rMEG and tMEG source-level connectivity; multimodal integration

In this practical session you are going to further explore processed MEG data and connectomes on the cortical sheet for both Task and Resting State paradigms. This practical should introduce to you the types and forms of connectomes that are computed from MEG data by the pipelines of the HCP and which will be distributed to the community. Additionally you will be provided with additional scripts that can perform various computations, such as group averaging.

- Group averages of MEG data in the source level.
- Common cross-modal data representation for MEG and fMRI data in source level.
- Dense connectivity results for Task MEG.
- Parcellation of the Task-MEG dense connectomes (This is the format in which
- Task-MEG connectome results will be distributed to the community).
- Connectomes of time-resolved, band-limited power correlation between a predefined seed and the rest of the brain in Resting State.
- Connectomes of non-time-resolved (stationary), band-limited power correlation in Resting State
- Connectomes of Imaginary Coherence in Resting State

The main directory of scripts, spec and scene files for this practical is:

/home/hcpcourse/day5-friday/practical2-afternoon/

TASK MEG

Exercise 1: Looking at the average Time Course across subjects

Learning objective of this exercise:

- Compute the average of MEG power maps on the cortical sheet across subjects. Observe the increased Signal-to-Noise ratio of this average relative to single subject results.

We saw in practical 1, using data from the motor task, that in single trials the brain activity shows very high variability. This variability is reduced by averaging across trials and unmasking in this way the Event Related activation relative to a stimulus or a task. Of course, there is still variability across subjects. In order to get the population average time-series of brain activation during a task, the individual brain activation maps can be averaged. In this exercise, you will see how existing time-series brain maps (in cifti format) can be averaged using wb_command and how the signal to noise ratio of the Event Related activation is increased when results are averaged across subjects.

Brain activity time-series are saved in ‘dtseries’ cifti files. Averaging time-series across multiple such cifti files is very straightforward using the -cifti-average mode of wb_command. For example, in order to

average acticity across files, A.dtseries.nii and B.dtseries.nii and put the result in GROUPAVG.dtseries.nii, one needs to execute:

```
wb_command -cifti-average GROUPAVG.dtseries.nii -cifti A.dtseries.nii -cifti \
B.dtseries.nii
```

When the number of subjects is large, the command becomes quite large. A sample script is provided that creates and executes the above command for 44 subjects and specifically for the power time-series derived from MEG data during the Right-Hand Motor Task.

- Using the file browser, navigate to /home/hcpcourse/day5-friday/practical2-afternoon.
- *Double-click* **P2E_WBavg_ERpow_RH.sh** and *select* **Run in Terminal**, to run the sample script.

This will output a group average time-series cifti file in /home/hcpcourse/day5-friday/practical2-afternoon/analysis:

GROUPAVG_MEG_Motort_srcavglcmv_[LM-TEMG-RH]_[IT-avg].power.dtseries.nii

Now that you have created the group average time-series, you can visualize it. For that we would need a subject-averaged brain surface. Here instead of trying to produce an average surface from the 44 subjects used in this MEG analysis, we instead use the average surface from 440 subjects , already released in the "Connectome Workbench v1.0 Tutorial " dataset.

The files are located in /home/hcpcourse/day5-friday/extradata/ and named:
Q1-Q6_R440.L.midthickness.32k_fs_LR.surf.gii

Q1-Q6_R440.R.midthickness.32k_fs_LR.surf.gii

For the current demonstration, we use the "midthickness" 32K surface. Of course this surface has 32K nodes per hemisphere while in the MEG analysis we have used surfaces downsampled from 32K to 4K points per hemisphere.

- To downsample the 32K average surface into the corresponding 4K one, use the file browser to navigate to **/home/hcpcourse/day5-friday/practical2-afternoon/**
- *Double-click* the **P2E_WB_resampSurf.sh** script. *Select* **Run in Terminal**.

You should see a window open for a split seconds and then disappear. The 32K average surfaces have been downsampled into the 4K ones in /home/hcpcourse/day5-friday/practical2-afternoon/analysis:

Q1-Q6_R440.L.midthickness.4k_fs_LR.surf.gii
Q1-Q6_R440.R.midthickness.4k_fs_LR.surf.gii

Now it's time to plot the group event related time-series from the MEG motor task on the average surface.

- In a terminal window, *enter*:

```
wb_view &
```

- *Select* **File->Open File** and set the **Files of type**: to "**Any File(*)**" in **/home/hcpcourse/day5-friday/practical2-afternoon/analysis/**
- select the anatomy files :

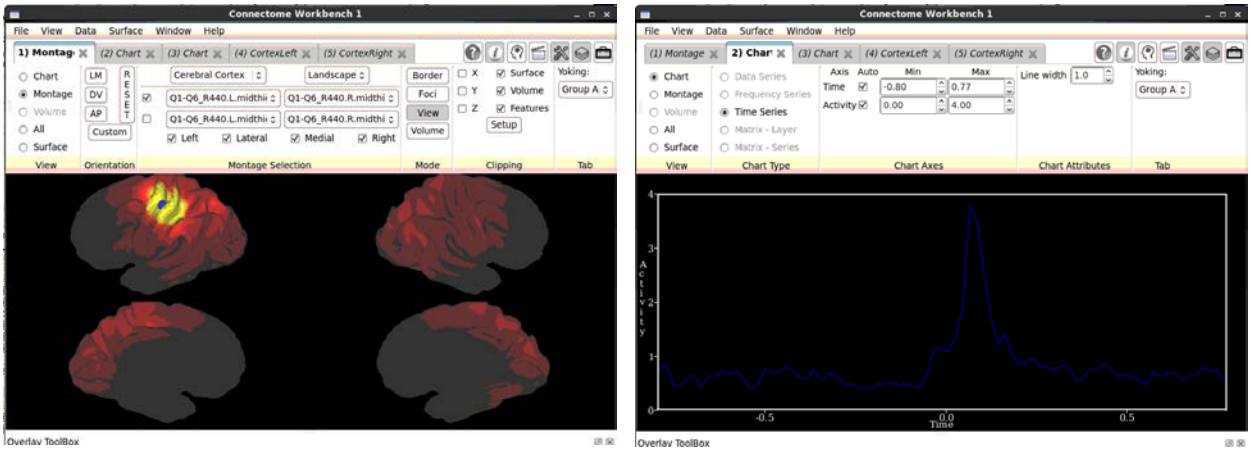
Q1-Q6_R440.L.midthickness.4k_fs_LR.surf.gii
Q1-Q6_R440.R.midthickness.4k_fs_LR.surf.gii

and the functional file:

GROUPAVG_MEG_Motort_srcavglcmv_[LM-TEMG-RH]_[IT-avg].power.dtseries.nii

- *Press* **Load**
- *Explore* the activation map across time in the same way you did for the single subject case in Exercise 4 of Practical 1.

Around 0.1 sec after movement onset you should be able to see a clear peak on the Left motor cortex. By plotting the time-series on a Chart you should be able to see how much clearer is the brain activation in the group average as compared to the one of a single subject, like in Exercise 4 of Practical 1.



- Don't close wb_view. Leave it open for the next exercise.

Exercise 2: Comparing MEG and fMRI data

Learning objective of this exercise:

- Show how MEG and fMRI activity maps on the cortical sheet can be converted to a common representation where they can be visualized (and analyzed) together.

One of the main utilities of the Human Connectome Project is that data is available from different modalities, which one should be able to compare and integrate.

In the previous exercise, we saw how one can plot the average time-series from MEG analysis of 44 subjects on the average cortical surface of 440 subjects, downsampled from 32K to 4K points.
The same downsampling can be also applied to functional maps defined on the 32K surface.

To demonstrate this, we use the Task FMRI average maps released in the "Connectome Workbench v1.0 Tutorial " dataset.

The cifti metric file is in directory /home/hcpcourse/day5-friday/extradata/
called:
HCP_Q1-Q6_R440_tfMRI_ALLTASKS_level3_zstat1_hp200_s2.dscalar.nii

This file contains average activation maps over 440 subjects for a multitude of different fMRI Tasks, including the motor task used here for the demonstration of the MEG data. These maps are defined on the 32K surface. We use wb_command to downsample them to the 4K representation.

Example linux commands for this operation can be found in the script file:

/home/hcpcourse/day5-friday/practical2-afternoon/P2E_WB_resampMetric.sh

- Use the file browser to *navigate* to /home/hcpcourse/day5-friday/practical2-afternoon and *double-click* **P2E_WB_resampMetric.sh**. *Select* **Run in Terminal**.

You should see a command window appearing only for a split second. This script has now created the downsampled 4K Task fMRI cifti file in /home/hcpcourse/day5-friday/practical2-afternoon/analysis/:
HCP_Q1-Q6_R440_tfMRI_ALLTASKS_level3_zstat1_hp200_s2_4K.dscalar.nii

Now we can compare MEG and fMRI results. You should still have open wb_view with the data from Exercise 1 above. (If not, please reopen wb_view and load the data from Exercise 1 before continuing.)

- In wb_view , go to **File-> Open File** , set **File Types** to "**Any File(*)**" , *select* and load file

  /home/hcpcourse/day5-friday/practical2-afternoon/analysis/

  HCP_Q1-Q6_R440_tfMRI_ALLTASKS_level3_zstat1_hp200_s2_4K.dscalar.nii
- In the **(1) Montage** Tab , in **Overlay Toolbox>Layers**, in the second row, *select*

  HCP_Q1-Q6_R440_tfMRI_ALLTASKS_level3_zstat1_hp200_s2_4K.dscalar.nii from the File selector.
- *Toggle* on this second row.

This is the file with the fMRI maps that was just downsampled. On the right, under the "Map" field you should be able to see displayed "**tfMRI_WM_2BK_BODY**". This is the name of the current functional

map which represents "Working Memory experiment and Trials with 2-Back Memory Load and Images with Body Parts".

- From the second row's Map menu, select "**tfMRI_MOTOR_RH**". This Map represents the activation during movements of the right hand in the Motor task (similarly to the MEG data).
- Make sure that on the **Overlay Toolbox**'s first row, **File** is set to **GROUPAVG_MEG_Motort_srcavglcmv_[LM-TEMG-RH]_[IT-avg].power.dtseries.nii** and *toggled on*. *Set* the timepoint in the **Map** section to **0.1 seconds**.
- Now compare the MEG and the Task activation by *toggling on and off* the "On" boxes on the very left of each entry. You should be able to see a coinciding activation of the Left Sensory/Motor cortex in both the fMRI and the MEG results. There are also some differences in these maps.
- Select different seeds on the fMRI map and examine the time-series from the MEG data using a Chart tab, similarly to Exercise 1 above.

Representing functional data from different modalities on the same spatial representation provides the opportunity to combine the different strengths of each recording method in order to understand brain dynamics.

Exercise 3: Cortico-cortical connectivity in Task MEG data

Learning objective of this exercise:

- Make yourself familiar with the form that Task MEG, time-resolved, DENSE connectomes are represented and produced by the HCP pipelines.

In Exercise 6 of Practical 1, it was shown that we compute the power time series in 8 different frequency bands. In Exercise 8 of MEG Practical 1, we showed that we examine the corticomuscular coherence time-series in the same 8 frequency bands. In the same fashion, we also examine cortico-cortical functional connectivity resolved in time and frequency.

Of course, connectivity results are much bigger in size. For this reason, we have computed connectivity matrices in 4 different time windows spanning the length of a trial, rather at a large number of time instances, as in the case of Task-MEG results in Practical 1.

In order to demonstrate the connectivity results, we use again the RH trials from the Motor Task. The connectivity metric we use here is "Imaginary Coherence". This is the magnitude of the imaginary part of coherency between 2 signals. It is used in MEG/EEG analysis due to the fact that a volume conducted signal in two different locations has no phase difference and is represented in the real part of coherency. So by examining the imaginary part, we look only at delayed interactions, not affected by volume conduction.

For the Task MEG, connectomes for different frequency bands are saved in different cifti files. Each of these files contains time-resolved connectomes (That is, the connectomes for each of the 4 time windows). Consequently they are saved as "dconnseries" files.

Currently, wb_view cannot display such time resolved dense connectomes. So we have constructed a simple script that splits a time-resolved connectome "dconnseries" file into separate "dconn" files, one for each time epoch.

This script is called:
P2E_SplitDconnseries.m and is executed by the "megconnectome" binary through running the wrapper script **P2E_SplitDconnseries.sh** in /home/hcpcourse/day5-friday/practical2-afternoon.

You don't need to run it now. We have already done this for you.

The original "dconnseries" file:
177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB-betalow].imcoh.dconnseries.nii

has been split into 4 files one for each epoch:

177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB-betalow]_epoch1.dconn.nii
177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB-betalow]_epoch2.dconn.nii
177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB-betalow]_epoch3.dconn.nii
177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB-betalow]_epoch4.dconn.nii

These files are located in /home/hcpcourse/day5-friday/extradata/Motort_tmegconne/

Epoch 1, 2, 3 and 4 correspond to time windows [-0.6 to -0.3 sec], [-0.3 to -0 sec], [0 to 0.3 sec] and [0.3 to 0.6 sec] relative to movement onset.

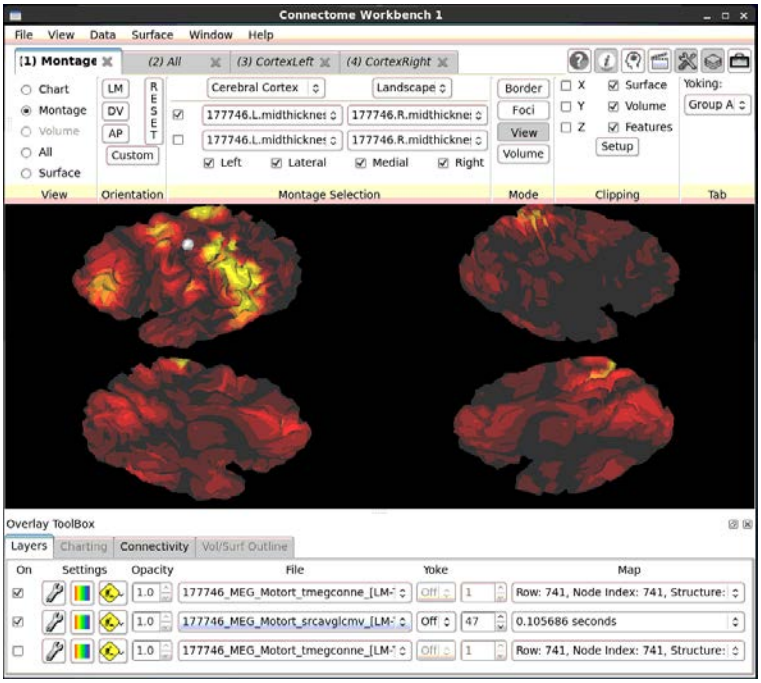
Let's visualize them:

- In wb_view, go to **File-> Open File**, set **File Types** to "**Scene Files (*.scene)**".
- *Select* and load the file:

/home/hcpcourse/day5-friday/practical2-afternoon/P2E_plotDconnepochs.scene

- In the **Scenes box** *double click* on the scene named "**plot dconn epochs**". After that is loaded close the Scenes box.

Now you should be able to see a seed location on the left motor cortex. The functional map is the imaginary coherence in the Low Beta frequency band from this seed location to the rest of the cortex in Epoch 1.



You can check the same connectivity for the rest of the epochs by going to the first row in the **Overlay ToolBox>Layers** and selecting in the **File** dropdown menu the functional data for each of the other 3 epochs. (Once you select one File in the dropdown menu then you can just use up and down arrows to scroll through the other functional map Files).

This connectivity data has been computed for the trials of Right Hand movement in the Motor task as in previous exercises. In the second row of **Overlay ToolBox>Layers**, you will see that the file with the average Event Related power time-series for the same subject is loaded. Also the time point has been set in the **Map** field to 0.10 seconds similar to Exercise 4 in Practical 1. You can see this map by toggling off layer one, which displays the connectivity results.

In this way you can use one type of functional data to select seeds for exploring another type of functional data.

- Try loading connectivity for other frequency bands for each of the 4 different epochs.

These files are located in **/home/hcpcourse/day5-friday/extradata/Motort_tmegconne/**.

For example, you could examine the imaginary coherence in the alpha frequency band by loading the following files into wb_view:

177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB-alpha]_epoch1.dconn.nii
177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB- alpha]_epoch2.dconn.nii
177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB- alpha]_epoch3.dconn.nii
177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB- alpha]_epoch4.dconn.nii

Exercise 4: Using parcellations with TMEG

Learning objective of this exercise:

- Make yourself familiar with the form and the process by which the Task MEG , time-resolved, DENSE connectomes are being parcellated in order to reduce their size, so that they can be realistically disseminated to the community. This is the representation in which it would be possible to fuse he released MEG connectomes with connectomes from other modalities.

In the previous exercise, we examined the dense connectivity series. The number of nodes in both cortical hemispheres used in the MEG analysis is 8004 resulting in a dense connectome of size 8004 x 8004. We also have 8 different frequency bands and four different time windows. And of course we also have multiple conditions, i.e. Left/Right Hand, Left/Right Foot. Not to mention that we have multiple connectivity metrics.

The pipeline for connectivity analysis of the Task MEG data (hcp_tmegconnebasic.m to be released in July) produces such dense connectome files. However all these multiple dimensions make the size of the results for all subjects and all possible combinations prohibitive for release. So it was decided that although the results are produced in dense connectivity format, they will be released in PARCELLATED CONNECTIVITY SERIES format or as it is called *pconnseries*.

The convention is the same. One pconnseries file for each frequency band. Within each such file there are four connectomes one for each different epoch. It was decided to use the parcellation by (Yeo et al J.Neurophys. 2011), which contains 107 contiguous parcels comprising 17 Networks related to Resting State and Task brain activity. Parcellation of the dense connectome series *dconnseries* into *pconnseries* (and of *dconn* into *pconn* files) is performed with wb_command.

We have constructed an example script:
/home/hcpcourse/day5-friday/practical2-afternoon/P2E_parcellateYeo11.sh

which parcellates the following dconnseries file, according to the Yeo11 parcellation:
177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB-betalow].imcoh.dconnseries.nii

into the pconnseries file:
177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB-betalow].imcoh.Yeo11.pconnseries.nii

IMPORTANT! : This pconnseries file format is the format in which the MEG connectomes will be released.

- Using the file browser *navigate* to **/home/hcpcourse/day5-friday/practical2-afternoon/** and *double click* on **P2E_parcellateYeo11.sh**

This should only take a few seconds to run. This script used wb_command to parcellate the dense connectome into parcellated connectome, which is also located in directory **/home/hcpcourse/day5-friday/extradata/Motort_tmegconne/**

This "pconnseries" file contains the 4 parcellated connectomes for the 4 different epochs during movement of the right hand by the given subject.

As with the dconnseries files, wb_view is not yet able to visualize connectome time series. So in order to visualize them, we need to split them in four separate non time-resolved "pconn" connectome files, in a similar fashion to the "dconn" files in the previous exercise.

We have constructed an example script that performs this split and is called **P2E_SplitPconnseries.m**. This script is executed by the "megconnectome" binary through running the wrapper script **P2E_SplitPconnseries.sh**.

You don't need to run it now. We have already done this for you.

The original *pconnseries* file :
177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB-betalow].imcoh.pconnseries.nii

has been split into 4 files one for each epoch:

177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB-betalow]_epoch1.Yeo11.pconn.nii
177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB-betalow]_epoch2.Yeo11.pconn.nii
177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB-betalow]_epoch3.Yeo11.pconn.nii
177746_MEG_Motort_tmegconne_[LM-TEMG-RH]_[CM-imcoh]_[FB-betalow]_epoch4.Yeo11.pconn.nii

These files are located in **/home/hcpcourse/day5-friday/extradata/Motort_tmegconne/**

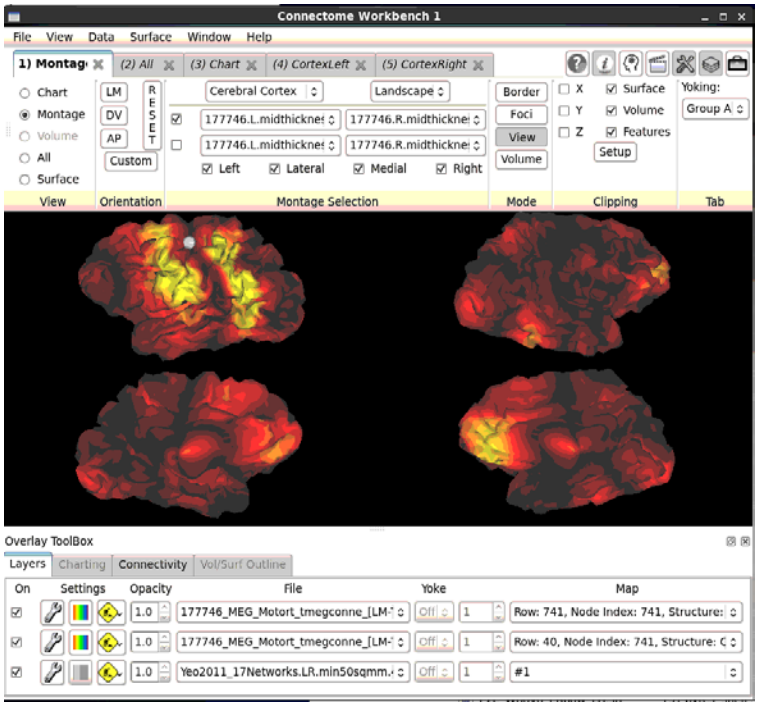
Let's visualize them.

- In wb_view , go to **File-> Open File**, set **File Types** to **"Scene Files (*.scene)"** , *select* and load file **/home/hcpcourse/day5-friday/practical2-afternoon/P2E_plotPconnepochs.scene**

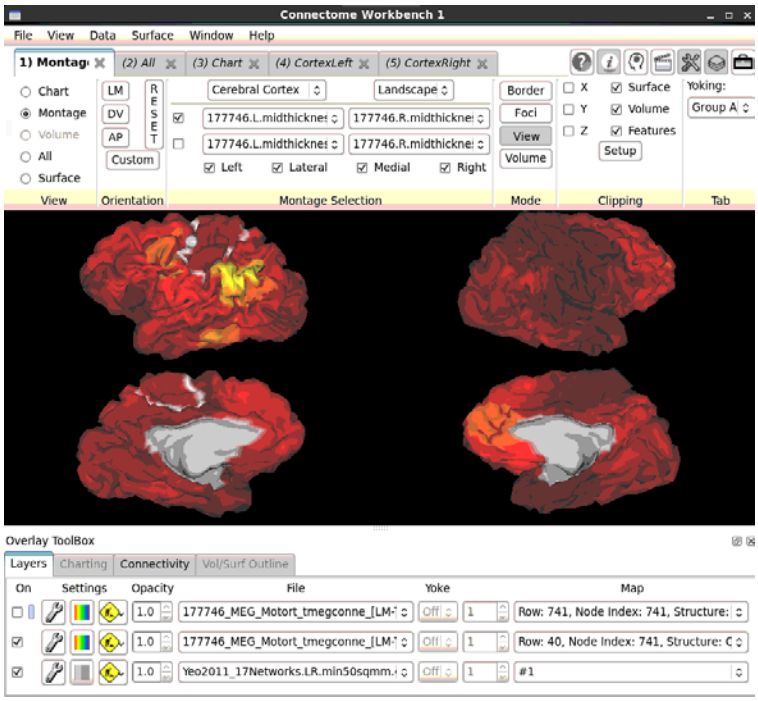
- In the **Scenes box**, *select* **P2E_plotPconnepochs.scene** scene file, then *double click* on the scene named "**plot pconn epochs**". After it is loaded, close the Scenes box.

Now you should be able to see a seed location on the left motor cortex. The functional map is the dense connectome of imaginary coherence in the Low Beta frequency band from this seed location to the rest of the cortex in Epoch 1.

- In the second layer of **Overlay ToolBox>Layers**, you can see loaded the parcellated connectome for the same epoch.



- If you *toggle off* the first layer, you will see this parcellated connectivity of the seeded PARCEL (seed denoted by the ID sphere on the surface).

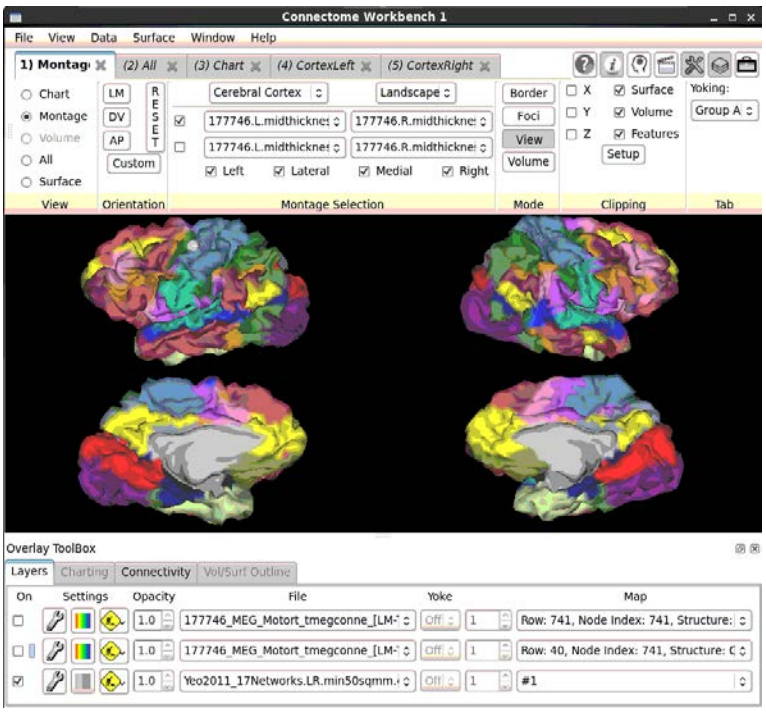


You can see with grey color the medial wall, which does not belong to any parcel in the Yeo11 parcellation. You can also see with the same grey color the border of the seed PARCEL that the seed vertex belongs to.

It is obvious that the size of the parcels within which connectivity is averaged creates a parcellated connectivity map that is smoothed relative to the sharper dense connectome map loaded in the first layer.

- In the third layer of the **Overlay ToolBox>Layers**, you can see loaded the labels of the Yeo parcellation, which you can see if you *untick* the "On" boxes in the above two layers.

In any of the three layers, you can also display the parcellated connectome for any of the other 3 epochs which already loaded in this scene.



By using parcellations, we are not only reducing the size of the connectivity results but we can also combine the information between fMRI, DTI and MEG. We saw in Exercise 2 of this practical that fMRI maps can be downsampled to 4K. In the same fashion, MEG functional maps can be oversampled to 32K. This number of thousands of vertices might provide the fine grained spatial resolution for each modality, but in terms of functional activity the current evidence shows that the functional nodes of the brain are more in the range to 10s to 100s. That is why existing parcellation schemes based on functional characteristics of the brain (including the Yeo11 presented above) converge on a number of parcels in this range.

Determining which parcellation is optimal and for which modality remains an open scientific question.

RESTING STATE MEG

Seed based Band Limited Power non-stationary correlation

In this part, course attendees will evaluate non stationary correlation between the BLP time course of one seed and the rest of the brain using a sliding window approach (i.e. seed-based non-stationary correlation). Both megconnectome binary and wb_view will be used. This exercise will show how the MEG functional connectivity might evolve across time. Using the suggested seed (R-vCs) one can show how the correlation patterns may strongly change, evolving for instance through states in which only the right hemisphere vertices are involved and states in which vertices of both hemisphere are strongly correlated.

Attendees will be able to change several settings: sliding window step can be chosen from 200 ms up to several seconds. The seed can be chosen among a list of 124 predefined vertices. Both a matlab script and workbench visualization will be used. The script ***P2E_blpenv_slidingw_corr.sh*** is located on ***/home/hcpcourse/day5-friday/practical2-afternoon/*** folder. The list of seeds we are providing can be found at the end of the practical.

Script parameters are:

- band (frequency band of interest): default alpha. Possible configurations 'delta', 'theta', 'alpha', 'betalow', 'betahigh', 'gammalow', 'gammamid', 'gammahigh', 'whole'
- step (step of the sliding window correlation evaluation in ms): **default step=200 ms**
- window (width of window for correlation computation in each step - in ms): **default window=10000 ms**
- seed (seed to be used in the seed-based correlation evaluation): **default seed='vCS'**
- hemisphere (L o R for left or right hemisphere): **default hemisphere='R'**. For example if seed='vCS' and hemisphere='R' the R-vCS seed is used.

Example: explicating the default command arguments:

```
sh P2E_blpenv_slidingw_corr.sh --band 'alpha' --seed 'vCS' --hemisphere 'R' \
--step 200 --window 10000
```

Exercise 5

Practical steps:

- In a terminal window, enter these commands:

  ```
  cd  /home/hcpcourse/day5-friday/practical2-afternoon
  sh P2E_blpenv_slidingw_corr.sh
  wb_view megdemo_rmeg_basic.spec &
  ```

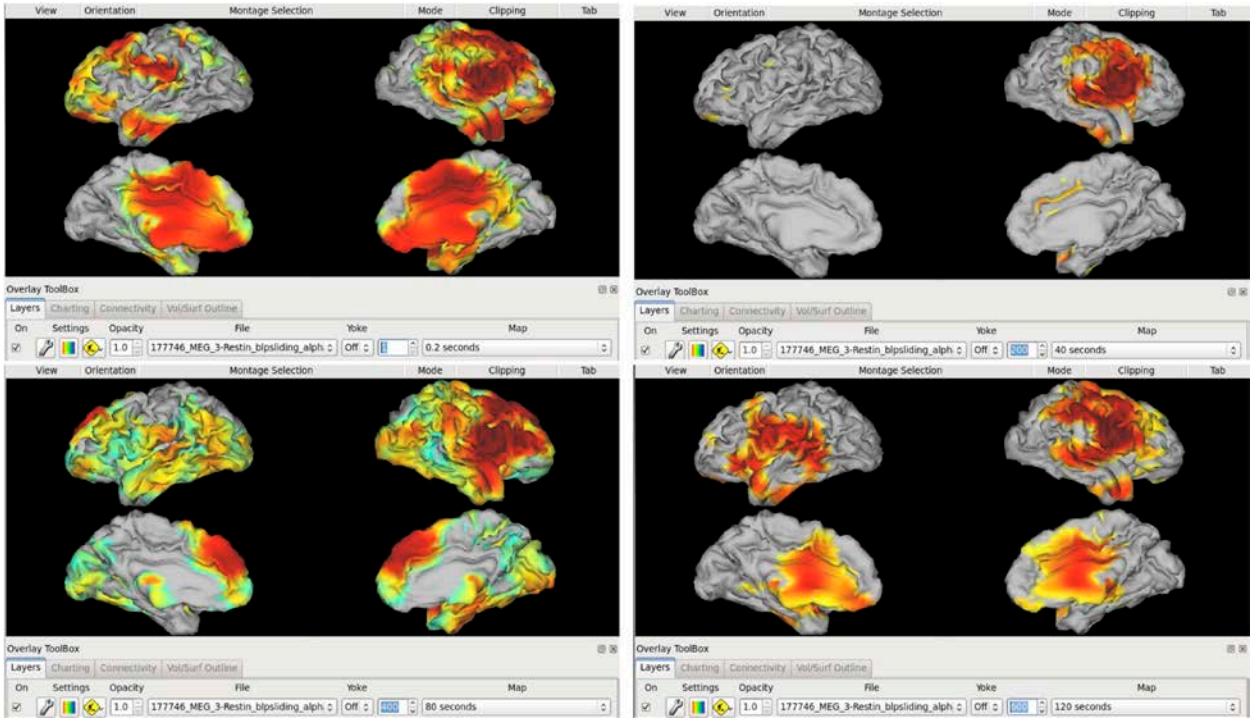
The output of this script will be a dense time series cifti file named **177746_MEG_3-Restin_blpsliding_<band>_<seed>_<step>_<window>.dcorr.dtseries.nii** in **/home/hcpcourse/day5-friday/practical2-afternoon/analysis/** folder. It contains the time-varying correlation between all vertices on the cortical sheet and the seed vertex, as computed by the parameters specified above.

This spec file loaded in the wb_view command contains midthickness cortical sheet and the seed dlabel file.

- *Load* the dtseries file you just obtained: **File: Open File: Files of type: Connectivity – Dense Data Series:/home/hcpcourse/day5-friday/practical2-afternoon/analysis/177746_MEG_3-Restin_blpsliding_alpha_R-vCS_200_10000.dcorr.dtseries.nii**.
- Make sure the top layer is *toggled on* and the top layer's File menu is *set* to the file just loaded.
- *Explore* how the topography of the correlation changes as a function of time by changing the time epoch. Notice the seed blur, i.e. the high value of correlation around the seed vertex.
- In wb_view**, File: Open Files: Files of type: Scene: P2E_blpenv_slidingw_R-vCS.scene**
- *Double-click* the scene **Palette**.

This shows a Tile tabs view of the timeseries map for timepoint 1 (0.2s) in the upper left; a chart view (upper right), and sample seeds for the left and right hemispheres in the lower panels. (It also entailed changing palette to JET256 and set thresholds to visualize only data between 0.5 and 1).

- *Click* on a seed location in one of the hemispheres (purple spots in lower panels). You will see the timecourse for that seed in the chart in the upper right.
- *Click* on Tab 1 (Montage) and change the map number for the top layer to different values to view maps for different timepoints on the cortical surface (upper left).



Band Limited Power stationary correlation (hcp_blpcorr pipeline)

hcp_blpcorr pipeline evaluate dense connectomes based on stationary correlation of the BLP for resting state data. Stationary correlation is obtained by using all the 3 resting state sessions. For each session the connectome is calculated by averaging the correlation of the BLP envelope in 25 seconds windows. Dense connectomes obtained in this way are the basis for the parcellated connectomes.

You will be able to inspect these data (we have 9 different bands) both using the wb_view and by inspecting figures we have already released. While wb_view will allow you to browse through cortex vertices to inspect connectome rows (i.e. correlation of one vertex time course with the rest of the brain), bitmap figures already obtained can be used to inspect dense and parcel based connectomes. Browsing through neighboring vertices, you will be able qualitatively explore the impact of volume conduction on the stationary correlation in MEG analysis. The list of predefined seeds can also be used.

Different frequency bands can be concurrently loaded and inspected. MATLAB figures will allow visual inspection of the dense connectomes. Figures already obtained have vertices ordered according to Yeo parcellation. You will be able to qualitatively evaluate features in the connectome matrices the vertices.

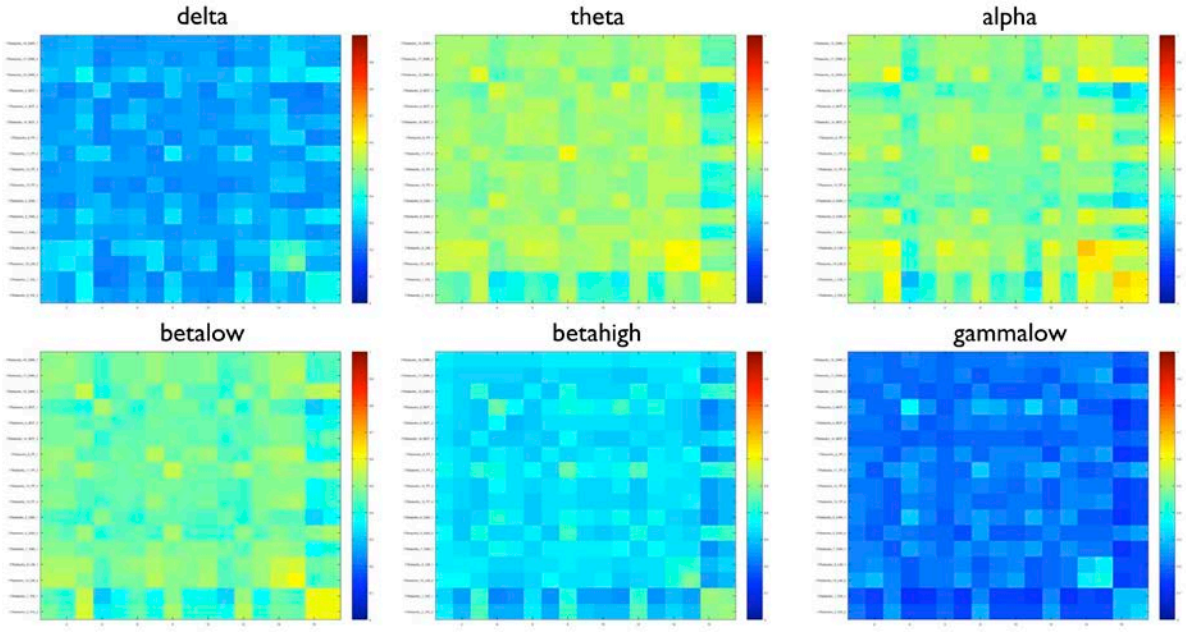
Exercise 6

In this exercise attendees will get familiar with hcp_icablpcorr outputs.

Practical steps:

- Inspect dense and parcellated bitmap figures, already obtained. Dense and parcellated connectomes in different bands can be compared. For instance a clearly visible feature is that average correlation is strongly varying between bands and may be related to the degree of stationarity of the BLP fluctuations in the considered band. Another very clear feature for instance is that parcels associated to visual areas show high degree of internal correlation in the alpha band, which is something one can expect in MEG data.
- In the figure below parcel-based (Yeo 17-Networks) blpcorr connectomes are plotted for six different frequency bands. Colormap extremes are 0-1. Parcel ordering can be seen when opening the figures:

  /home/hcpcourse/day5-friday/extradata/177746_MEG_Restin_icablpcorr_<band>.blpcorr_parc.png

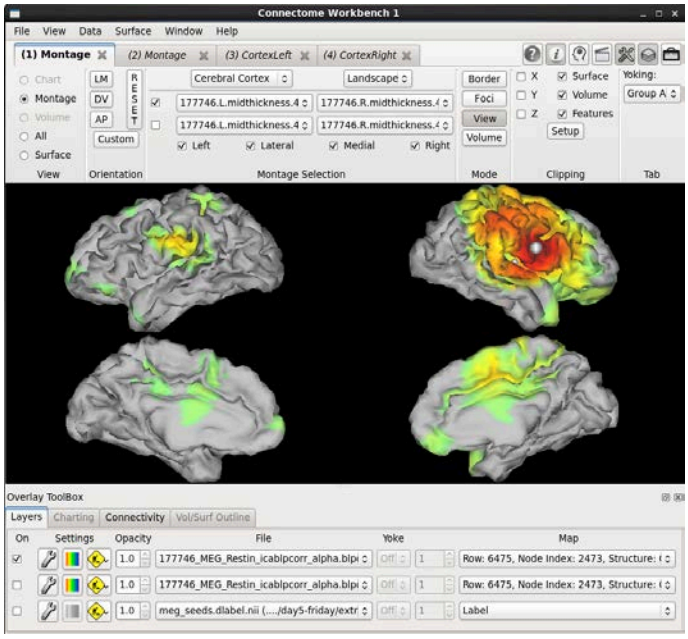


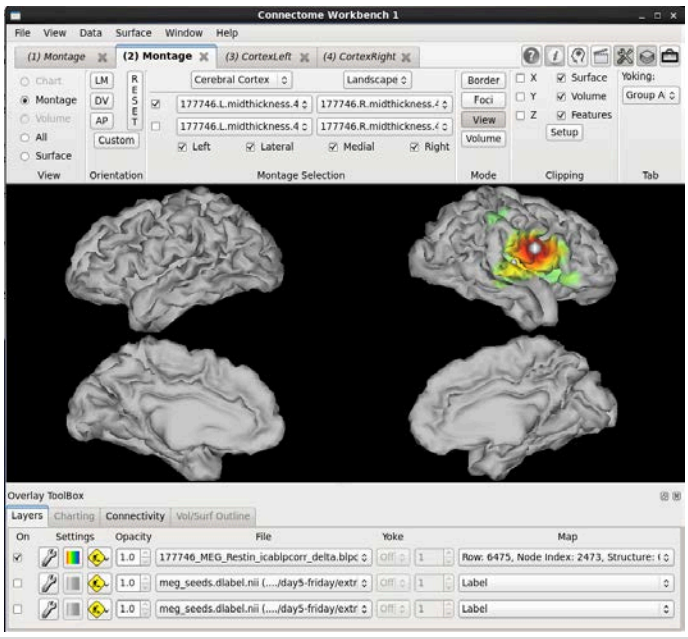
Exercise 7

In this exercise you will use wb_view to browse through dense connectome rows by selecting vertices on the cortical sheet. This allows to inspect stationary correlation for different seeds in different bands. Seed selection can be done arbitrarily or by selecting them from the list we provide. One interesting thing may be to qualitatively evaluate the impact of the volume conduction in MEG data by selection of very proximate seeds.

Practical steps:

- In **wb_view. File: Open File: Files of type: Specification Files: /home/hcpcourse/day5-friday/practical2-afternoon/*P2E_icablpcor.spec.*** This spec file contains the midthickness cortical sheet, the seed dlabel file and icablpcorr connectomes in all the bands.
- Click **Load Scenes**.
- In the Scenes box, *double click* the "R-vCs" scene to load setting for R-vCS example.
- *Click between* tabs (1) and (2) to compare the stationary correlation maps with R-vCS seed in alpha and delta bands as an example.
- *Toggle on* the second layer and select meg_seeds.dlabel.nii from the File menu. Click the purple spots (seeds) to see the pattern for the seeds provided.
- *Browse* through cortex vertices to qualitative inspect BLP correlation by changing them manually. *Select,* for instance, alpha band and browse through close vertices to explore how and if the connectivity varies.
- Do the same for each file (different bands) on the top overlay's File drop-down menu.





- Open png figures to inspect dconn blpcorr output in different bands

MIM based frequency resolved connectomes (hcp_icaimagcoh)

hcp_icaimagcoh pipeline generates frequency specific connectomes based on the "Multivariate Interaction Measure (MIM)" (Ewald et al., 2012; Marzetti et al., 2013) for source level data from non artifactual independent components (as estimated from the *hcp_icamne.m* pipeline). The "Multivariate Interaction Measure" maximizes the imaginary part of coherence between MEG signal at a given reference voxel with respect to the signal at any other target voxel. More specifically, the estimated MEG signal at each brain voxel is a vector quantity that can be represented, in a given reference system, through its three components and the MIM is designed to maximize the imaginary part of coherence between vector quantities.

You will be able to inspect these data (on 9 different bands) both using the wb_view. wb_view will allow the users to browse through cortex vertices to inspect connectome rows (i.e. correlation of one vertex time course with the rest of the brain). Different frequency bands can be simultaneously loaded and inspected. By loading previously discussed blpcorr connectomes, you can compare the two different connectivity measures.

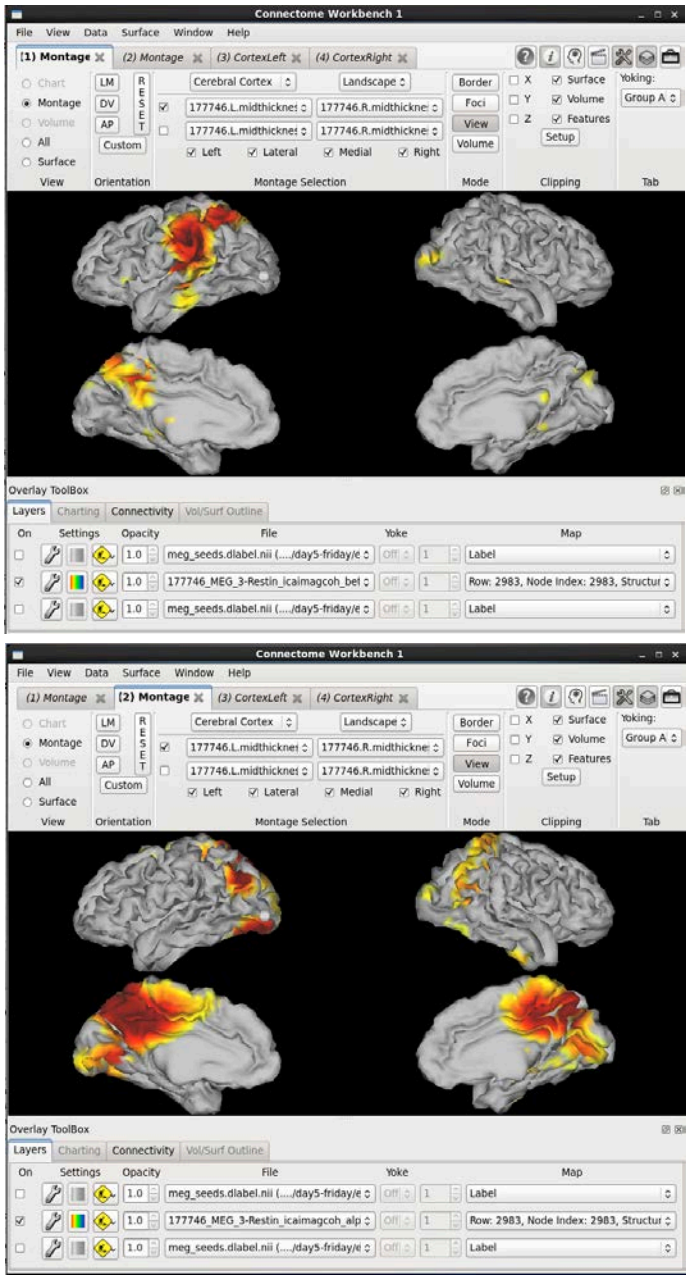
Exercise 8

In this exercise you will browse through cortex vertices to inspect MIM maps in different bands. One of the things you may notice is that MIM measures show connectivity patterns very different from correlation patterns. For instance, the MIM measure is intrinsically not affected by the very high connectivity blur around the seed. Often, obtained patterns are non-trivially explainable.

Practical steps:

- In **wb_view. File: Open File: Files of type: Specification Files: /home/hcpcourse/day5-friday/practical2-afternoon/P2E_icaimagcoh.spec.** This spec file contains the midthickness cortical sheet, the seed dlabel file and the icaimagcoh connectomes in all the bands.
- *Press* the **Load** button to load the files in the spec.
- *Toggle on* the top layer in the **Overlay toolbox** and from the **File** drop-down menu select **177746_MEG_3-Restin_icaimagcoh_alpha.dconn.nii**.
- *Click* on different parts of the surface to inspect MIM patterns. (If you don't see a pattern, make sure the threshold on the top layer's settings [wrench icon] is turned off.)

- Do the same for each file (different bands) on the top overlay's File drop-down menu.
- Select **Toolbar: Scene** icon to inspect the MIM pattern for L-MT seed. As can be seen from the **tab (1)**, a strong connectivity between parietal and somatosensory cortices of the same hemisphere is found (see figure right).
- In **tab (2)** the same measure for alpha band is shown. In this case, the connectivity involves right posterior parietal cortex and other regions of both hemispheres (comprising L-V4 and L-AG).



Authors:

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Seed regions (network, hemisphere, location) in the *meg_seeds.dlabel.nii* file

VFN L Fovea-LO
VFN L LO
VFN L MT
VFN R V3A
VFN R LO-RV3A
VFN R V4v
VFN R LO
VFN R LO
VFN R V4v
VFN R LOMT
VFN R LOMT
VFN R VOIT
VPN L V1d-V2d
VPN L V3-V3A
VPN L V3A
VPN L POSd
VPN L V7
VPN L V1v
VPN L VP
VPN L V7-POSd
VPN R V1d
VPN R V1
VPN R V3-V3A
VPN R V3-V3A
VPN R POSd
VPN R V1v-RV2v
VPN R VP
VPN R V4v
VPN R POSv
DAN L FO
DAN L PrCe
DAN L FEF
DAN L dPrCe
DAN L vPoCe-SMG
DAN L dPoCe
DAN L aIPS
DAN L ITG
DAN L mIPS
DAN L vIPS
DAN L MT
DAN L pIPS-SPL
DAN R IFG
DAN R PrCe
DAN R FEF
DAN R vPoCe-SMG
DAN R dPoCe
DAN R mIPS
DAN R ITG
DAN R pIPS-SPLd
DAN R MT
DAN R pIPS-SPL
DAN R vIPSd
DAN R vIPS
MN S MA
MN L dPrCe1
MN L dPoCe
MN L SMA1
MN L dmSPL
MN L dCS
MN L cPrCe
MN L CS
MN L SMA2
MN L vPoCe
MN L vCS
MN L S2
MN L mI
MN L mI2
MN R dPoCe
MN R SPL-preCun
MN R dPrCe
MN R mdSPL
MN R SMA
MN R CS
MN R vPoCe
MN R vCS
MN R mI2
AN L mI3
AN L mI
AN L mI
AN L pI
AN L mSTG
AN L STG1
AN L pI
AN L STG2
AN R mI
AN R mI
AN R mI
AN R STG2
AN R pI
AN R pI
AN R STG1
CON D ACCmsFC
CON L aTha
CON L aI
CON R preSMA
CON R aTha
CON R aIfO
VAN L AI
VAN L vIFG
VAN L PC
VAN L SMG
VAN R aPFC
VAN R IFG-AI
VAN R AC
VAN R vPrCe
VAN R vIFG
VAN R AI
VAN R MFC2
VAN R AC2
VAN R SMG
VAN R STG
LN L IFG
LN L ifg1
LN L ifg2
LN L mfg
LN L mfc4
LN L stg1
LN L stg2
LN L stg3
LN L stg4
LN R ifg1
LN R ifg2
LN R stg2
LN R stg1
FPN M Cing
FPN L aPFC
FPN L dlPFC
FPN L FC
FPN L IPL
FPN L IPS
FPN L prCu
FPN R dlPFC
FPN R dPrCe
FPN R IPL
FPN R IPS
FPN R prCu
DMN R mPFC2
DMN L AC1
DMN R mPFC1
DMN L mSFG3
DMN L mPFC2

DMN L AC3
DMN L mSFG2
DMN R AC2
DMN R PC2
DMN R PreCun
DMN L MFG2
DMN L AC2
DMN L SFG
DMN L mSFG1
DMN L MFG
DMN L ITG
DMN L STS
DMN L preCunPC
DMN L ag
DMN L AG
DMN R SFG2
DMN R SFG
DMN R MTG2
DMN R MTG1
DMN R STS
DMN R PCPreCun
DMN R AG
DMN L PCC