

Intro to wb_view & Imaging File Types

Part 1: Demo & Quick Connectome Workbench (wb_view) Orientation

Note: Part 1 is a “guided tour”, in which you are asked to watch Jenn Elam’s presentation while concurrently following each of her steps on your own computer, using the instructions below.

Connectome Workbench (often shortened to ‘Workbench’) is a freely available software platform for visualization and analysis of neuroimaging data being developed as part of the HCP. It is customized for handling data from the HCP, including functional and structural connectivity and task-fMRI, using combined surface and volume visualization.

The Workbench platform includes **wb_view**, the brain visualization graphical user interface, and **wb_command**, a set of command line tools for performing simple to complex operations using volume, surface, and grayordinate data. **wb_command** is a required program for running the [HCP pipelines](#) (released Sept 2014) that we will discuss later today (Practical 2).

This section and the accompanying demo provides a quick orientation to the Workbench GUI, **wb_view**, while exploring individual and group average data from the HCP. Watch the demo and follow along in the written instructions here.

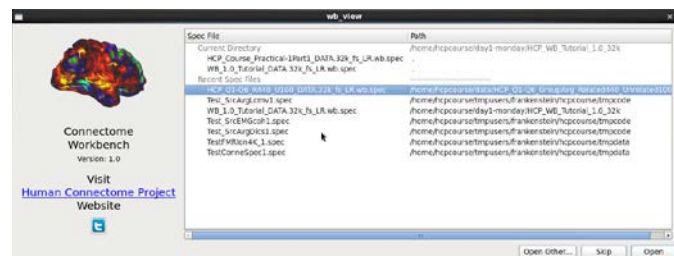
More information on the file types that one can view in **wb_view** will be in Part 2. A more extensive step-by-step orientation to **wb_view** is available in the WB 1.0 Tutorial provided as additional material.

Launching wb_view

In a terminal window: *change (cd)* to the **day1-Monday/HCP_WB_Tutorial_1.0_32k** directory, then enter:

wb_view

When you launch Workbench, by default a splash screen opens (**right**), showing a list of Specification files in your current directory path. (Each “Spec File” organizes a set of data files for loading into **wb_view** at one time.) If you have launched Workbench before, recently opened Spec Files are also listed.



Connectome Workbench Splash Screen

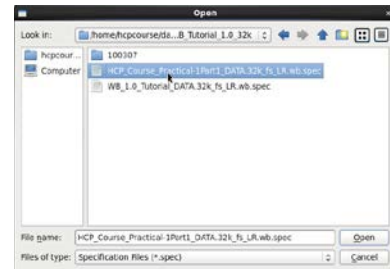
- Click **Skip** to launch Workbench without opening a spec file.

Opening a File and Loading Scenes

- In the File Menu, select **Open File...** (shortcut cmd/ctrl + O) to display the **Open File Dialog**.

- In the **Open File Dialog (right)**, select:
- *Select* the file: **HCP_Course_Practical-1Part1_DATA.32k_fs_LR.wb.spec** and *click* the **Open** button.

The **Open Spec File Dialog (right)** will appear, showing the files listed in this particular spec file.



The Open File Dialog

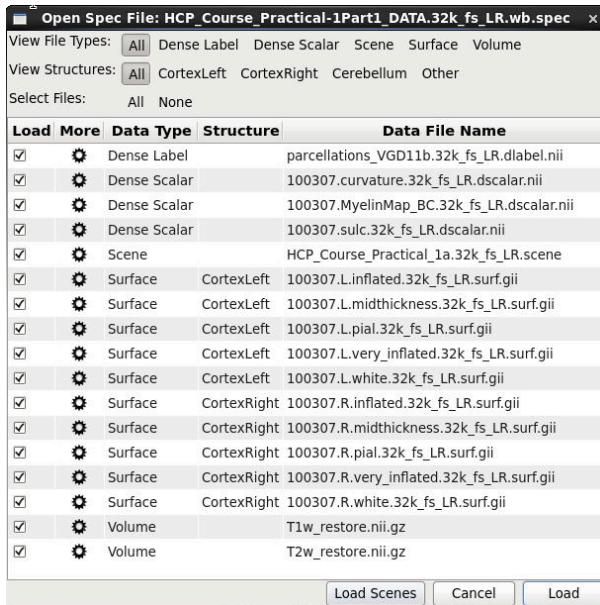
- *Click* **Load Scenes** at the bottom of the dialog to open the scene file we'll use in the practical.

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 (right)** will appear. In the Scenes field the scene:

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

- *Click* **Show** to load the scene.



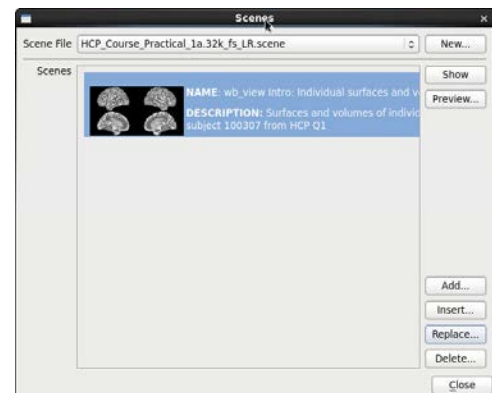
The Open Spec File Dialog

This scene shows cortical surfaces (plus volumes – stay tuned) of an individual HCP subject (100307) and illustrates the high quality of structural data obtained at the single-subject level.

- *Close* the Scenes box.

Workbench Window Layout

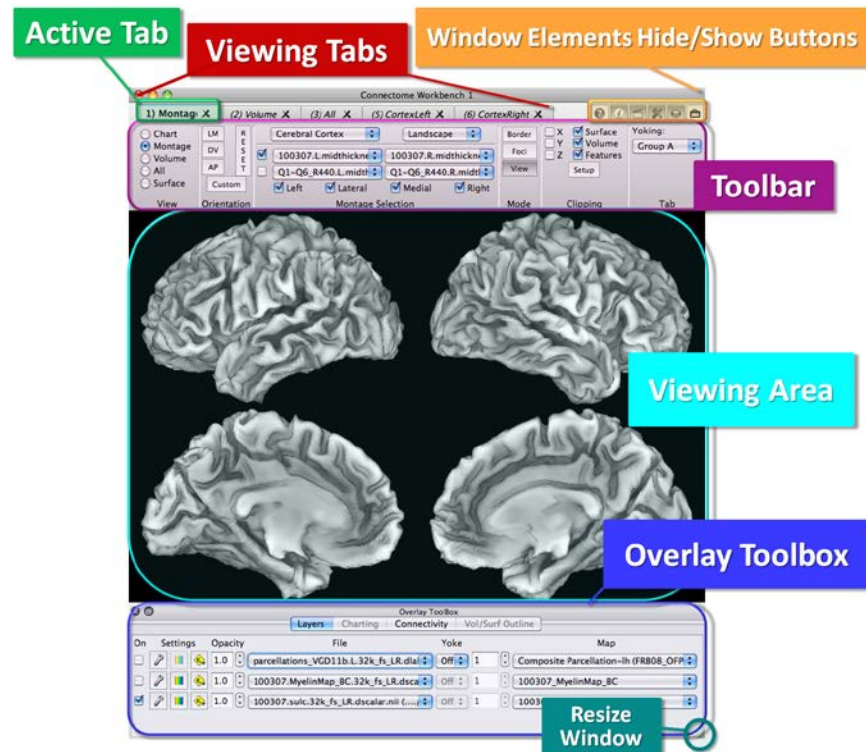
The scene opens with a “montage” view of the left and right hemisphere anatomical midthickness cortical surfaces (halfway between the pial and white matter surfaces) of the HCP subject 100307 in the **Viewing Area** of the **Workbench Window** (“Connectome Workbench 1”). Components of the Workbench Window are shown **on the top of the next page**.



The Scenes box

- At the top of the window, you see the 5 tabs of loaded surfaces and volumes in this scene. 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. *Click* through the tabs and notice that the options in the **Toolbar**



The Workbench Viewing Window in Horizontal Orientation

change when you switch tabs/views.

- The **Overlay Toolbox**, at the bottom of the window in the figure **above**, 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 buttons in the upper right of the window.

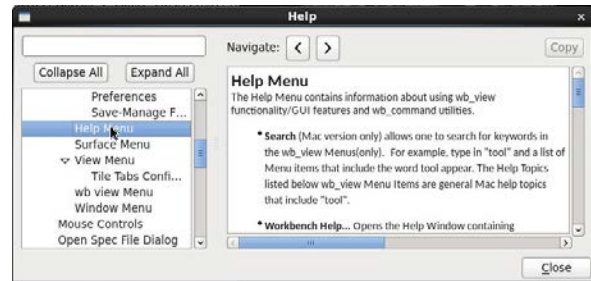
Help: Information box: Identify Brainordinate box: Scenes box:
Toolbar: Overlay Toolbox: Features Toolbox:

- 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 highlighted **Tooltip** pops up describing the function of the control.
- Click* on the **Help** **button**. The Help box will appear that has a glossary of terms and help information for both wb_command and wb_view.

- Scroll down on the left and *click* on the **Help Menu** entry. Information and helpful images will appear on the right (right). *Close* the Help box.

Basic Navigation using Mouse Controls

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



The Help box

- In the first **Viewing tab** labeled (1) *Montage*, move your **mouse** into the viewing window depicting the brain surfaces. *Hold down* the **left mouse button**, *drag* your **mouse** back and forth and up and down to rotate the surfaces.
- To zoom, *hold down* the **control key**, *hold down* the **left mouse button**, and *drag* your **mouse** up and down. If you have a **mouse wheel**, you can also zoom by *moving* your mouse into the Viewing Area and *scrolling up* to zoom out or *scrolling down* to zoom in.
- To pan (move the brain surface to a different part of the [Viewing Area](#)), *hold down* the **shift key** on the keyboard, *hold down* the **left mouse button**, and *drag* your **mouse** left, right, up, or down.
- Use the **Reset button** in the **Toolbar** to return to the default zoom, pan, and orientation.
- 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. (A “brainordinate” refers to a vertex or a voxel somewhere within the brain. A “grayordinate” refers to a vertex or a voxel specifically within cortical or subcortical gray matter.)
- *Click* on the **Properties button** in the **Information Box** to change the color and size of the ID sphere (*try ID Symbol Color: Fuchsia and Most Recent ID Symbol Diameter: 12 mm*)
- *Click* a second brainordinate and note that the symbol diameter of the most recently identified brainordinate is by default larger than previously identified brainordinates.
- By *reclicking* precisely on a sphere that identifies a brainordinate, you can deselect that brainordinate; the sphere will disappear. By *right-clicking* anywhere in the **Viewing Window**, you can select an option to **Remove All Vertex Identification Symbols**.
- *Close* the **Information Properties** box.
- *Click* on **Tab 2** at the top of the **Workbench Window**, labeled (2) *Volume*. Move your mouse cursor into the Viewing Area. This shows coronal, horizontal, and parasagittal views concurrently.
- *Zoom* on the displayed **Volume** slice as above, by *holding down* the **control key**, *holding down* the **left mouse button**, and *dragging* your **mouse** up and down, or *scrolling* up or down with your **mouse wheel**.

- *Pan* the **Volume** slice as above by *holding down* the **shift key** on the keyboard, *holding down* the **left mouse button**, and *dragging* your **mouse** left, right, up, or down.

Note that the mouse-controlled rotation 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. The crosshairs will move to the identified voxel and the **Information box** shows information of the particular brainordinate (voxel) that was clicked.

Tile Tabs

The **Tile Tabs** view allows concurrent visualization of all tabs available in the Workbench window.

- *Click* on the **View menu** (at the top of the Window) and select **Enter Tile Tabs**. Now all 5 tabs are showing as “panes” in the same window.
- Use the shortcut *Ctrl + M* to toggle back and forth from Tile Tabs to normal view

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

- *Click* on the  and  buttons to hide the Toolbar and Overlay Toolbox, respectively, allowing for a larger display.
- *Reclick* on the  button to display the Overlay Toolbox.

Surface Layers

- If you are still in Tile Tabs view, *use Ctrl + M* to return to normal view.
- *Click on* tab **(5) CortexRight** at the top of the **Workbench Window** to switch the view to the **right hemisphere**. This tab is set to display the inflated right hemisphere surface of subject 100307 with the top layer displaying a map of myelin content obtained from running the HCP structural pipeline on this subject.
- Rotate the surface (*hold down the left mouse button and drag your mouse*). Red and orange represent heavily myelinated regions, purple and black represent areas of low myelin content ([Glasser & Van Essen, 2011](#)).
- *Move the cursor down* to the **Overlay Toolbox** below the **Viewing Area**. There are 4 tabs in the **Overlay Toolbox**. You are currently viewing the **Layers** tab.

Layers of displayed data 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 “dlabel” file showing a parcellation from [Van Essen et al. 2011b](#) is listed on top (but is toggled off), the second layer is the “dscalar” Myelin Map file that you are viewing, and the third layer is a dscalar file representing cortical shape based on sulcal depth (FreeSurfer’s ‘sulc’ map). These file types will be explained more in Part 2. Each of these CIFTI files can include surface data for both left and right hemispheres even though the associated geometric surfaces on which they are displayed are separate “GIFTI” files for each hemisphere (see Part 2). CIFTI files can also contain volume data for subcortical gray matter voxels (see Part 2).

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

This concludes Part 1. Remember that a more extensive step-by-step orientation to wb_view is available in the WB 1.0 Tutorial, provided as additional material.

Part 2: NeuroImaging File types

Part 2a: The next two pages are informational; there are no action items on your computer until Part 2b (p.9).

DICOM, NIFTI, and DCM2NII

Images are collected on the scanner in the **DICOM** (Digital Imaging and Communications in Medicine) format. A single DICOM file contains both a header (which stores information about the patient's name, the type of scan, image dimensions, etc), as well as all of the image data (which can contain information in three dimensions).

DICOMs are very unwieldy (many uncompressed small files, often contain Protected Health Information, PHI), therefore HCP does not release these. DICOMs do contain useful header information that is needed to run the HCP Pipelines if you are working with your own data. This DICOM header viewer is useful for looking at this information: <http://nrg.wustl.edu/software/dicom-browser/>.

If you envision (eventually) sharing your data publicly, it is important to make some of the non-PHI information available to users. For HCP, some of the subject-specific info is in ConnectomeDB and is released with the individual subject structural packages (see Thursday’s practical). Relevant scanning protocol DICOM info that is identical across subjects is released as [Appendix 1 in the HCP Reference Manual](#).

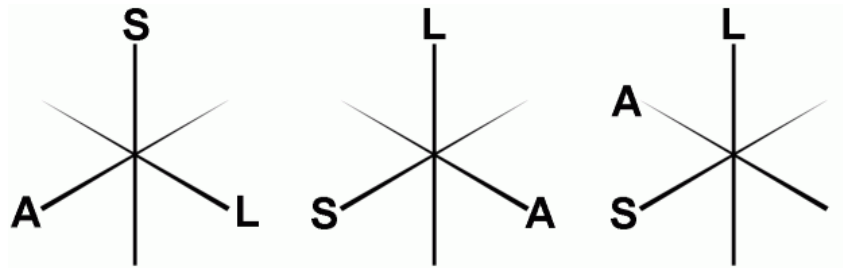
HCP data are converted from DICOM to NIfTI format before further processing. The NIfTI image format standard was designed for scientific analysis of brain images (see <http://nifti.nimh.nih.gov/nifti-1>) using a simple, compact and versatile format. The images are generally stored as a single file (nii), though the standard also supports a header/image pair format for older tools that expect ANALYZE images. Programs like FSL, MRICron, and Connectome Workbench can also read compressed images (nii.gz). A valuable NIfTI feature is that the format includes spatial information about the voxels, allowing for alignment of volume files having different fields of view (bounding boxes), among other things.

The program DCM2NII converts images from the proprietary DICOM scanner format to the NIfTI format used by FSL, Workbench, SPM5, and many other brain imaging tools. DCM2NII is a stand-alone program that is distributed with MRICron (<http://www.mccauslandcenter.sc.edu/mricro/>, Chris Rorden).

Reorienting to canonical spatial axis orientations

The NIfTI format stores spatial transforms so that software can determine the orientation of the image. This enables some programs (including wb_view) to automatically display the image in an intuitive orientation.

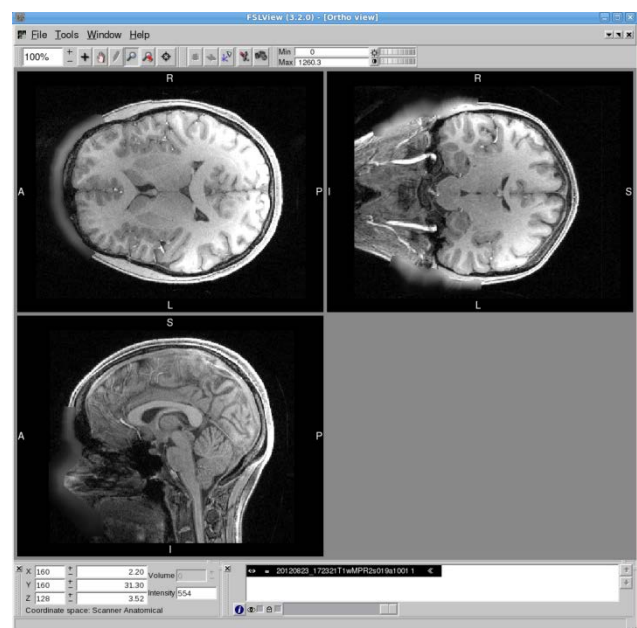
However, many programs ignore these transforms, and display the images as they are saved to disk (e.g. FSLview, MRICro) - this means that a sagittally acquired scan (e.g., structural scans in HCP protocol) appears very differently from an axially acquired scan (functional and diffusion scans). In fact, the three spatial dimensions (left-right, anterior-posterior, superior-inferior) can be saved in 48 different orthogonal orientations. The drawing above shows three exemplars of the possible orientations.



Using the default settings of DCM2NII, sagittally collected HCP structural images, FSLview will show the images in a non-intuitive orientation (right).

For your own data, you can deal with this in several ways:

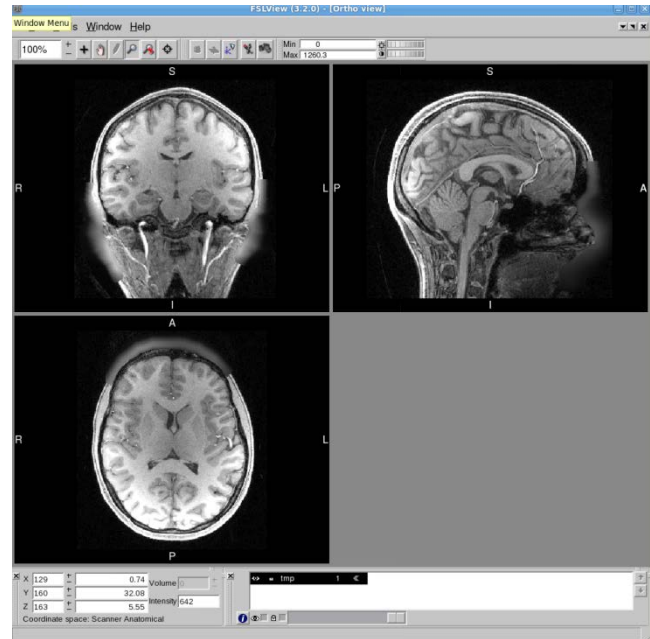
1. You can set dcm2nii to reorient all images so they are all aligned to the nearest orthogonal



direction to 'canonical space' (i.e. as close as possible to the rotation matrix $\begin{bmatrix} 1 & 0 & 0; 0 & 1 & 0; 0 & 0 & 1 \end{bmatrix}$). This enables programs like FSLview and MRICro to display the images in a sensible orientation, regardless of the acquisition.

2. The HCP structural pipeline uses the FSL command “fslreorient2std” to orthogonally rotate the NIFTI image to match the orientation of the standard template images (MNI152).

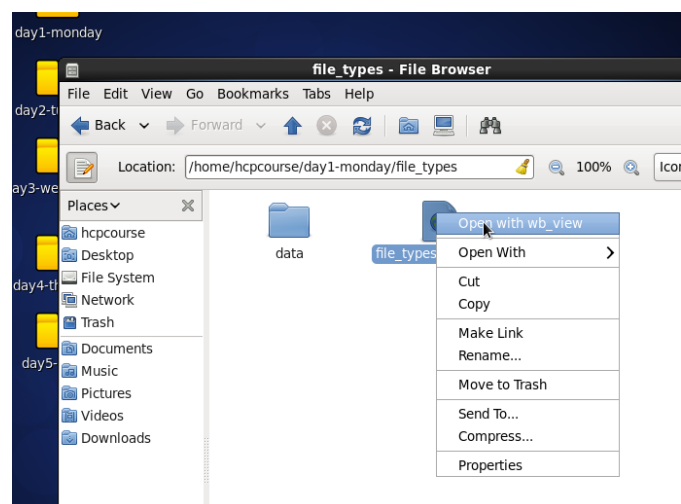
3. The “wb_command -volume-reorient” command can reorient a volume into any of the 48 possible orientations. The most often used orientations are LPI and RPI. Here’s the same image (right) in FSL view after reorientation to RPI (right-left [RL], posterior-anterior [PA], inferior-superior [IS]).



Part 2b: Go through the practical independently, in ‘asynchronous’ mode.

NIFTI

- Double-click the **day1-Monday** shortcut on the Desktop, then double-click the **file_types** directory, and double-click or right-click **file_types_1.0.scene**, to open the scene in wb_view:

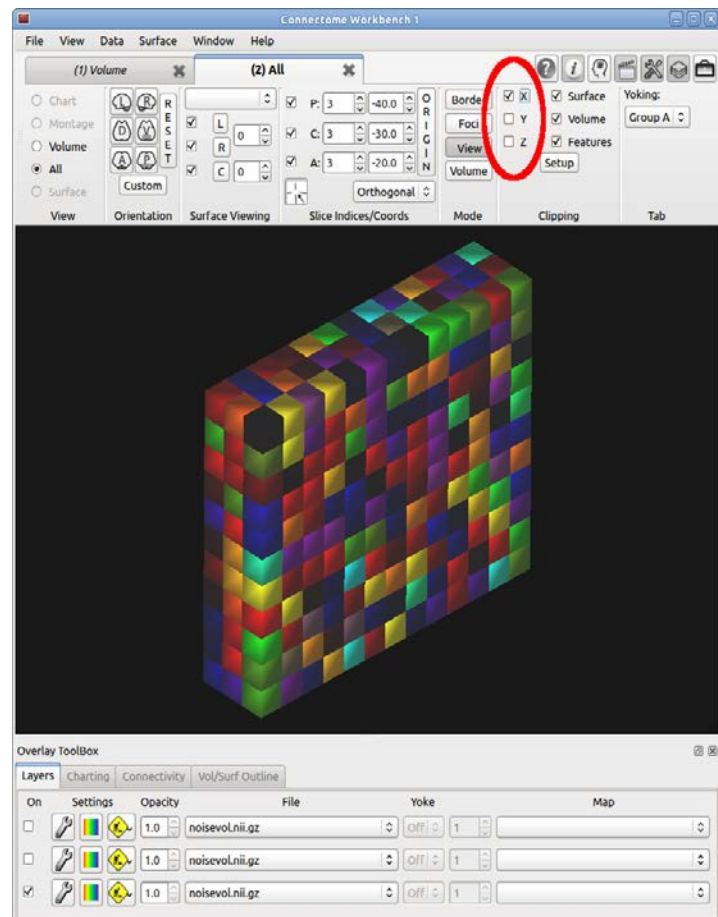
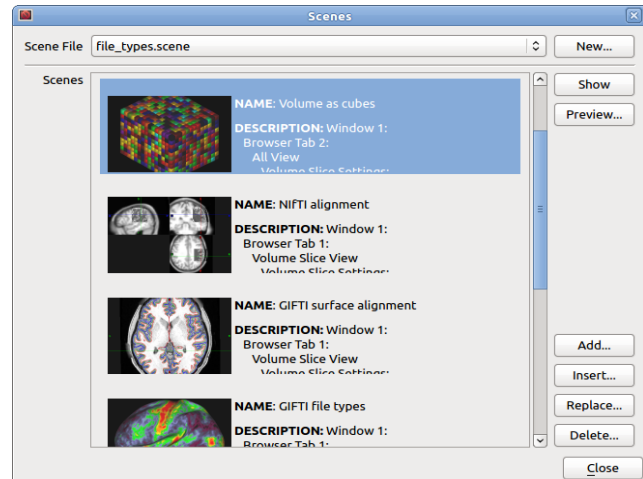


- Double click the “**Volume as cubes**” scene in the **Scenes box** (or click “Show”).
- Drag the scenes box to the side.
- Put your cursor over the main image, hold down the left mouse button, and drag the mouse to rotate the figure.

This is a NIfTI volume file (extension .nii.gz, sometimes just .nii). It consists of “voxels”, which are usually cubes, stacked in a regular grid.

Side note: if the edges of the volume look like they are not parallel when rotating it, don't worry, it is an optical illusion. Workbench draws 3D figures using orthographic projection, rather than in perspective, so instead of parallel lines converging in the distance, they stay parallel. For a deeper explanation, see the end of this document.

- Toggle the X, Y, and Z checkboxes on and off in **Clipping**, as shown in the image (right), to view portions of the cube by removing volume slices.
- Return to the **Scenes box**, double click “**NIfTI alignment**”, and toggle the circled checkbox (‘Layers’) in the image below to turn the T2 weighted section image layer on and off.



Note that despite the different resolution (voxel size) and spatial dimensions, the anatomical features align (these files are derived from the same subject):

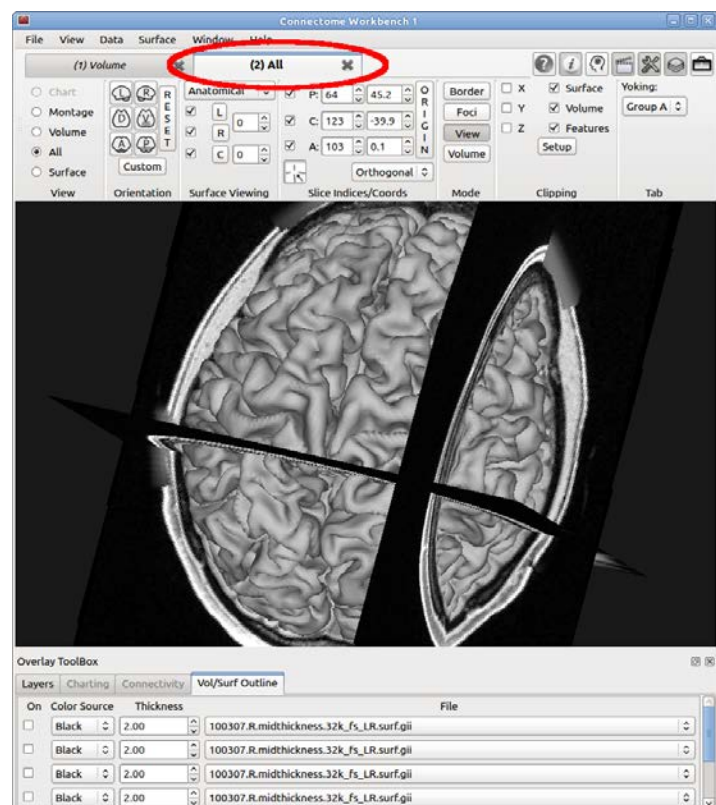
This demonstrates that the NIfTI files each contain information on the size and location of the voxels, such that volumes of different resolution and bounding box size can align properly, by using their voxel coordinates in millimeters. This is a major reason why the NIfTI-1 file format was created. (Some previous widely-used formats, notably ANALYZE, did not have enough information to do this kind of alignment properly, and would instead show the the T2 section volume with its corner aligned to the corner of the low resolution T1, shifted to the inferior, posterior, right side of the head.)

This flexibility regarding alignment comes with some complexity. Many tools have a set of preferred orientations for volume files (wb_view prefers LPI and RPI, FSL prefers RPI, freesurfer prefers RAS). As noted above, NIfTI volumes can be reoriented using, e.g., wb_command -volume-reorient.

GIFTI:

In the **Scenes box**, double click on “**GIFTI surface alignment**”. The three colored contours are the intersections of the white, midthickness, and pial surfaces (red, green, and blue, respectively) for the volume slice being viewed.

- Click the “**All**” tab to see the surfaces in 3D with volume slices drawn through them:



- Drag the mouse with the left button held down to rotate the figure.
- Click on the surface or a volume slice to change which volume slices are drawn.

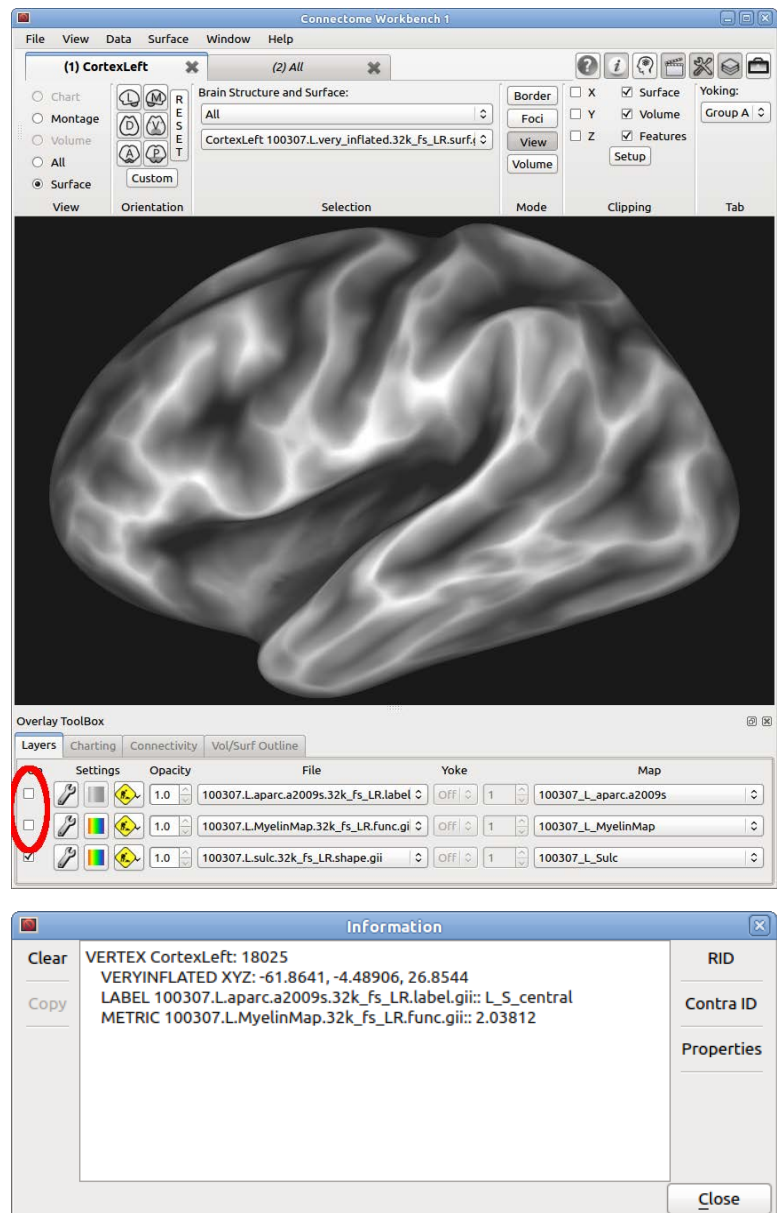
GIFTI surface files (extension .surf.gii) consist of a mesh of triangles, each containing one hemisphere (in these scenes, the left and right hemispheres are separate files loaded simultaneously).

- In the **Scenes box**, double click “**GIFTI file types**” to view Freesurfer’s sulc map displayed on the very inflated left hemisphere surface of HCP subject 100307.

The inflated and very inflated surfaces facilitate visualization of buried cortex and thus have advantages over the anatomical surface types mentioned previously (pial, white, and midthickness).

- Click the circled checkboxes to turn the myelin map and the label file (which is a FreeSurfer-generated map of gyri and sulci) on and off.

The files in this scene show two different types of GIFTI surface data files: “metric” files (their extensions are .func.gii and .shape.gii), and “label” files (extension .label.gii). Metric files contain real-valued data, whereas label files contain integer-valued data, with a name associated with each integer used. Clicking on the surface will show the name (“label”) associated with the integer that exists at the clicked location, in the Information box (right).



- In the **Scenes box**, double click the “**GIFTI surface triangles**” scene.

This scene shows the triangle structure of the surface file, with data displayed on it. Data in both metric and label files exists on the vertices of the mesh. If you click on the surface, you will notice that the identification symbol is centered on the vertex.

CIFTI:

- In the **Scenes box**, *double click* the “**CIFTI grayordinates**” scene.

This scene displays a single CIFTI file, a “dtseries” file (extension .dtseries.nii), which contains data for both hemispheres, and also contains voxels for gray matter in the cerebellum and various subcortical structures. This represents the standard HCP grayordinate space. (The data is a resting-state fMRI timeseries file, about which you will learn a lot more in Tuesday’s session.)

The CIFTI file format serves multiple needs, most notably to enable flexible representation of data associated with multiple geometric structures (surfaces and portions of volumes). GIFTI and conventional NIFTI files are not designed for cross-structure measures, nor can they include both surface and voxel representations, and nor can they exclude irrelevant parts of the image from taking up space in the file (e.g., white matter, CSF/skull/background, or the non-cortical surface along the ‘medial wall’ of each hemisphere).

By taking only the data elements that are relevant and simply concatenating them, the interesting data can be stored in a single 2D matrix (the other dimension can be timepoints, contrasts, etc.), but it is essential to be able to translate back to what each index means. The CIFTI format solves this problem by including both the 2D matrix and an XML representation of this translation information.

In order to store the data matrix and this XML, the NIFTI-2 format is used, because it is similar to the already widely-used NIFTI-1 (volume files), but without having NIFTI-1’s 32,767 limit on dimension length (roughly equal to a single fMRI-resolution surface’s number of vertices). Because CIFTI files use the NIFTI-2 format, the file names must end in .nii, but they have 2 parts, similar to GIFTI files (i.e. .surf.gii), to reflect the multiplicity of CIFTI file subtypes.

- Load (*double-click* on) the “**CIFTI dense file types**” scene.

“Dense” CIFTI files store values for each voxel and surface vertex (collectively known as brainordinates) as separate elements in the file, even if they have the same value (for instance, label data).

- *Toggle the checkboxes* by the layers to turn on and off the various types of dense CIFTI files.

Label data is in .dlabel.nii files (distinct from GIFTI ‘label.gii’ files).

Files of the .dscalar.nii type have independent names for each map, whereas .dtseries.nii files have data arranged as regularly spaced samples, for instance timeseries or frequency series.

- Load (*double-click* on) the “**CIFTI dconn (remote loading)**” scene, and enter your ConnectomeDB username and password at the prompt that shows up (*do not check* “save password to preferences”):

If you get an error that says “Error opening URL, response code: 401”, it means your username or password was typed incorrectly, try loading the scene a second time to re-enter them. Note that if the

internet connection is not good, this may take a long time, or fail with a different response code. If you can't get it to load without an error, skip the following instruction.

- *Click on a surface* (or in the volume within the represented voxels) to load connectivity data from the clicked point.

The dense connectome file type ("dconn") is viewed interactively. Each row in the file is the connectivity from one vertex or voxel to all other vertices or voxels. Since the typical mode of viewing these kinds of files is to look at one row at a time, we can retrieve each row individually from a remote server as they are accessed, as each row is relatively small. A similar strategy is used when viewing a dconn that is a local file, in order to avoid loading the entire file into memory.

- *Open the "CIFTI parcellated file types" scene.*

Parcellated file types use one value in the file for multiple brainordinates. This shows a parcellated version of the myelin map that was shown earlier.

- *Toggle on* the top layer to see a parcellated connectivity file that represents resting-state functional connectivity between areas in the brain, as will be discussed in detail on Tuesday.
- *Click* on various parcels to see that while the values in each parcel change, the edges between areas do not move, because their locations were set when the file was parcellated.
- *Select* the **"(2) Chart"** Viewing tab to see a representation of the entire parcellated connectivity matrix.

Summary of File Types:

DICOM: only volume (voxel) data, full rectangular FOV, sometimes multi-file format (1 slice per file), often contains PHI from scanner

NIFTI: only volume data, full rectangular FOV, single file format

GIFTI: only surface data, only one structure per file

CIFTI: surface and volume data in one file, multiple structures, exclude vertices and voxels without interesting data, can store parcellated data with description of parcel locations

End of Practical 1.

Authors:

The authors of this practical were Jennifer Elam and Tim Coalson, with contributions from Matt Glasser, Greg Burgess, Donna Dierker, and David Van Essen.



Extra information:

If you want to know more about the internal details of the file types, here are some resources to look into:

NIfTI:

The official specification of NIfTI-1 is inside the C header file:

<http://nifti.nimh.nih.gov/pub/dist/src/niftilib/nifti1.h>

More information is available on the same website: <http://nifti.nimh.nih.gov/nifti-1>

NIfTI-2, which is used by the CIFTI format, is also described on the site, mostly it changes some of the fields in the NIfTI-1 header to have a larger size (and hence larger maximum value), and otherwise leaves their meaning the same: <http://nifti.nimh.nih.gov/nifti-2>

You can output most of the NIfTI header on a file (version 1 or 2, including CIFTI) in text form with “wb_command -nifti-information -print-header”.

GIFTI:

The specification of the GIFTI format is here: <https://www.nitrc.org/projects/gifti/>

It is an XML-based format, unlike NIfTI which uses a binary format. This means you can view it as a text document, and read some of the information in it.

CIFTI:

The specification of CIFTI-2 is in pdf files attached to these forum posts on NITRC:

http://www.nitrc.org/forum/forum.php?thread_id=4380&forum_id=1955

http://www.nitrc.org/forum/forum.php?thread_id=4381&forum_id=1955

The CIFTI-1 specification is within the NITRC wiki:

<http://www.nitrc.org/plugins/mwiki/index.php/cifti:Cifti-1>

There is code available for using the CIFTI format in C++ or Matlab:

http://www.nitrc.org/frs/?group_id=454

Orthographic Projection Illusion:

Since perspective drawing matches how we see real objects, orthogonal drawing can look strange to us, especially while rotating the figure. While rotating it, it looks more 3D, and thus we expect it to look more realistic, including having perspective. The lack of the expected perspective makes it look as though the part of the rectangular prism that is farthest from us is flared outward, especially when rotating it across an end-on view.

