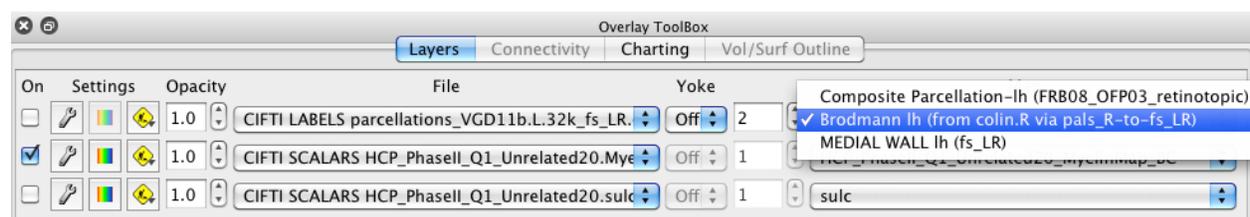
The layers set in the Layers Tab apply to all surface types of the structure displayed in the Viewing Area (e.g. if you set layers for an Anatomical surface then switch to an Inflated surface, the layers will remain the same).

By default, Workbench loads 3 layers into the **Toolbox**. The top layer of displayed data is listed first, the second layer below that, etc., like a layer cake.

- Click to *check and uncheck* the **checkboxes** under **On** at the left side of the Layers Tab. The data loaded into each layer will be toggled off and on on the displayed surface. When a top layer is unchecked, you see the layers underneath that layer displayed on the surface. Leave all 3 layers unchecked.
- In the **File pull-down** you can set what file you want to view from the data files that loaded when you opened your spec file. Each file contains one or more brain maps that can be displayed on the surface.
- Check the top layer **On** and set **File** to:  
**CIFTI LABELS parcellations\_VGD11b.L.32k\_fs\_LR.dlabel.nii**
- Click the **Map pull-down button** in the top layer, *select* Brodmann lh (Figure 2.14).

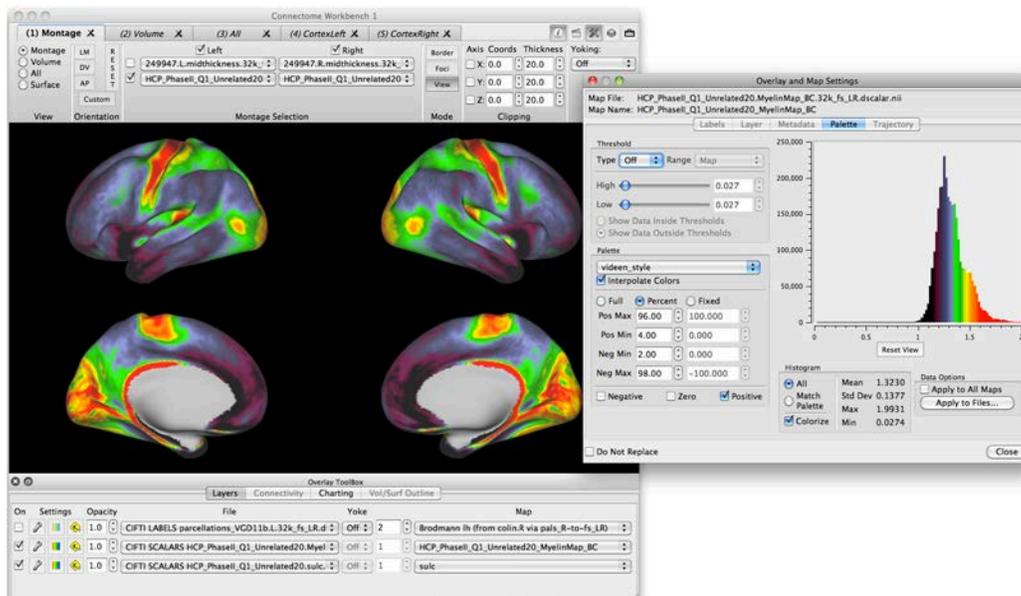
The top layer will now display the classical [Brodmann \(1905\)](#) architectonic parcellation. This map is derived from a mapping of the Brodmann areas onto the colin.R and colin.L atlas subsequently registered (deformed) to the fs\_LR atlas.

- *Uncheck* the **‘On’ checkbox** at the left of the top layer.



**Figure 2.14 – Overlay Toolbox: Layers Tab, Map Selection**

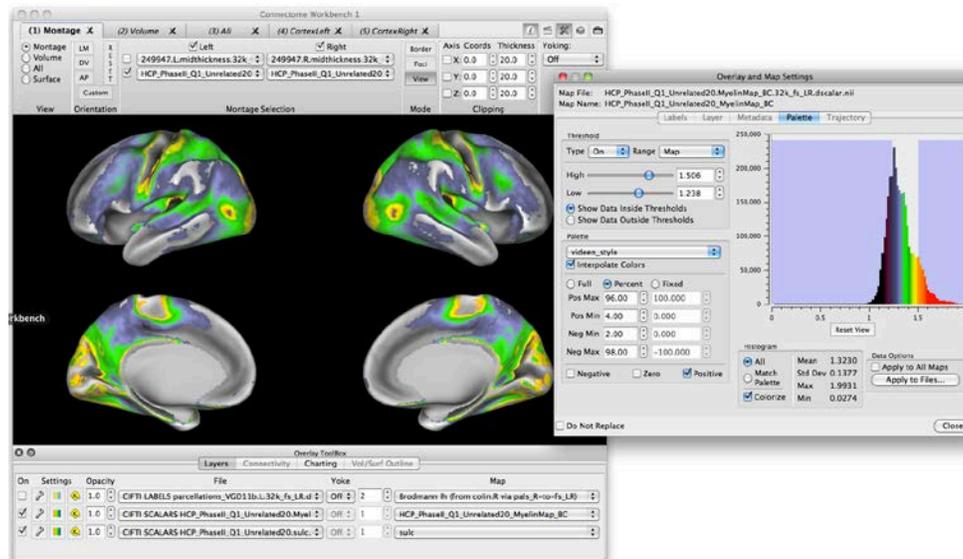
- Check **On** the second layer and you should now see **CIFTI SCALARS HCP\_PhaseII\_Q1\_Unrelated20.MyelinMap\_BC. 32k\_fs\_LR.dscalar.nii**
- Also check **On** the third layer and set **File** to **CIFTI SCALARS HCP\_PhaseII\_Q1\_Unrelated20.sulc.32k\_fs\_LR.dscalar.nii**
- Click the **Settings**  button in the second layer, to the right of the checkbox.
- A popup window will appear, as seen in **Figure 2.15**. If you'd like to reposition this box, *left click and drag* the top of the popup to the desired position on your screen.



**Figure 2.15– Layers Settings: Non-Thresholded Data**

- The **Overlay and Map Settings** box allows you to set attributes of the map selected for the layer for which the settings button was clicked. Currently, there are five tabs in this box: **Labels**, **Layer**, **Metadata**, **Palette**, and **Trajectory**.
- The **Labels**, **Metadata**, and **Trajectory** tabs are currently under development. The **Labels** tab will allow you to edit the color and name of map labels; the **Metadata** tab will allow you to add descriptive metadata to a map; the **Trajectory** tab will allow you to set properties for display of a Fiber Trajectory file.
- The **Layer** settings tab is currently only active (not greyed out) for Volume layers in the All (whole brain) view. Here, you can set whether voxels are drawn on the slices or as 3D cubes (only applies in the All viewing mode).
- Click on the **Palette** tab, if not already selected. Here, you can change the thresholds applied to the map being viewed, change the color palette (spectrum) of the displayed data, and view a histogram of the data being mapped.
- Click on the **Type** pull-down in the **Threshold** section of the **Palette** tab. **Select On**.

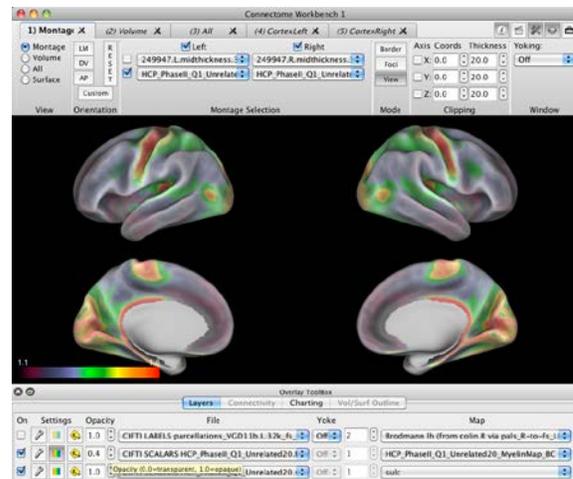
- Move the **High and Low sliders** to adjust the high and low thresholds. The default is to show **Data Outside the Thresholds**. Select the **Show Data Inside Thresholds** radio button. In both cases, data excluded by the thresholds is shaded blue in the histogram graph.
- Again move the **High and Low sliders** to adjust the thresholds. The display in the Viewing Area should look something like **Figure 2.16**.



**Figure 2.16 – Layers Settings: Thresholded Data**

- To change the palette, or color spectrum, of the data displayed on the surface, *hover over the palette selector* below the Threshold settings and *scroll* to browse the different palettes available (or *left click and select* from the pull-down). *Reset* to the original **videon\_style** palette.
- The **Range** pull-down menu allows you to set the range of data controlled by the Threshold sliders by range of data values in the File or Map or by Unlimited values.
- The settings below the **Palette selector** allow you to set the range of data you want represented in the palette. Selecting:
  - **Full** shows the full range of the data.
  - **Percent** shows the range of data set by percentage in the settings below it (here the spectrum positive maximum is set to 96% and the positive minimum is set to 4%, therefore the top and bottom 4% of data values are not represented in the spectrum).
  - **Fixed** shows a range of data in real data values set by the user (for this myelin map data, a positive max of 1.6 and a positive min of 1.1 makes sense).
- Set the **Palette selector pull-down** back to **videon\_style**, set the **Threshold Type pull-down** back to **Off**, and close the **Overlay and Map Settings popup** by *clicking* the red **X button** in the top left or right, or the **Close button** in the bottom right.

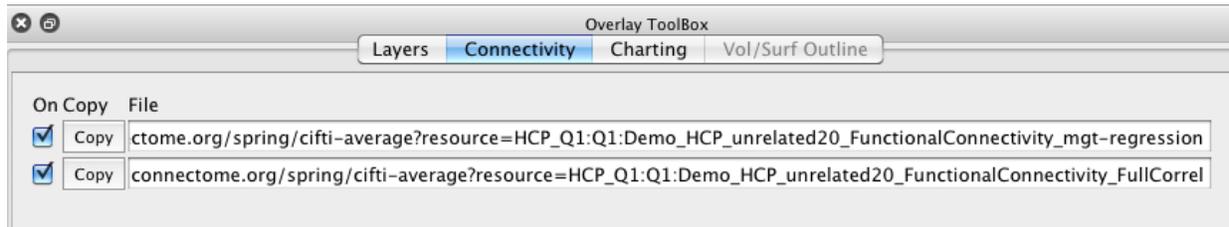
- Back in the **Layers Tab**, the **Colorbar**  **button** shows a colorbar of the data spectrum set in the **Settings Box**. If thresholds are set, the colorbar will reflect the high and low thresholds.
- The **Add/Move/Remove Layer**  **button** opens a dropdown with options to add new layers, move layers up and down, and remove layers.
- The toggle box to the right of the layer add/move button allows you to set the **Opacity** for the layer.
- Use the down arrow to set the Opacity of the **CIFTI SCALARS HCP\_PhaseII\_Q1\_Unrelated20.MyelinMap...** layer to 0.40. The Viewing Area should look like that of **Figure 2.17**. Notice the **Tooltip** for opacity in the yellow box on **Figure 2.17**.
- *Click* on the top layer's **File** dropdown and *select* **DATA\_SERIES CP10101\_HCP\_Pilot-1.fMRI.dtseries.nii**.
- *Click* the **On** checkbox for the first layer.
- You are now viewing the first (time 0 seconds) BOLD activation frame of the resting state time series. The default ROY-BIG palette (as in [Figure 1.9](#))—shows high BOLD signal in yellow/orange/red and low BOLD signals in cyan/green/violet/blue (after regressing at the global mean signal).
- In the frame number field, *click the up arrow* (or mouse scroll up) and watch the BOLD maps change for successive time frames.
- The **Yoke** option allows you set a yoke group (identified by Roman numerals in the Yoke pull-down) to link viewing the maps of more than one data series file by “frame” to ease display. This is especially useful for viewing and comparing two files containing the same type of data for (e.g. comparing the same task activation between two or more subjects over various experimental conditions, or comparing two or more types of processing for data from the same subject). Yoking groups are active between Workbench Windows and Tabs.



**Figure 2.17 – Setting Layer Opacity**

## Connectivity Tab

The Overlay Toolbox **Connectivity Tab** lists connectivity files that are loaded in your Workbench session. The Connectivity Tab is greyed out (inactive) if no connectivity files are loaded, as we have here in chapter 2. In chapter 1 of this tutorial, when we access the dense functional connectivity via the **Open Remote File dialog** as described in [Scene 4: Functional Connectivity from RS-fMRI surfaces and volumes](#), the links to the functional connectivity data appear in the Connectivity Tab (**Figure 2.18**).



**Figure 2.18 – Overlay Toolbox: Connectivity Tab**

The checkboxes to the left of the listed connectivity files control whether the connectivity is refreshed when you identify a brainordinate. Turning these off can be important when many connectivity files are loaded or when your internet connection to remote files is slow or disabled.

## Charting Tab

The Overlay Toolbox **Charting tab** lists all dense scalar and dense data series files that contain multiple maps currently loaded into your Workbench session. Both of these file types contain continuous (real numbers) for some or all brainordinates (cortical hemisphere vertices and/or sub-cortical voxels).

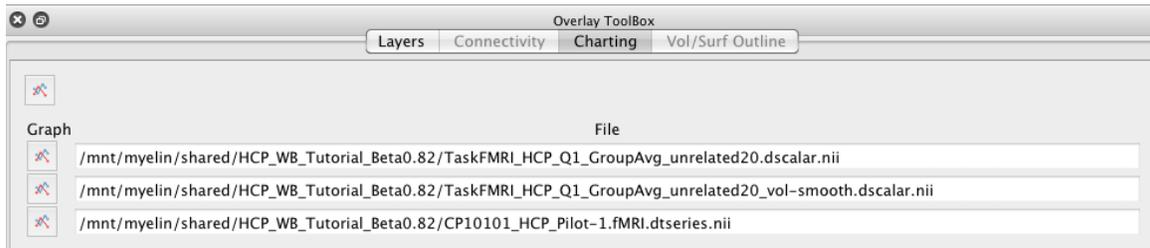
A dense data series file contains a sequence of related data with one measurement for the brainordinates in each of many maps (frames) and each map (frame) is in the same data units. The names of the map in a data series file indicate the position within the sequence of the data. The most common data series file we use for HCP is the time series file (commonly resting state data) and its map names are the time corresponding to frame in the MRI data. Other non-temporal data sequences may be added in the future.

In contrast, a dense scalar file contains one or more maps of related or non-related data and the data in each map may be of different units. The names of the maps in a dense scalar file are text describing the data within the map. Examples of dense scalar files include myelin data, rfMRI/tfMRI contrast maps, ICA components, or cortical shape data.

Both files types have their data colored by a color palette and the user may adjust the settings that are used to apply the color palette. Since a dense data-series file contains multiple frames of related data, there is a single color palette within the data series file that is used to color all frames within the file. In contrast, since dense scalar files usually contain unrelated data, each map in the dense scalar file contains a color map so that the data within each map may be uniquely colored. Lastly, all maps within a single data series or scalar file must always contain the same number of brainordinates.

### Comparison of File Attributes

Attribute	Dense Data Series	Dense Scalar
Maps/Frames	Sequence of Related	Unrelated
Palette Mapping	One per file	One per map
Maps	Many Frames	Smaller number of maps
Units	All Frames same units	Each map may be different units

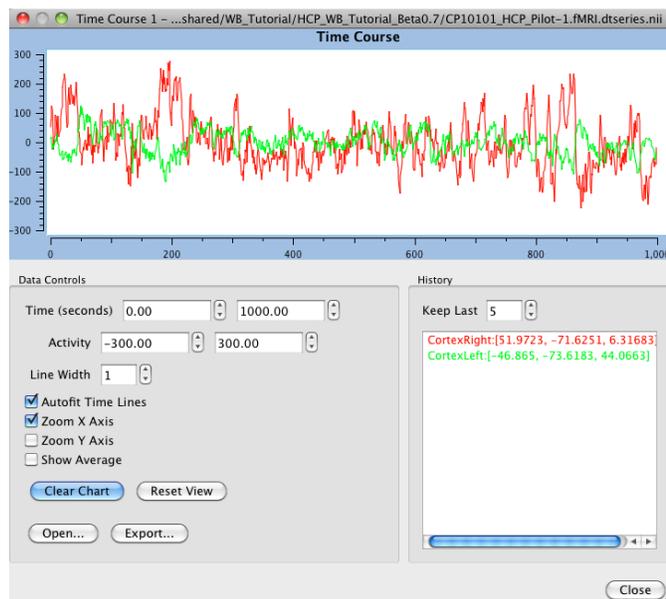


**Figure 2.19 – Overlay Toolbox: Charting Tab**

- Click on the **Overlay Toolbox: Charting tab**.
- When the **HCP\_beta0.83\_tutorial.32k\_fs\_LR.wb.spec** Spec file was loaded, three dense data series files were loaded and are listed in the Charting tab (**Figure 2.19**).

The first file contains grayordinate-smoothed HCP Q1 group average task fMRI contrast maps. The second contains a single frame grayordinate-smoothed myelin map. The third file contains volume-smoothed HCP Q1 group average task fMRI contrast maps with the same number/types of contrasts as the first file. The last file is the BOLD fMRI dense time series file from the individual subject CP10101.

- The **Graph button** for each row activates the time course graph function for the data series file listed. When a grayordinate is identified, a popup box appears that shows variation of the activity signal over the time course. This is especially useful for analysis of resting-state fMRI BOLD signals in different brain regions.
- Click the graph button for the bottom **CP10101...** file.
- Click anywhere on the brain surface. A **Time Course** graph will pop up (**Figure 2.20**).
- Click *again* on the surface. The time course for that grayordinate is shown in a different color along with the first on the graph.
- Move your mouse over the graph and scroll up and down to zoom along the X axis. Alternatively, adjust the high and low **Time** fields at the top left of the **Data Controls** to adjust the time range of data you want to view (X axis).



**Figure 2.20 – Data Series Time Course Graph**

- Click the **Zoom Y Axis checkbox** (and *deselect* the **Zoom X Axis checkbox**) to enable Y axis zooming with your scroll wheel in the graph area. Alternatively, adjust the high and low **Activity** fields in the Data Controls to adjust the activity range of data you want to view (Y-axis).

- Click **Reset View** to reset the zoom to the defaults defined by the data.
- Click the **Show Average checkbox** to show an average of the two (or more) time courses viewed on the graph.
- The **History** section allows you to interactively set the number of time course plots you want to keep on the graph before they are overwritten and shows X, Y, Z coordinate values of the grayordinates you clicked color-coded to match their displayed time course plots.
- The **Open...** button allows you to open a timeseries Dvars .txt file for viewing as a chart.
- The **Export...** button allows you to save an image of the graph currently displayed or save the data for a particular plot as a .txt file.
  - To save the graph currently displayed, *click Export...*
  - Choose a file name with the image file type extension (e.g. .jpg) you want (default is .bmp), make sure that Image files is chosen as the file type, and *click Save*.
  - To save the data from a particular plot (one column of data from the CIFTI dscalar or dtseries file), first *select* the desired plot by *clicking on the corresponding coordinate in the History section* (e.g. **CortexRight:[51.9723, -71.6251, 6.31683]**), then *click Export...*
  - Choose a file name, change the file type to **Dvars files (\*.txt)**, and *click Save*.
- Click **Close** to close the Time Course Graph window.
- Back in in the **Charting tab**, *click* the pressed down (darkened) **Graph button**  *again* to turn off the Time Course Graph popup.

## Volume/Surface Outline Tab

The Overlay Toolbox **Volume Surface Outline Tab** (Vol/Surf Outline for short) allows you to set parameters for viewing brain surface outlines on volume slices in the **Volume** or **All** (Whole Brain) **Viewing Tabs** (the Vol/Surf Outline tab is inactive in the Surface and Montage Views). This is useful for comparing your Freesurfer or otherwise reconstructed surface with your T1-weighted structural maps as a check of the quality of the surface. It is also useful for viewing Connectivity data (dense connectivity and BOLD dense data series files) on both the cortical ribbon and in subcortical voxels (see [Scene 3: Resting State fMRI Time Series surfaces and volumes](#) in Chapter 1).

- Click on Viewing **Tab 2, (2) Volume**.
- Click on the **Overlay Toolbox: Layers** tab and switch the first layer to VOLUME T1w\_restore.nii.gz (individual subject 249927).
- Click on the **Overlay Toolbox: Vol/Surf Outline** tab.

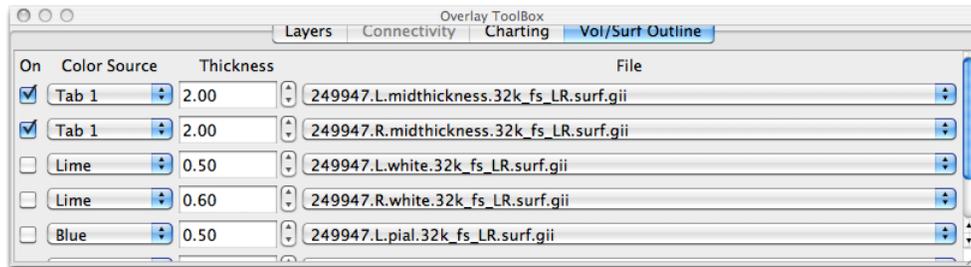


Figure 2.21 – Overlay Toolbox: Vol/Surf Outline Tab

- Click the top two outline selections **On**, change the **Color Source** for both to Tab 1, the **Thickness** to 2.00 and the **Files** to the individual left and right midthickness surfaces (249947.L.midthickness.32k\_fs\_LR.surf.gii and 249947.R.midthickness.32k\_fs\_LR.surf.gii) as shown in **Figure 2.21**.
  - We are now viewing the surface outline for the individual time-series BOLD activation for CP10101 (which is the top layer for Tab1 montage) for both hemispheres (**Figure 2.22**).
  - Click the up and down arrows in the **Thickness** column to adjust the thickness of each outline. The default thickness of 5.00 is approximately the width of the cortical gray matter ribbon. Thickness is centered at the average cortical midthickness.
  - Toggle off these first two surface outlines and toggle on the third, fourth, fifth, and sixth outlines.
- The third and fourth outlines show the white matter/ gray matter boundary surface for this individual in lime green. The fifth and sixth show the pial surface in blue.
- In the **Toolbar**, scroll or toggle through the Axial (A) slice indices and watch the outline change with the volume (**Figure 2.23**).

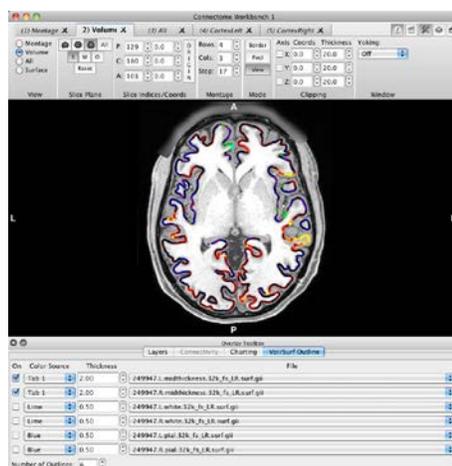


Figure 2.22 – Volume Surface Outline: Top layer of Viewing Tab 1

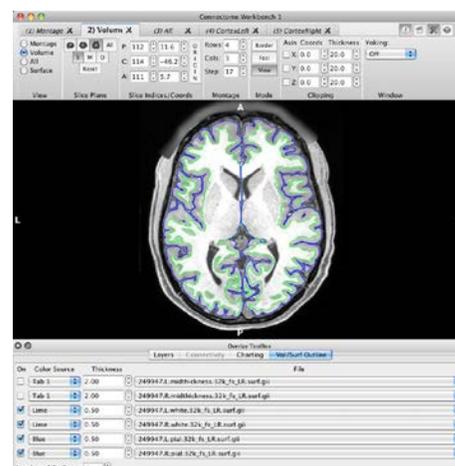


Figure 2.23 – Volume Surface Outline: White and Pial surfaces

## Features Toolbox

The **Features Toolbox** allows viewing of additional features such as borders and foci on top of data layers set in the **Overlay Toolbox**.

- Click on Viewing **Tab 1, (1) Montage**.
- Click off the top layer to display layer 2, the group average Myelin Map.
- To open the **Features Toolbox**, click the **Features Toolbox icon**  in the upper right corner of the **Toolbar**.
  - Alternatively, in the Menu bar, select **View ► Features Toolbox ► Attach to Right**.
- To detach it from the right side of the **Viewing Area**, place your cursor on the top of the **Features Toolbox** hold down the left mouse button and drag the **Toolbox** to the side off the **Workbench Window**. This will also restore the full size of the Viewing Area.
- The **Group dropdown** allows you to set the Features group for your current Active Viewing Tab.
- Grouping tabs allows you to change the Features that you are displaying in several Viewing Tabs all at once. For example, you may want to display a particular set of borders in tabs 2, 3, and 5 only (Group A) and another set of borders and foci in tabs 1 and 6 (Group B).
- When the Group dropdown is set to 'Tab', the settings in the Features Toolbox will apply *only* to the Active Tab.

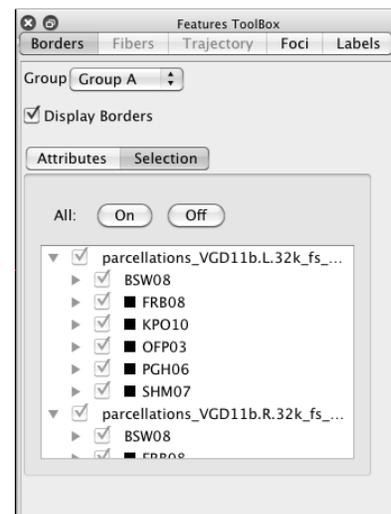
## Borders Tab

The **Borders Tab** in the **Features Toolbox** allows you to display and view an organized selection list of loaded and newly created borders on brain surfaces.

*Note:* Currently, borders are only viewable on surface structures. Future versions of Workbench will enable this feature in brain volumes as well.

- **Toggle on Display Borders** in the **Borders: Attributes tab**.
- Click on the **Borders: Selection tab**. We are viewing the borders from the **parcellations\_VGD11b...border** file for each hemisphere (recall VGD11b is from the [Van Essen et al. 2011b](#) publication).
- Loaded borders are organized by border file (top tier) and class (second tier) (**Figure 2.24**).

These borders are derived from a composite cortical parcellation based on architectonic or retinotopic fMRI maps ([Van Essen et al. 2011b](#)). Border class abbreviations (FRB08, OFP03, etc.) refer to the publication that defined



**Figure 2.24 – Borders Selection**

a particular cortical area in the map (cf. Table 3 of [Van Essen et al. 2011b](#)).

- If they are not displayed already, in the **Layers** tab of the **Overlay Toolbox**, change the top layer to:

CIFTI LABELS parcellations\_VGD11b.L.32k\_fs\_LR.dlabel.nii

- The borders match the Composite Parcellation map from the Labels file.
- *Click off* the second layer in order to see these parcellations more clearly.
- *Zoom and pan* to get a close up view of some of the borders on the surface.
- *Click back* on the **Borders: Attributes tab**.
- *Toggle on and off* the **Contralateral checkbox**. This button displays the borders of the contralateral hemisphere on top of the borders from the hemisphere you are viewing. Notice the differences in the parcellation borders between the two hemispheres.
- *Toggle off* **Display Borders** and *Reset* the orientation.

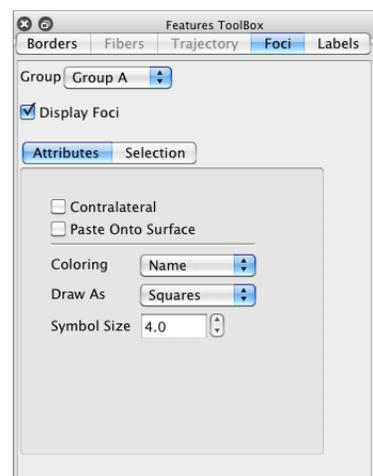
## Foci Tab

The Foci Tab in the **Features Toolbox** allows you to display and view an organized selection list of loaded foci on brain surfaces.

*Note:* Currently, foci are only viewable on surface structures. Future versions of Workbench will enable this feature in brain volumes as well.

- In the **Features Toolbox**, *switch to* the **Foci: Attributes tab** (**Figure 2.25**)
- *Toggle on* **Display Foci**, *change* the **Size** to 8.0.
- The default shape of foci is **Squares** to differentiate foci from identified brainordinates. *Change* **Draw As** to **Spheres**.
- *Change* the **Coloring** to **Class**, now all the foci should be displayed in black since all are in the same class.
- *Switch to* the **Foci: Selection tab**.

Just as with the borders, loaded foci are organized by foci file (top tier) and by class (second tier).



**Figure 2.25 – Foci Attributes**

- Foci from the **Parcels\_GV11...foci** file are located at the center of mass of the probabilistic cytoarchitectonic areas (originally defined by [Amunts and Zilles](#)) used by [Glasser and Van Essen 2011](#) for comparison to areas defined by myelin mapping.
- *Toggle off* **Display Foci**.
- *Click On* the second layer (Myelin Map) in the **Overlay Toolbox: Layers tab**.

## Labels Tab

The Labels Tab in the **Features Toolbox** allows you to display and view an organized selection list of loaded labels (named colored regions) on brain surfaces. Therefore, when labels are displayed, regions appear painted on the brain surface. The parcellation map (parcellations\_VGD11b) in the top layer is made up of many of these labels that describe and color cortical areas.

*Note:* Currently, labels are only viewable on surface structures. Future versions of Workbench will enable this feature in brain volumes as well.

- In the **Features Toolbox**, *switch to* the **Labels: Selection tab** (Figure 2.26).

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 list is the red label **hOc5\_MT** for area MT in the occipital lobe on the left hemisphere. *Try toggling* this label *off and on* and notice how this label roughly lines up with an orange/yellow patch on the myelin map of the HCP\_Q1\_Unrelated subjects, indicating high myelin content.
- Scroll up and *click* the **Attributes tab**.
- *Click* the **Draw as: dropdown** and *select* **Outline**. Now only the edge of the label is shown as a colored outline.
- *Switch* back to **Selection tab** and *click* **All: Off**
- *Click* the 'X' in the top left corner of the **Features Toolbox** to close it.

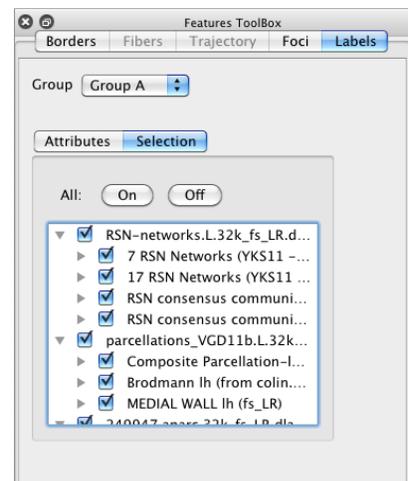


Figure 2.26 – Label Selection

## Save/Manage Files

The **Save/Manage Files dialog** allows you perform several operations on the files loaded into your Workbench session, including saving modified files.

- Select File **Menu** ▶ **Save/Manage Files...** (or the shortcut: command + S) to open the dialog (Figure 2.27).

The bars at the top of the dialog contain buttons that filter the listed files as we saw in the Open Spec File dialog (Figure 1.3).

- Checkboxes in the **Save column** the left allow you to choose which files will be saved/overwritten once you press the **Close** button in the lower right.

- A **YES** in the **Modified** column indicates that there have been changes to the listed file that need to be saved or discarded.
- The checkboxes in the **In Spec** column indicate whether the file is currently being saved as part of the Specification file shown at the top of the list. You can use these to add or take files out of a spec file.
- *Click* on a few of these **In Spec checkboxes** and notice that a **YES** appears in the Modified column for the Specification file because you have indicated that you want to remove files from the spec file.

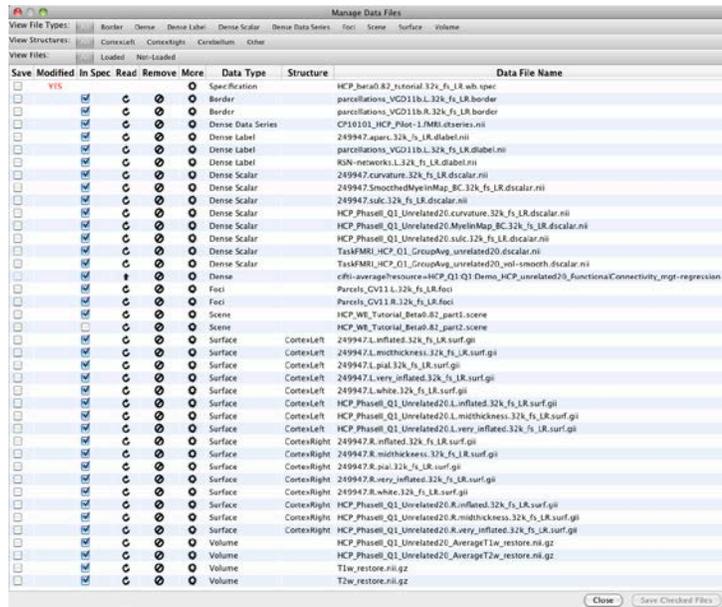


Figure 2.27 – The Save/Manage Files dialog

- If you wanted to save these changes, you would need to *click* the **Save checkbox** for the spec file and *click* the **Save Checked Files button** at the bottom right.
- The **Read** column allows you to:
  - reload files that are currently loaded into memory (indicated by )
  - load files that are currently not loaded (indicated by )
- The **Remove** column  removes a previously loaded file from memory but not from the spec file itself. This is useful if you are running other applications that are memory intensive.
- The **More** column  gear buttons allow you to edit the metadata associated with a file or change the name of a file. If you edit the metadata, you will see that that is sufficient to trigger the **YES** in the Modified column.
- Remember, if you want to save the changes to any file you modified here or elsewhere in Workbench, you need to click the Save checkbox for the file, and click the Save Checked Files button (or hit Return).

## Help Menu

The Help menu (File Menu ► Help...) (Figure 2.28) gives you options to search Workbench, launch the HCP website and Submit feature requests to the developers of Workbench software.

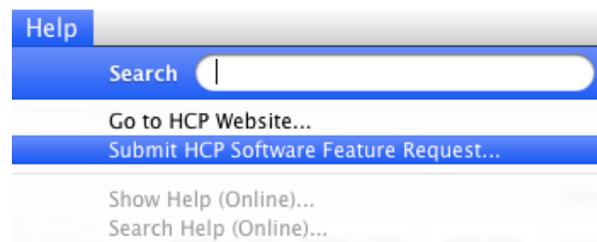
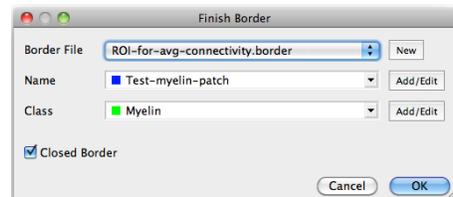


Figure 2.28 – Help menu



- Click the **Border button** in the **Toolbar: Mode section**. This opens the Border drawing and editing tools at the top of the **Viewing Area**.
- The loaded border files are automatically displayed on the surface. To turn them off before drawing a new border, click the **Features Toolbox icon**  in the upper right hand corner of the Workbench Window to pop up the Features Toolbox on the right edge of the Viewing Area.
- Click the **Borders:Selection tab**.
- Click the **down arrow** beside the border files (parcellations\_VGD...) to collapse the list of borders and **deselect** their checkboxes. This will turn off every border within that file.
- When you start Border Mode, the **Draw** tools are selected by default (at the top of the Viewing Area) and the cursor becomes a pen icon, indicating that you are ready to draw a border.
- Now use the myelin map as your guide to draw an outline around the MT patch. *While holding down the alt/option key and the left mouse button*, trace around the entire green and yellow patch that is identified as MT with your mouse in a clockwise direction.
  - You can draw multiple short sections (these just all need to be drawn in the same direction) in order to make a complete border or you can draw a single, continuous line.
  - Reminders of the mouse and key strokes used to draw a new border, or erase, extend, or replace a border you have already drawn are available as **Tooltips**. *Hover your mouse over the **New**, **Erase**, **Extend**, or **Replace** buttons* for the tooltips to appear.
  - The mouse controls for rotating, panning and zooming a structure in the Viewing Area are still active in Border mode.
- When you have completed drawing the border, click the **Finish** button. A popup box will appear (**Figure 3.2**).
  - You can either add the new border to an existing **Border File** or you can create a new border file. Since we drew the border around an ROI in order to get average connectivity for that region (in a upcoming step), we will create a new border file.
  - Click on the Border File **New button**, enter the name “ROI-for-avg-connectivity.border”, and Click **Save**.
  - Click **Name Add/Edit** button to create a name for the new border. In the popup, click **New** and enter “Test-myelin-patch” in the **Name:** field.
  - Select a color for your border with the scroll bars (choose Blue = 255 for tutorial purposes).
  - Click on the **Class Add/Edit** button. Select **New** and enter the Name “Myelin”. Select a color with the scroll bars (Green = 255) and click **OK**.
  - Select the **Closed Border** checkbox, since this is a fully closed border.



**Figure 3.2 – Finish Border popup box**

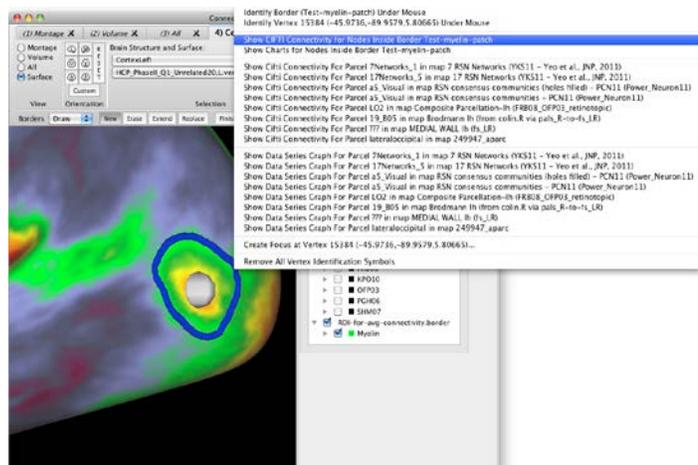
- Press **OK**.
- Your new border will turn blue on the surface and the new border file and class will show up in the **Features Toolbox**. The start point and end point of the border are marked as green point on the border for reference.

## Viewing Average Connectivity of a border encompassed region

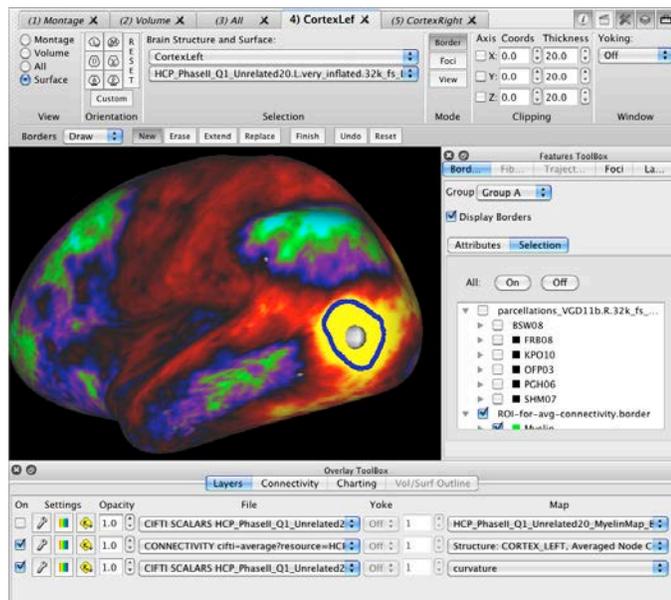
- RIGHT *click* on the border you just drew. A popup will give you a few options (**Figure 3.3**).
- Click on ‘**Show CIFTI Connectivity for Nodes Inside Border Test-myelin-patch**’.

The calculation for viewing the average connectivity for this ROI will take a few moments.

- Click the  icon in the right top corner to turn the **Overlay Toolbox** back on.
- *Deselect* the top CIFTI SCALARS layer in order to show the **CONNECTIVITY** layer underneath. You are now viewing the Average Connectivity for the brainordinates within the area of Test-myelin-patch (**Figure 3.4**).

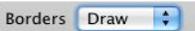


**Figure 3.3 – Selecting Connectivity Averaging for a newly created ROI**



**Figure 3.4 – Average Connectivity for area within border ‘Test-myelin-patch’**

## Editing Borders

Once you have drawn a border you can adjust/correct just a portion of a border that you otherwise are happy with while still in Draw mode .

## Editing Closed Borders

We will start by editing the closed border we just created, erasing and redrawing a section.

- *Pan and zoom* to focus on the **Test-myelin-patch** border we created above.

- Click the **Erase** button. Then *click the mouse twice*, once at the beginning of the section that is to be removed and once at the end of the section. Then *click* the **Finish** button. The section of border that you clicked on either side of will disappear (**Figure 3.5A,B**).
- Click the **Replace** button. *While holding down the alt/option key and the left mouse button*, draw a new section in the same direction as the border you are replacing was drawn (clockwise). Your trace will appear in red (**Figure 3.5C**). If you make a mistake, *hit Reset* and *redraw*.
- When you are satisfied with your replaced border section, *hit Finish* and the completed edited border will be shown in a single color (**Figure 3.5D**).

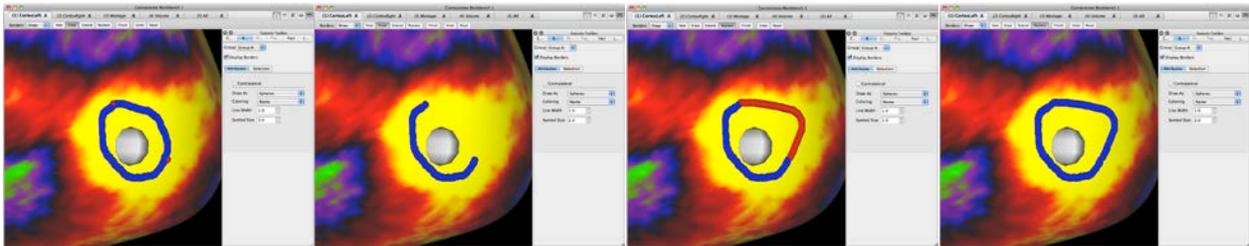


Figure 3.5 – Erasing and replacing a section of the closed border ‘Test-myelin-patch’.

A) Points selected (red) defining section of the border to be erased, B) Erased section, C) Replacement section is drawn, D) Edited border.

## Editing Open Borders

Now, we will draw a non-encompassing, or open, border defining the boundary between Brodmann area 44 and area 6 (**Figure 3.6**).

In **Overlay Toolbox: Layers**, set the top layer to CIFTI LABELS parcellations\_VGD11b.L.32k\_fs\_LR.dlabel.nii and *change* the Map to Brodmann lh. Turn the second (connectivity) layer off.

- *Zoom and pan* the surface to have Brodmann areas 44 and 6 in the center of the viewing area (purple and dark fuchsia regions on the surface).
- *While holding down the alt/option key and the left mouse button* draw a border between these two areas in the ventral to dorsal direction. *Click* the **Finish** button.
- In the **Finish Border** popup (**Figure 3.6**):
  - Click the **New** button for Border File and enter the new name of “Boundries.border” and *click Save*.
  - Click the **Add/Edit** button next to Name.

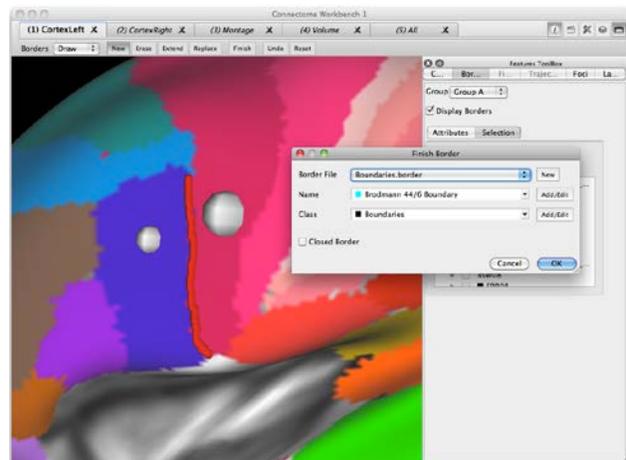


Figure 3.6 – Drawing/finishing the Brodmann 44/6 Boundary border

- In the **Edit Name attributes popup** click **New** and enter “Brodmann 44/6 Boundary” in the **Name field**.
- Use the scroll bars to select a color, we’ll use light blue here.
- Similarly *click* the **Add/Edit button** next to Class, and the **New button** in the **Edit Class Attributes popup** and *enter a new Name* of “Boundaries”, keep the default color of black, *hit OK*.
- *Deselect* the **Closed Border** checkbox.
- *Click OK*.
- In the **Features Toolbox**, *click* on the **Borders: Attributes Tab** and in the **Coloring pull-down**, select **Name**. Now the new border is colored the light blue color you set when you named the boundary.

For demonstration purposes, we will **Erase** part of this border, **Extend** it with an intentional mistake and then **Replace** the section with the mistake.

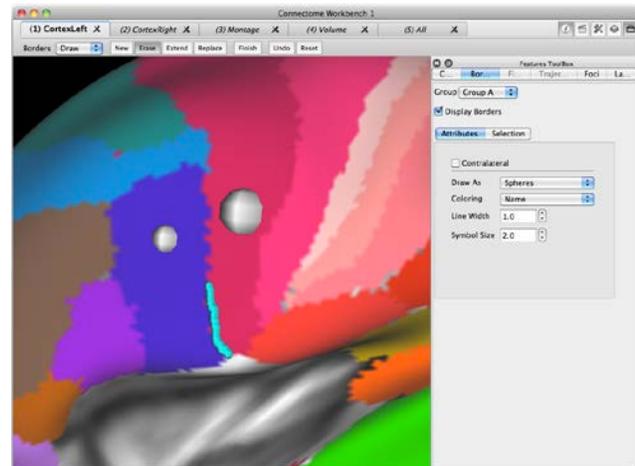


Figure 3.7 – Erasing a Portion of the border

- *Click* the **Erase** button. Then *click the mouse twice*, once at the beginning of the section that is to be removed and once at the end of the section. Then *click* the **Finish** button. The section of border that you drew along will disappear (**Figure 3.7**).
- *Click* the **Extend** button and draw in the missing section of the border with an intentional bump and *click* **Finish**. The inaccurate extension will be displayed (**Figure 3.8A**).
- *Click* the **Replace** button and *draw* where the border should be (**Figure 3.8B**). Make sure to start with your cursor on a border point that you want to keep and end on the opposite end of the error, on a border point you want to keep. The function needs to know where exactly the replacement is going. *Click* **Finish**. The inaccurate section is properly replaced (**Figure 3.8C**).

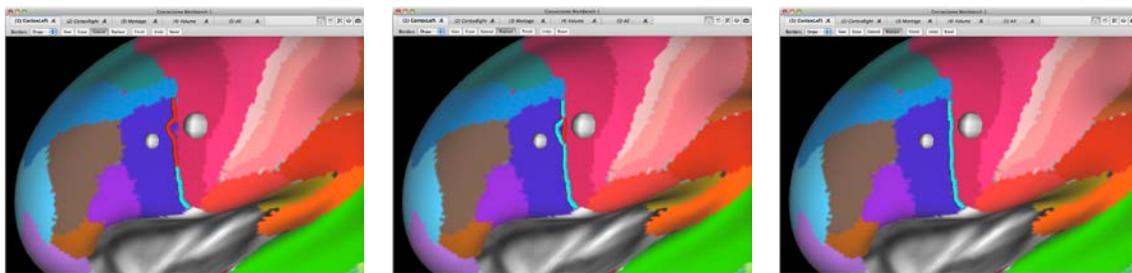
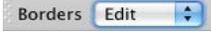


Figure 3.8 – Border extension and replacement. A) Extension with intentional mistake, B) Replaced extension, C) Finished border

- To delete just a few border points, before you have “Finished” the border, *click* the **Undo** button while the border is still red. One click per border point.
- If you want to delete a border before you have “Finished” it, *click* the **Reset** button while the border is still red.

Editing borders, while in the Edit mode  makes it possible to delete completed/ “Finished” borders and edit the Properties for completed borders.

- In the **Borders mode pull-down select Edit**.
- *Click* the **Delete** button and then *click* on the border that you wish to delete. It disappears.
- *Click* the **Properties** button and then *click* on a desired border. This brings up a box that allows you to edit the properties of that border (**Name, Class**, and associated colors).

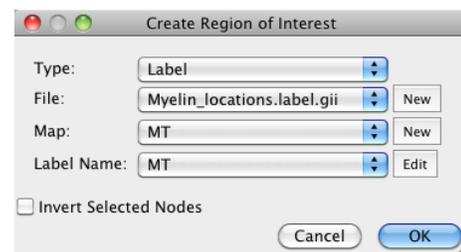
This popup also allows you to change the order of the border points by clicking the **Reverse Point Order** checkbox.

## Creating a Region Of Interest (ROI)

There are two options for creating regions of interest using Create an ROI: create a **Label ROI** or a **Metric ROI**.

For Label ROIs, you may be interested in creating your own or making additions to current Label files by creating unique ROIs. This is possible through the **Borders function: ROI**.

- *Click Off* the first layer (CIFTI LABELS parcellations\_VGD11b.L.32k...) in the **Overlay Toolbox**. *Switch* the third layer to CIFTI SCALARS HCP\_PhaseII\_Q1\_Unrelated20.sulc.32k\_fs\_LR.dscalar.nii
- In the **Borders mode pull-down select ROI**. 
- In the **Features Toolbox: Borders: Selection**, make sure the checkbox for the ROI-for-avg-connectivity: Myelin: Test-myelin-patch border we drew previously is selected.
- *Left click* on the border.
- A popup box will appear (**Figure 3.9**)
  - Leave the **Type** as the default “Label”.
  - *Click* the **File: New** button. In the box that pops up, you are able to change both the **File Name** and the **Map Name**. Both of these default to the border name often convenient)M, but to save some confusion we will rename them.
    - Change the File Name to Myelin\_locations.label.gii and the Map Name to MT and *Click OK*.



**Figure 3.9 – Create ROI popup box**

- Click the **Edit** button for **Label Name**, click **New**, enter **MT** as the **Name** and select a color for the new **Label** (here, we're using light blue (Green = 255 + Blue = 255), don't choose red, since the Composite Parcellation Label File that we compare below has MT colored red). Click **OK**.
- Click **OK**.
- Back in the **Overlay Toolbox**, click the top layer **CIFTI LABELS parcellations... On** and set the **Map** to **Composite Parcellation...**
- Set the second layer to the new file **LABEL Myelin\_locations.label.gii**, click this layer **On**
- Toggle layers 2 and 3, only, **On** to see the new Myelin\_locations: MT label displayed on the surface (**Figure 3.10**).
- Now toggle layer 1 on in order to see the Composite Parcellation location MT (red) compared with the Myelin label map over MT (light blue) (**Figure 3.11**).

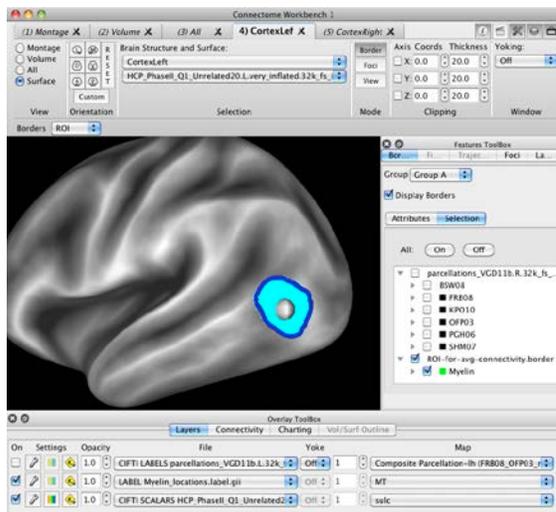


Figure 3.10 – The newly created MT ROI

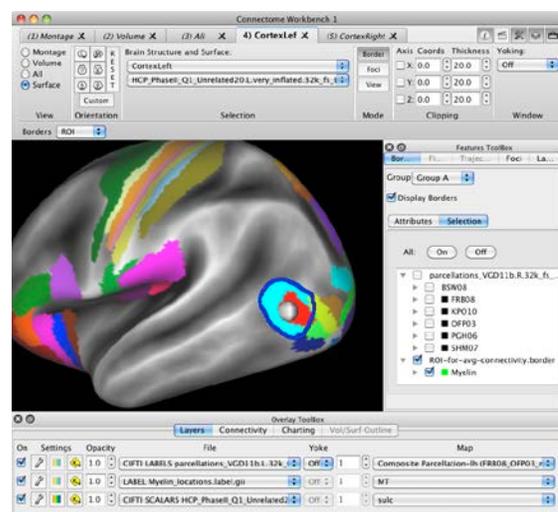


Figure 3.11 – Comparison between new MT ROI and the Composite Parcellation

- Click off **Display Borders**
- Click the information icon at the top of the Workbench window and click the RID button to clear the identified vertex.

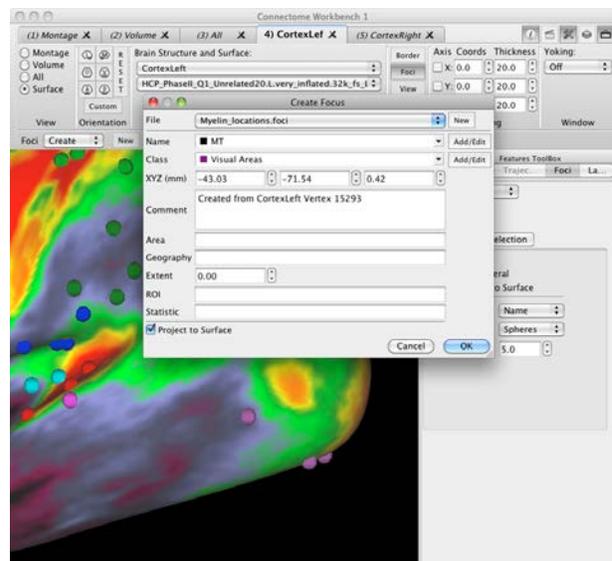
## Foci Mode

### Creating a Focus

Now we will demonstrate how to create a focus at the center of the myelin patch at MT in the Q1 Unrelated 20 myelin map.

- Switch to **View mode** in the **Toolbar**. If the Toolbar is off, turn it on with the  in the upper right corner.
- In the **Overlay Toolbox**, *turn off* the top layer and *set the second layer* to **CIFTI SCALARS HCP\_PhaseII\_Q1\_Unrelated20. MyelinMap\_BC...** Click the **X** in the upper left of the **Overlay Toolbox** to close it.
- If it isn't open already, open the **Features Toolbox**  in the **Toolbar**.
- Click on **Display Foci** in **Features Toolbox:Foci:**. The foci from the loaded file **Parcels\_GV11...** are displayed.
- Click on **Paste Onto Surface** and *set Coloring* to **Name** and **Draw As** to **Spheres** and changed **Symbol Size** to **5.0**. Notice that none of the identified foci from the **Parcels\_GV11...** file mark the myelin patch over area MT.
- *Pan and zoom* to focus on MT.
- Switch to **Foci mode** in the **Toolbar**.
- The **Foci: Create** mode is now active. *Left click* the center of the orange myelin patch over MT.
- The **Create Focus popup** appears with the XYZ coordinates for the spot you just clicked filled in (**Figure 3.12**).

- Click the **New** button to the right of the **File** field. Enter the new File name '**Myelin\_locations.foci**' and click **Save**.
- Click the **Add/Edit** button next to the **Name** field. Click the **New** button. In the **Name** field, delete the default and enter '**MT**'. Keep the black focus default color. Click **OK**.
- Click the **Add/Edit** button next to the **Class** field. Click the **New** button and enter '**Visual Areas**' in the **Name** field, and *slide* the Red and Blue color sliders halfway to set a dark purple class color. Click **OK**.
- Make sure the **Project to Surface** checkbox is clicked on, then *hit* **OK**.
- A black focus should show up where you had clicked (**Fig 3.13**).



**Figure 3.12 – Create Focus popup**

- Anytime you *left click* in **Foci: Create mode**, the **Create Focus popup** will appear.

If you instead just want to identify a vertex to see information on it, *right click* and select the first option to **Identify vertex... under mouse** (Fig 3.13).

Further down the list of right click options, is one to **Create Focus** at the nearest vertex to the place on the surface you right clicked (without clicking the Foci: Create New button). This option to create a focus is active in any mode (**View**, **Border**, or **Foci**) when you *right click* a structure.

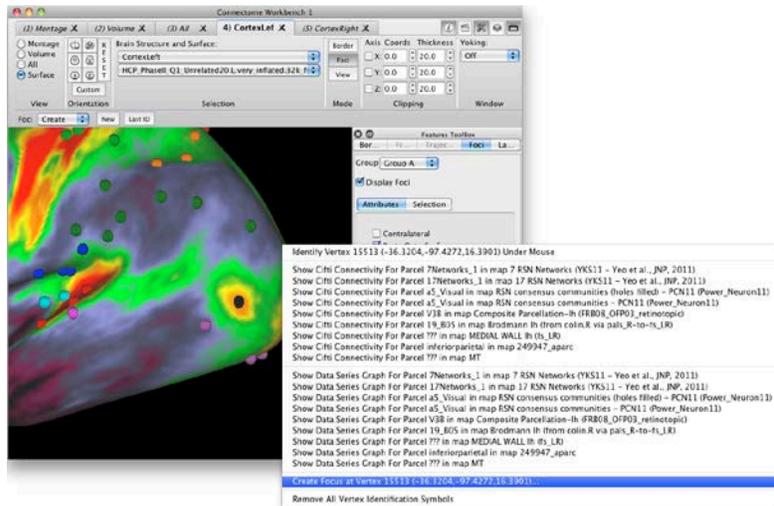


Figure 3.13 – Right click options in any mode

- To create a focus for a particular set of coordinates (rather than directly clicking on a structure), *click* the **New** button next to **Foci:Create**.
  - Click **Name: Add/Edit**.
  - In the popup (**Figure 3.14**), click **New**, enter the name '**V1/V2**', and set the color to blue. *Click OK*
  - Keep the **Class** as 'Visual Areas'.
  - In the **XYZ** fields, *enter coordinates* -16.00, -95.00, -19.00.
  - In the **Comment** field, enter "Created from coordinates at an area of high myelin content on the boundary between V1 and V2".
  - *Click OK*. A blue focus should appear at the coordinates you entered in the middle of a patch of high myelin content at the border between V1 and V2. (Turn the surface to a

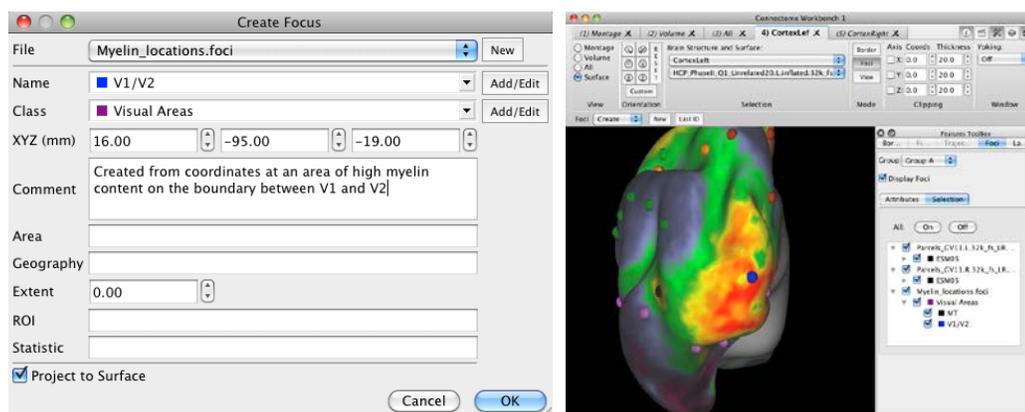


Figure 3.14 – Create New Focus from coordinates

posterior view to see the focus clearly).

- You can also create a focus from the last vertex you ID'd (with a *left click*) in **View mode**.
  - *Click* on **Foci Mode**, then *click* on the **Last ID** button.
  - *Enter* the desired name, class and associated colors in the **Create Focus popup** and *hit OK*.
- **Foci:Edit** mode allows you to **Delete** a focus or edit its **Properties** using the appropriate buttons.
  - To delete, *click* the **Delete** button and *left click* on the focus you want to delete. The focus will disappear from the structure and its name and color will be removed from the list in the **Foci:Selection** tab.
  - Similarly, to edit the properties of a focus, *click* the **Properties** button and *left click* on the focus you want to edit. An Edit Focus popup will appear and allows you to edit all fields set when the focus was created.

Note: When you close Workbench, you will be notified that you have modified files. If you wish to save the test files, *click* on **File ► Save/Manage Files...** at the top of the Workbench Window. In the **Manage Data Files** dialog that pops up, *click* on the appropriate **Save** and **In Spec** checkboxes to save the files and add them to the Spec file, respectively.

## Chapter 4: Using `wb_import` and `wb_command`

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Besides the main GUI application, the Workbench software package provides command line interface programs `wb_import` and `wb_command` that allow you to perform many operations on data files. The command line interface allows for significantly improved efficiency when analyzing a large number of datasets.

**`wb_import`** is a tool that is used to convert files into a format compatible with Workbench.

**`wb_command`** is a program containing a growing number (currently, 124) operations that can be applied singly, or in combination, to process surface and/or volume data.

Either program must be launched from the terminal (Linux/Mac) or Command Prompt (Windows). For convenience of running the programs from any terminal or command window and within any directory, it is useful to set a user-specific environment variable path for `wb_import` and `wb_command`.

### Setting the Command Line Environment

#### **For Mac users:**

- Open a terminal window.
- When you downloaded Workbench, if you moved the Workbench folder to Applications, add an environment variable path in your `.cshrc` or `.bash` file for `wb_import` and `wb_command`, such as (for `tcsh/csh`):

```
setenv PATH /Applications/workbench/macosx64_apps/wb_import.app/Contents/MacOS:$PATH
```

```
setenv PATH /Applications/workbench/macosx64_apps/wb_command.app/Contents/MacOS:$PATH
```

#### **For Linux users:**

- Open a terminal window.
- Set your path to whatever directory you placed the unzipped `workbench_linux64.beta_0.83/workbench/bin_linux64` folder.
  - To set the PATH in Bash shell, enter this command:  

```
echo 'export path=$path:/my/workbench/path' >> ~/.bashrc
```
  - To set the PATH in `tcsh/csh` shell, enter this command:  

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

where `'/my/workbench/path'` is the path to the `workbench/bin_linux64` folder.

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

### **For Windows users:**

Within the 'workbench\_windows64.beta\_0.83' folder you unzipped when you downloaded the program, is the workbench\bin\_windows64 folder that contains the executables for the 'workbench' application, 'wb\_import', and 'wb\_command'.

wb\_import and wb\_command must be run from the Command Prompt program in Windows. In order to launch them from any directory at the Command Prompt, we must set an environment variable path.

- *Right click* on the '**Computer**' or '**My Computer**' icon on your Desktop. *Left click* on **Properties**.
- *Click* on **Advanced System Settings**.
- *Press* the **Environment Variables...** button at the bottom of the popup.
- *Press* the **New...** button under User variables.
- Enter the following in the New User Variable dialog:

Variable Name: PATH

Variable Value: "C:\my\path\workbench\_windows64.beta\_0.83\workbench\bin\_windows64"

where '\my\path' is the path to the directory in which you downloaded the program

- *Press* the **OK** button in the New User Variable dialog.
- *Press* the **OK** button in the Environment Variables dialog.
- *Press* the **OK** button in the System Properties dialog.
- Using the Start Menu button, move the mouse over All Programs, and from the Accessories Menu, select Command Prompt.
- In the Command Prompt Window, enter the command 'wb\_import'. If the Path Environment variable has been set correctly, wb\_import will launch. If not, check the previous steps.

## **wb\_import: Converting Files to Workbench Format**

In addition to the files provided in this tutorial, you may want to convert your own structure, volume, and data files into Workbench format for visualization. This requires the use of **wb\_import**, that is distributed with Connectome Workbench and is launched through the terminal interface (Linux/Mac) or Command Prompt (Windows).

### **Converting Caret 5 Spec Files**

If you have Caret 5 format specification files, you can easily convert them (and the files listed within them) to Workbench format in one step. These tutorial instructions use the sample Caret5 spec files Conte69\_atlas.L.164k\_fs\_LR.c5.spec and Conte69\_atlas.R.164k\_fs\_LR.c5.spec as examples. Find your Caret5 spec files on your computer and note the full path of the directory in which they are located.

In Mac OSX or Linux:

- Open a new terminal window so the environment for the `wb_import` command is activated.

In Windows:

- Open the folder containing the Caret5 file(s) on your computer.
- Add a New folder to this directory and call it 'wb\_spec'
- Open the wb\_spec folder
- Open the Command Prompt from this folder by *holding down Shift + right click*, then *left clicking* on '**Open command window here**' in the dropdown menu that appears.

All platforms:

- At the prompt, type 'wb\_import' to launch the program.
- Some basic information on running the tool will appear, including the two commands available:

```
CONVERT DATA FILE TO WORKBENCH FORMAT    -data-file
CONVERT SPEC FILE AND ITS DATA FILES TO WORKBENCH FORMAT    -spec-file
```

- Type 'wb\_import -spec-file'
- More information about this command will appear, including the correct syntax for running the command:

```
wb_import -spec-file <structure-name> <spec-file-name>
```

- As noted in the command information, you will need to run this command once for each structure in the spec file that you are converting. You need to specify which structure (left, right, cerebellum) as part of the command.
- This command will output a file in Workbench format with the same name as the input file. Therefore, it is best to run the command from a newly created, empty directory on a spec file in a different location to minimize the chances that any file is overwritten or corrupted if the command fails.
- Mac/Linux users: create a new directory named 'wb-spec' and change to that directory (If you are following the directions for Windows, you should already be in the wb-spec directory):

```
mkdir wb-spec
cd wb-spec
```

- Run the command with this syntax:

```
wb_import -spec-file left /my_path/Conte69_atlas.L.164k_fs_LR.c5.spec
```

where "/my\_path/..." is the directory that contains the left hemisphere spec file you are converting.

The log from the spec file conversion will appear. *Note:* You will see error messages for conversion of types of files (such as .topo or .scene files) because they are not file types currently supported in Workbench (aka. Caret7). These errors will not affect the conversion of allowed file types.



- Type 'ls' at the prompt to list the files in your wb-spec directory (or look at the contents of the directory in a Finder or explorer window). All the files that were converted by wb\_import are written out to this directory in workbench format with the same name as they had in the Caret5 format spec file.

- Now run the command for the right hemisphere:

```
wb_import -spec-file right /my_path/Conte69_atlas.R.164k_fs_LR.c5.spec
```

Again, the log from the conversion will appear with error messages for unsupported file types.

- Now that these spec files are in Workbench format, you may want to change their names using the move command to indicate the new format:

```
mv Conte69_atlas.L.164k_fs_LR.c5.spec Conte69_atlas.L.164k_fs_LR.wb.spec
```

```
mv Conte69_atlas.R.164k_fs_LR.c5.spec Conte69_atlas.R.164k_fs_LR.wb.spec
```

- Now, each of these new spec files can be opened in Workbench separately. However, you may want to merge them into a single file containing information for both hemispheres.

- To merge two spec files, you can use the wb\_command operation `-spec-file-merge`. Type:

```
wb_command -spec-file-merge
```

to get an explanation of how to run the command.

- To merge the two spec files above, you would use this syntax:

```
wb_command -spec-file-merge /my_path/wb-spec/Conte69_atlas.L.164k_fs_LR.wb.spec
```

```
/my_path/wb-spec/Conte69_atlas.R.164k_fs_LR.wb.spec
```

```
/my_path/wb-spec/Conte69_atlas.LR.combined.164k_fs_LR.wb.spec
```

## wb\_command: Making and manipulating Workbench files

wb\_command allows you to perform apply many operations on data files singly, or in combination, to process surface and/or volume data. The command line interface allows efficient, batch processing of neuroimaging data.

- In a terminal or Command Prompt window, type 'wb\_command' to launch the program.

```
>wb_command
```

```
Level: CONFIG
```

```
Method: static void caret::VolumeFile::setVoxelColoringEnabled(bool)
```

```
File:
```

```
/Users/caret/caret7_development/mac64/caret7_source/src/Files/VolumeFile.cxx
```

```
Line: 69
```

```
Text: Volume coloring is disabled.
```

```
Workbench
```

```
Version: Beta 0.83
```

```
Qt Compiled Version: 4.8.3
```

```
Qt Runtime Version: 4.8.3
```

```
commit: fa2a65ebfacf903f413891fb23145e333fc55936
```

```
commit date: 2013-08-12 10:27:48 -0500
```

```
Compiled Debug: NO
```

```
Information options:
```

```
-help
```

```
print this help info
```

```
-arguments-help    explain how to read the help info for subcommands
-version          print version information only
-list-commands    print all non-information (processing) subcommands
-all-commands-help  print all non-information (processing) subcommands and
                   their help info - VERY LONG
```

- As indicated, a list of the commands currently available and short description of each will appear when you type:

```
>wb_command -list-commands
```

```
-add-to-spec-file      ADD A FILE TO A SPECIFICATION FILE
-backend-average-dense-roi  CONNECTOME DB BACKEND COMMAND FOR CIFTI
AVERAGE DENSE ROI
-backend-average-roi-correlation  CONNECTOME DB BACKEND COMMAND FOR CIFTI
AVERAGE ROI CORRELATION
-cifti-average        AVERAGE CIFTI FILES
-cifti-average-dense-roi  AVERAGE CIFTI ROWS ACROSS SUBJECTS BY ROI
-cifti-average-roi-correlation  CORRELATE ROI AVERAGE WITH ALL ROWS THEN
AVERAGE ACROSS SUBJECTS
-cifti-change-timestep  CHANGE THE TIMESTEP OF A CIFTI FILE
-cifti-convert        CONVERT TO OR FROM CIFTI
-cifti-convert-to-scalar  CHANGE A CIFTI DIMENSION TO NAMED SCALAR MAPS
-cifti-correlation    GENERATE CORRELATION OF ROWS IN A CIFTI FILE
-cifti-correlation-gradient  CORRELATE CIFTI ROWS AND TAKE GRADIENT
-cifti-create-dense-timeseries  CREATE A CIFTI DENSE TIMESERIES
-cifti-create-label   CREATE A CIFTI LABEL FILE
-cifti-cross-correlation  CORRELATE A CIFTI FILE WITH ANOTHER CIFTI
FILE
-cifti-dilate        DILATE A CIFTI FILE
-cifti-extrema       FIND EXTREMA IN A CIFTI FILE
-cifti-gradient      TAKE GRADIENT OF A CIFTI FILE
-cifti-label-import  MAKE A CIFTI LABEL FILE FROM A CIFTI FILE
-cifti-math          EVALUATE EXPRESSION ON CIFTI FILES
-cifti-merge        MERGE CIFTI TIMESERIES, SCALAR, OR LABEL
FILES
-cifti-merge-dense  MERGE CIFTI FILES ALONG DENSE DIMENSION
-cifti-pairwise-correlation  CORRELATE PAIRED ROWS BETWEEN TWO CIFTI FILES
-cifti-palette       SET PALETTE ON A CIFTI FILE
-cifti-parcellate    PARCELLATE A CIFTI FILE
-cifti-reduce        PERFORM REDUCTION OPERATION ALONG CIFTI ROWS
-cifti-reorder       REORDER THE PARCELS OR SCALAR/LABEL MAPS IN A
CIFTI FILE
-cifti-replace-structure  REPLACE DATA IN A STRUCTURE IN A CIFTI FILE
-cifti-resample      RESAMPLE A CIFTI FILE TO A NEW CIFTI SPACE
-cifti-roi-average   AVERAGE ROWS IN A SINGLE CIFTI FILE
-cifti-rois-from-extrema  CREATE CIFTI ROI MAPS FROM EXTREMA MAPS
-cifti-separate      SEPARATE A CIFTI MODEL INTO METRIC OR VOLUME
-cifti-separate-all  SEPARATE MULTIPLE CIFTI COMPONENTS AT ONCE
-cifti-smoothing     SMOOTH A CIFTI FILE
-cifti-transpose     TRANSPOSE A CIFTI FILE
-class-add-member    ADD MEMBER AND GETTER/SETTER TO SOURCE CODE
FILES (.h and .cxx)
-class-create        CREATE CLASS SOURCE CODE FILES (.h and .cxx)
-class-create-algorithm  CREATE SOURCE CODE CLASS FILES (.h, .cxx) FOR
ALGORITHM
-class-create-enum   CREATE SOURCE CODE CLASS FILES (.h, .cxx) FOR
ENUMERATED TYPE
-class-create-operation  CREATE SOURCE CODE CLASS FILES (.h, .cxx) FOR
OPERATION
-convert-affine      CONVERT AN AFFINE FILE BETWEEN CONVENTIONS
-convert-fiber-orientations  CONVERT BINGHAM PARAMETER VOLUMES TO FIBER
ORIENTATION FILE
-convert-matrix4-to-matrix2  GENERATES A MATRIX2 CIFTI FROM MATRIX4
WBSPARSE
-convert-matrix4-to-workbench-sparse  CONVERT A 3-FILE MATRIX4 TO A WORKBENCH
SPARSE FILE
```



-convert-warpfield	CONVERT A WARPFIELD BETWEEN CONVENTIONS
-create-signed-distance-volume	CREATE SIGNED DISTANCE VOLUME FROM SURFACE
-estimate-fiber-binghams	ESTIMATE FIBER ORIENTATION DISTRIBUTIONS FROM
BEDPOSTX SAMPLES	
-fiber-dot-products	COMPUTE DOT PRODUCTS OF FIBER ORIENTATIONS
WITH SURFACE NORMALS	
-foci-list-coords	OUTPUT FOCI COORDINATES IN A TEXT FILE
-gifti-convert	Convert a GIFTI file to a different encoding
-label-dilate	DILATE A LABEL FILE
-label-mask	MASK A LABEL FILE
-label-resample	RESAMPLE A LABEL FILE TO A DIFFERENT MESH
-metadata-remove-provenance	REMOVE PROVENANCE INFORMATION FROM FILE
METADATA	
-metadata-string-replace	REPLACE A STRING IN ALL METADATA OF A FILE
-metric-convert	CONVERT TO OR FROM METRIC FILE
-metric-dilate	DILATE A METRIC FILE
-metric-extrema	FIND EXTREMA IN A METRIC FILE
-metric-fill-holes	FILL HOLES IN AN ROI METRIC
-metric-gradient	SURFACE GRADIENT OF A METRIC FILE
-metric-mask	MASK A METRIC FILE
-metric-math	EVALUATE EXPRESSION ON METRIC FILES
-metric-merge	MERGE METRIC FILES INTO A NEW FILE
-metric-palette	SET THE PALETTE OF A METRIC FILE
-metric-reduce	PERFORM REDUCTION OPERATION ACROSS METRIC
COLUMNS	
-metric-regression	REGRESS METRICS OUT OF A METRIC FILE
-metric-remove-islands	REMOVE ISLANDS FROM AN ROI METRIC
-metric-resample	RESAMPLE A METRIC FILE TO A DIFFERENT MESH
-metric-rois-from-extrema	CREATE METRIC ROI MAPS FROM EXTREMA MAPS
-metric-smoothing	SMOOTH A METRIC FILE
-metric-vertex-sum	SUM VALUES ACROSS VERTICES IN A METRIC FILE
-nifti-convert	Convert a NIFTI 1 file to a NIFTI 2 file
-nifti-information	Display information about a Nifti/Cifti File.
-probtrackx-dot-convert	CONVERT A .DOT FILE FROM PROBTRACKX TO CIFTI
-set-map-name	SET THE NAME OF A MAP IN A FILE
-set-map-names	SET THE NAME OF ONE OR MORE MAPS IN A FILE
-set-structure	SET STRUCTURE OF A DATA FILE
-show-scene	OFFSCREEN RENDERING OF SCENE TO AN IMAGE FILE
-signed-distance-to-surface	COMPUTE SIGNED DISTANCE FROM ONE SURFACE TO
ANOTHER	
-spec-file-merge	MERGE TWO SPEC FILES INTO ONE
-surface-affine-regression	REGRESS THE AFFINE TRANSFORM BETWEEN SURFACES
ON THE SAME MESH	
-surface-apply-affine	APPLY AFFINE TRANSFORM TO SURFACE FILE
-surface-apply-warpfield	APPLY WARPFIELD TO SURFACE FILE
-surface-average	AVERAGE SURFACE FILES TOGETHER
-surface-closest-vertex	FIND CLOSEST SURFACE VERTEX TO COORDINATES
-surface-cortex-layer	CREATE SURFACE APPROXIMATING A CORTICAL LAYER
-surface-create-sphere	GENERATE A SPHERE WITH CONSISTENT VERTEX
AREAS	
-surface-distortion	MEASURE DISTORTION BETWEEN SURFACES
-surface-flip-lr	MIRROR A SURFACE THROUGH THE YZ PLANE
-surface-flip-normals	FLIP ALL TILES ON A SURFACE
-surface-generate-inflated	SURFACE GENERATE INFLATED
-surface-geodesic-distance	COMPUTE GEODESIC DISTANCE FROM ONE VERTEX TO
THE ENTIRE SURFACE	
-surface-geodesic-rois	DRAW GEODESIC LIMITED ROIS AT VERTICES
-surface-inflation	SURFACE INFLATION
-surface-information	DISPLAY INFORMATION ABOUT A SURFACE
-surface-match	SURFACE MATCH
-surface-modify-sphere	CHANGE RADIUS AND OPTIONALLY RECENTER A
SPHERE	
-surface-resample	RESAMPLE A SURFACE TO A DIFFERENT MESH
-surface-smoothing	SURFACE SMOOTHING
-surface-sphere-project-unproject	DEFORM A SPHERE ACCORDING TO A REGISTRATION
-surface-vertex-areas	MEASURE SURFACE AREA EACH VERTEX IS
RESPONSIBLE FOR	
-surface-wedge-volume	MEASURE PER-VERTEX VOLUME BETWEEN SURFACES

-unit-test	Unit Testing
-volume-affine-resample	APPLY AFFINE TRANSFORM TO VOLUME AND RESAMPLE
-volume-dilate	DILATE A VOLUME FILE
-volume-extrema	FIND EXTREMA IN A VOLUME FILE
-volume-fill-holes	FILL HOLES IN AN ROI VOLUME
-volume-gradient	GRADIENT OF A VOLUME FILE
-volume-label-import	IMPORT A LABEL VOLUME TO CARET FORMAT
-volume-label-to-surface-mapping	MAP A LABEL VOLUME TO A SURFACE LABEL FILE
-volume-math	EVALUATE EXPRESSION ON VOLUME FILES
-volume-merge	MERGE VOLUME FILES INTO A NEW FILE
-volume-palette	SET THE PALETTE OF A VOLUME FILE
-volume-parcel-resampling	SMOOTH AND RESAMPLE VOLUME PARCELS
-volume-parcel-resampling-generic	SMOOTH AND RESAMPLE VOLUME PARCELS FROM
-volume-parcel-smoothing	SMOOTH PARCELS IN A VOLUME SEPARATELY
-volume-reduce	PERFORM REDUCTION OPERATION ACROSS SUBVOLUMES
-volume-remove-islands	REMOVE ISLANDS FROM AN ROI VOLUME
-volume-reorient	CHANGE VOXEL ORDER OF A VOLUME FILE
-volume-rois-from-extrema	CREATE VOLUME ROI MAPS FROM EXTREMA MAPS
-volume-smoothing	SMOOTH A VOLUME FILE
-volume-to-surface-mapping	MAP VOLUME TO SURFACE
-volume-warpfield-resample	RESAMPLE VOLUME USING WARPFIELD
-wbsparsed-merge-dense	MERGE WBSPARSE FILES ALONG DENSE DIMENSION
-zip-scene-file	ZIP A SCENE FILE AND ITS DATA FILES
-zip-spec-file	ZIP A SPEC FILE AND ITS DATA FILES

- For a full explanation and the syntax used to run each command, type:

```
wb_command [-command-name]
```

## Creating a New or Add to an Existing Spec file

You can create a new spec file, or add a file to an existing spec file, using the `wb_command -add-to-spec-file` operation.

- Type the following to get a description of the operation:

```
>wb_command -add-to-spec-file
```

```
ADD A FILE TO A SPECIFICATION FILE
wb_command -add-to-spec-file
<specfile>
<structure>
<filename>
```

The resulting spec file overwrites the existing spec file. If the spec file doesn't exist, it is created with default metadata. The structure argument must be one of the following:

```
CORTEX_LEFT
CORTEX_RIGHT
CEREBELLUM
ACCUMBENS_LEFT
ACCUMBENS_RIGHT
ALL_GREY_MATTER
ALL_WHITE_MATTER
AMYGDALA_LEFT
AMYGDALA_RIGHT
BRAIN_STEM
CAUDATE_LEFT
CAUDATE_RIGHT
CEREBELLAR_WHITE_MATTER_LEFT
CEREBELLAR_WHITE_MATTER_RIGHT
CEREBELLUM_LEFT
CEREBELLUM_RIGHT
```



```
CEREBRAL_WHITE_MATTER_LEFT  
CEREBRAL_WHITE_MATTER_RIGHT  
CORTEX  
DIENCEPHALON_VENTRAL_LEFT  
DIENCEPHALON_VENTRAL_RIGHT  
HIPPOCAMPUS_LEFT  
HIPPOCAMPUS_RIGHT  
INVALID  
OTHER  
OTHER_GREY_MATTER  
OTHER_WHITE_MATTER  
PALLIDUM_LEFT  
PALLIDUM_RIGHT  
PUTAMEN_LEFT  
PUTAMEN_RIGHT  
THALAMUS_LEFT  
THALAMUS_RIGHT
```

Descriptions of parameters and options:

```
<specfile> - the specification file to add to  
<structure> - the structure of the data file  
<filename> - the path to the file
```

- Create the new spec file “test.spec” (that contains the sample left cortex file Conte69.L.inflated.164k\_fs\_LR.surf.gii) in your wb-spec directory :

```
>wb_command -add-to-spec-file test.spec CORTEX_LEFT  
Conte69.L.inflated.164k_fs_LR.surf.gii
```

- Note: the structure argument (e.g. CORTEX\_LEFT) must be typed in all caps.
- Check the contents of your wb-spec directory to see that test.spec was created.
- Now add another file (the inflated right cortex file Conte69.R.inflated.164k\_fs\_LR.surf.gii) to this newly created spec file with the command:

```
>wb_command -add-to-spec-file test.spec CORTEX_RIGHT  
Conte69.R.inflated.164k_fs_LR.surf.gii
```

- Check the contents of your wb-spec directory to see that test.spec was created.
- To open the test.spec file in workbench, type:  

```
>workbench test.spec
```
- Both the CortexLeft and CortexRight inflated surface files should be listed in the Spec File Data File Selection dialog. Press the **Load** button.
- Four Viewing Tabs should automatically open: (1) *Montage*, (2) *All*, (3) *Cortex Left*, and (4) *Cortex Right* and you should be able to interact with both left and right inflated surfaces in the tabs.
- If desired, continue to add other files to the test.spec file using the `–add-to-spec-file` command and open them in Workbench. Note: All data files must have a structure designated in the command (e.g. CORTEX\_LEFT) to be added to the spec file.

## Adding to an Existing Spec file in the Workbench GUI

The GUI interface of Workbench affords another way to add files to an existing spec file. Here we use the example of adding a label file to a spec file. With the example test.spec file open in the Workbench GUI:

- Click on **File ► Open File...** at the top of the Workbench Window.
- Change Files of type: to Label Files (\*.label) in the Open file dialog.
- Select **parcellations.L.composite-cortical.164k\_fs\_LR.label.gii** by holding down the command/control key as you left click.
- Press **Open**.
- You should see the new label file appear as a file selection option in the Layers tab of the Overlay Toolbox.
- Click on **File ► Save/Manage Files...** at the top of the Workbench Window.
- The label file you just opened is listed in the **Manage Data Files** dialog, *but it is not added to the spec file by default*. If you want to save the file to the test.spec file, *check* the '**In Spec**' checkbox to the left of the file name.
- Check the **Save** checkbox beside the Spec file name to save the changes to the spec file (the addition of the new file).

## Appendix: Tutorial for Q1 Unrelated 20 Dataset (v1b)

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# Connectome Workbench Tutorial for HCP Group-Average Demo Version 1b Data (Q1 Unrelated 20)

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11 June 2013

***\*\*This Tutorial for HCP Group-Average Demo Version 1b Data (Q1 Unrelated 20) is compatible with Workbench Beta v0.83\*\****

## 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 the HCP group-average demo version 1b (Q1 unrelated 20) task-fMRI and functional connectivity data originally released on 5 March 2013 and updated on 11 June 2013. The updated dataset includes files in CIFTI file format that are compatible with Workbench Beta 0.83 (see below). Note that this HCP Q1 group-average demo dataset was processed using Version 1 preprocessing pipelines (plus additional processing), rather than the Version 2 preprocessing pipelines that have been applied to all Q1 and Q2 individual subjects in the Q2 data release (see the [HCP Q2 Release Reference Manual](#) for more information).

For a more extensive introduction to using Workbench, [download the Connectome Workbench Beta v0.83 Tutorial and User Guide and associated dataset](#).

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](mailto:hcp-users@humanconnectome.org).

## ConnectomeDB and Tutorial Data

Besides handling locally stored data files, Workbench can access data files stored in [ConnectomeDB](#), a web-accessible database that handles all HCP data modalities (MRI, MEG/EEG, and behavioral data). This interactivity will be critical, given the complexity of the datasets and the large file size for some data types (e.g., ‘[dense connectome](#)’ files currently exceed 30 GB per subject). To circumvent downloading of these large files, connectivity maps for user-selected subjects and regions of interest can be extracted on the fly from ConnectomeDB and transmitted within seconds to Workbench through an internet connection. For this tutorial, using Workbench Beta v0.83, the Workbench interaction with ConnectomeDB involves a single step: opening a dense connectome file from ConnectomeDB through the Open Location option in the File menu (see [Viewing Functional Connectivity](#) below).

- This tutorial uses dense functional connectome data that are for demonstration purposes only. You will need to [register and accept a Data Use Agreement](#) that acknowledges this stipulation. (This restriction is necessary because the advanced methods used to analyze the connectivity data have not been published or fully vetted). This restriction does not apply to the group-average task-fMRI, myelin maps, and other surface and volume data that are part of the tutorial dataset.
- Unprocessed and minimally processed image data and behavioral data being released as part of the HCP Quarter 2 Data release is available for download and can be used freely by registering and accepting a separate Data Use Agreement at <http://humanconnectome.org/data/>.

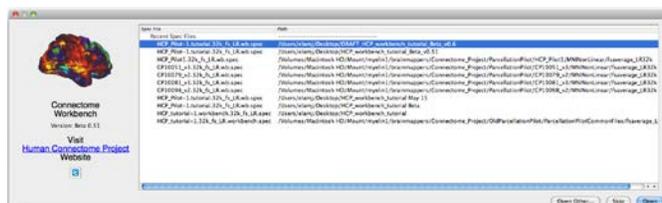
## Workbench Orientation

This section is to provide a quick orientation to Workbench (and its associated file types) for the purposes of exploring the group average HCP Q1 data provided. For a more comprehensive introduction to Workbench, please download and check out the Workbench Beta 0.83 tutorial.

One major enhancement in Workbench Beta 0.83 is the utilization of 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**.
- In the **Open File Dialog (Figure 2)**, Navigate to the folder or directory that contains the data, the **HCP\_WB\_Tutorial\_Beta0.83** folder.
  - The default file type filter is Specification Files (\*.spec).
  - Note: if you started from a terminal window in the directory containing the tutorial dataset, the tutorial spec file would already be available.

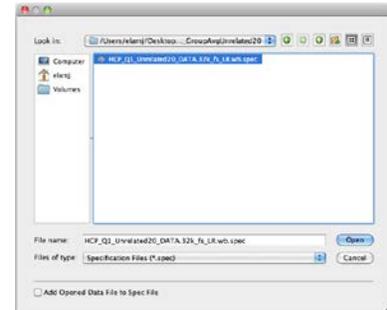


Figure 2 - The Open File Dialog

- Select* the desired file: **HCP\_beta0.83\_tutorial.32k\_fs\_LR.wb.spec** and *click* the **Open** button. The Open Spec File Dialog (**Figure 3**) will appear, showing the files in this particular spec file, grouped into 9 types: Border, Dense, Dense Label, Dense Scalar, Dense Data Series, Foci, Scene, Surface and Volume.

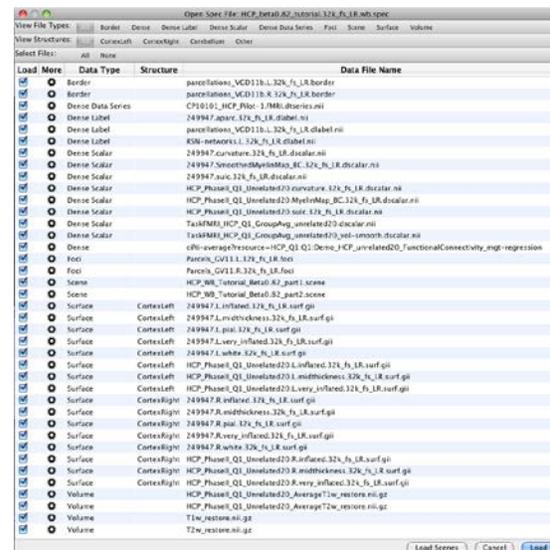


Figure 3 - The Open Spec File Dialog

- 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).

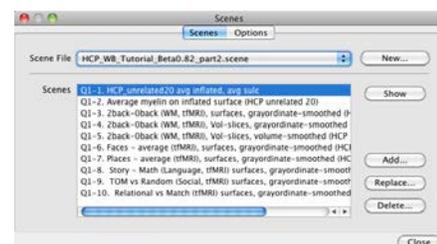


Figure 4 - The Scenes box

- The **Scenes box (Figure 4)** will appear.

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 Q1 data provided and many features of Workbench.

- In the Scene File drop-down menu, *select* HCP\_WB\_Tutorial\_Beta0.83\_part2.scene. In the Scenes field our first scene: “HCP\_unrelated20 avg inflated, avg sulc” should be highlighted, indicating that it is selected.
- *Click Show* to load the scene.

## Scene 1: HCP\_unrelated20 avg inflated, avg sulc

This scene shows group average surfaces and volumes of a set of 20 unrelated Q1 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 with a montage of lateral and medial views of the group average inflated cortical surfaces of both hemispheres in the [Viewing Area](#) of the [Workbench Window](#) (“Connectome Workbench 1”).

The Workbench Window contains five [Viewing tabs](#): (1) Cortex Left, (2) Cortex Right, (3) Montage, (4) Volume, and (5) All. (You may not see the 5<sup>th</sup> until the window is enlarged.)

The [Viewing Area](#) defaults upon opening to view [tab 3](#) (the [Active Tab](#)) showing a montage of lateral and medial views of the surfaces of both hemispheres. Components of the Workbench Window are shown in [Figure 5](#).

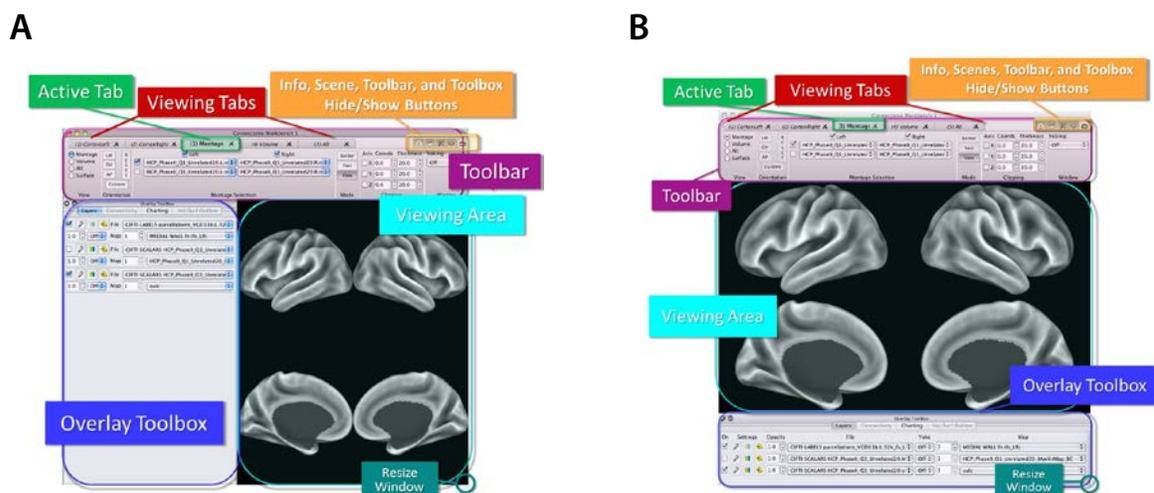


Figure 5 - The Workbench Viewing Window A) Vertical Orientation B) Horizontal Orientation

The [Overlay Toolbox](#) 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.

- *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 (1) Cortex Left**. This shows the inflated left cortical surface. Click on **Tab (2)**, which shows the inflated right cortical surface.*
- *Click on **Tab (4)**. This shows a montage of 9 group average volume slices. Note that even though this is a group average volume, there are clear boundaries between the gray and white matter regions reflecting the high quality of the HCP data.*
- *Click on **Tab (5) All**. Drag the surface up and to the left to rotate the surface and volume (whole brain) and see that group average midthickness surfaces of both hemispheres and all 3 volume planes (parasagittal, coronal, axial) are visible.*
- *Click through the tabs again and notice that the [Toolbar](#) changes when you switch tabs/views.*
- *Try out the other buttons and dropdowns in the **Toolbar** to get a sense of what they do.*
- *Click back to **Tab (3) Montage**. The **Montage Selection** section of the **Toolbar** lets you switch between brain structures for each hemisphere. For this data, you can select very inflated, midthickness (halfway between the white matter boundary and the pial surface), and inflated population-averaged surfaces for the HCP\_Q1 Unrelated 20 subjects.*

**\*\*Tip:** Whenever you encounter any **dropdown menu** in Workbench, you can *click* or *hover your mouse over* the menu and quickly browse through selections using your mouse scroll wheel, or by typing a letter to search through selections by name.

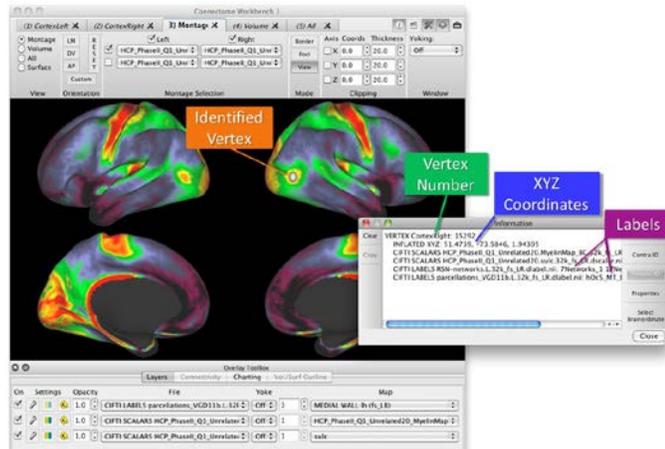
## Scene 2: Average Myelin on inflated surface

- In the **Scenes Dialog**, select **“Average Myelin on inflated surface (HCP unrelated 20)”** 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 **clipboard**  **button** in the upper right of the **Workbench Window**.

This scene shows the same group average surfaces from Scene 1, but now overlaid with a map of myelin content averaged across the 20 unrelated subjects.

- 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 for the structures being viewed, whether or not they are currently being displayed.



**Figure 6 – Vertex Identification and the Information Box**

**Note:** The next eight scenes show different types of task contrasts from the HCP Task-fMRI analyses. If you want to skip some or all of these exemplar Task-fMRI scenes, you may proceed at any time to the [Viewing Functional Connectivity](#) section near the end.

## Scene 3: 2back – 0back (WM, tfMRI), surfaces, grayordinate-smoothed

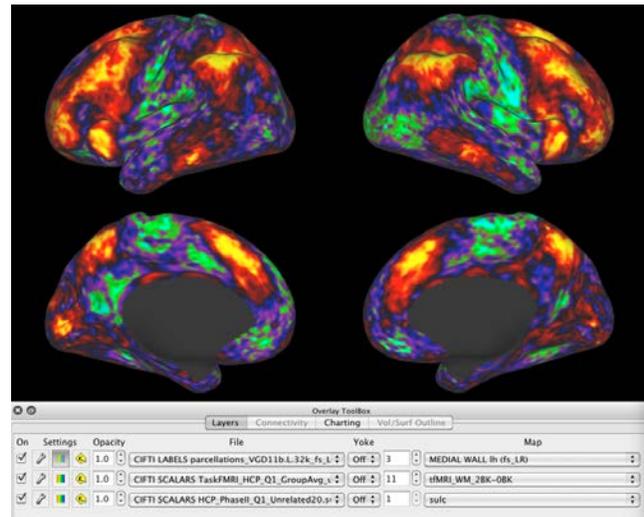
- Select “**2back – 0back (WM, tfMRI), surfaces, grayordinate-smoothed (HCP unrelated 20)**” in the **Scenes Dialog box** and click **Show** to load the scene. Leave the **Scenes Dialog** open.

This scene shows the group average 2back-0back contrast of the HCP Working Memory task on the inflated surfaces. The fMRI data processing included grayordinate-constrained smoothing (4 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, which in which the cerebral cortex is better aligned across subjects because of surface-based registration.

**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 4.5 and minimum of -3.8. (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 0.7 tutorial.)

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).

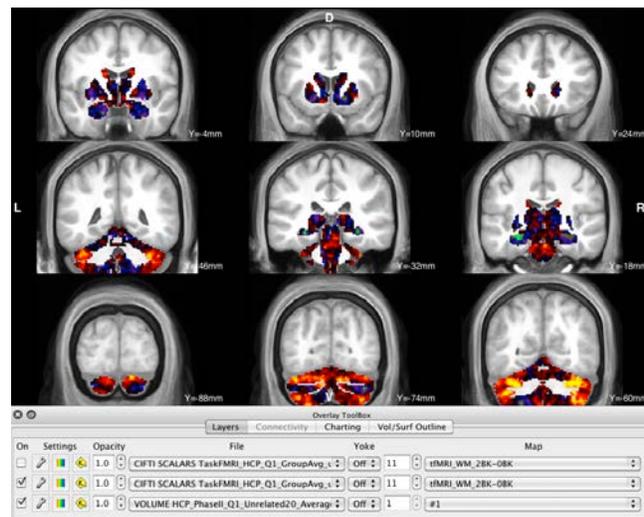


**Figure 7 – Cortical surface montage, showing group-average task contrast for the 2-back vs 0-back HCP working memory task.**

## Scene 4: 2back – 0back (WM, tfMRI), Vol-slices, grayordinate-smoothed

- *Select “2back – 0back WM, tfMRI), Vol-slices, grayordinate-smoothed (HCP unrelated 20)” in the Scenes Dialog box and click Show to load the scene. Leave the Scenes Dialog open.*

This scene (**Figure 8**) shows the same 2back-0back contrast of the HCP Working Memory task in Volume slices, but only showing subcortical grayordinates (gray-matter voxels, including the cerebellum). Prominent bilateral activations are evident in lateral cerebellar cortex.



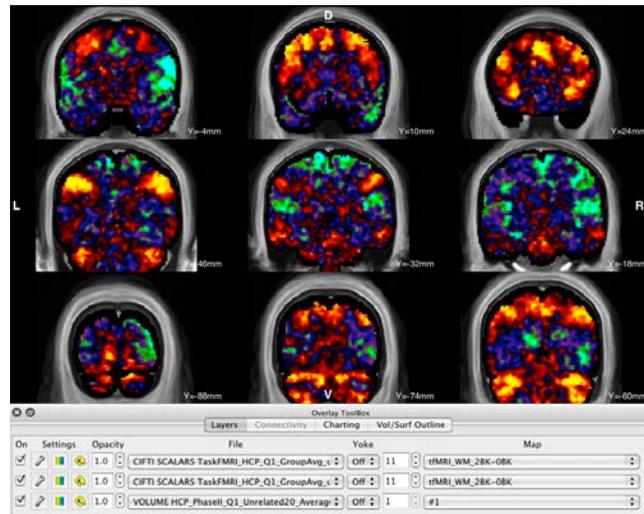
**Figure 8 – Volume slice montage, showing group-average task contrast for the 2-back vs 0-back HCP working memory task displayed on subcortical grayordinates.**

## Scene 5: 2back – 0back (WM, tfMRI), volume-smoothed

- Select “**2back – 0back (WM, tfMRI), volume-smoothed (HCP unrelated 20)**” in the **Scenes Dialog box** and **click Show** to load the scene.

This scene (**Figure 9**) shows the same 2back-0back contrast of the HCP Working Memory task in conventional volume slices. For this analysis, smoothing (4 mm FWHM) was done in volume space, which increases spatial blurring across sulcal banks. Similarly, cortical activations across subjects in volume space induces greater blurring.

Activations are visible in lateral prefrontal, anterior cingulate, lateral parietal, and cerebellar cortex, similar to those shown in the preceding two figures. The peak z-statistic from the volume-average analysis is 4.2 (not shown here, but revealed by pressing the color bar icon in Overlay Toolbox: Layers), which is lower than that from the grayordinate-constrained analysis shown above. Various advantages of surface-based compared to volume-based analysis and visualization are discussed elsewhere ([Glasser et al. 2013](#)).



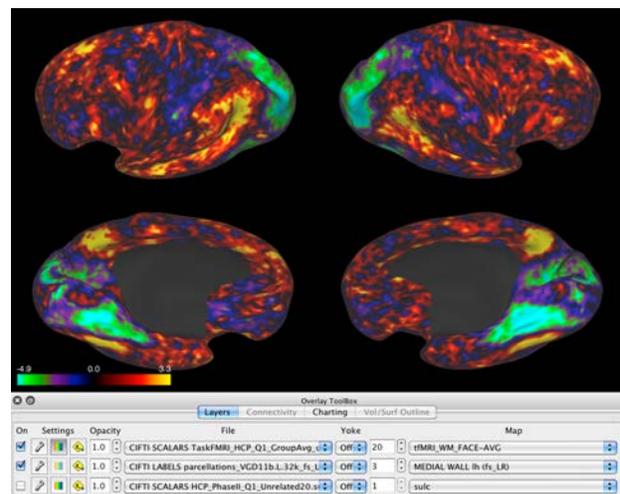
**Figure 9 – Volume slice montage, showing group-average task contrast for the 2-back vs 0-back HCP working memory task generated by a volumetric analysis (4mm FWHM volume smoothing).**

## Scene 6: Faces – average (tfMRI), surfaces, grayordinate-smoothed

- Select “**Faces – average (tfMRI), surfaces, grayordinate-smoothed (HCP unrelated 20)**” in the **Scenes Dialog box** and **click Show** to load the scene.

This scene (**Figure 10**) shows the grayordinate-smoothed analysis of the group-average Faces vs. Average contrast of the HCP Working Memory task displayed on the inflated surfaces.

The surfaces have been rotated in the montage view so that you can see the strongest task activation in ventral occipito-temporal cortex, in



**Figure 10 – Group-average task contrast for the Faces vs average of all objects from the HCP working memory task. The inflated cortical surfaces are rotated to better show the face-selective activation in ventral temporal cortex (lower panels).**

the general location expected from numerous published studies. The peak z-statistic is 3.3, indicating a weaker overall task activation compared to the 2-back vs. 0-back task.

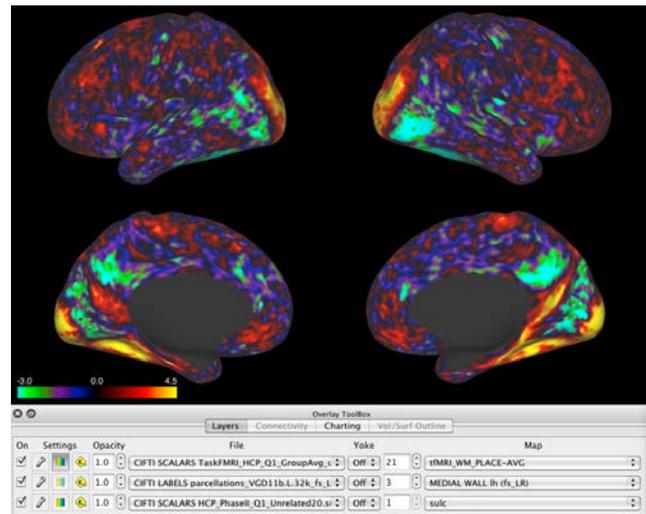
This contrast is part of the same working memory task described above, but compares the 0-back + 2-back memory of pictures of Faces with the 0-back + 2-back memory of the average of all the pictures presented (places, tools, faces and body parts).

## Scene 7: Places – average (WM, tfMRI), surfaces, grayordinate-smoothed

- Select “Places – average (tfMRI), surfaces, grayordinate-smoothed (HCP unrelated 20)” in the **Scenes Dialog box** and *click Show* to load the scene.

This scene (**Figure 11**) shows the group-average Places vs. Average contrast of the HCP Working Memory task from the 20 unrelated subjects, displayed on the inflated surfaces. This data is grayordinate-smoothed as above. Strong activations are visible in three regions of posterior cortex, including the parahippocampal cortex, the inferior part of the anterior bank of the parieto-occipital sulcus, and cortex in and around the transverse occipital sulcus, similar to activations reported in previous studies (e.g., [Nasr et al. 2011](#)). The peak z-statistic is 4.5, substantially stronger than that for the face activation map.

This contrast is part of the same working memory task described above, but compares the 0-back + 2-back memory of pictures of Places with the 0-back + 2-back memory of the average of all the pictures presented (places, tools, faces and body parts).



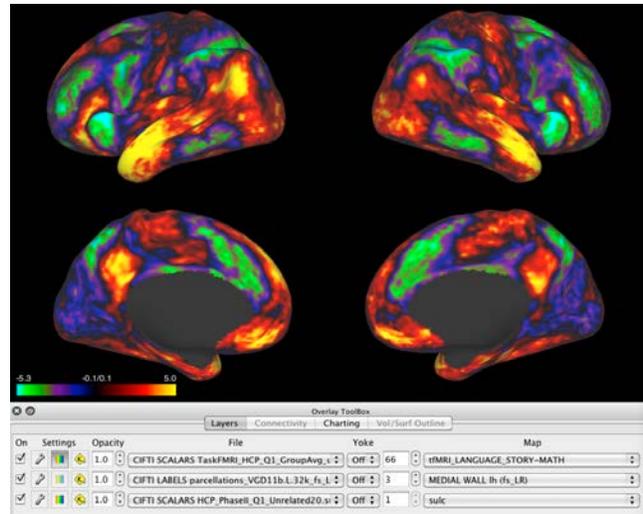
**Figure 11 – Group-average task contrast for the Places vs average of all objects, from the HCP working memory task.**

## Scene 8: Story – Math (Language tfMRI), surfaces, grayordinate-smoothed

- Select “**Story – Math (Language tfMRI), surfaces, grayordinate-smoothed (HCP unrelated 20)**” in the **Scenes Dialog box** and **click Show** to load the scene.

This scene (**Figure 12**) shows the group-average Story vs. Math contrast of the HCP Language Processing task, displayed on the inflated surfaces. Strong activations are evident in many regions, including anterior temporal cortex, posterior parietal cortex, and posterior cingulate cortex. The peak z-statistic is 5.0.

In this task, participants were presented a story task (brief auditory stories, followed by a 2-alternative forced-choice question that asks participants about the topic of the story) or a math task (auditorially presented addition and subtraction problems, followed by two choices for the correct arithmetic answer, e.g., “twenty-nine or twenty-six”).



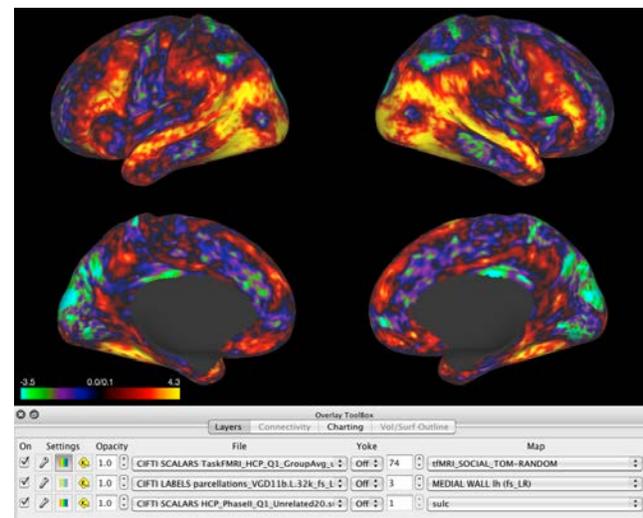
**Figure 12 – Group-average map for the Story vs Math task contrast from the HCP Language task.**

## Scene 9: TOM vs Random (Social, tfMRI), surfaces, grayordinate-smoothed

- Select “**TOM vs Random (Social, tfMRI), surfaces, grayordinate-smoothed (HCP unrelated 20)**” in the **Scenes Dialog box** and **click Show** to load the scene.

This scene (**Figure 13**) shows the group-average TOM (theory of mind) vs. random motion contrast of the HCP social cognition (theory of mind) task. Strong activations (up to  $z = 4.3$ ) are evident in the superior temporal sulcus, area 45 of lateral prefrontal cortex, and several other regions of occipital-temporal cortex.

In this task, participants were presented with objects (squares, circles, triangles) that either



**Figure 13 – Group-average map for the Theory Of Mind (TOM) vs Random movement task contrast from the HCP Social task.**

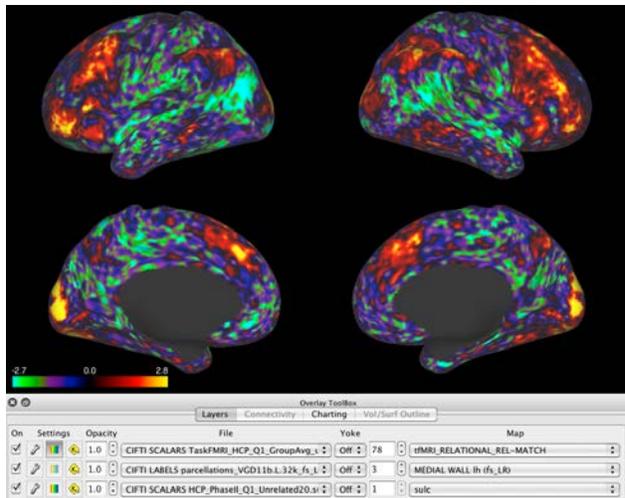
interacted in some way, or moved randomly on the screen, then participants judged whether the objects had a mental interaction (an interaction that appears as if the shapes are taking into account each other's feelings and thoughts), Not Sure, or No interaction.

## Scene 10: Relational vs Match (tfMRI), surfaces, grayordinate-smoothed

- Select “**Relational vs Match (tfMRI), surfaces, grayordinate-smoothed (HCP unrelated 20)**” in the **Scenes Dialog box** and *click Show* to load the scene.

This scene (**Figure 14**) shows the group-average contrast comparing relational activations (subjects judging whether one pair of objects are related in shape or texture to another pair of objects) with match activations (subjects matching the shape or texture of one object with one of a pair of presented objects).

This task did not generate strong activations (peak z-statistic = 2.8), but candidate activations which may be validated using a larger sample size include a swath of dorso-lateral prefrontal cortex as well as a patch of dorsal occipital cortex.



**Figure 14 – Group-average map for the Relational vs Match task contrast from the HCP Relational task.**

## Return to Scene 1: Viewing Functional Connectivity

Now we return to Scene 1, which provides a template for viewing resting-state fMRI “dense” functional connectivity retrieved from ConnectomeDB the group average inflated surfaces.

- Select Scene 1 (“**HCP\_unrelated20 avg inflated, avg sulc**”) in the **Scenes Dialog box** and *click Show* to load the scene.

This section shows how to access, display, and interact with group averaged functional connectivity data from the HCP Q1 20 unrelated subjects on the cortical surface and in subcortical volumes.

Functional connectivity data is derived from correlations between grayordinates in the resting state BOLD data. [Dense connectome](#) files that show functional connectivity are REALLY big (~30 GB for current resolution). Because of their size, these files are stored in [ConnectomeDB](#), which can tap into these large files as needed to view particular connectivity maps of interest.

- In the **Menu bar**, select **File►Open Location...** (shortcut for Mac: command + L, Linux/PC: control + L).
- A popup will appear as shown in **Figure 15**. Enter your ConnectomeDB username and password (same as you used to download data for Workbench).
- Press Open Location: Standard. The default selection should be: “**HCP-Q1\_ Correlation with Mean Gray Regression (Avg 20)**” (If a different choice is shown, use the pull-down menu to make this selection.)



**Figure 15 – Open Location Dialog**

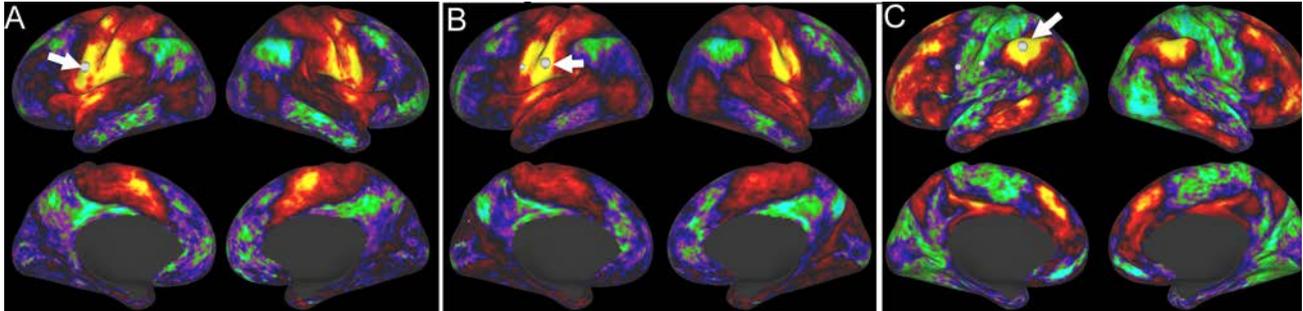
As a reminder, the dense connectome data are for demonstration purposes only. The [Q1 Open Access Data Use Agreement](#) you agreed to in order to access the tutorial data acknowledges this stipulation. (This restriction is necessary because the advanced methods used to analyze the functional connectivity data have not been published or fully vetted).

- *Click OK*. It will take a few seconds to access the file over the internet. This step makes the selected 30 GB dense connectome file accessible, but (fortunately!) does not attempt to load the file.

The dataset is from 80 scan sessions (20 subjects, 15 min/scan, for a total of 20 hours of scan time). Data were averaged across subjects using surface based registration for cerebral cortex and nonlinear volume registration for subcortical and cerebellar voxels. Minimal spatial smoothing (2mm FWHM) was done. Preprocessing and de-noising were carried out as described in [Glasser et al. 2013](#) and [Smith et al., 2013](#).

- *Click* on the **Layers tab**.
- Use the top layer’s **File** dropdown and *select* **CONNECTIVITY cifti-average?resource=HCP-Q1:Q1:Demo\_HCP\_unrelated20\_FunctionalConnectivity\_mgt-regression**
- *Toggle* the top layer ‘**On**’.

- Click on the left hemisphere surface in the ventral part of the precentral gyrus, approximately the same place as the highlighted vertex in **Figure 16A (white arrow, upper left)**.



**Figure 16 – Comparing functional connectivity for three brain locations.**

This shows a map of functional connectivity map associated with the face representation in motor cortex. 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 yellow location on the postcentral gyrus (**white arrow in Figure 16B**) to view the similar functional connectivity map for the face representation of somatosensory cortex.
- Now click a green or blue area in the supramarginal gyrus (**white arrow in Figure 16C**). You will see a much different connectivity pattern than for either of the previous maps (**Figure 16C**). This demonstrates how nearby brain regions can have very different functional connectivity from each other in the resting state.

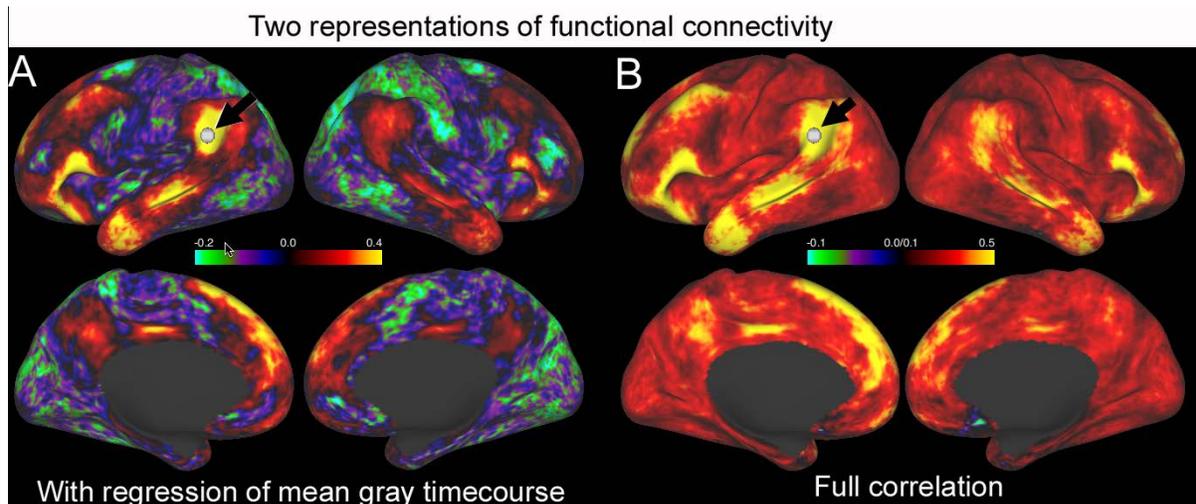
### ***Comparing functional connectivity maps: full correlation vs. regression of the mean gray timecourse.***

- Select **File ► Open Location...**
- Select **"HCP-Q1 Full Correlation (Avg 20)"** from the pull-down menu under "Standard".

This dense connectome is from the same dataset as the preceding one, except that regression of the mean gray timeseries was not carried out.

- Use the second layer's **File** dropdown and select **CONNECTIVITY cifti-average?resource=HCP-Q1:Demo\_HCP\_unrelated20\_FunctionalConnectivity\_FullCorrel**
- In Toolbox Overlay: Layers, turn the second layer **On**
- In the **Information box**, click on **RID** to remove any previously selected vertices
- Click on a vertex in the left supramarginal gyrus, close to that shown in **Figure 17A**.
- In Toolbox Overlay: Layers, turn the first layer **Off**.

The functional connectivity map should appear similar to that in **Figure 17B**. Most of the map will show positive correlations, but a few locations show negative values, indicating an anti-correlation even without regression of the mean gray timeseries (MGT).



**Figure 17 – Alternative representations of functional connectivity maps using an exemplar seed in the left supramarginal gyrus (black arrows). A. Functional connectivity map after regression of the mean gray timecourse (MGT). B. Full correlation functional connectivity map for the same seed location.**

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.

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\*\* Further details on the data acquisition and analysis methods are available in eight manuscripts in press 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.

## Glossary

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**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 scalar (\*.dscalar.nii), 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 Connectome** refers to connectivity matrix CIFTI files that contain correlations between every surface or volume brainordinate and every other surface or volume ordinate in our model of the brain. For example, a grayordinates x grayordinates dense connectome file contains a connectivity value between every grayordinate and every other grayordinate. Because dense connectivity files can be very large (~32.5 GB for HCP-generated dense connectomes), it is noteworthy that they can be accessed interactively by reading out only one row at a time or an average across a user-selected subset of rows, as needed, from a file that is stored remotely (e.g., in the ConnectomeDB database). Dense

connectomes can also be asymmetric, such as a structural connectivity matrix between grayordinates (all gray matter structures) and whiteordinates (all white matter structures).

**Dense label** CIFTI files (grayordinates  $\times$  label maps) contain a name and/or color label for every brainordinate. These files will be useful for mapping combined cortical and subcortical parcellations.

**Dense scalar** CIFTI files contain real-valued data for every brainordinate mapped to a color palette. A dense scalar file can contain one map or frame (such as a single cortical myelin map) or a series of spatial maps (e.g. tfMRI contrast maps or ICA component spatial maps) that can have distinct labels for each frame.

**Dense time series** is a type of dense scalar CIFTI file (grayordinates  $\times$  time) that can be viewed as a series of maps (or animated movie) displayed on cortical surfaces and subcortical volume slices or as a timecourse graph for a selected grayordinate, using the timecourse graph window (and as an average timecourse for all grayordinates within a selected ROI). This type of file is particularly useful for viewing resting state fMRI time series.

**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 pull-downs (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](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.