

# ISTAART Brain visualization Webinar

Visualization of neuroimaging data  
using R and the connectome workbench

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# Learning objectives

- Learn to import nifti files in R
- Extract ROI based data from nifti files in R
- Map ROI based data to surface data
- Render surfaces in R and in the connectome workbench



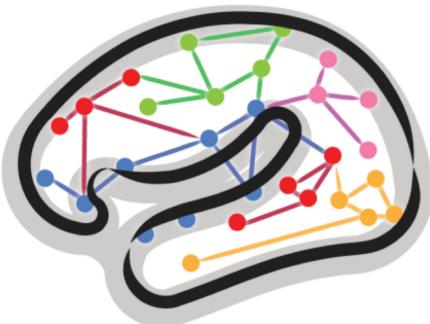
All materials and slides  
can be found on GitHub



[https://github.com/nfranz  
me/Tutorials](https://github.com/nfranzme/Tutorials)

# Introducing the connectome workbench

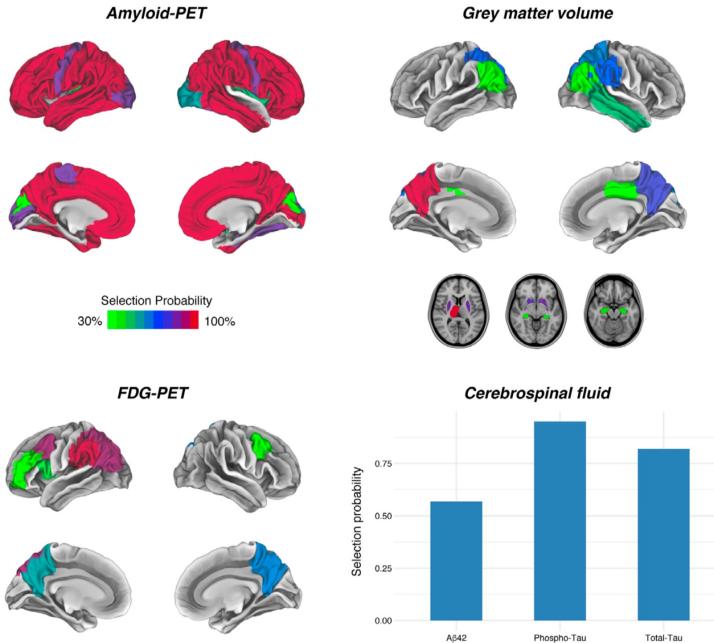
- Developed within the Human Connectome Project ([www.humanconnectome.org](http://www.humanconnectome.org))
- Open source visualization tool for neuroimaging data
- Includes a GUI and command line tools for mapping and manipulation of neuroimaging data
- Works with volumetric (i.e. nifti) and surface based imaging data (i.e. cifti)
- Available for Mac OS, Linux and Windows
- Download here: <https://www.humanconnectome.org/software/connectome-workbench>



HUMAN  
**Connectome**  
PROJECT

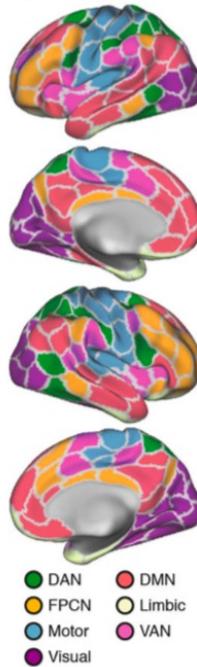
# Example images

**B: Feature selection probabilities of the AFGC model**

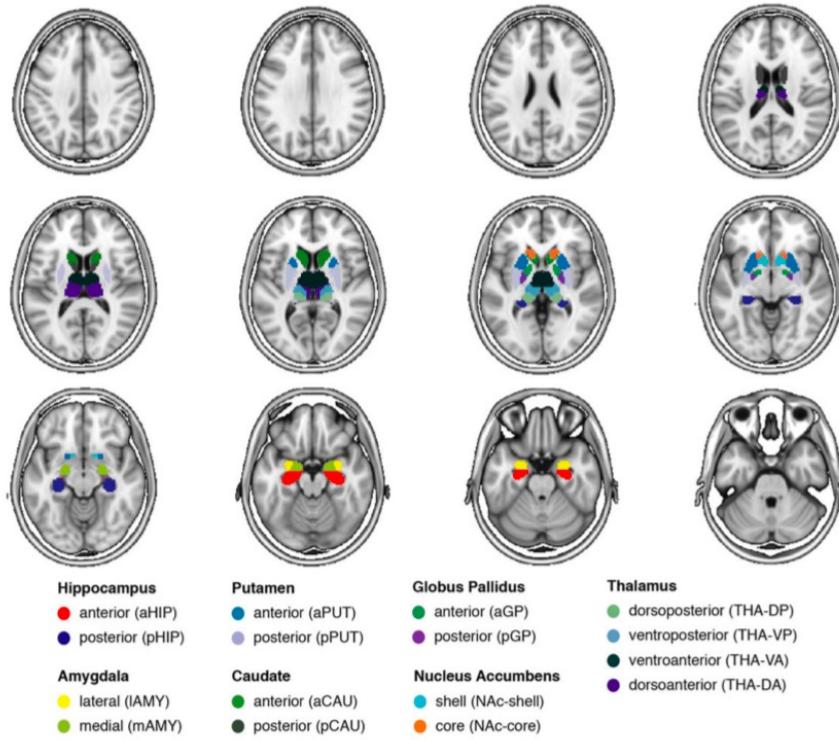


*Regions of interest (ROIs) for atlas-based analyses*

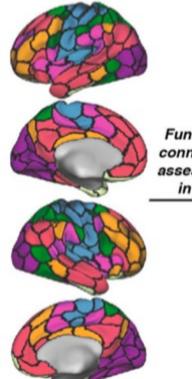
**G: Cortical parcellation**



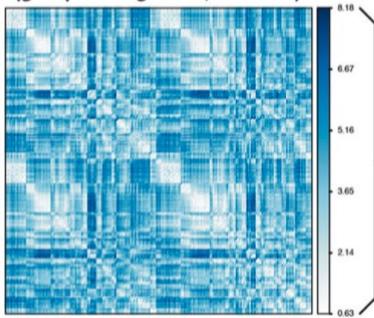
**H: Subcortical parcellation**



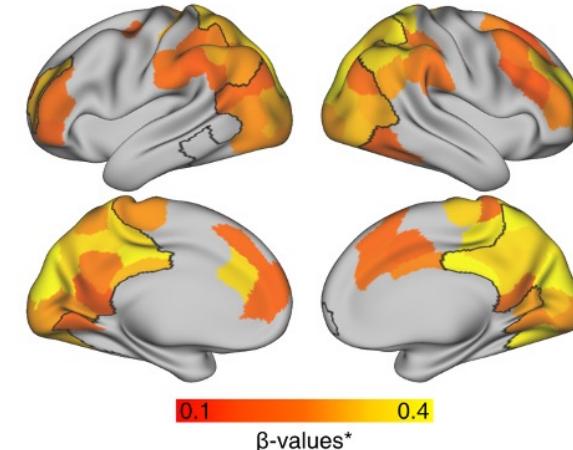
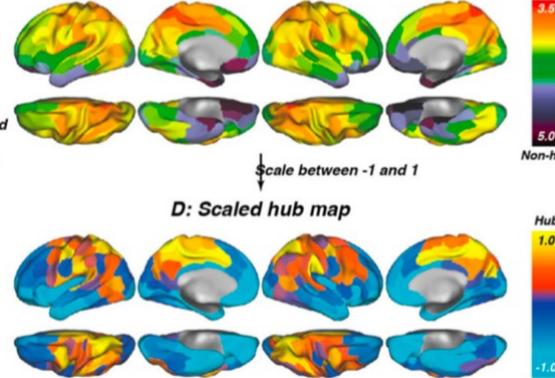
**A: 200-ROI brain atlas**



**B: Connectivity-based distance (group-average HCP, n = 1000)**

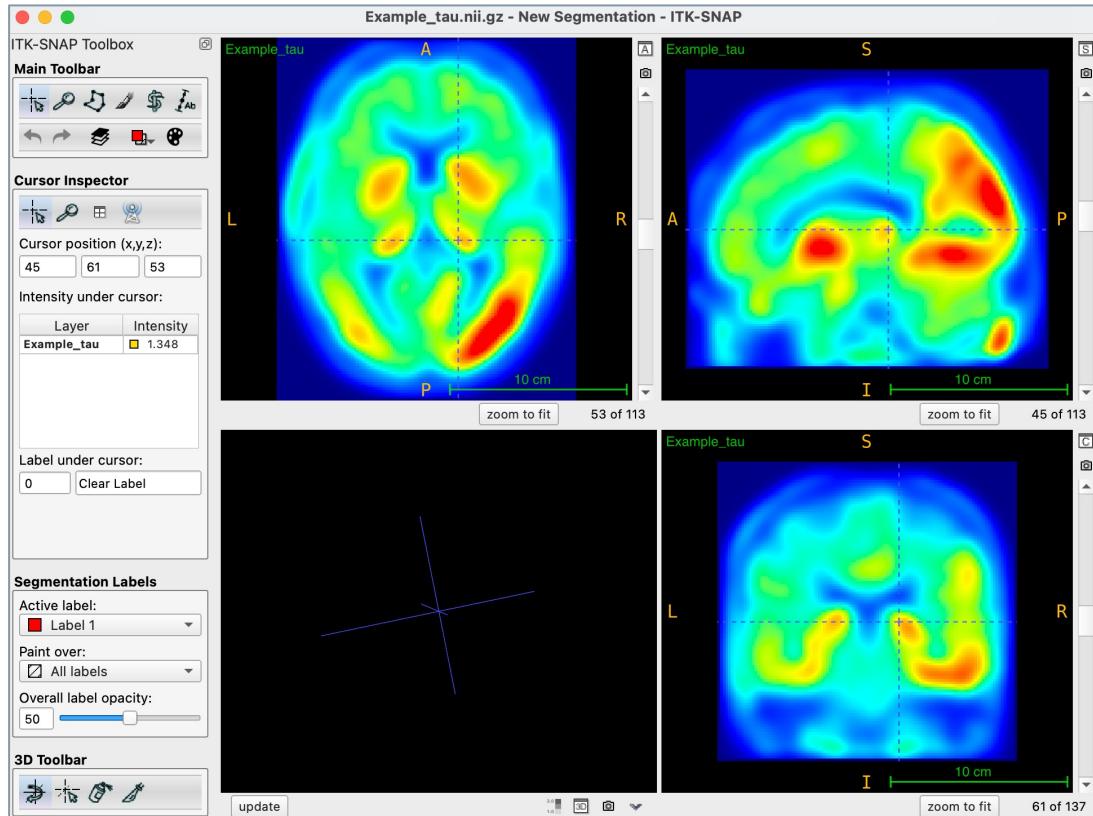


**C: Weighted degree (global functional connectivity)**

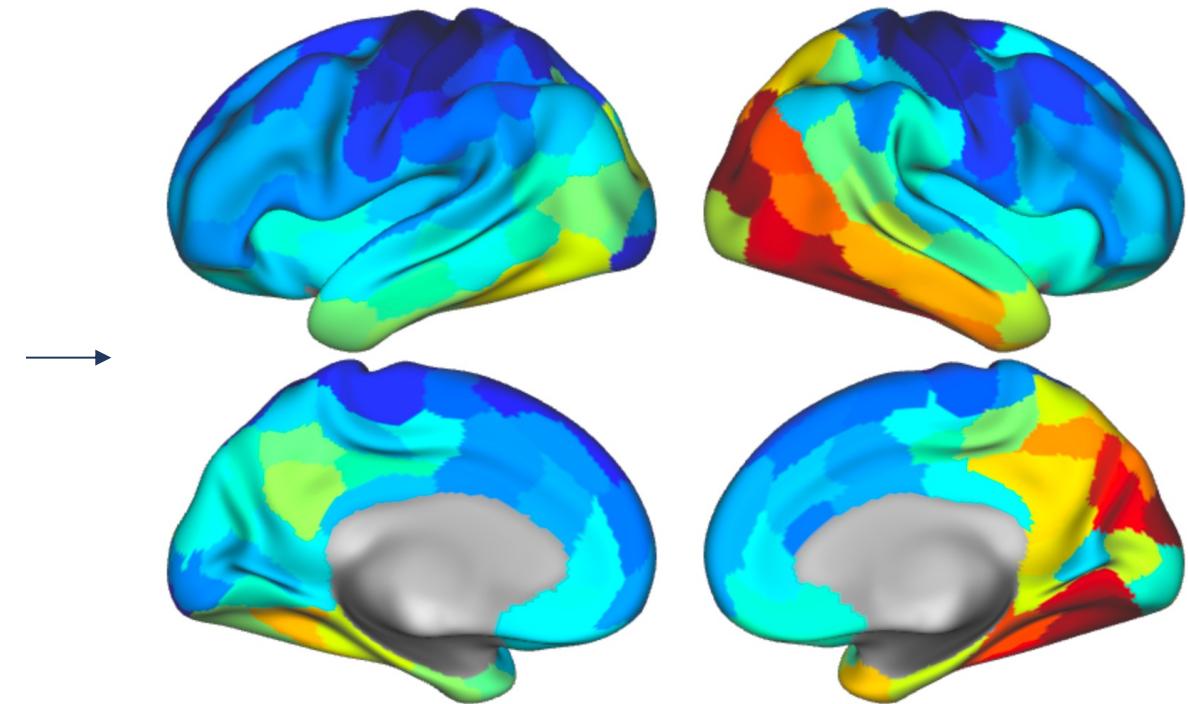


# Agenda for today – Map 3D nifti images to ROI-based surfaces

Source Image (Tau-PET in MNI space)



Target



# Lesson 1: Extracting ROI based data in R

All R code can be found on Github in an R-Markdown file

Tutorials / Connectome\_workbench / Map\_nifti\_to\_ROIs / 

Add file 

Name	Last commit message	Last commit date
..		81d737a · 5 hours ago 
Example_data	Add files via upload	5 hours ago
Example_surface.dscalar.nii	Add files via upload	5 hours ago
R_connectome_workbench_tutorial.Rmd	Add files via upload	5 hours ago
R_connectome_workbench_tutorial.html	Add files via upload	5 hours ago

# Lesson 1: Extracting ROI based data in R

## TUTORIAL

### Mapping Voxel-based niftis to ROI-based surface data

#### prepare environment and load libraries

Make sure you have installed the latest version of the connectome workbench, which you can download here:

<https://www.humanconnectome.org/software/connectome-workbench>

```
#### load required libraries ####
require(neurobase) ← Reading/Writing nifti files with R (https://cran.r-project.org/web/packages/neurobase/neurobase.pdf)
require(ciftiTools) ← Working with gifti/cifti files in R (https://github.com/mandymejia/ciftiTools)
require(plyr)
require(dplyr)

#### set path to workbench (example for a MacOS environment) ####
ciftiTools.setOption('wb_path', '/Applications/workbench/bin_macosx64')
```

```
## Using this Workbench path: '/Applications/workbench/bin_macosx64/wb_command'.
```

# extract ROI-based data

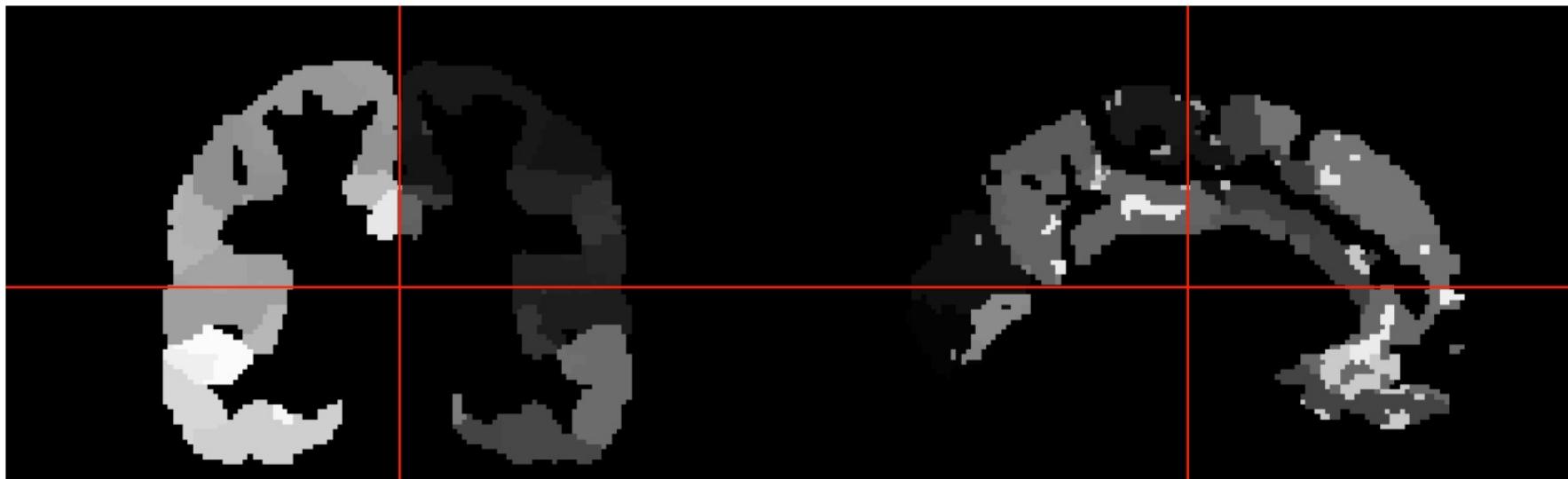
For this example, we will extract ROI based data from a tau-PET image using the 17 network version of the Schaefer 200 ROI atlas. The atlas including the reference (Schaefer et al., Cerebral Cortex, 2018) can be found here:

[https://github.com/ThomasYeoLab/CBIG/tree/master/stable\\_projects/brain\\_parcellation/Schaefer2018\\_LocalGlobal](https://github.com/ThomasYeoLab/CBIG/tree/master/stable_projects/brain_parcellation/Schaefer2018_LocalGlobal)

## read in images

### read in atlas

```
# load the atlas
atlas_readin <- neurobase:::readnii(
  file.path(sdir, "/Example_data/rSchaefer2018_200Parcels_17Networks_order.nii.gz")
)
neurobase:::ortho2(atlas_readin)
```

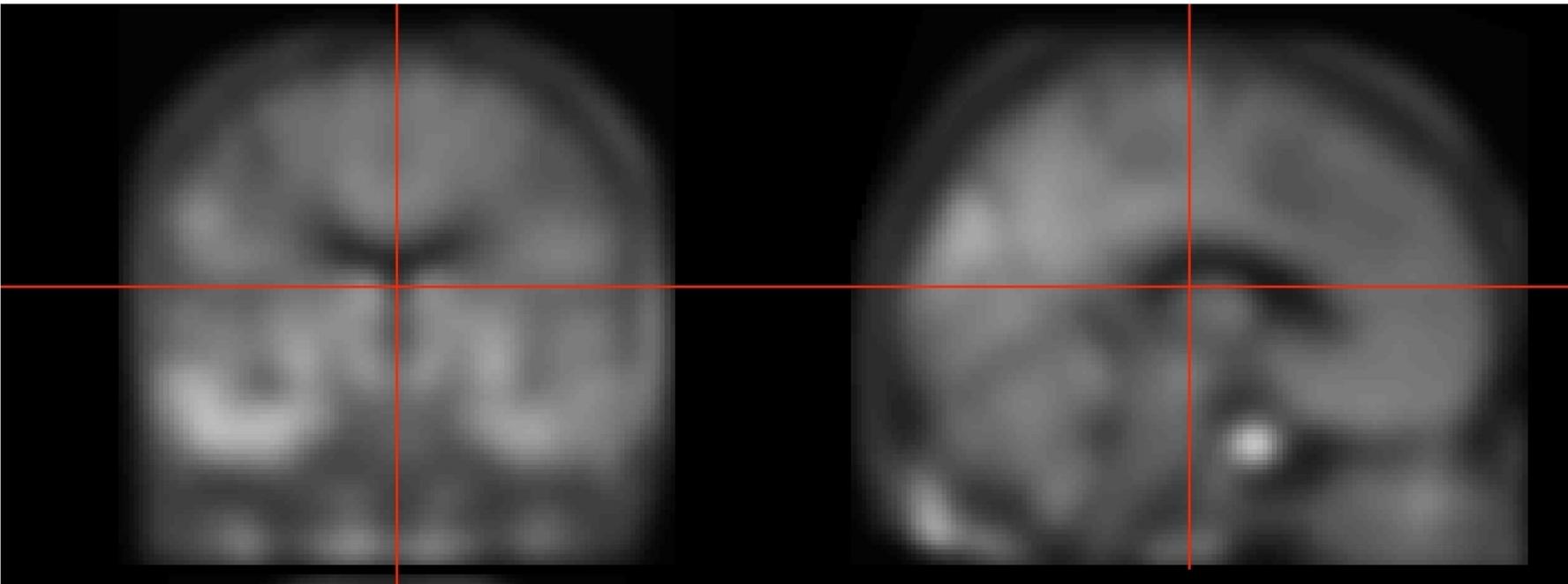


## read in the PET image

```
# load the atlas  
pet_readin <- neurobase:::readnii(  
  file.path(sdir, "/Example_data/Example_tau.nii.gz")  
)
```

```
## Warning in datatyper(nim, warn = warn): Need to change bitpix and datatype to  
## FLOAT64 due to NAs
```

```
neurobase::ortho2(pet_readin)
```

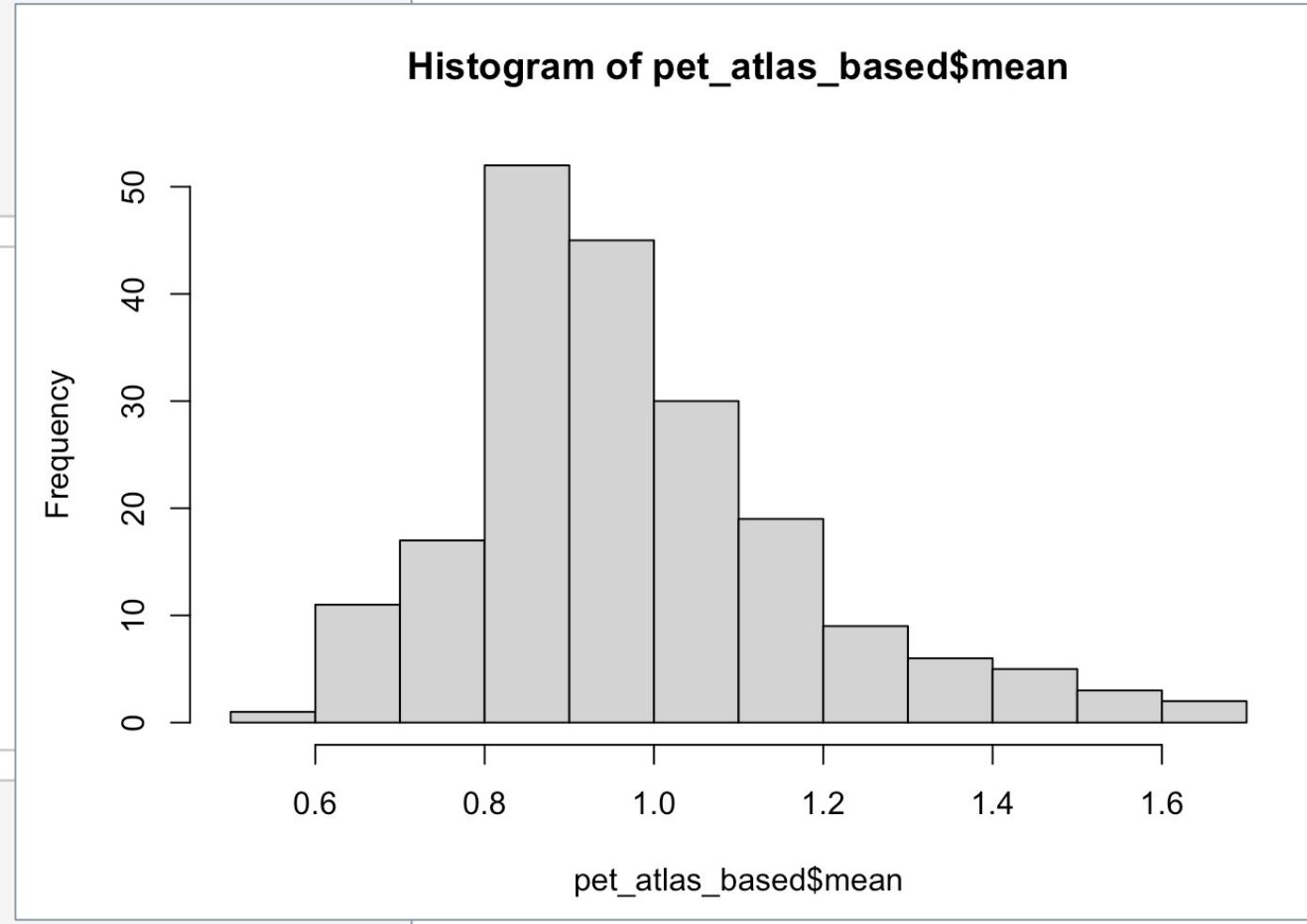


# extract ROI-based mean values

```
pet_atlas_based =  
  data.frame(pet = as.vector(pet_readin@Data),  
             atlas_idx = as.vector(atlas_readin@Data)) %>%  
  filter(atlas_idx != 0) %>%  
  group_by(atlas_idx) %>%  
  summarize(mean = mean(pet))  
head(pet_atlas_based)
```

```
## # A tibble: 6 × 2  
##   atlas_idx  mean  
##       <int> <dbl>  
## 1          1  1.11  
## 2          2  0.742  
## 3          3  0.860  
## 4          4  0.904  
## 5          5  1.09  
## 6          6  1.16
```

```
# show distribution of SUVR data  
hist(pet_atlas_based$mean)
```



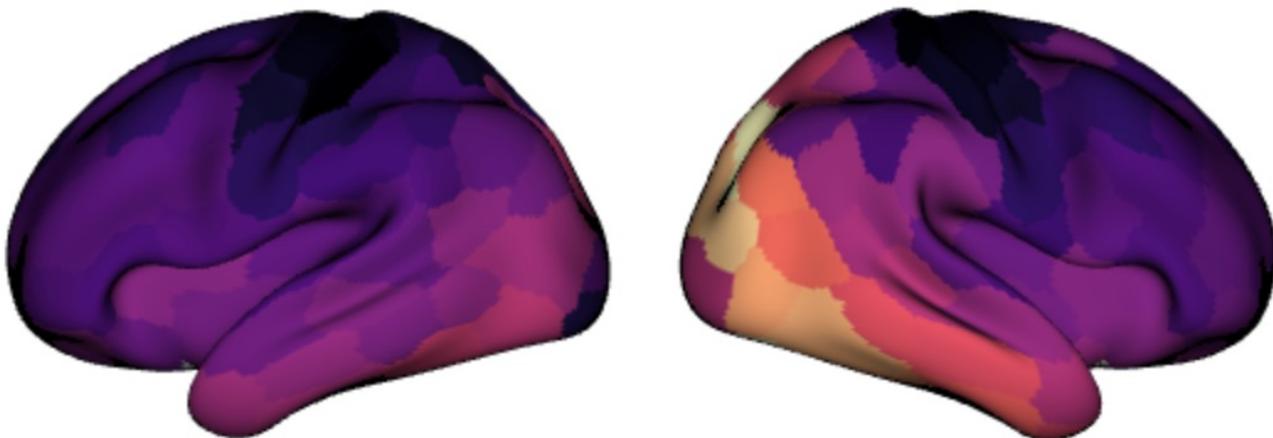
## map to xifti file

```
# read in atlas
atlas_dscalar <- read_xifti(file.path(sdir, "/Example_data/Schaefer2018_200Parcels_17Networks_order.dscalar.nii"))
atlas_dscalar_vec <- c(as.matrix(atlas_dscalar))

# determine values to map to surface
vector_to_map = pet_atlas_based$mean

# map ROI-based PET data to cifti
xii_to_map <- c(NA, vector_to_map)[atlas_dscalar_vec + 1]
xiil <- select_xifti(atlas_dscalar, 1)
xii_to_map <- newdata_xifti(xiil, xii_to_map)

# view cifti directly in R
view_cifti_surface(xii_to_map, colors = "magma", zlim = range(vector_to_map),
                    borders = T)
```



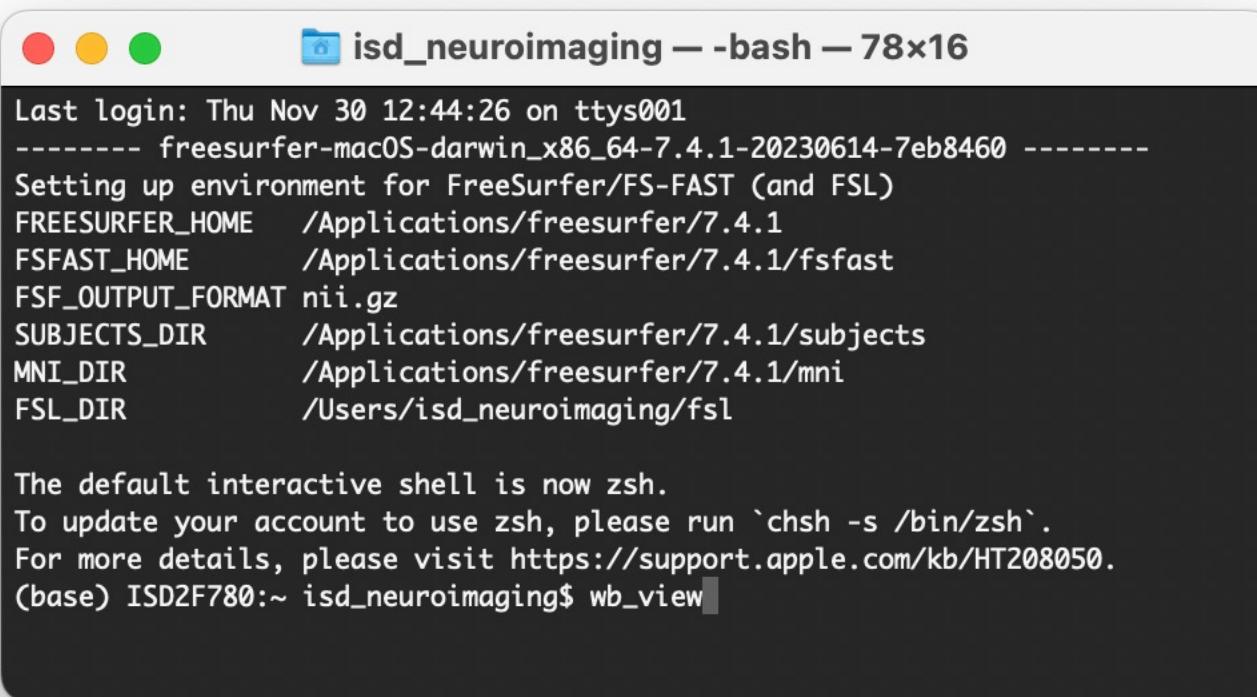
Direct visualization of data/results in R is quicker than moving to workbench Every time. Moving to workbench is useful if you like to create final Figures/images

# Moving to Connectome Workbench

## write cifti to disk

```
ciftiTools:::write_cifti(xii_to_map, file.path(sdir, "/Example_surface"))
```

```
## Writing left cortex.  
## Writing right cortex.  
## Creating CIFTI file from separated components.
```

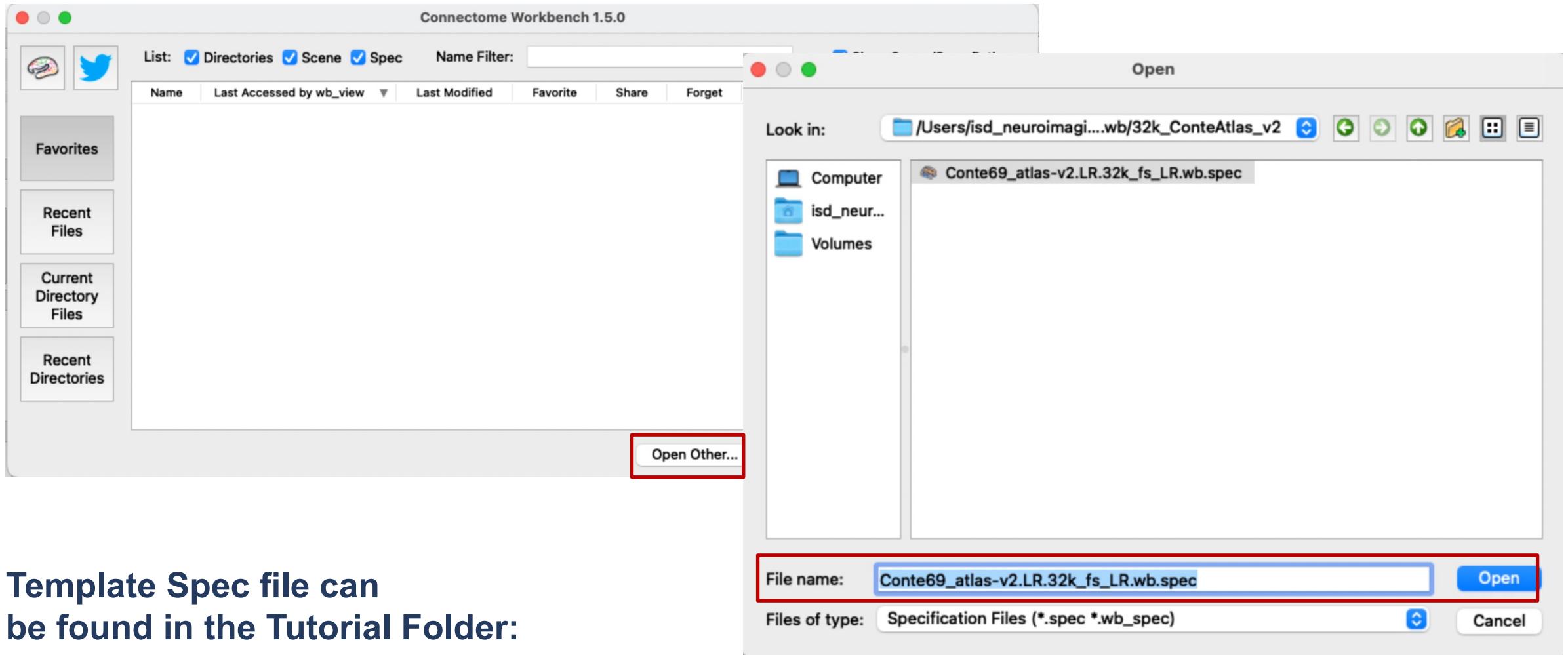


A terminal window titled "isd\_neuroimaging — bash — 78x16". The window shows the following command-line session:

```
Last login: Thu Nov 30 12:44:26 on ttys001  
----- freesurfer-macOS-darwin_x86_64-7.4.1-20230614-7eb8460 -----  
Setting up environment for FreeSurfer/FS-FAST (and FSL)  
FREESURFER_HOME /Applications/freesurfer/7.4.1  
FSFAST_HOME /Applications/freesurfer/7.4.1/fsfast  
FSF_OUTPUT_FORMAT nii.gz  
SUBJECTS_DIR /Applications/freesurfer/7.4.1/subjects  
MNI_DIR /Applications/freesurfer/7.4.1/mni  
FSL_DIR /Users/isd_neuroimaging/fsl  
  
The default interactive shell is now zsh.  
To update your account to use zsh, please run `chsh -s /bin/zsh`.  
For more details, please visit https://support.apple.com/kb/HT208050.  
(base) ISD2F780:~ isd_neuroimaging$ wb_view
```

If you installed the workbench correctly,  
You can open the GUI via the command line,  
By typing in `wb_view`

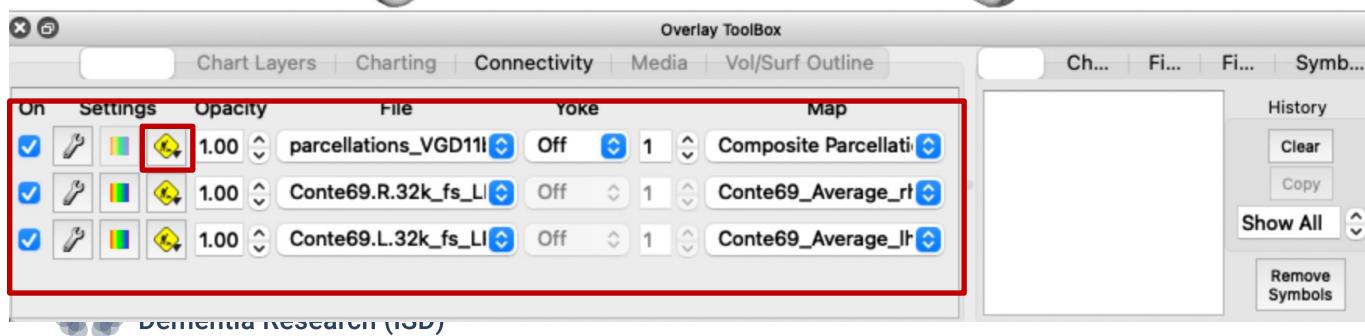
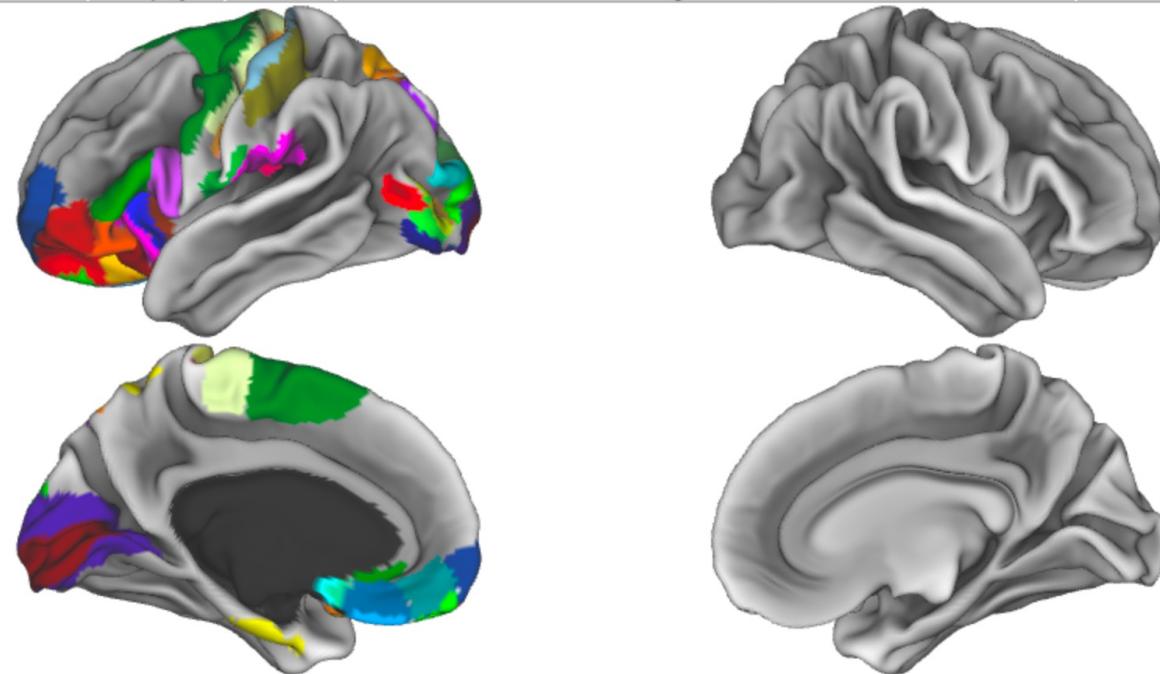
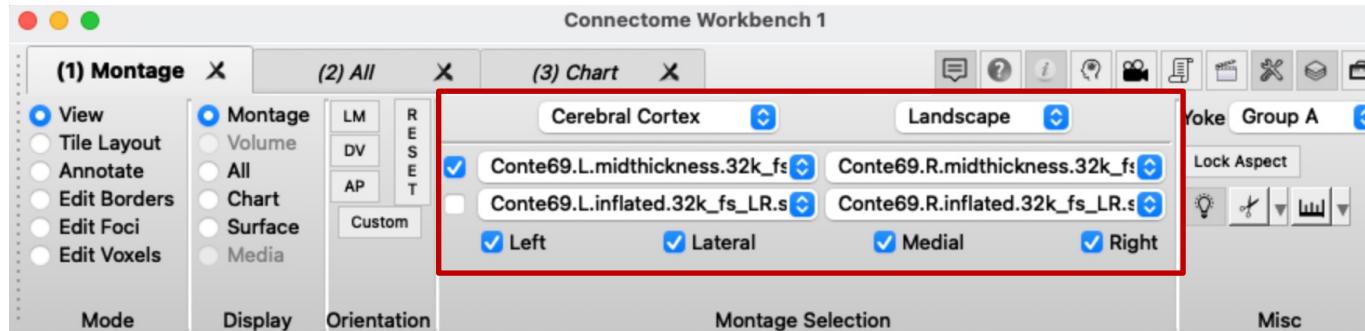
# Connectome workbench requires a Surface Template to work with



**Template Spec file can  
be found in the Tutorial Folder:**

Connectome\_workbench/Map\_nifti\_to\_ROIs/

Conte69\_atlas-v2.LR.32k\_fs\_LR.wb/32k\_ConteAtlas\_v2/Conte69\_atlas-v2.LR.32k\_fs\_LR.wb.spec



## Montage selection plane:

- Select the template you want to display (**Midthickness**, inflated or very inflated)

## Overlay Toolbox

- Select the overlay planes you would like to display
- Overlays can be added and moved

New Window ⌘ N  
New Tab ⌘ T  
Duplicate Tab ⌘ D  
Reopen Last Closed Tab ⌘ ⌘ T

---

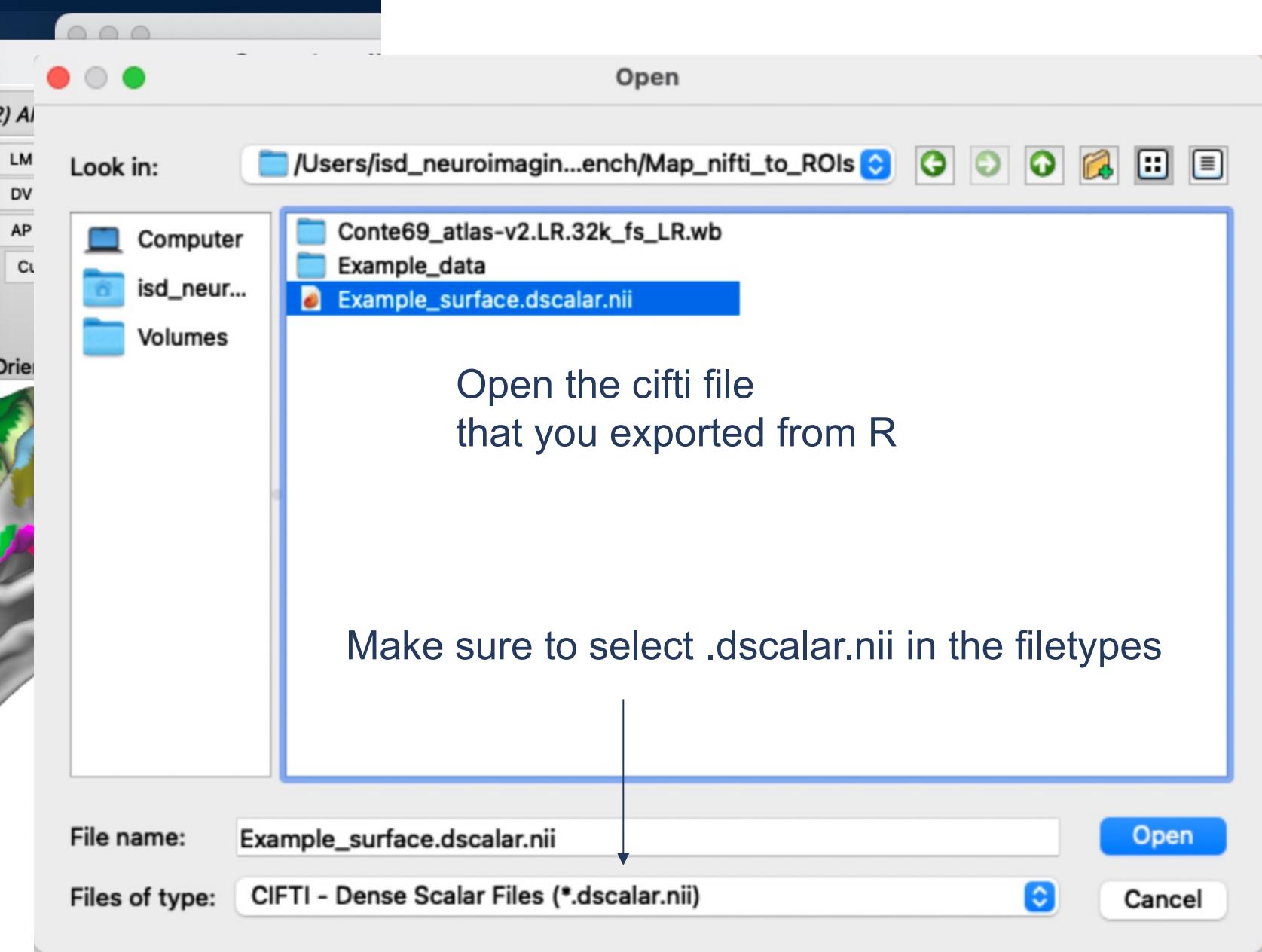
**Open File...** ⌘ O  
Open Recent... ⌘ ⌘ O  
Open Location... ⌘ L  
Save/Manage Files... ⌘ S  
Close All Files

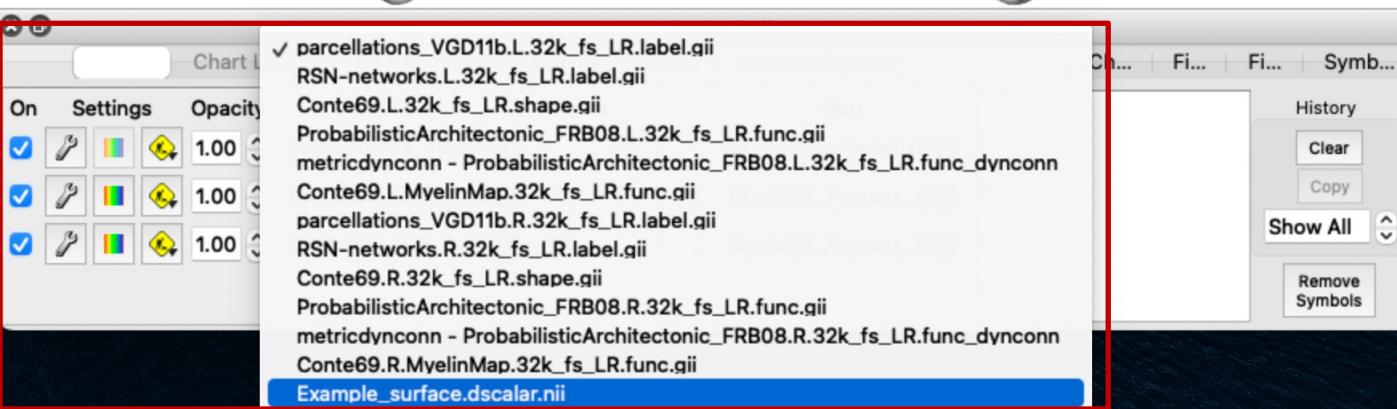
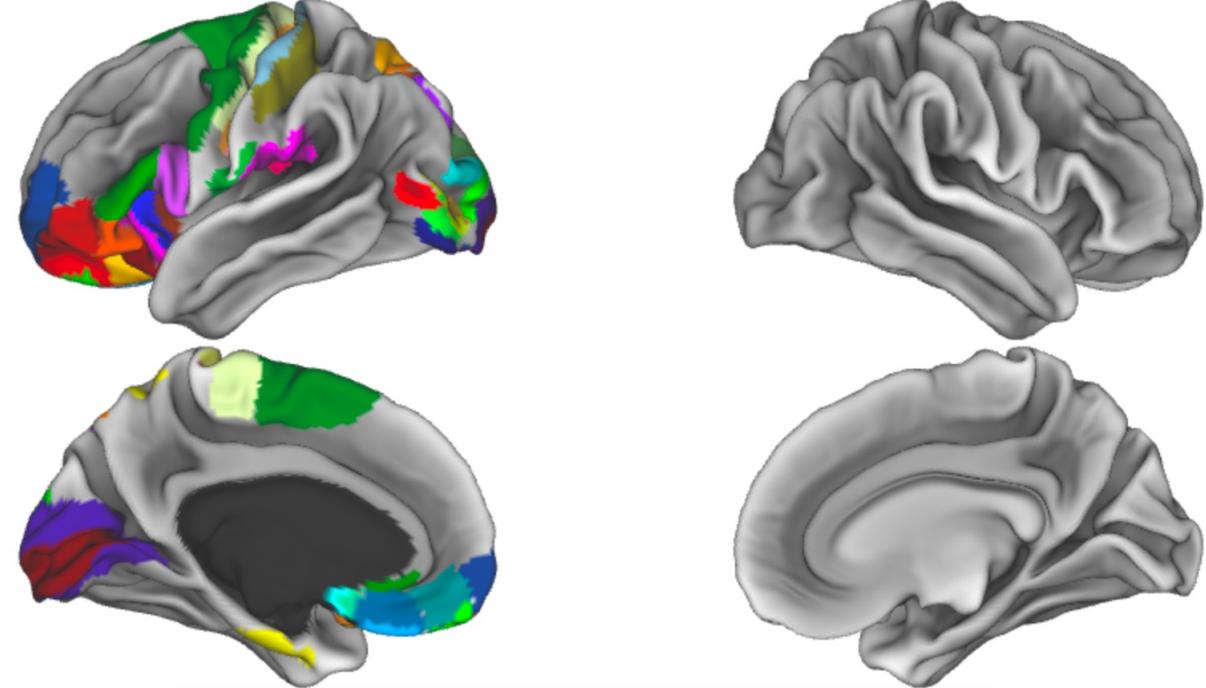
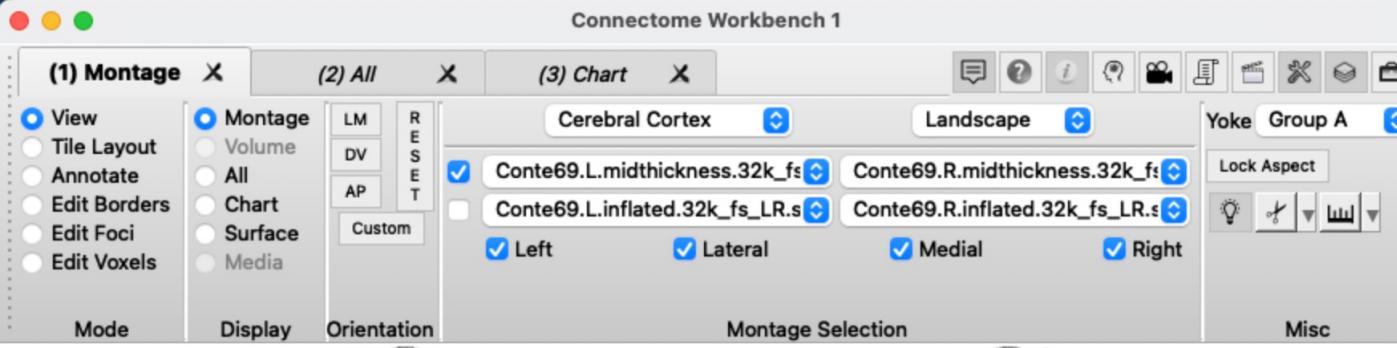
---

(obsolete) Animation Control...  
Capture Image...  
Movie Recording...

---

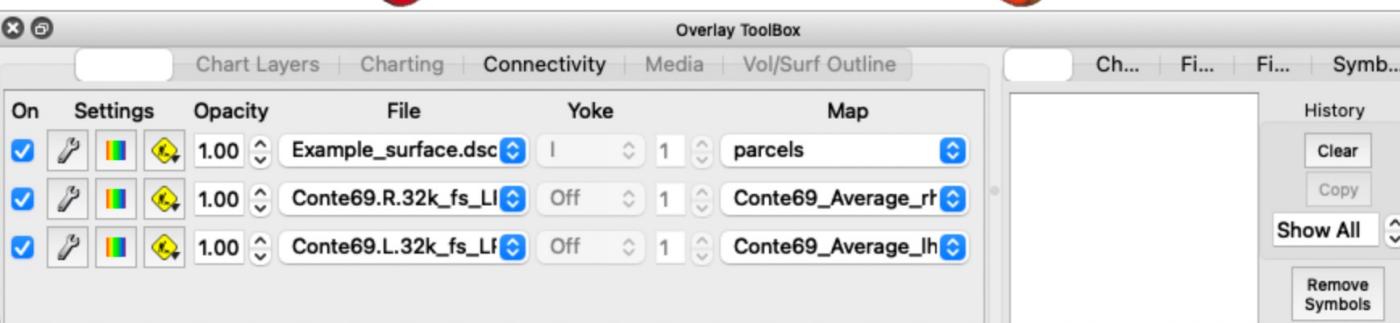
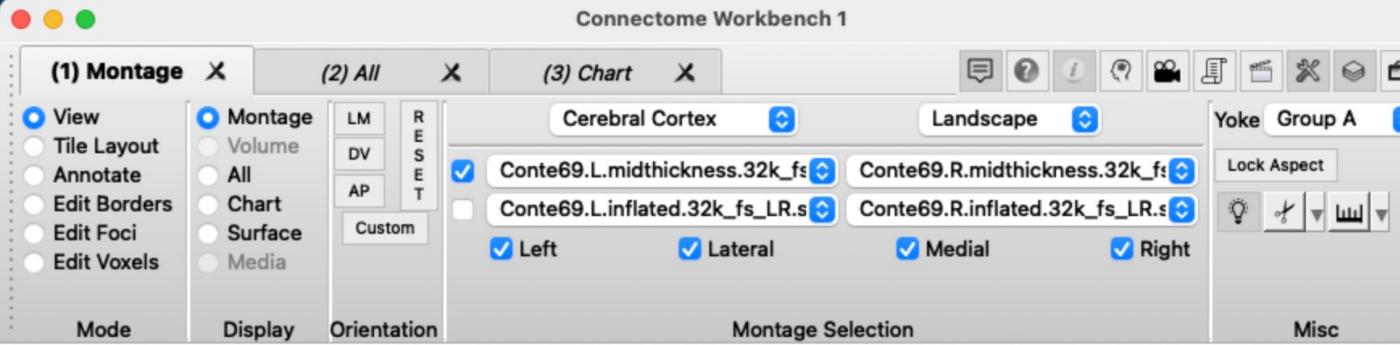
Close Tab ⌘ W  
Close Window... ⌘ ⌘ W

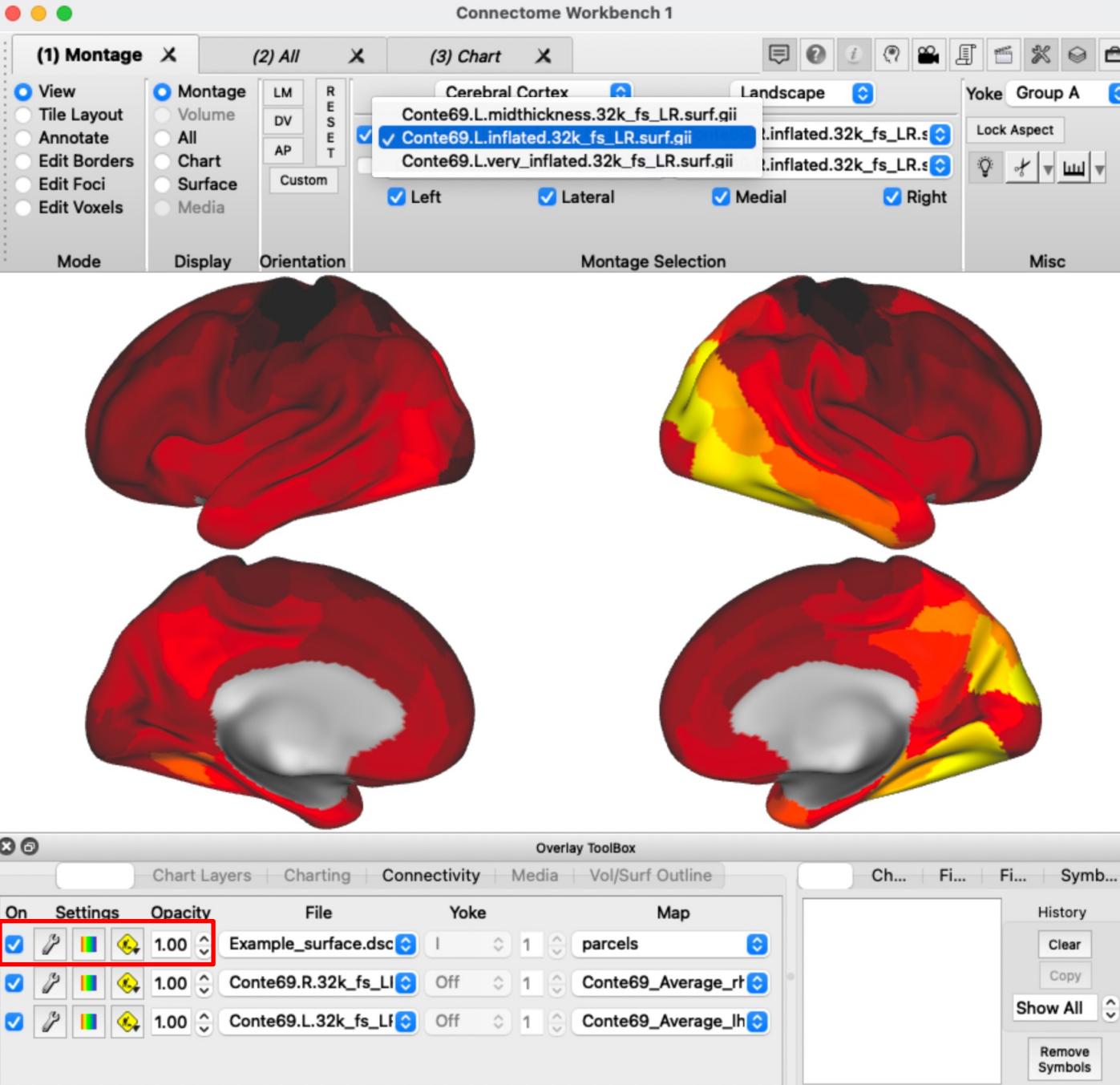




## Overlay Toolbox

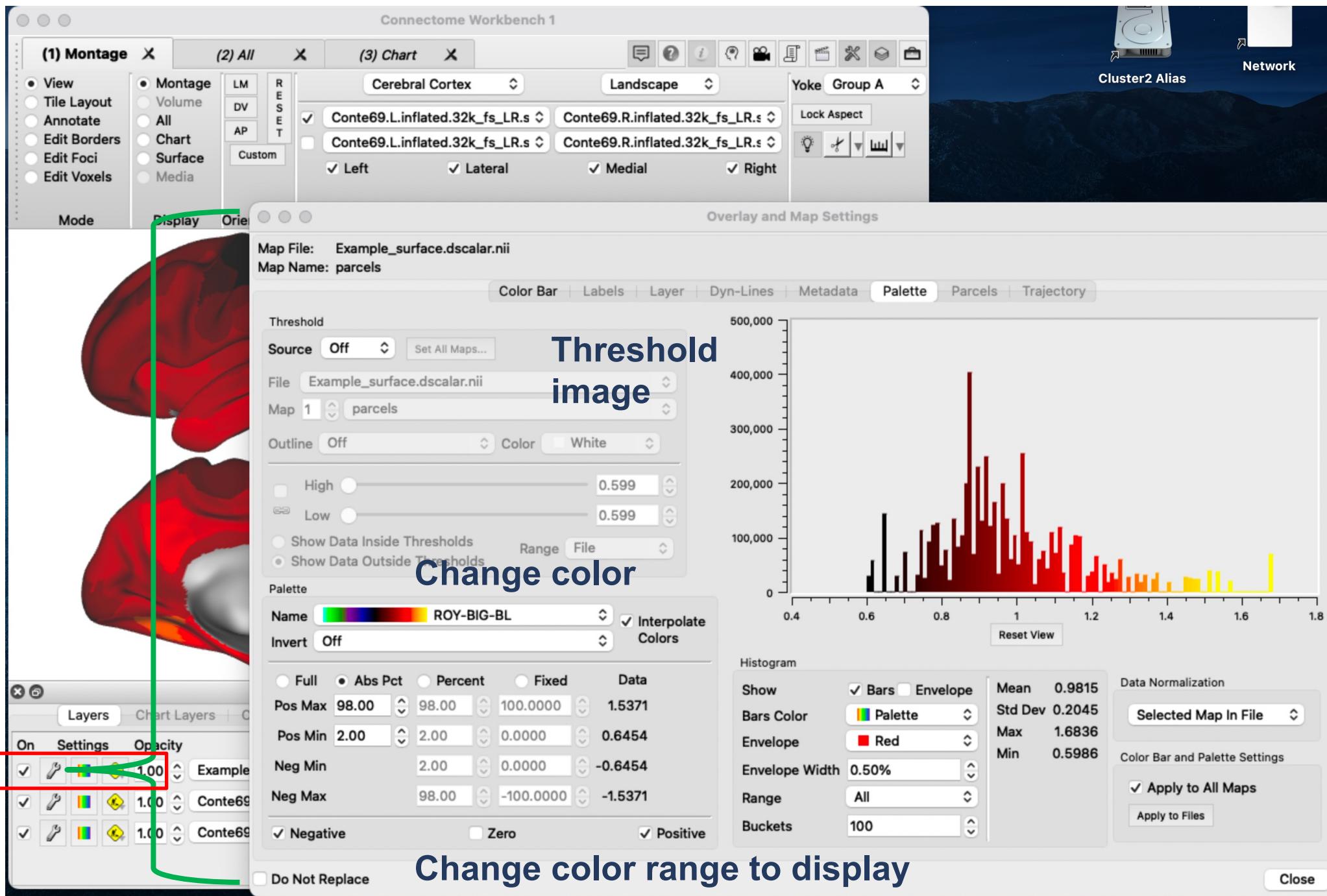
- Select the new overlay as the top overlay (overlays are stacked from top to bottom)

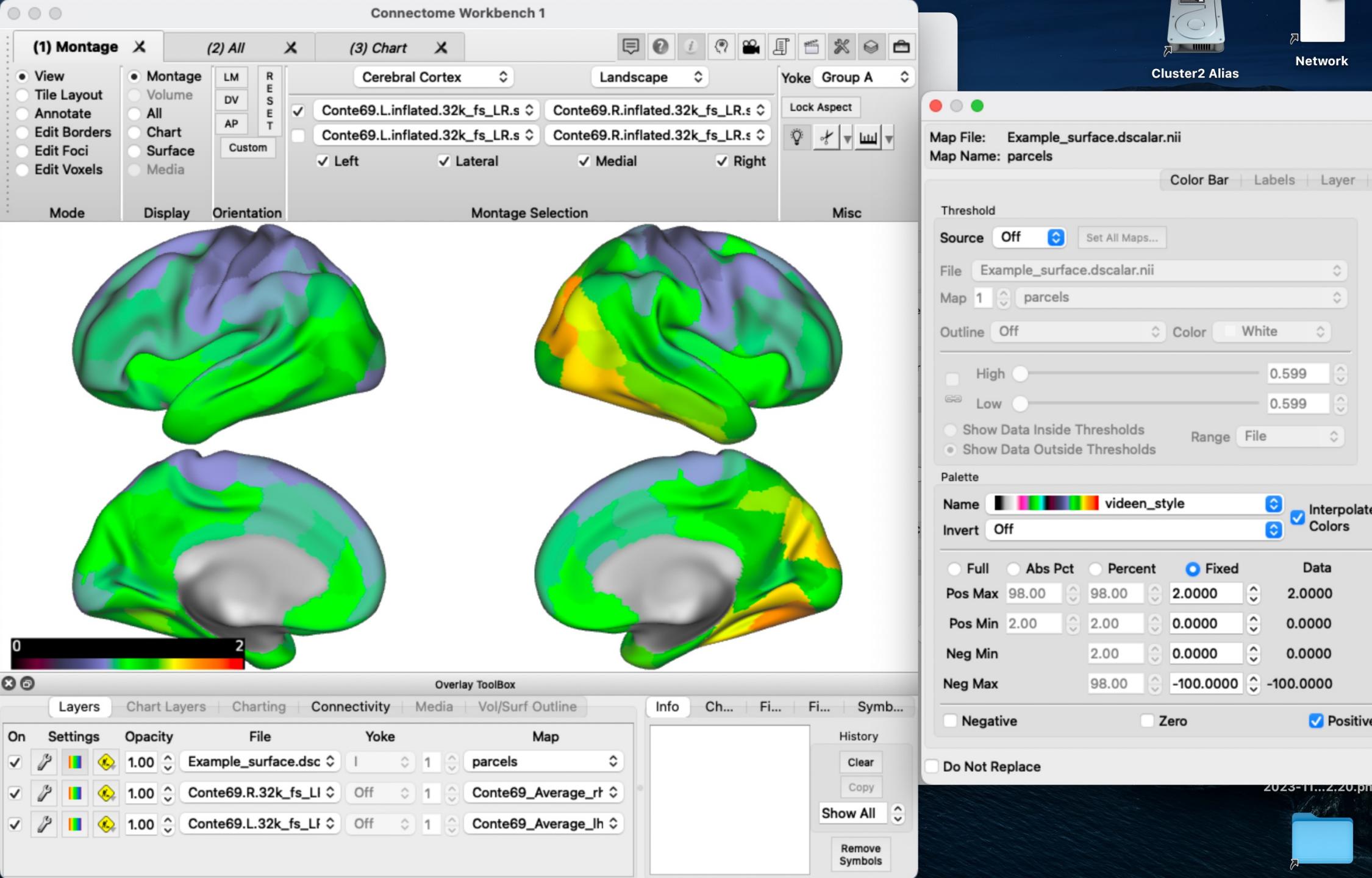


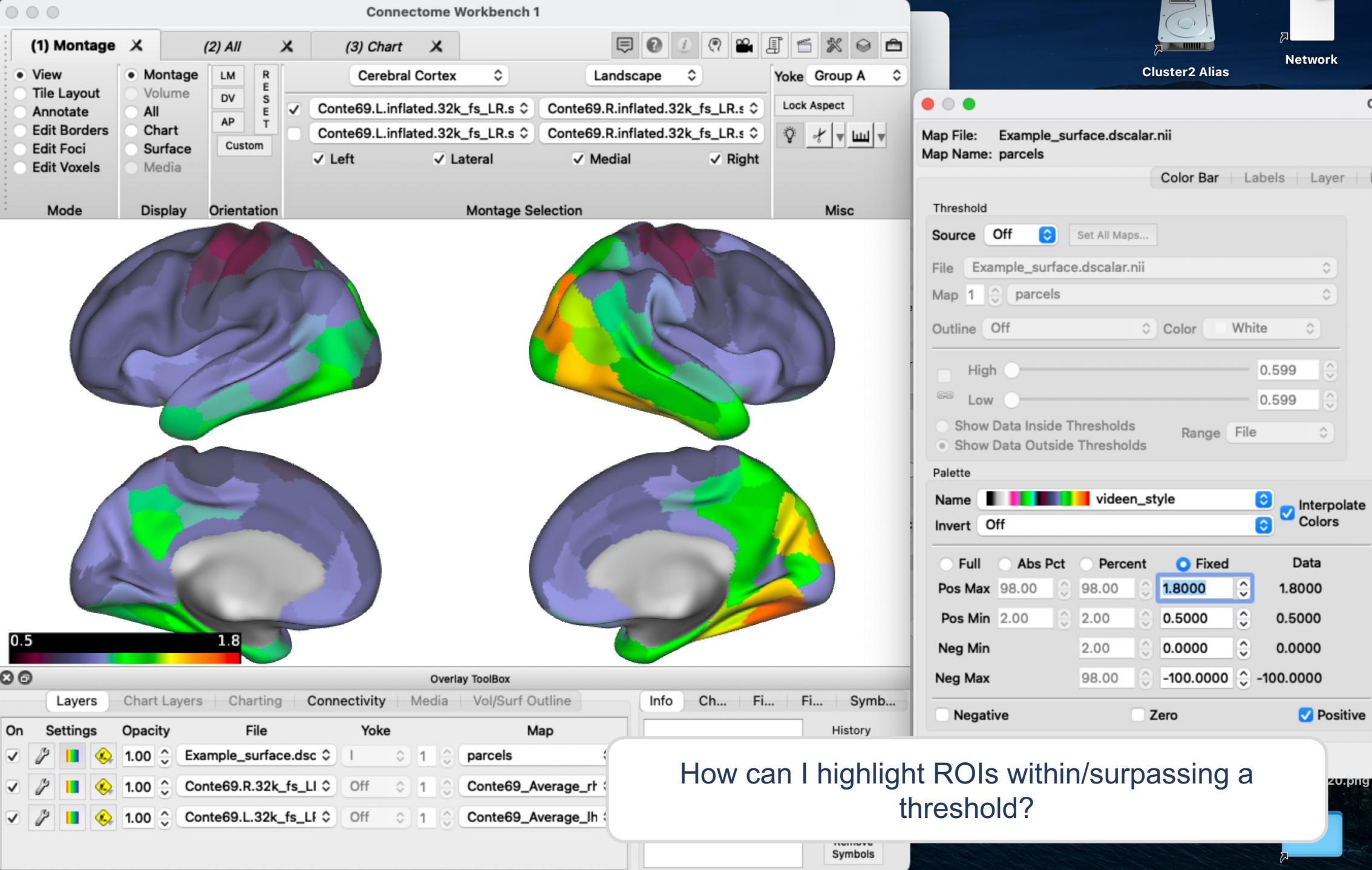


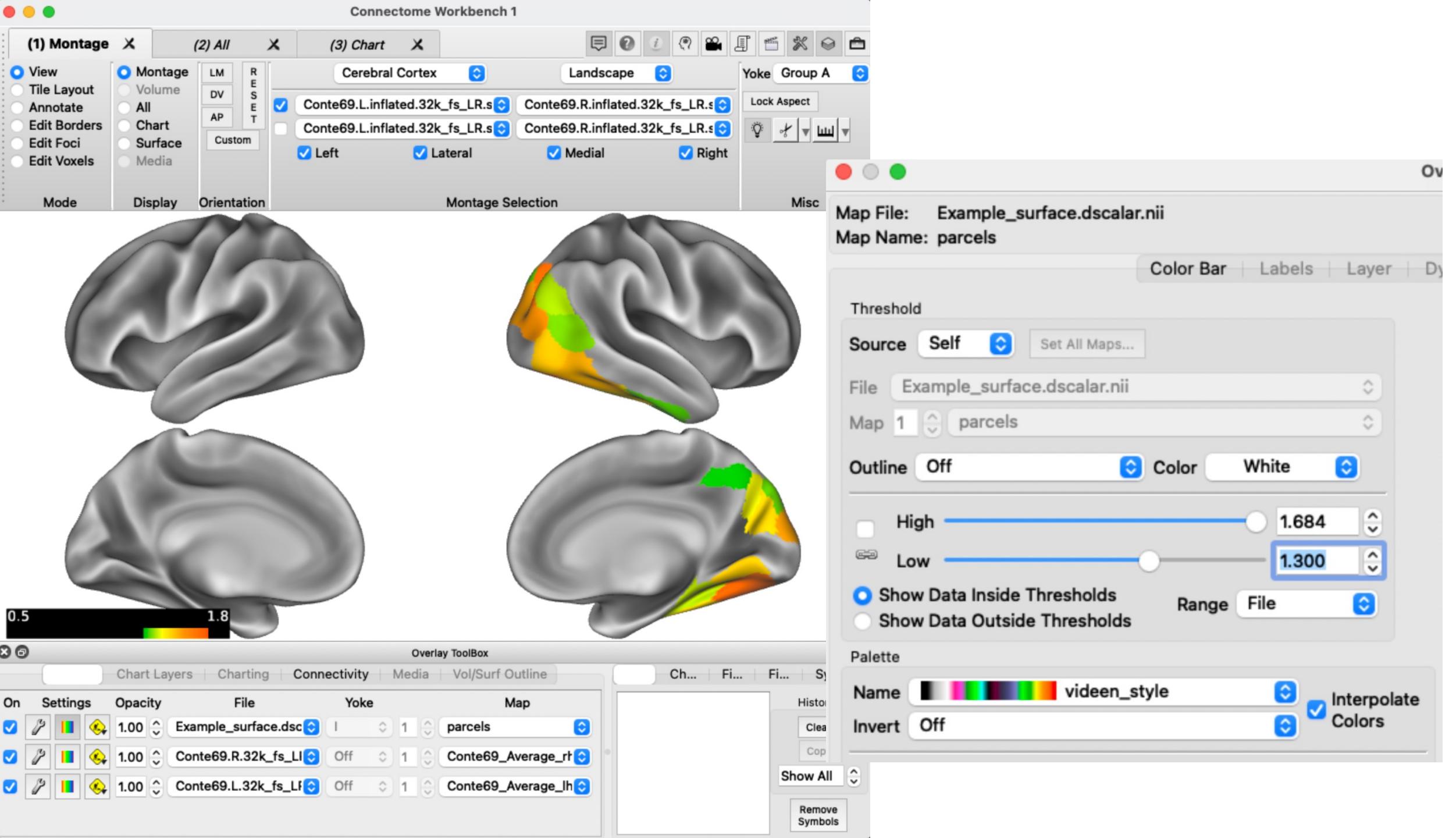
## Montage selection plane:

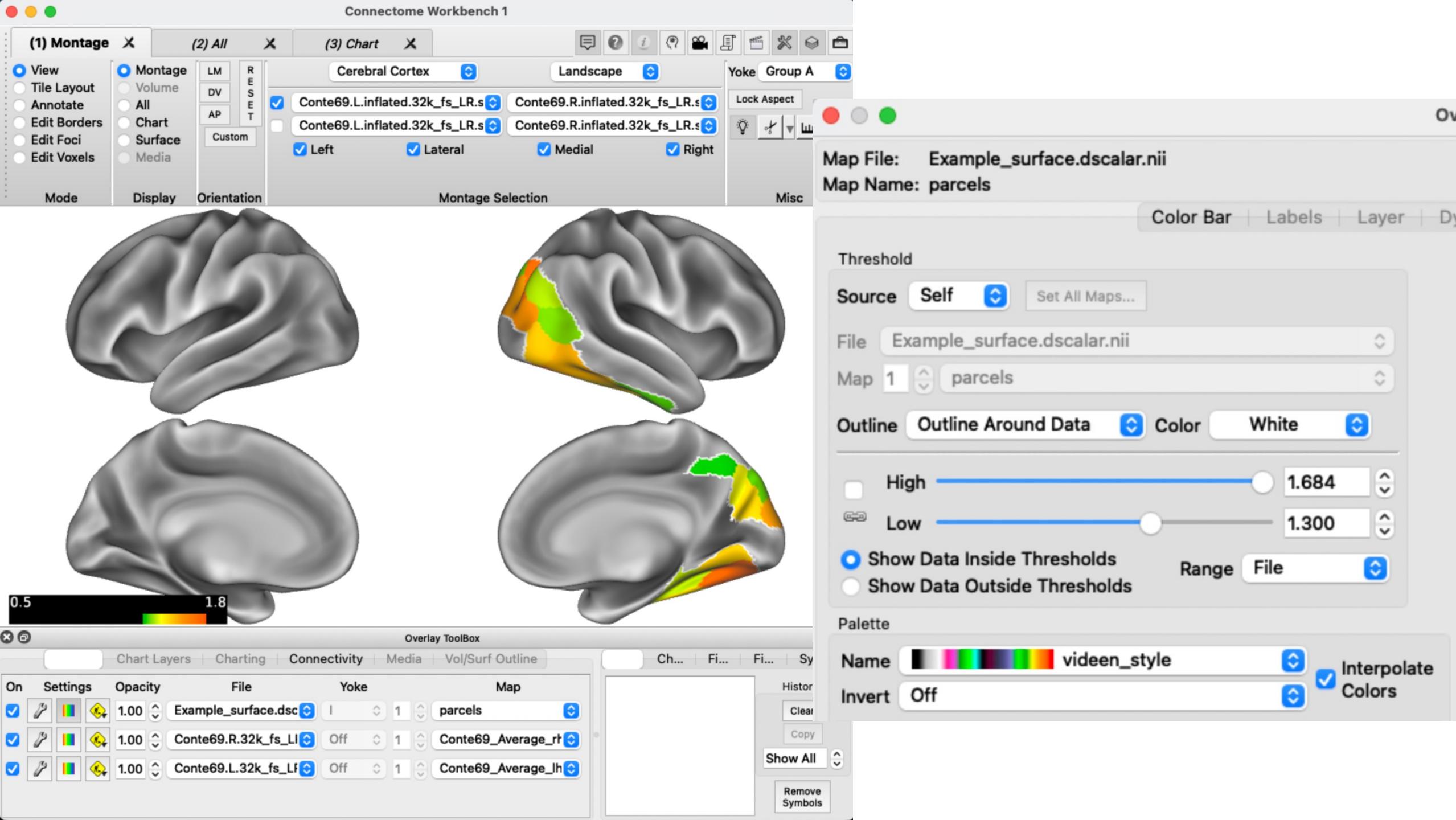
- Select the template that you prefer

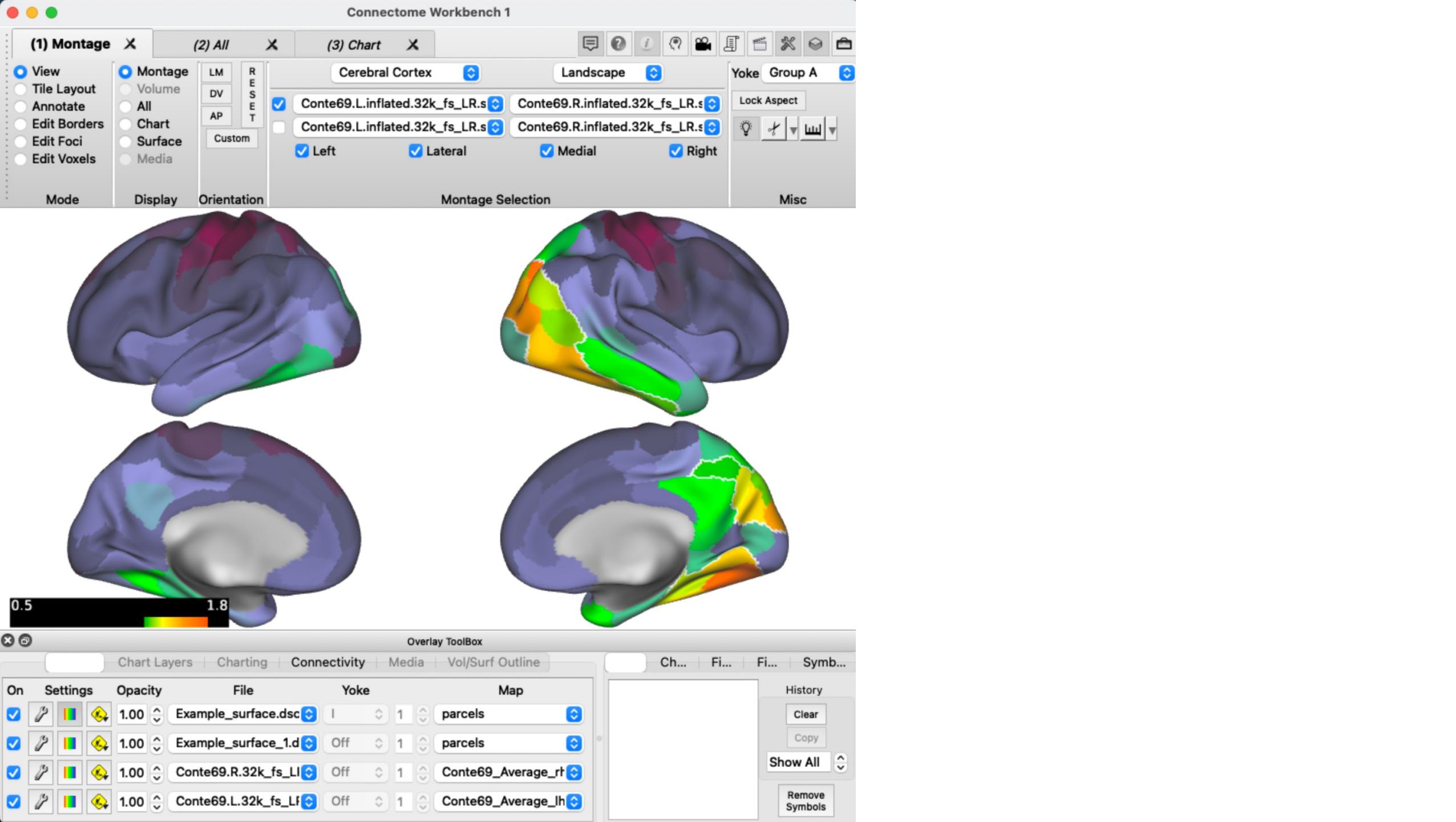


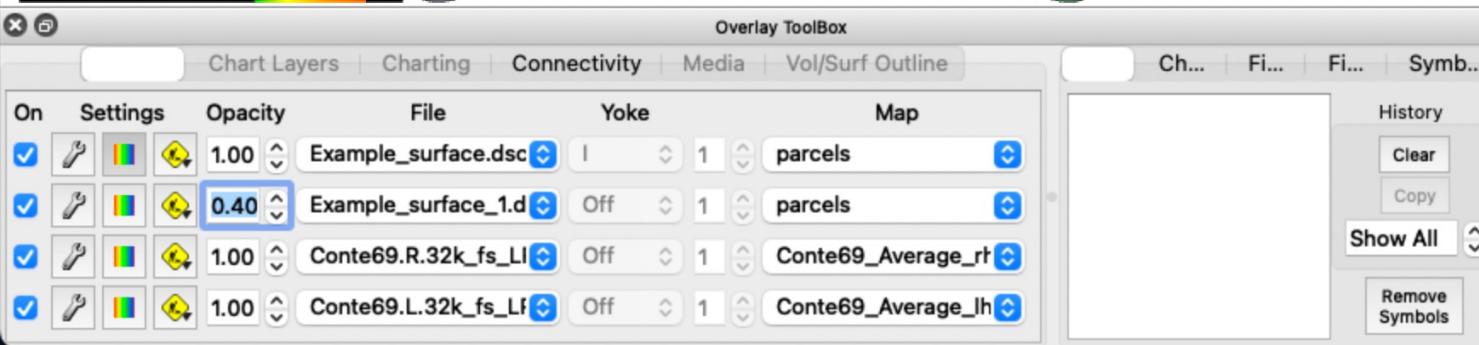
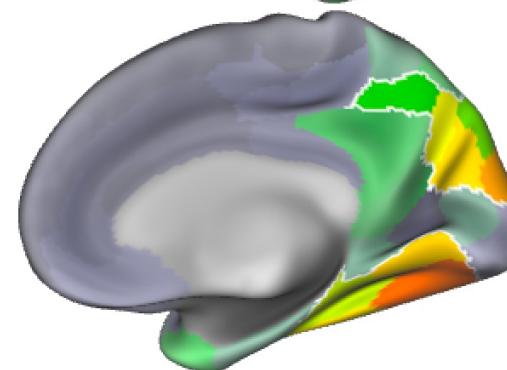
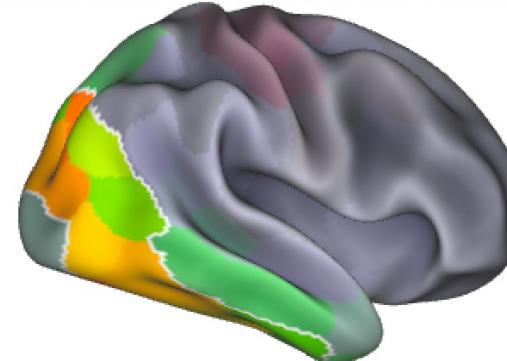
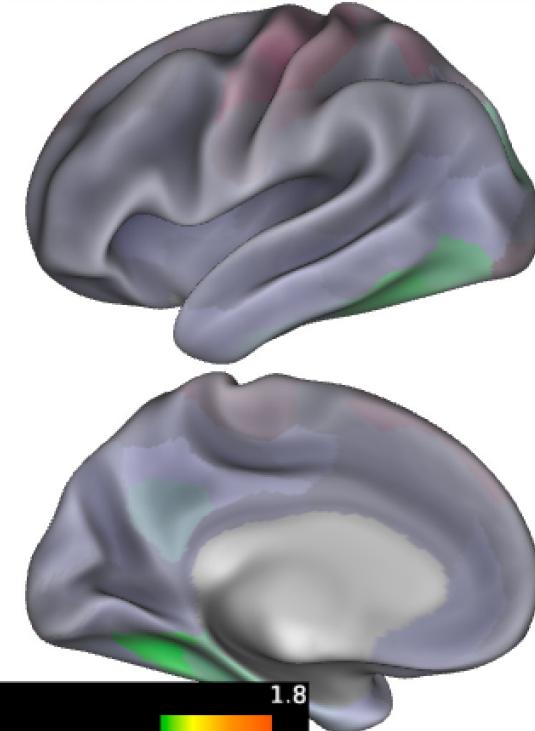
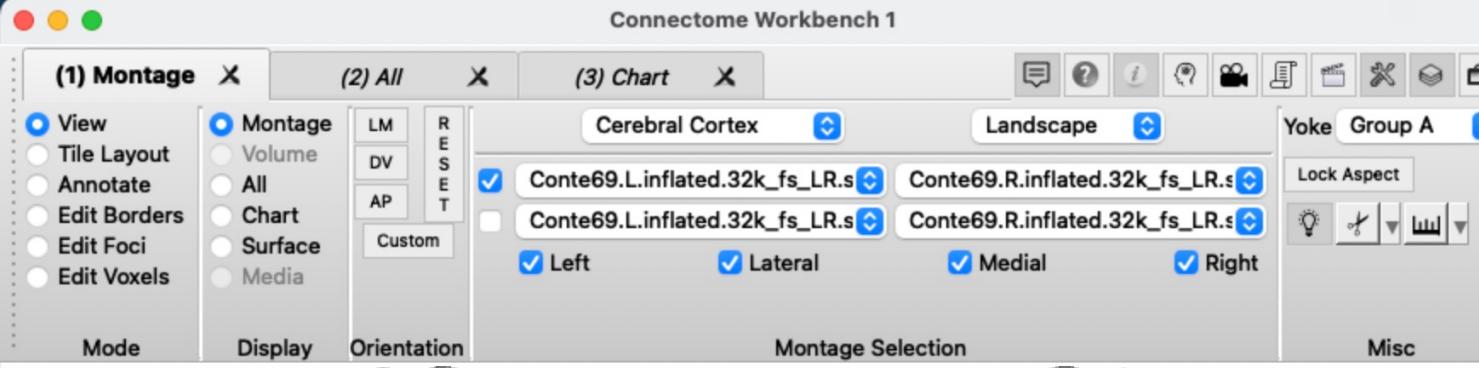


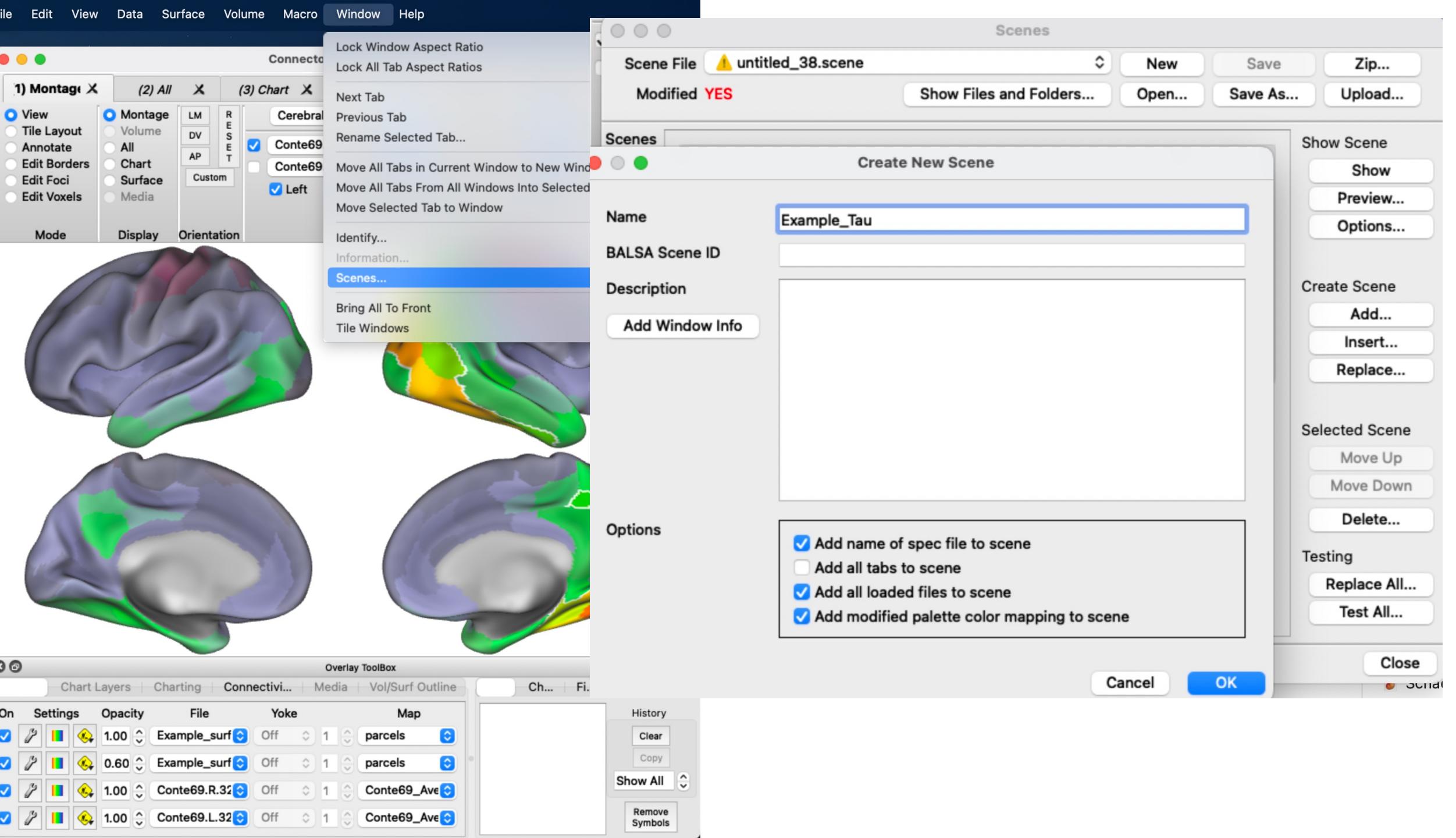










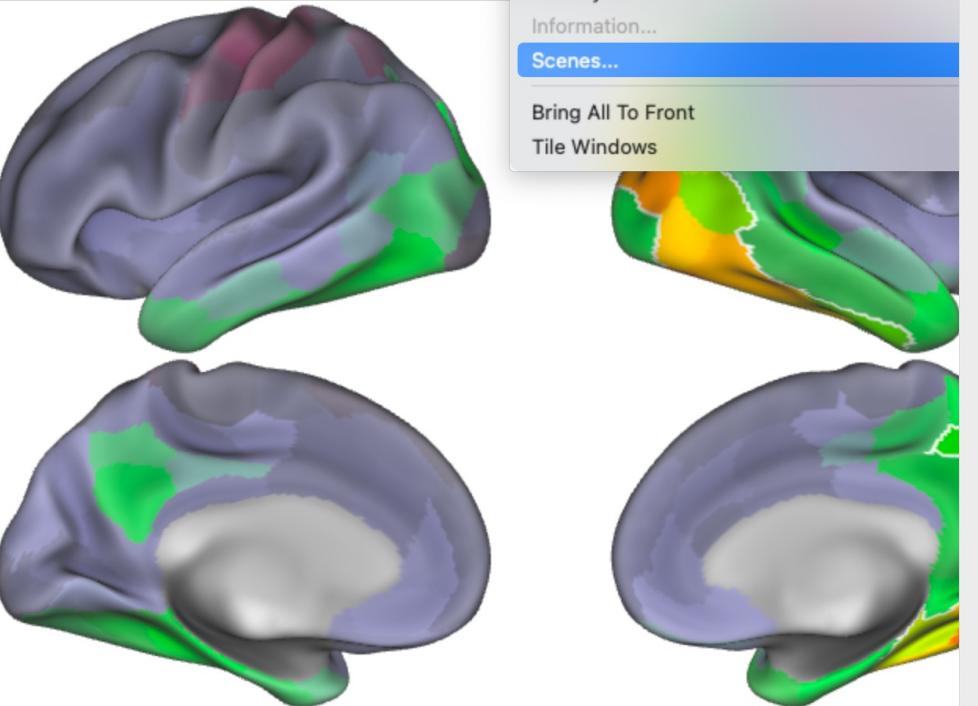


File Edit View Data Surface Volume Macro Window Help

**1) Montage X** (2) All X (3) Chart X

View Montage LM Cerebral  
 Tile Layout Volume DV  
 Annotate All AP  
 Edit Borders Chart RESET  
 Edit Foci Surface Conte69  
 Edit Voxels Media Left

Mode Display Orientation



Lock Window Aspect Ratio  
 Lock All Tab Aspect Ratios  
 Next Tab  
 Previous Tab  
 Rename Selected Tab...  
 Move All Tabs in Current Window to New Window  
 Move All Tabs From All Windows Into Selected Window  
 Move Selected Tab to Window  
 Identify...  
 Information...  
**Scenes...**  
 Bring All To Front  
 Tile Windows

Scenes

Scene File **⚠️ untitled\_38.scene**

Modified YES

Show Files and Folders... Open... Save As... Upload...

**Current Scene**  
**NAME (1): Tau\_Example**  
**BALSA SCENE ID:**

Show Scene  
 Show Preview... Options...

Create Scene  
 Add... Insert... Replace...

Selected Scene  
 Move Up  
 Move Down  
 Delete...

Testing  
 Replace All... Test All...

Overlay ToolBox

Chart Layers | Charting | Connectivi... | Media | Vol/Surf Outline

Help

On Settings Opacity File Yoke Map

Example\_surf 1.00 Off 1 parcels

Example\_surf 0.60 Off 1 parcels

Conte69.R.32 Off 1 Conte69\_Ave

Conte69.L.32 Off 1 Conte69\_Ave

History  
 Clear  
 Copy  
 Show All  
 Remove Symbols

Close

New Window ⌘ N  
New Tab ⌘ T  
Duplicate Tab ⌘ D  
Reopen Last Closed Tab ⌘ ⌘ T

Open File... ⌘ O  
Open Recent... ⌘ ⌘ O  
Open Location... ⌘ L  
Save/Manage Files... ⌘ S  
Close All Files

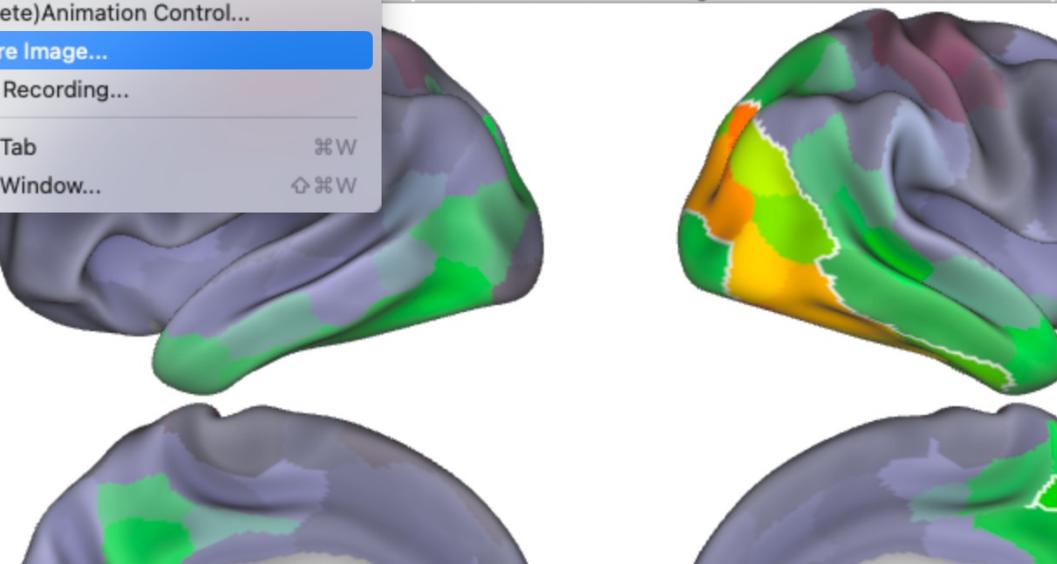
(obsolete)Animation Control...

Capture Image...

Movie Recording...

Close Tab ⌘ W

Close Window... ⌘ ⌘ W



Connectome Workbench 1

(3) Chart X

Cerebral Cortex Landscape

Y R E S E T

Conte69.L.inflated.32k Conte69.R.inflated.32k

Conte69.L.inflated.32k Conte69.R.inflated.32k

Left Lateral Medial Right

Montage Selection

Image Capture

Source

Workbench Window: 1

Crop to Tab/Window Lock Aspect Region

Dimensions

Size of Window (778 x 453 pixels)

Custom

Pixel Dimensions

Width: 2250

Height: 1310

Scale Proportionally

Image Dimensions

Width: 7.50 inches

Height: 4.37

Resolution: 300.00 pixels/inch

Uncompressed Image Memory Size: 8.84 Megabytes

Image Options

Automatically Crop Image

Margin 10

Destination

Copy to Clipboard

Save to File: Example\_tau.png Choose File...

Capture Close

This screenshot shows the Connectome Workbench 1 interface with a 'Chart' tab selected. A context menu is open over a brain model, with 'Capture Image...' highlighted in blue. To the right, an 'Image Capture' dialog is displayed, allowing users to set dimensions for the captured image. The dialog includes fields for pixel dimensions (Width: 2250, Height: 1310), image dimensions (Width: 7.50 inches, Height: 4.37), and resolution (300.00 pixels/inch). Other options include 'Automatically Crop Image' (unchecked) and 'Copy to Clipboard' (unchecked). The 'Save to File' field contains 'Example\_tau.png', and a 'Choose File...' button is available. At the bottom are 'Capture' and 'Close' buttons.



# Further reading

## Workbench Tutorial

[https://www.humanconnectome.org/storage/app/media/documentation/tutorials/Connectome\\_WB\\_Tutorial\\_v1.5.pdf](https://www.humanconnectome.org/storage/app/media/documentation/tutorials/Connectome_WB_Tutorial_v1.5.pdf)

## Guide to annotations

[https://www.humanconnectome.org/storage/app/media/documentation/tutorials/Guide\\_to\\_WB\\_Annotations\\_1.5.pdf](https://www.humanconnectome.org/storage/app/media/documentation/tutorials/Guide_to_WB_Annotations_1.5.pdf)