rfMRI Preprocessing

rfMRI preprocessing occurs in the HCP Functional pipelines (fMRI Volume Pipeline, followed by fMRI Surface Pipeline) as outlined in the lecture. Once the pipelines have been run, we recommend looking at the output SBRef for each run to check the alignment with the brain surfaces generated from the structural data (in the Structural pipeline).

Viewing SBref volume/surface alignment of REST1_LR (subject 100307)

- In a terminal window: *cd* to the **day2-tuesday/rfMRI_Practical_1** directory, then enter:

```
wb_view rfMRI_1.scene &
```

- *Click* **Show** to show the highlighted first scene.

Launching a pre-generated scene saves time, but it doesn't teach you how to configure a convenient layout like this when starting from scratch. At the end of the practical you will learn these steps.

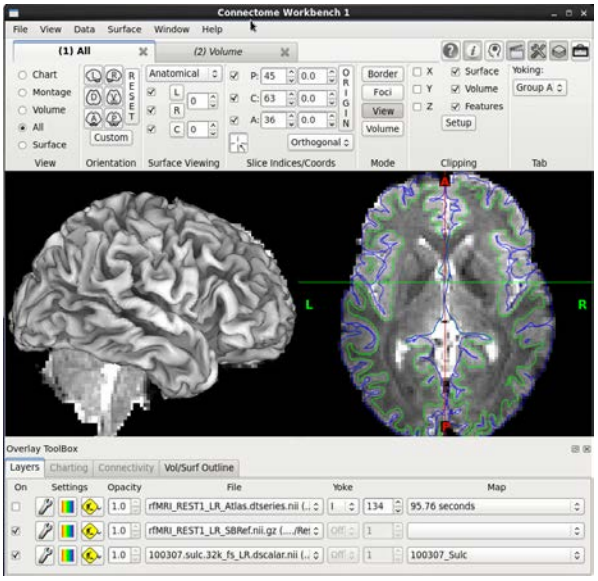
- *Move* the **Scenes box** out of the way (*click on the top of box and drag*), but leave it open.

The scene opens in Tile Tabs view with All view in the left tab displaying the midthickness cortical surface of subject 100307 (output from the HCPpipelines –MSM Sulc) overlaid on the SBRef volume for that subject's REST1_RL fMRI run.

In the right tab Volume view, is an axial slice of the same 100307 SBRef volume (**right**).

- In the (1) All tab, **Surface Viewing** section of the **Toolbar** (top of window), *toggle* the checkbox left of the **R** (right hemisphere) button off and on.

You can see the alignment of the right hemisphere surface with the underlying SBRef parasagittal volume slice.



- *Click* on the (2) Volume tab at the top of the Toolbar.
- In the **Overlay Toolbox** (below the viewing area), *click* on the **Vol/Surf Outline** tab.
- *Scroll down on the right* to show the checked surface outlines that are displayed on the volume.

The white matter surface contour is outlined in **lime green** and the pial (outer grey) surface contour is **blue**.

- *Toggle these surface contours off and on* for the left and/or right hemisphere. Note how well these surfaces are aligned with the white and gray matter in the SBRef axial volume slice underneath. Good alignment is crucial for accurate mapping of the fMRI data to the gray matter ribbon!

Dense timeseries for an individual-subject resting-state fMRI BOLD signal.

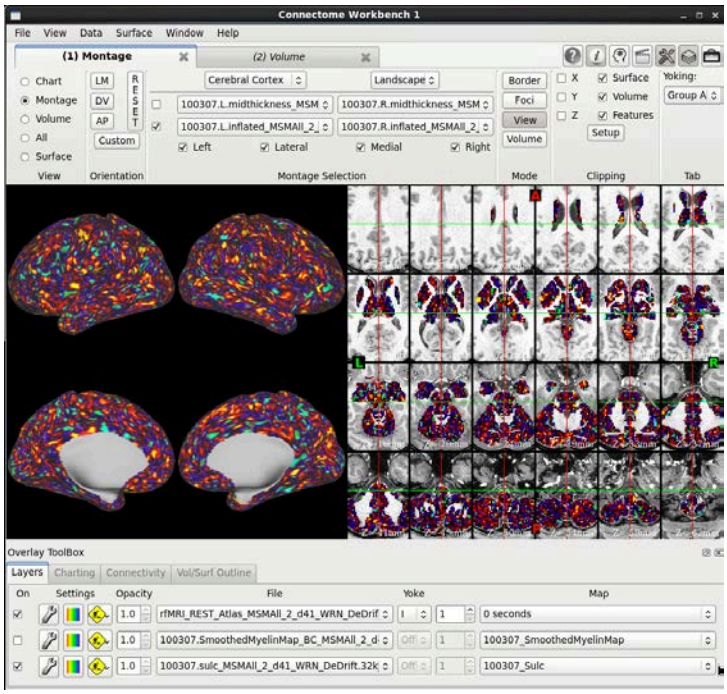
- Back in the **Scenes box**, *double click* on the 2nd scene. Keep the scenes box open.

This shows 60 frames (~43 s) of resting-state BOLD signal, part of the dense (all grayordinates) timeseries of the REST4_RL run (i.e., one subject's fourth rfMRI 15-minute dataset) on the (MSM-All registered) inflated surfaces and in the subcortical gray matter (axial volume slices). The complete 4800 frames (~58 min) is too large for the course computers to handle, so for this practical we truncated this timeseries *.dtseries file to include only frames 4640-4700.

- In the first row of Layers in the **Overlay Toolbox**, where the .dtseries file is listed, *click* the up arrow next to the Map number (now showing 1).

These 1st and 2nd timepoints of this dtseries show a relatively irregular and noisy-appearing BOLD signal.

- *Continue to click* the up arrow for the map number.



Around frame 8 you'll start to notice some BOLD signal in task positive network brain regions and anticorrelation in the default mode network.

- *Continue to click* the up arrow for the map number until you reach the end of the timeseries, noticing the activations and fluctuations across the timeseries.

As you can see, the activation signals frequently change and are quite noisy at the dense timeseries level for a single subject, even after the denoising steps described in lecture. In a later exercise, it will be easier to see resting state correlations using the dense connectome derived from this dense timeseries, both at the single subject and group levels. However, we first take a closer look at the critical process of denoising (reduction of spatial artifacts).

- *Exit* Workbench (**File: Exit**), as we will relaunch it for the next section.

Spatially Specific Denoising: ICA+FIX

In this section of the practical, you will see examples of noise (artifact) ICA Components that we want to remove from our fMRI data. ICA separates the strongly structured and spatially specific signals in the fMRI data into component spatial maps and timeseries. FIX classifies these components as noise or signal, so that structured noise can be regressed out of the data. The ICA+FIX pipeline performs a very gentle highpass filter (longer than the run length), runs melodic ICA, classifies the resulting components, and then regresses 24 motion parameters and the

noise components out of the data. Some other possible methods of denoising (e.g. band pass filtering, global/WM/CSF signal regression, and scrubbing) are less purely data-driven, and hence many of the following components could still be lurking in your data!

- *Enter these commands* in a terminal window:

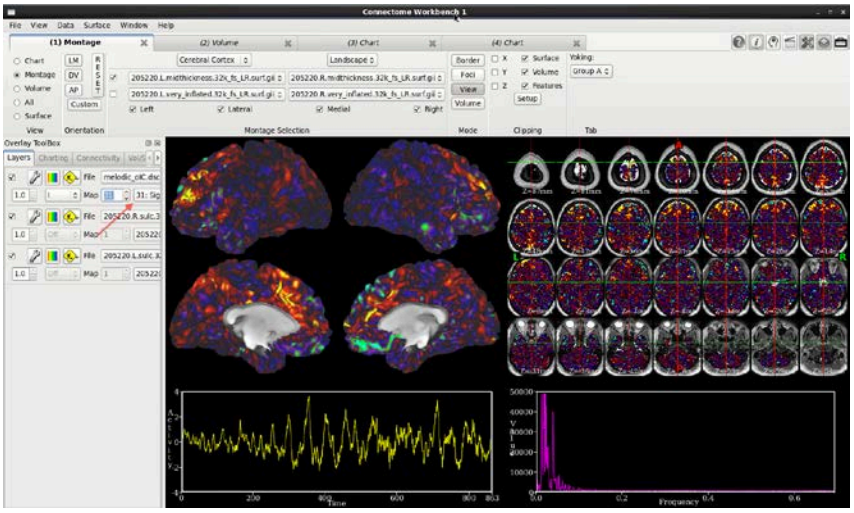
cd **day2-tuesday/rfMRI_Practical_1** (if your terminal isn't already in that directory)

wb_view What_FIX_Removes.scene &

- In the **Scenes box**, *double-click* the first scene, **Sample Signal Component (#31)**.
- *Drag the 'Scenes' window over to the far left* so it doesn't obstruct your view of the main window. Alternatively, you can close the scenes window by toggling it off on the 'scenes' icon in the top right of the Toolbar (4th from right), then remember to toggle it back on when you need to view another scene.

Viewing Signal Components

To understand what is considered noise, first it helps to know what is considered neurobiological signal, so in the first scene we will consider several signal components. This scene shows a montage view of four wb_view tabs for ICA component #31 (in one of the four 15min rfMRI scans from HCP subject 205220).



In the top left, the component spatial maps are displayed on the cortical midthickness surfaces; in the top right, the component spatial maps are overlaid on axial volume slices that extend from top to bottom of the brain. Both views are useful for seeing the difference between signal and noise.

The bottom left panel shows the component timecourse (intensity of component signal [y-axis] vs. time [x-axis]), and the bottom right shows the timecourse's power spectrum (the amount of variance that exists at different temporal frequencies, power [y-axis] vs. frequency [x-axis]). Finally, the map name (red arrow in Overlay Toolbox on the left) says whether FIX identified the component as signal or noise.

Signal components are unlike any noise components. Most importantly, they specifically follow the cortical grey matter ribbon and/or localize to subcortical grey matter (most noise sources are not specific to a particular tissue type). This means that they show up very strongly on the surface view. Generally, signal components form discrete "patches" on the cortical surface or in subcortical nuclei, and often are present bilaterally in spatially corresponding (mirror-image) locations.

- In the viewing tabs above the toolbar, *click* on the **Volume** tab.
- In the **Overlay Toolbox** on the left, *toggle on and off* the top layer ("**melodic_oIC_vol.dscalar.nii**") to reveal the anatomical underlay below the component spatial map in the volume slices.

This should convince you that this signal component is largely within the cortical grey matter. Signal component timeseries tend to have a regular (smoothly oscillating), relatively low frequency pattern, which is reflected in their power spectra, which is concentrated at low (but not the very lowest) frequencies (mostly below 0.1hz).

- In the **Scenes box**, *double-click* the **Sample Signal Component** scene again to restore the original view.
- *Using the arrow buttons* or by entering text in the map number, *inspect* the following component numbers: 35, 42, 45, 47, 54, 55, 56, 59. The left and right windows are conveniently yoked, (the displayed top layers are set to change together, as set in the "Yoke" option just left of the map number).

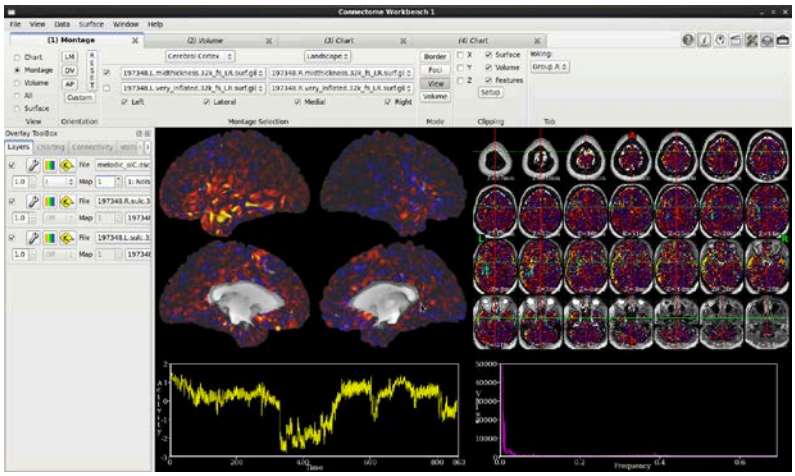
Notice that while these signal components represent different resting state networks, they generally share the following common features:

- Spatial maps include well-defined patches on the cortical surface (upper left) and in the volume (upper right).
- Symmetry between left and right hemispheres (usually, but not always)
- Power spectra (lower right) are "clean" and dominated by low frequencies.
- Time course (lower left) lacks motion-related spikes or other obvious artifacts.
- Spatial maps are consistent with known RSNs.
- Similar components are evident across runs (same subject, different datasets)

Viewing Noise Components

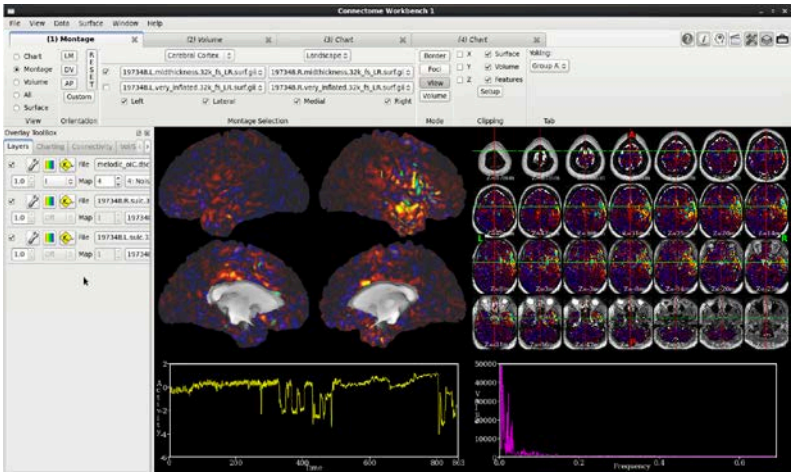
Noise components are basically anything that doesn't look like a signal component, but they arise from a variety of different sources. Head motion can cause a variety of serious artifacts in fMRI images. In addition to reducing global motion effects by regressing out 24 motion parameters (xyz translations, xyz rotations, derivatives of these, and squares of everything) , ICA+FIX also addresses spatially specific nonlinear motion artifacts by modeling them as a collection of linear components.

Motion often shows up as "ring-like" components that are strongest around the edges of the brain (which move the most). Also, motion components tend to be mostly very low temporal frequencies (dramatic spike at the lowest frequencies in the power spectrum [right bottom graph] and large changes in the timeseries [left bottom graph] alongside periods of relative stability).



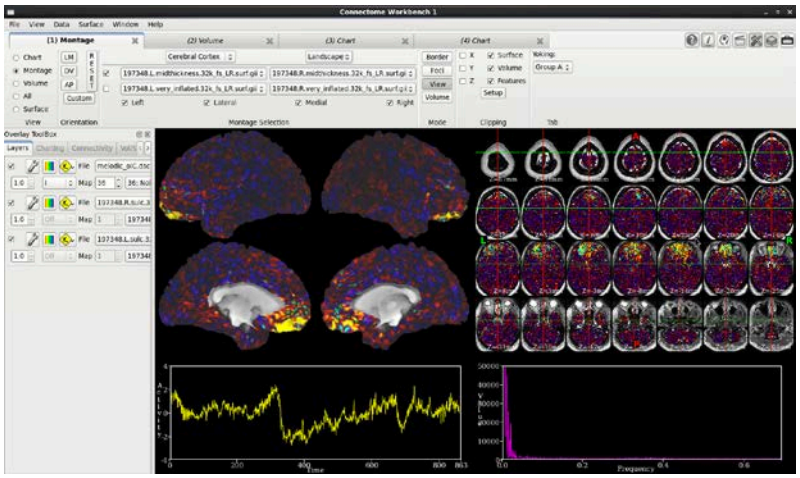
- *Double-click* the **Motion**

generated rings: Example #1 scene to see an example of ring-like noise caused by motion (in HCP subject 197348, a different subject than in the first scene).

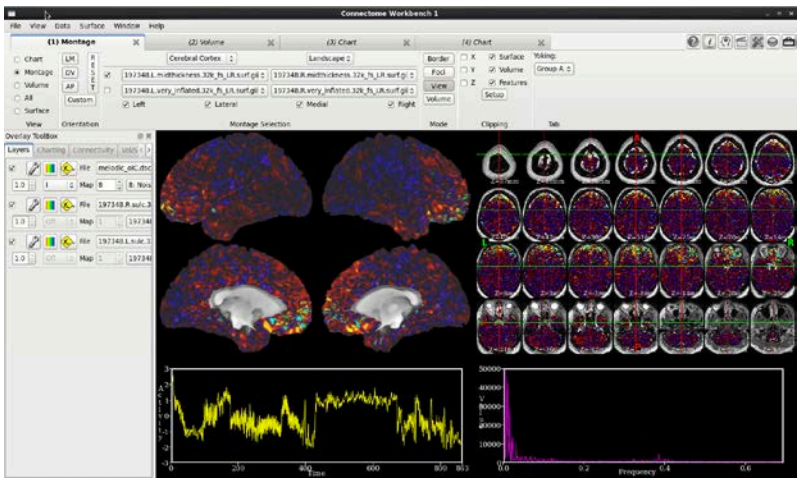


- In the top layer of the **Overlay Toolbox**, *use the arrow buttons* or enter the map number to *select* **map #4** to see another example having a different spatial pattern (including artifacts into the interior of the right hemisphere).

Motion and susceptibility-induced signal loss can interact in non-linear ways, particularly in orbitofrontal and anterior temporal cortex. One should be suspicious of such components (even though they are sometimes reported to be RSNs in the literature!). As with ring-like components, these components often have spikes at the lowest frequencies (right bottom graph).

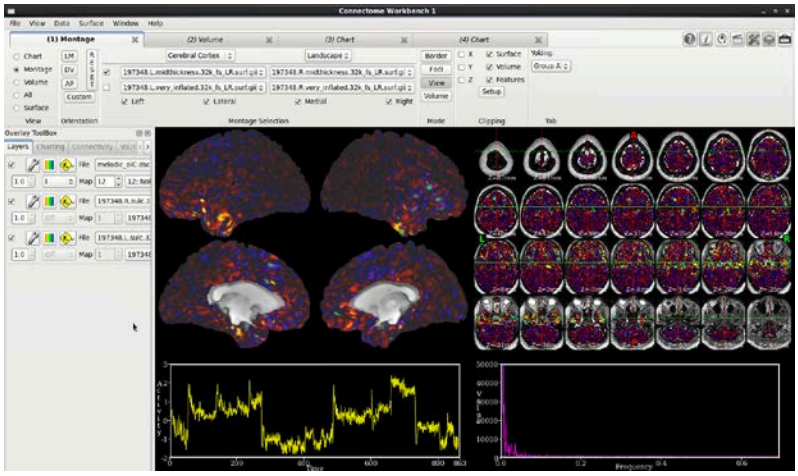


- *Double-click* the **Orbitofrontal noise: Example #1** scene to see an example in orbitofrontal cortex (HCP subject 197348).



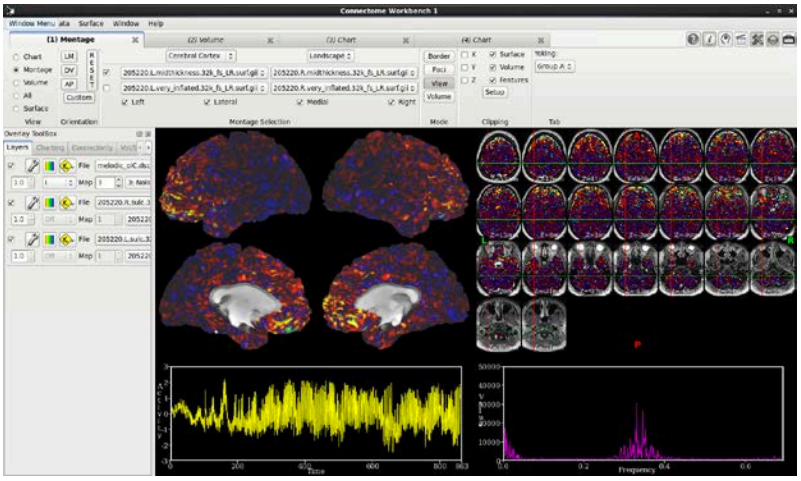
- *Enter* **map #8** in the Overlay Toolbox (top layer) to see another orbitofrontal example in this scan.

- *Double-click* the **Anterior-temporal noise** scene for an example in anterior temporal cortex.



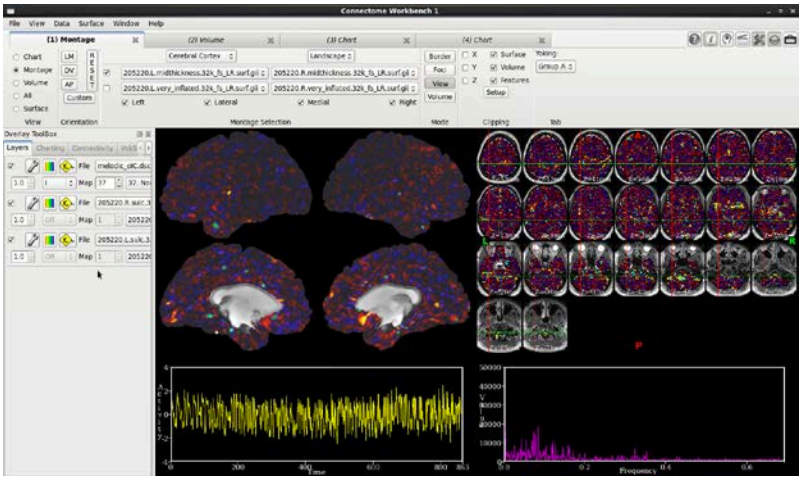
In addition to moving while in the scanner, living subjects have other annoying habits such as breathing and heartbeats. Fortunately, ICA+FIX can identify artifactual components related to these physiological processes as well. They tend to have higher temporal frequencies than either movement artifacts or resting state signal components. Breathing causes the magnetic field to change as air enters and exits the lungs, and these changes can influence signal intensities in the head.

- *Double-click* the **Respiration-related artifact** scene to see a prominent respiratory artifact (in HCP subject 205220).



Also, cardiac pulsations cause artifacts near brain arteries (e.g. around the circle of Willis where blood is distributed to the main cerebral arteries).

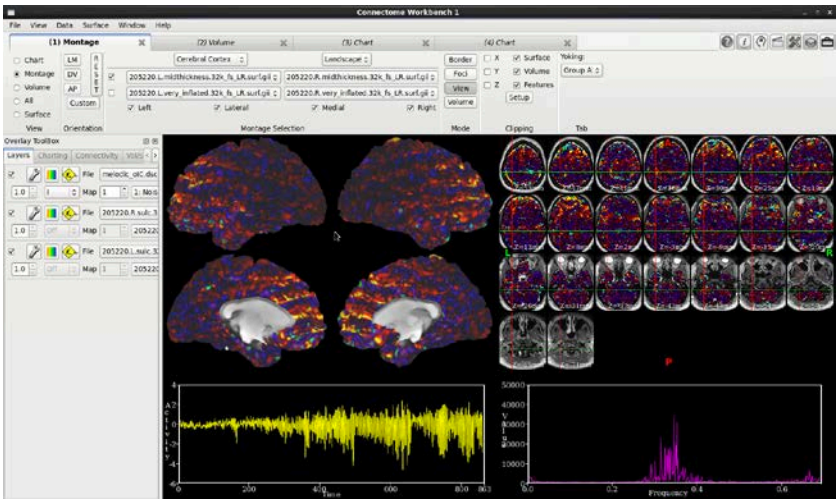
- *Double-click* the **Cardiac pulsation artifact** scene.



- *Increment* the Map number from 37 to 38 to see another example (not shown).

If a moving, breathing, pulsating brain isn't bad enough, the scanner is sometimes uncooperative, by generating artifacts related to the physics of MRI. One example of this is a banding artifact found in some subjects, presumably related to the multiband fMRI pulse sequences, though the exact mechanism is not understood.

- *Double-click* the **Banding Artifact** scene to see an example of this type of artifact.



Now that you've seen some example signal and noise components, spend a little time scrolling through the remaining components of this scene. (You may want to look back at scene 1 to refresh your memory on signal components). Do you generally agree with FIX's classification of the ICA components? Did you find any noise components that didn't fit into the above categories?

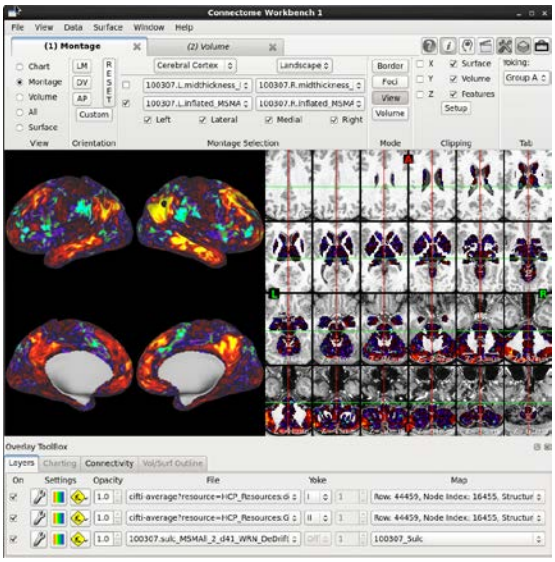
On the high quality, fairly long (15min) HCP rfMRI datasets, FIX is on average 99.6% sensitive and 98.9% specific at identifying signal and noise components as compared with a trained rater, which we think is a pretty good job! On more "standard" datasets the classification accuracy is still good (often around 95%) [Salimi-Khorshidi NeuroImage 2014]. Keep in mind, if you aren't using a method like ICA+FIX to identify and remove spatially specific structured noise in a data-driven way, you're likely to be leaving in a substantial amount of artifacts in your data, which might lead you to make incorrect interpretations.

The publicly released HCP FIX pipeline generates a melodic_oIC.nii.gz volume image, similar to what is shown on the upper right portion of this scene. It also outputs FSL-generated web pages (html, png) of the time course and power spectrum for each component. We plan in a future pipeline release to incorporate automatically generated scenes and associated files of the type shown in this section, as they help in analyzing the types of noise in your own data and how well FIX has done in identifying and regressing out structured noise components.

Single subject and the R468 group average Dense connectomes for Seed-based visualization

The dense timeseries for each REST run are demeaned, artefact-cleaned, concatenated and processed (correlating every grayordinate's timeseries with every other) to generate a full correlation dense connectome matrix *.dconn file with correlations between all 91282 grayordinates. These files can be read by wb_view for interactive seed-based connectivity visualization. These *.dconn files are large (33GB each!) so on the limited space of the course

computers, we will be interactively calling these files remotely from ConnectomeDB over the internet (hopefully the venue Wifi will cooperate!) . This might mean that there will be a delay when clicking seeds as you do this exercise.



In a terminal window: *cd* to the **day2-tuesday/rfMRI_Practical_1** directory (if it isn't already there, then enter:

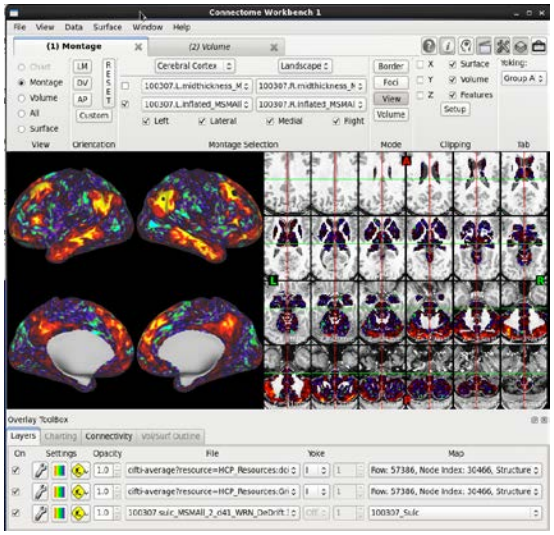
wb_view rfMRI_1.scene &

- In the **Scenes box**, *double click* on the third scene.

A pop up will ask for your Username and Password. You will need to use your ConnectomeDB credentials to login, just as in yesterday's first practical.

After loading, the scene will display, showing, for the single subject 100307, the functional connectivity of the selected seed (black circle) near the angular gyrus in the right hemisphere.

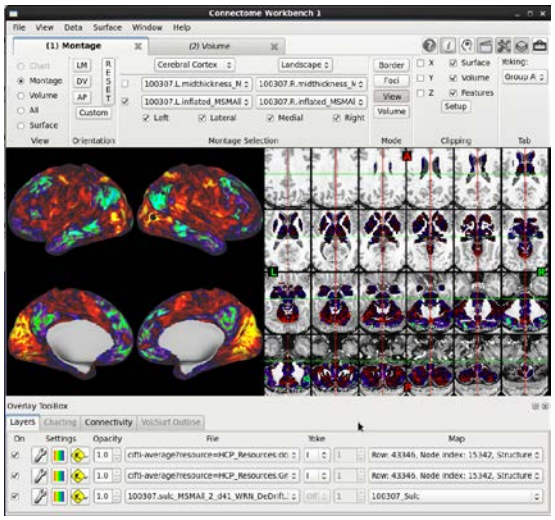
- *Click* on the large yellow/red patch correlation (with the seed) in the right frontal cortex (strong functional connectivity with the parietal seed).



Notice that the correlation pattern does not change much for this region, which is part of the same resting state network.

- *Click* on the small patch of cyan (anti-correlation) in the right occipital lobe.

Notice how the correlation pattern changes dramatically, showing functional connectivity among a completely different set of regions.

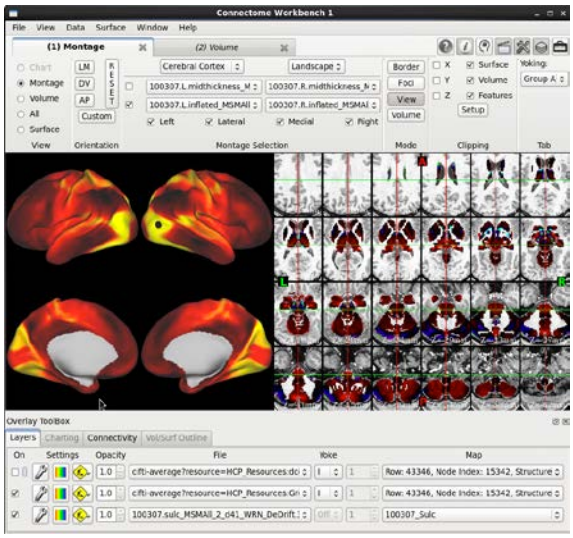


- *Toggle the top layer* (100307 dense connectivity) off to reveal the correlation with the same (last clicked) seed location, for the group average (from 468 HCP subjects).

The group average maps are much smoother, but show the same general pattern of correlation.

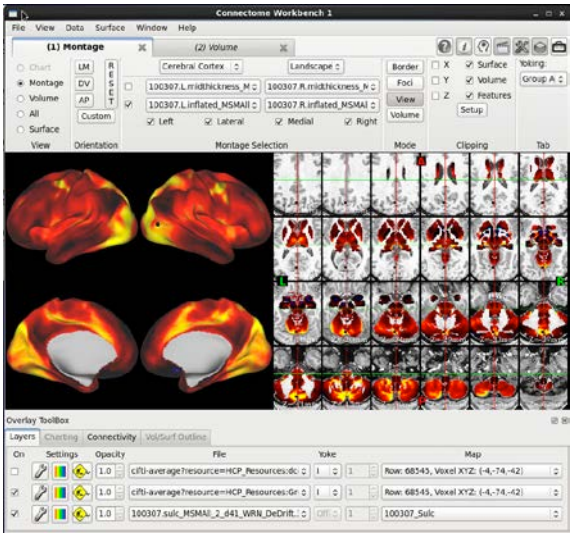
Workbench also allows you to select subcortical voxels from a *.dconn file.

- *Click* on a cerebellar location near the bottom of subcortical volume slice Z=41mm (bottom left of panel of the volume slice montage).



Note how the cerebellar seed shows strong correlations with the contralateral cerebellum and with selected regions of the cerebral cortex.

- *Explore* several more seed locations and toggle between the individual (top layer) and group average (middle layer) to compare.
- *Exit* Workbench (File: Exit) when you are done, as we will relaunch it in the next section.



Viewing & working with "PTN" data (Parcels, node-Timeseries, Netmats)

The PTN data release also contains node-average timeseries: one timeseries per node, per subject. For a given subject, and parcellation dimensionality N (e.g., 50 or 200), we have N nodes' timeseries, and can then estimate parcellated-connectomes (a.k.a. network matrices, or netmats). In the next practical, we will show how these are estimated and viewed in wb_view. For now, we can view the group-averaged netmats associated with the group-average dense connectome we were just looking at in wb_view.

Generating scenes from scratch. We will take a longer road to get there, because we'll start from scratch, rather than using a pre-generated scene, so you learn more about what's under the hood. This entails many discrete steps, but the lessons learned will be generally useful for navigating wb_view and for generating your own customized scenes.

Note that if you run low on time, or if something goes awry (computer crashes), there is a pre-existing scene file (**../day2-Tuesday/frMRI_Practical_1/HCP_rfMRI_Practice.scene**) that will let you enter mid-stream into this process and avoid having to restart from scratch.

In a terminal window, enter the following two commands:

cd /home/hcpcourse/day2-tuesday/rfMRI_Practical_1

wb_view &

- *Press* **Skip.**
- *Select* **File: Open File**: then navigate to: **/home/hcpcourse/data/HCP_Q1-Q6_GroupAvg_Related440_Unrelated100_v1**
- *Select* **Files of Type: Surface Files** at the bottom of the Open file dialog.
- *Highlight* all 6 files, then *press* **Open** to load six group-average surfaces. The group average midthickness surfaces will appear in "montage" view by default.
- *Select* **File: Open File: Files of Type**: **Connectivity – Dense Scalar Files** (the fourth of the Connectivity subtypes).
- *Select* **Q1-Q6_R440.sulc.32k_fs_LR.dscalar.nii** *and* **Q1-Q6_R440.MyelinMap_BC.32k_fs_LR.dscalar.nii** then press **Open**. (Or you can open and load them sequentially.) It would have been easy to select and load even more group average data (e.g., curvature and thickness maps), but we're keeping it simple here.
- In the **Overlay Toolbox**, *toggle* the lowest of the 3 layers on.
- *Toggle* the second layer on, and change the file in that layer to: **Q1-Q6_R440.MyelinMap_BC.32k_fs_LR.dscalar.nii** to view the group average myelin map.
- In the **Toolbar** along the top, in **Montage Selection**, in the top row, *select*: **Q1-Q6_R440.L.inflated.surf.gii** *and* **Q1-Q6_R440.R.inflated.surf.gii** to see the myelin maps on inflated rather than midthickness surfaces.
- To save the work you've done loading and displaying files, *press* the **Scenes** button in the upper right corner (4th from far right, clapboard icon).
- In the **Scenes** box, *press* **New**, then enter **HCP_rfMRI_Practice.YourName.scene** [using your name or initials] and *press* **Save.**
- In the Scenes box, *press* **Add**.
- In the **Create New Scene** popup, under **Scene name**, enter "**HCP Group average surfaces (Q1-Q6_R440), sulc, myelin maps**" [or an alternative descriptive name], then *press* **Save**.

You have just created and saved a scene within the scene file that is currently loaded in memory, but the newly created scene is *not yet saved to disk*. To carry out this important step:

- *Select* **File: Save/Manage Files**

The popup **Manage Data Files** dialog is useful for many purposes. Many options are reasonably intuitive, and you can explore them whenever you have time and interest. For now, let's settle for saving the modified scene file. Note that your new scene file (Data File Name on the right; in alphabetical order in Data Type: Scene) has a red check mark in the 'Save' column on the far left.

- *Press* **Save Checked Files** in the lower right of the Manage Data Files dialog, then *press* **Close**.

Congratulations! You've saved your first scene (at least for this course), which can serve as a workhorse launching pad for more complex analyses. Note that the scene file (i) stores the identity and relative directory location of a variety of files that are in various directories; (ii) saves all of the wb_view settings needed to restore the exact viewing specifics; but (iii) does not store the data files themselves in the scene file. However, there is a wb_command command that can zip a scene file and its contents (and another to zip a spec file and its contents), which is useful for data transfer purposes.

- *Select* **File: Open File: Volume Files**.
- *Select* **Q1-Q6_R440_AverageT1w_restore.nii.gz** and *press* **Open** to load the group average T1w volume.
- In the **Toolbar**, *press* Tab **(2) All**.
- *Press* **Toolbar: View: Volume** to see an axial slice of the group average volume.
- *Press* **Toolbar:Slice Plane: C** for a coronal view.
- *Press* **Toolbar:Montage: On** for a Montage view (default 4 rows, 3 columns)
- Use the arrow keys or the text entry to *change* the Montage settings to 3 rows and 4 columns, and the step size to 14.
- In **Slice Indices/Coords**, *set* **C: 134** to adjust the middle coronal slice to be at slice 134 (Y = -32mm). The volume montage now spans all of the subcortical regions (including cerebellum) but excludes much of frontal cortex. This is useful when viewing subcortical regions in CIFTI files.
- In **Slice Indices/Coords**, *toggle* the 'crosshair' icon off (not 'depressed') in the lower left corner.
- *Hover the mouse over this icon* if you want a description of how it controls the crosshairs in the volume slices and the links to other tabs when they are yoked.
- Use the zoom (scroll wheel up or Ctl + move left clicked mouse up) and pan (shift + move left-clicked mouse) controls to zoom in on each volume montage panel and center it on the subcortical portions of that slice (see image, right).
- *Press* '**X**' at the top right of tabs **(3) Cortex Left** and **(4) Cortex right** to close them (they open by default, but we don't need them).
- *Select* **View: Enter Tile Tabs** to view the surface and volume displays concurrently.
- Back in the **Scenes** box, *select* **Add**, and enter "**HCP group average surfaces and volumes montage**" or some other descriptive text.
- *Select* **File: Save/Manage Files**, then press **Save Checked Files** and *click* **Close**.

You have now created and saved another generic scene that can be useful for general analyses. If you decide to change details such as the number of rows and columns in the volume montage, it can be much easier to edit an existing scene than to generate a new view or new scene from scratch!

Now it's finally time to look at connectivity-related data from the PTN dataset.

- *Select* **File: Open File: Files of Type: Connectivity – Dense Scalar Files**, then navigate up two directories (up arrow), then down four subdirectories to:

day2-tuesday/rfMRI_Practical_2/PTN/groupICA/groupICA_3T_Q1-Q6related468_MSMsulc_d50.ica/

(Note, that although we are still doing practical 1, we just told you to navigate to the practical 2 folder.)

- Select and open **melodic_IC.dscalar.nii**
- In the **(2) Volume** tab, in the Overlay Toolbox, set the second layer (lowest 'unused' layer) to File:

  melodic_IC.dscalar and *toggle* it on.
- In that layer, just to the right of the file name, *select* **Yoke: I**.
- *Switch* to the **(1) Montage** tab, *set* the first ('lowest unused') layer of Overlay Toolbox, to File: **melodic_IC.dscalar** and *toggle* it on.
- *Select* **Yoke: I** in this top layer.

You should now see the group average ICA component #1 in combined surface and subcortical volume view.

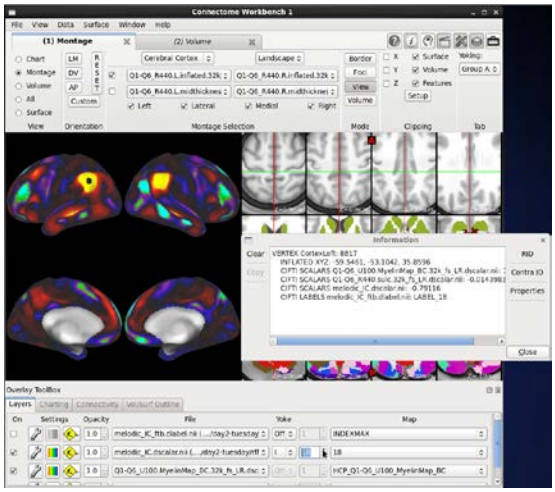
- *Click* on the up arrow button in the **Map** number field (just to the right of Yoke) to view additional ICA components.
- *Set* the **Map** number back to **1**, so that we can save this as a starting point for a scene.
- Back in the **Scenes** box, *select* **Add**, and enter "**HCP R468 d50 ICA components on group average surfaces and volumes montage**" or some other descriptive text.
- *Select* **File: Save/Manage Files**, then *press* **Save Checked Files** and *click* **Close**.

You will examine the **melodic_IC.dscalar.nii** file again in more detail in rfMRI Practical 2, so let's move on. Next, we'll load and view a 'find the biggest' map that shows which ICA component is the dominant one for each grayordinate.

- *Select* **File: Open File: Files of Type: Connectivity – Dense Label Files** (second of the Connectivity subtypes).
- Open **melodic_IC_ftb.dlabel.nii** (it is in the PTN/groupICA/groupICA_3T_Q1-Q6related468_MSMsulc_d50.ica directory where your open file manager should already be pointed).
- In the **Montage** tab, in the **Overlay Toolbox** top layer, *click* on the yellow diamond construction sign under **Settings**, and *select* **Add Overlay Above**.

- In this newly created topmost layer, *select* **melodic_IC_ftb.dlabel.nii** and *toggle* this layer on to view a 'hard' parcellation of cortex based on the group average ICA results.
- Switch to tab **(2) Volume**, in the top layer of the Overlay Toolbox, *select* **melodic_IC_ftb.dlabel.nii** and toggle this layer on. You should now see the hard parcellation for both surface and subcortical grayordinates.
- *Click* on the light yellow lateral parietal parcel in the left hemisphere.
- The popup information box should include a line that reports:

  "**CIFTI LABELS melodic_IC_ftb.dlabel.nii: LABEL_18**". This indicates that component 18 is the largest ICA component at this location.



- In tab **(1) Montage**, *deselect* (*toggle off*) the top layer (**melodic_IC_ftb.dlabel.nii**)
- In the second layer (melodic_IC.dscalar), *set* the **Map** number to **18** and note that this ICA component is indeed centered on the selected node in lateral parietal cortex. (You may need to scroll up in the Overlay Toolbox to see the Map column header).
- In the **Information** box, click **RID**, to remove the identification symbol (gray spot-- black spot in figure).
- Back in the **Scenes** box, *select* **Add**, and enter "**HCP R468 d50 ICA parcellation on group average surfaces and volumes montage**" or some other descriptive text.
- *Select* **File: Save/Manage Files**, then *press* **Save Checked Files** and *click* **Close**.

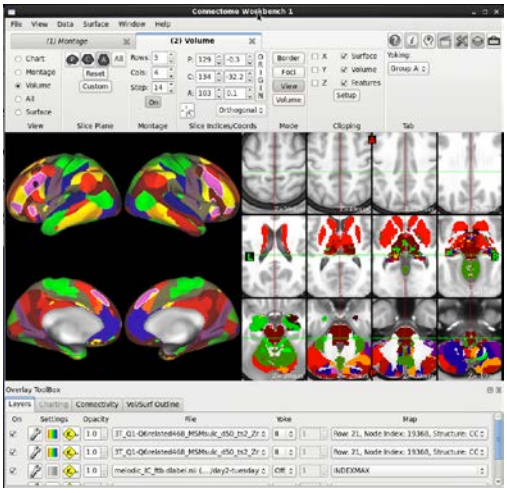
Next, we'll load and view group average parcellated connectomes ("pconn") files that were generated from the group average ICA. (You'll learn more about this process this afternoon.)

- Select **File: Open File: Files of Type: Connectivity – Parcel Files** (sixth from the bottom of the Connectivity subtypes)
- *Navigate* up two levels, then down two levels to **day2-tuesday/rfMRI_Practical_2/PTN/netmats/**
- *Select* and *open* both pconn files: **3T_Q1-Q6related468_MSMsulc_d50_ts2_Znet1.pconn.nii** *and* **3T_Q1-Q6related468_MSMsulc_d50_ts2_Znet2.pconn.nii**

The 'Znet1' pconn file is the full correlation matrix; the 'Znet2' pconn file is the partial correlation matrix. More about distinction between them is covered in the lectures and in Practical 2.

- In the Montage tab, in the Overlay toolbox top layer, *click* on the yellow diamond construction icon under **Settings** and *select* **Add Overlay Above**.

- *Repeat this* so that you have two new layers to play with.
- *Select* the **"…Znet1…"** file for the top layer and the **"….Znet2…."** file for the second layer.
- *Select* **Yoke: II** for both layers.
- Repeat this setup for the volume: *select* tab **(2) Volume**; in the Overlay toolbox top layer, *click* on the yellow diamond construction icon under **Settings** and *select* **Add Overlay Above**.
- *Repeat this* so that you have two new layers to play with.
- *Select* the **"…Znet1…"** file for the top layer and the **"….Znet2…."** file for the second layer.
- *Select* **Yoke: II** for both layers.
- To view the parcellated connectivity maps, *click* on any location of interest in the surface or volume.



Notice, if you clicked on the surface, that the parcel you clicked on is now outlined in white on both hemispheres to indicate that it is the seed parcel for the connectivity map being shown (see image, above). When you click on a "seed parcel", all other parcels get colored according to their connectivity/correlation with the seed parcel. You may find it easier to understand the colorings by using a simpler colormap. Press the wrench/spanner next to the overlay being viewed (Znet1 or 2), and then change the Palette to "FSL". You can now easily distinguish between positively (red-yellow) and negatively (blue) correlated parcels (relative to the seed parcel).

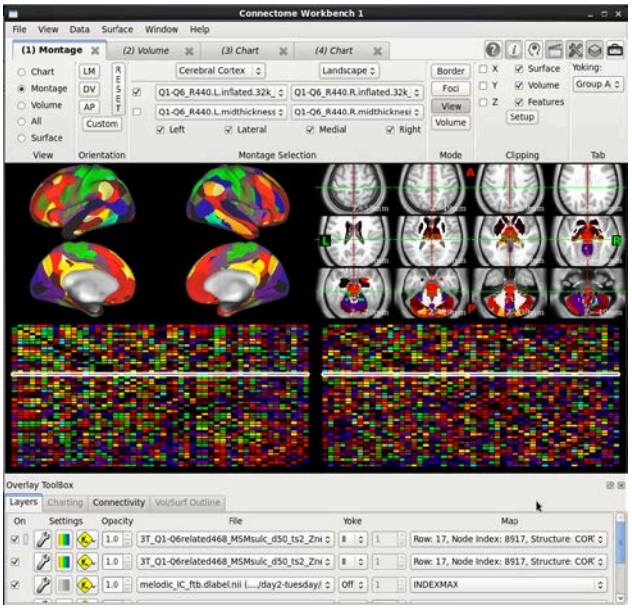
- Back in the **Scenes** box, *select* **Add**, and enter "**HCP R468 d50 Parcellated connectivity on group average surfaces and volumes montage**" or some other descriptive text.
- *Select* **File: Save/Manage Files**, then *press* **Save Checked Files** and *click* **Close**.

Now we'll set up wb_view so you can view the parcellated connectivity matrix as well as the connectivity maps.

- *Select* **File: New Tab** to create a third tab.
- *Repeat* (**File: New Tab**) to create a fourth tab.
- *Select* **View: Exit Tile Tabs** to return to single-tab mode.
- *Select* tab **3**, in the **Toolbar**, *select* **View: Chart**.
- In the **Overlay Toolbox***, Charting tab,* under **Matrix Loading** *set* the Matrix File to be the **…Znet1…** file.
- Select tab **4**, in the **Toolbar**, *select* **View: Chart**.
- In the **Overlay Toolbox***, Charting tab,* under **Matrix Loading** *set* the Matrix File to be the **…Znet2…** file.
- *Select* **View: Enter Tile Tabs**.

- *Select* **View: Tile Tabs Configuration: All Tabs (Default)**.

You should now see surfaces, volume slices, and separate connectivity matrices for the Znet1 (full correlation) and Znet2 (partial correlation) data.



- Back in the **Scenes** box, with "**HCP R468 d50 Parcellated connectivity on group average surfaces and volumes montage**" (or whatever you titled the last scene) highlighted, *select* **Replace**.
- Enter "**HCP R468 d50 Parcellated connectivity maps and matrices on group average surfaces and volumes montage**" or some other descriptive text.

The scene you created above will now be updated (overwritten) with the chart displays of parcellated connectivity added.

- *Select* **File: Save/Manage Files**, then *press* **Save Checked Files** and *click* **Close**.
- *Click* on various locations on the surfaces and/or volumes to see the full correlation connectivity maps associated with each parcel.
- *Select* tab 1 and *toggle off* the top layer to see the partial correlation connectivity maps in layer 2.
- When you are done, *click* the **X** button at the top right of the **Workbench Window** to exit wb_view. Note that the warning when you exit Workbench reminds you of the value of saving scenes to start where you left off when you open wb_view again.

End of rfMRI Practical 1.

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