The GPS Cookbook

Bruna Olson and Reid Vancelette
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*for more detailed information about any of these processes, please refer to the GPS Manual

Setting Environment via *Terminal*:

- Download and save all the files within the GPS folder that can be found at :

  https://www.nmr.mgh.harvard.edu/software/gps

  https://www.martinos.org/software/gps

- Go to *Applications -> System Tools -> Terminal*
- Once *Terminal* is open, type: *gedit ~/.cshrc*
- Once the file is open, at the end of the document type the following:
    - *alias GPS source /cluster/dgow/setup_GPS*
- Save the file and return to the *Terminal* command line

Opening up *Matlab* via *Terminal*:

- Enter the *Terminal* command line and type *GPS*
- The command *GPS* will set the necessary environment to run *Freesurfer* and *MNE* commands, and additionally will open the version of *Matlab* specified within the .cshrc file

Opening up *GPS* via *Matlab*:

- Type in the following in your *Matlab Command Window*: *GPS*
- This will open up the *GPS* suite and provide you with four different options:
    - Analysis – GUI that contains the commands to pre-/post-process your data
    - Editor – interface that allows you to edit the structure of a pre-existing study
    - Regionator – GUI that enables you to create Regions of Interest (ROIs) based off of Maximal Activity, MNE, and other metrics
    - Plot Drawer – GUI in which you can plot your Granger computations for already determined ROIs

Adding a Study in GPS

- After typing in *GPS* into the *Matlab Command Window*, click on the *Analysis* button. This will open up the GPS1.8's *Analysis* GUI.
- Under the *Studies* box, click on the button labeled *New*. This will open up a dialogue box that contains lines for three types of necessary information: *Name*; *Base Directory*; *Block Names*.
- Type in the name of your study in the Name box.
- Under *Base Directory*, type in the path to your study's directory. This will be the folder in which all of your data and analyses will be saved. If you do not have a folder for your base directory yet, at the end of the path type in the studies name. The GUI will automatically create a base directory for you the first time you import your data. For example, if your study is called BMD and its base directory will be located on the cluster under dgow, the path would be:
    - /autofs/cluster/dgow/BMD
- Under *Block Names*, type in the name of each block the same way it was saved in your raw data files. Usually, we name our blocks: B1; B2; B3.
- Once all of this information has been added, press *OK* and your study will be added to the

Studies list.

Setting up the parameters for your Study in GPS

GPS automatically applies default settings for your study. If your study contains different settings, you are free to change them. You can change them on three different hierarchies: Studies; Subjects; Conditions.

- Studies: contains the settings that will be used for every single subject for each study.
- Subjects: contains the settings that will be used specifically for each subject. For example, if you cannot use a block for one of your subjects, you can delete that condition from the subject's list.
- Conditions: contains the settings that will be used specific to each condition. Items that need to be changed are:
    - the event codes – within your study's event extraction program (*Extract Events* under *Stages* and *MEG Preprocessing*) it will change the triggers of interest from your raw.fif file into event code numbers. These numbers should be added to each condition in order to process these conditions separately and properly;
    - the level – use the number 1 for your primary conditions, 2 for your secondary (sub-) conditions, 3 for your tertiary (subsub-) conditions. This will allow you to do higher level and more detailed analyses with your data. If you do not have any secondary conditions, then simply use the number 1 for all your conditions. For example, in BMD the condition All is considered the primary condition and Correct as the secondary condition. The primary condition(s) will always show up in bold.
    - Subjects- you can select what subjects you would like to use in a specific condition. This is important because when averaging MRI, the average brain will be done only among these subjects.
    - the Brain – this parameter can be found within *cortex*. This field allows you to specify how you want the average brain for that condition to be named. Furthermore, all the analyses within that condition will be done using the brain you chose. For single subject analyses, once you input the subject name on the Subject field within the condition's parameters, the GUI will recognize that is does not need an average subject brain.
    - the ROI set - this field allows you to specify what ROI set you want to be used for the analyses of this condition. For secondary conditions, the ROI set is usually the same as the ROI set of its primary condition. This is done so comparisons between conditions can be drawn. For example, in BMD the ROI set for the primary condition All is named "All" and the ROI set for the secondary condition Correct is also named "All". For single subject analyses the ROI used will have the same name as the condition.

- Once finished with your changes to the three hierarchies, press the *Save & Exit* button and all your changes will be saved.

Checking the status of your stages

- It is very important to check the stages of your data processing. This will allow you to know what has been done and what still needs to be done. On the bottom of the screen, check the box next to *Refresh Status*. *Green* means that the stage is ready to go. No coloring means that the

stage isn't ready to be processed. *Blue* means that the stage has already been finished and was successful. If a stage needs to be repeated, you can check the box next to *Override*. This will allow you to repeat any stage that is in blue. Be very careful with *Override*. You do not want to *Override* a process that has been finished and does not need to be redone.

MRI Processing

Importing your MRI data

- Make the correct subject is selected.

- Under Stages, click on the *MRI* button. This will give you access to all the MRI related processes. Click on the first stage Import and a dialogue box will open up with the two opens: *Bourget*; *CD/Select Dir*. The first open, *Bourget*, will automatically find your subject's data on the Martinos MRI server. If you have a CD and did not save the raw MRI data on the Bourget server, select the second open *CD/Select Dir*. If you are using a Linux computer, follow the following steps:
    - Go to *Look In* and go a few levels below to /. Once you are in here, find the folder *Media*. Within *Media*, go within the Subject specific folder, go within the folder labeled *dicom*, then within the next folder and the next folder. This will bring you to the place in which all MRI related material is located. Press the *OK* button and GPS will automatically import the raw MRI data for you and copy it into your Subject's *MRIraw* directory.

Processing your MRI

- If you are processing the MRI for a single subject, check the boxes next to the following buttons: Find *MPRAGE*; *Organize*; *Build Surfaces*; F*S Average*; *Source Space*; *Setup Coreg*; *BE Model*; *BE Model to .fif*. To process all of these sequentially, once each box is checked press the Batch button. The processing of the routines for an average subject will be explained later. Also, each specific step is explained in great detail within the GPS Manual. Please note that these steps might take over 3 hours to be completed.

MEG Preprocessing

Importing your MEG data

Under Stages, click on the *ME*G button. This will give you access to all the MEG related processes. Click on the first stage *Import* and a dialogue box will open up. Please type in the MEGraid in which you saved your data. This will change depending on the system. Once you type the MEGraid in, it will automatically find your subject specific data on the Martinos server. If it isn't able to find the right files it will prompt the user to locate the correct directory containing the MEG recordings.

Extract Events

- Extract events will take the timing, sampling rate, and trigger codes from the raw .fif files saved during your MEG scanning session and save them in a separate .eve file. To do so, click the *Extract Events* button.

Process Events

- Press the Process Events. This will run a routine specific to each experiment to extract the trigger numbers and replace them with specific condition codes. These codes should be

specified before doing any MEG data processing. The program will take the .eve file created during the *Extract Events* process. Once the *Process Events* process has been done, GPS will be able to properly extract each event and relate it to each condition that you have. To change the manner of processing your events, you will need to 1. change the event processing Matlab program, and then 2. change the condition codes located within the *Edit* structure for *Conditions* on the top of the GPS GUI.

Bad Channels

- The button *Bad Channels* in the *MEG Preprocessing* stream only accepts a list of bad channels detected for both MEG and EEG. In order to find out what are the bad channels within the raw data file, click on *Utilities* under *Stages* and then on *mne_browse_raw*.
- Once the *mne_browse_raw* program is open, go to *File*, then *Open*. Make sure you are in the subject's folder that contains the raw.fif files that were imported over during the *Import* stage of *MEG Preprocessing*. Select one of the block's raw.fif files and then press *OK*. This will open up the raw MEG and EEG data, alongside the EOG data.
- Scroll through all the channels and determine whether or not each channel is conspicuously bad. Write down the bad channels as you proceed through this checking process. Make sure also that the channels that were determined bad during the data acquisition process are indeed bad.
- As an additional check and also should be done with extremely high-frequency data, look at the raw.fif emptyroom file. This will give you the bad channels affected by tuning issues or introduced by the environment.
- If the MEG/EEG data are too high-frequency, you will need to apply MaxFilter-ing. You can refer to the instructions written on the Wiki.
- Once all the bad channels have been identified and written down, close the *mne_browse_raw* program by going to *File* and then *Quit*.
- Return to the *MEG Preprocessing* stage and click on *Bad Channels*. A dialogue box will open up. Please enter both the *Bad EEG* and *Bad MEG* channels in their respective boxes and then press *OK*. This will create a .txt file within the subject's directory under the MEG folder that contains the bad channels and additionally will mark these channels bad (as can be seen by their black color in mne_browse_raw) in each of the blocks' raw.fif files.

EOG Projections

- The *EOG Projections* button under the *MEG Preprocessing* stage requires a file that contains all saved EOG projections. To begin and create this file, go to *Utilities* under *Stages* and click on *mne_browse_raw*. EOG projections will not be successful unless you have already marked the bad channels.
- Go to *File* and *Open* to load the raw data from one of the blocks.
- Once a block has been loaded, scroll down to the bottom to find the EOG's, labeled under *EOG 061* and *EOG 062*.
- On the bottom of the *mne_browse_raw* screen, you will notice several buttons. The most important button for our purposes is the *Pick to:* button. Next to the *Pick to:* button you will notice a number. At first this number is set to 1000. Change this number to whatever number you like. Essentially, we are going to identify as many EOG's as possible and save them to this number.
- Once you have selected a number, go through the block, select an eye-blink by click in the middle of the curve, and then press *Pick to:* to save the eye-blink. Continue to do this for as many eye-blinks as possible. The more *n* equals, the better the projections will be later on.

- After selecting and saving, click on the beginning of the upward-rising EOG, jot down the time located next to t at the bottom of the screen, then click on the middle (apex) of the upward-rising EOG and jot down the time. Calculate the time it took to go from the beginning of the EOG to the middle. This will be used in the next step to create projections.
- Click on *Process*, then *Create a new SSP Operator*. This will open up a dialogue box containing several options. In the first box, *Start time (s)*, type in the time the length from the middle of the eye-blink that was just calculated. You are going to need to make this number negative. The middle of the eye-blink is considered the beginning of the SSP Operator calculation (0 ms), thus the beginning will be negative and the end will be positive. Once you have entered in the start and end times, type in the number that you saved your EOG projections to and press *OK*.
- The *Evaluate new projection* box will open and give you several different options for creating EOG projections: planar and axial (the two different types of MEG sensors); and EEG.
- Under *Existing items*, click on the box next to each of the projection options. These are mandatory projections that the program has identified for you.
- Under *New items*, click on each of the options while looking at the MEG/EEG data to see which projections help decrease the noise introduced by the eye-blinks. Try to be as minimal as possible as the more projections you use, the more you data will become smooth.
- Once you have found the best projections for your data, press *Accept*.
- Next, you will need to save the data. Go to *File*, *Save projections*. Within the dialogue box, you can specify where you want it saved, how you want to call the file. Before pressing *OK* to save, make sure to click on the box Include *EEG average reference*.
- Quit the program, go to *MEG* under *Stages* and click on the *EOG Projections* button under *MEG Preprocessing*. This will bring up a dialogue box. In this box, type in the location and name of the file that contains the projections that you just created. Press *OK*.

Coregistration

- In order to perform the coregistration, both the MRI needs to be fully processed and the MEG data need to be preprocessed.
- First, go to *Utilities* under *Stages* and click on the *mne_analyze*.
- In order to load the brain, go to *File*, *Load Surface...* A dialogue box will open with many different options. Make sure that under the Available subjects, your specific subject for coregistration is highlighted. Under available surfaces, select *inflated*. You will not need to select anything else. Press *OK*. You will now see the inflated brain in the center of your screen.
- Next, go to *File* and *Load digitizer data...* Go into the folder in which the subject's raw.fif files are located. Select a raw.fif file and then press *OK*. A dialogue box will open *Good for you to know...*, telling you how many digitized points it is loading. Press *OK* to continue. This will load all of the digitizer data from the scanning session.
- Now, go to *View* and *Show viewer*. This will open a window containing the MNE's version of your MEG reconstruction.
- Also, go to *Adjust* and *Coordinate* alignment... This will open a window with options on how to adjust your digitized data to the MRI reconstruction.
- To start, we will first align the digitized data according to the Fiducials. In the *Adjust coordinate alignment* box, press on *LAP* (Left Periauricular) and then in the *Viewer* window, point and click on where the *LAP* is located. Next click on *Nasion* in the *Adjust coordinate alignment* window and then click on the nasion in the *Viewer* window. Do the same for the *RAP*. Now, in the *Viewer* window, press on *Options* and click on the box to the left of *Transparent* for the *Scalp*. Now, click on the *Align using fiducials*. You will notice that the digitized data will get

closer to the actual skull. The larger the dots (digitized data) are the farther away from the scalp, either inside or outside of it. Next, in the *Adjust coordinate alignment* window, we are going to perform an *ICP (*Iterative closest point) alignment. This will give you a better coregistration between the digitized points and the MRI. Next to *ICP align*, type in the amount of steps you want the program to perform. Usually, our group uses that number 100. You can do more if you want. Once you have typed in your steps, click on *ICP align*. It should take a few moments, but you will notice the digitized data getting closer to the MRI scalp.

- Once the *ICP align* has finished click on *Omit...* Omit will go through the digitized data and delete all the digitized data farther than the number specified. Our lab uses 5.0 mm, but you can change it to the needs of your lab. Once you have typed in your maximum distance allowed, click *Done*.
- For security sake, our group performs one last *ICP align* after performing the *Omit*. Sometimes digitized points that are extremely far from the scalp can bias the data. Perform another ICP in order to make sure the digitized data is as close to the MRI scalp as possible.
- Once finished, click on *Save MRI set*. In the window *Good for you to know...* write down the name of the MRI set, Press *OK* and close *mne_analyze*.
- Under *Stages*, click on *MEG* and then *Coregistration*. Find the saved MRI set, select it, and press *Open*. This will let GPS know where your coregistration data are saved.

MNE (Minimum Norm Estimates)

*All commands will be performed on the *MNE* selection under *Stages*.

- Select the desired subjects. More than one subject can be selected for this stage and the program will do the function for each of the selected subjects.

Average Waves

- Click on Average Waves. This will perform several functions:
    - Combine the *MEG* and *EEG* data for better a signal-to-noise ratio. This will only be done for your primary condition, which is set with in the Conditions structure
    - High-pass filter your data (filter that passes high-frequency signals, but attenuates and filters out signals with frequencies lower than the threshold specified. Compare this to low-pass filters)
    - Create the emptyroom covariance matrix if an emptyroom measurement was taken (very important to have one!)

Forward Solution

- Click on *Forward Solution*. This will perform the *MNE* command for creating a forward solution for your dataset.

Inverse Solution

- Click on Inverse Solution. This will perform the MNE command for creating an inverse solution for your dataset.

Evoked Trials

- Click on *Evoked Trial*. This function will gather the evoked trials and place them into groups based off of your event code set during the Process Events step.

Make .stc

- Click on *Make .stc*. This function will create .stc files (source timecourses) for your primary conditions. In these .stc files will contain MNE data from sensor averages and the inverse solution created.

Single Subject Analysis

*This section will include the additional steps needed to perform a single subject analysis

The main difference between group analyzes and single subject analyzes is set when choosing the parameters for conditions.

- Once the study parameters have been added, add the subject and condition.
- Under the condition list press *edit*. A dialog box will open with five dropdown menus. Make sure you have the correct condition selected and then on the next dropdown menu click *subject*. The only subject that should be listed under this parameter is the subject you wish to single analyze.
- Next, within that same dropdown menu click on cortex. A new dropdown menu on the right will be available. Under this parameter, the brain listed should be the name of the subject. This will assure that for that specific condition, the brain used for analysis will be the subject's brain rather than an average brain.
- Next, click on roiset and make sure that the ROI set used for that condition is the correct one.

MEG steps will be the same as group analysis.

MRI steps will be the same as group analysis, however the last step: *Average subject*, will not need to be done.

MNE- all the steps will be the same with the exception of the two last step : *Morphed .stc Average Subject.* These steps do not need to be done for a single analyses.

Granger- steps will be the same as group analysis.

ROIs- steps will be the same as group analysis.

Average Subject Analysis

*This section will include the additional steps needed to perform an average subject analysis

MRI – Average Surface

- Go to *MRI* under *Stages*. Next, under Subjects make sure that all the subjects that you want to be in the analysis are listed. Under Conditions make sure the correct primary condition is selected. If all the other conditions have the same brain as the average brain, there is no need to repeat the step.
- Click on the *Average Surface* button under *MRI Processing*; you do not need to highlight all subjects to perform this function, it will automatically do it for all. This will create an average surface from all of your subjects' MRIs that will be needed later for ROI detection process.

MNE – Morphed .stc

- Go to *MNE* under *Stages*. Next, select all subjects and all conditions that you want to perform this function; the function does this process subject specific and condition specific. Now, click on the *Morphed .stc*. This function will create .stc files for each subject for the primary condition and each other condition selected.

MNE – Average Subject

- Go to *MNE* under *Stages*. Next select each condition on which you want to perform this function; you do not need to select all subjects as it will do it for all of them even if only one subject is selected. Now, click on *Average Subject*. This function will morph all the .stc files created from *Morphed .stc* onto the average subject's brain.

GPS: ROIs

*This section will be for both Single Subject Analyses and Average Subject Analyses and will detail how to create ROIs based off of MNE

Opening GPS: ROIs

- Go to Utilities under Stages and click on GPS:ROIs. Two windows will open up:
    - *GPS rois data figure <<Do not close>>* contains all the current variables. If you want to perform a different analysis but with the same parameters (such as thresholds for MNE, Max Activity, Similarity, etc.), then do not close this window.
    - *Graphical Processing Stream: Regions of Interest* is the main GUI for processing ROIs.

Selecting Your Dataset

- Under *Panel Selection*, select *Dataset*. Under *Data*, select your *Study*, *Subject*, *Condition*, and *Set* (if you have one). For *Subject*, if you are doing *Single Subject Analyses*, select the subject. If you are performing *Average Subject Analyses*, select the a*verage* subject.
- Press *Load* next to *MNE* under *Measures*. This will open up the MNE maps created in past steps. If you get the warning dialogue box "You do not have a STC or MAT file listed for the mne measure," you will have to press *Browse* and manually find and select the .stc file needed to open up MNE. The .stc files are located under your study directory, MNE, subject or average (depends on whether you are doing single subject or average subject analyses), stcs. You should use the lh.stc file. You can press *Load* now.

Viewing the Brain

- At first, you will not be able to see the brain or any of the other windows related to creating ROIs. In order to see these windows, uncheck *Pause Auto Draw* under *Quick Display*. Other instructions on how to visualize different hemispheres and different layers (pial, inflated, etc.) are located in the Manual.

Selecting Your Metrics: MNE

- Make sure under *Metrics*, *Minimum Norm Estimates* is selected. Under *Time Windows (ms)*, type in your *Start* time and your *Stop* time. These numbers basically reflect during which periods in milliseconds after the onset of your condition you want to define your ROIs.

Selecting Your Metrics: Maximal Activity

- Make sure under *Metrics*, *Maximal Activity* is selected. Under *Time Windows (ms)*, type in the *Start* and *Stop* that you specified in the selecting your MNE metrics.

Creating Centroids

- Under *Panel Selection*, click on *Centroids*. Make sure that *Spatial Exclusion* is selected. The default for this is 5 mm. This can be changed depending on your study. Basically, this will make sure that each centroid is at least 5 mm from one another.
- Also, make sure *White Matter* is selected and Percentile is 95.
- Now, click on *Find from Maximal Activity*. Once finished, by clicking *Show Centroids* you can look at all the potential ROIs on the brain.

Selecting Your Metrics: Similarity

- Go to *Metrics* under *Panel Selection*.
- Under Metrics, click on the pop-up menu and select Similarity.
- Make sure that the *Start* and the *Stop* under *Time Window (ms)* are the same for your MNE and Maximal Activity settings.
- Under *Standardizing*, click on the *Standardize* box. Under the pop-up menu select *windows: Vertices*. This should be the default.

Creating ROIs

- Under *Panel Selection*, click on *Regioning*. Under Regioning, you will notice a list of areas in the brain. These are the centroids just defined. You will even see on the bottom the number of centroids defined. There will be a 0 next to ROIs. This will change once we constrain out centroids.
- Under *Redundancy*, adjust the criterion to the requirements of your study. The more negative the number, the more the computation of creating ROIs will rely on redundancy and will constrain your dataset. This metric takes into consideration similarity in waveforms in one centroid compared to other centroids. If one centroid is considered similar to another, then it will be excluded depending on your redundancy criterion.
- Under *Similarity*, adjust the criterion to the requirements of your study. Like *Redundancy*, the more negative the number, the more the computation will rely on similarity and constrain your dataset. This metric takes into consideration similarity within each centroid separately. It will look at all the vertices within each centroid and exclude vertices (winnowing down the size of a centroid) that are too similar in wave form depending on your similarity criterion.
- Under *Continuity*, adjust the criterion to the requirements of your study. Continuity represents the number of millimeters a point must be from other neighbors to be considered an ROI.
- Under *Spatial Weight*, type a number from 0 to 1; 0 means that there is no weighting whatsoever; 1 means that there is 100% spatial weighting. In short, the more the spatial weighting you have, the more the computation will take into consideration the differences in neural activity by location. For example, if you have spatial weighting, then similar activity in the L and R hemisphere will not knock each other out, but without spatial weighting whichever hemisphere has the neural activity with the highest frequency will knock the other out.
- Press the *Make All ROIs* button to start the ROI creation process.

Saving ROI labels

- Go to *Saving* under *Panel Selection*. Next to the *Save Labels* button, press on *dir*. This will open

up the directory in which you will save all your ROI labels. ROIs for your study should be saved in your study's directory, the *Granger* folder, the *rois* folder, and your condition specific folder. If you are going to save multiple sets of ROIs with different metrics used, make sure to name their folders differently. Once finished, press *OK*.

- Press S*ave Labels*. In your Matlab screen, it will tell you when your ROIs have been fully saved.

Granger

*All Granger-related processes will be performed under the Granger button under Stages.

- Select the conditions you want to be analyzed. Both primary and secondary conditions should be selected.

Processing Your ROIs

- Press on the *Process ROIs* button. This will perform three tasks:
    - create .mat files from the labels saved during the ROI creation process
    - spin back the ROIs from the average cortical surface to each individual subject
    - locate the vertices with the highest cortical activation within each region

MNI Coordinates

- Click on *MNI Coordinates*. This function will create MNI (Montreal Neurological Institute) coordinates for each ROIs central vertices for publication. These coordinates are located the study's folder, *Granger* folder, *rois* folder, condition folder, average folder (folder in which you saved your ROI labels). In this folder, the file will be called *mni_coordinates.txt*.

ROI Timecourses

- Click on *ROI Timecourses*. This function will create waveforms based off of the processed ROIs from *Process ROIs* and the activation from the .stc files created during the *MNE/Evoked Trials* step.

Consolidate timecourses

- Click on *Consolidate*. This function will create a single input file that contains the timecourses for each subject.

Compute Granger

- Click on *Compute*. This function will take the single input file containing each subject's timecourses and use them in creating the Kalman Filters and computing Granger Causality. The output file can be used to look at Granger Causality between defined ROIs in *GPS: Plot* without having to perform the next two steps. The output file can be found in the study's folder, *Granger* folder, *results* folder.

Null Hypotheses

- Click on *Null Hypotheses*. This function will perform a 2000 run iterative process that will calculate the significance between each ROI. Careful: this process can take a few hours to several days depending on how many ROIs were defined. The output of this process is located in the study's folder, *Granger* folder, *results* folder, *nullhypothesis* folder.

Get Significance

- Click on *Get Significance*. This function will calculate α-values and perform p-values between each ROI.

Plot Drawer:

Single Condition Plots

Opening the Plot Drawer:

- On the *MATLAB Command Window* type: GPS.
- On the GPS suit click on the button *Plot Drawer*.

Dataset

- The GUI will open with *Dataset* already selected.
- On the Dataset interface click on the dropdown menu *Study and* select the study desired.
- Under the dropdown menu *Condition* select the condition desired. This will open a search window. Once the conditions have been selected, click on *open* and then click on '*Load'*.
- On the *Activation* dropdown menu, select the condition and then load the data following the same steps as above. This allows visualization of brain activity on the cortex surface.

Surface

- Once the mat. files have been loaded, click on *Surface*. This button will give the option of generating 2 kinds of picture analyses:

1. **Cortex**: A image of the average subject's inflated brain.
2. **Circle**: A circle graph with the image of all ROIs previously determined for this condition.

In both cases, Bubbles showing accumulative activation on ROIs and arrows showing directional causality can be added. For a single condition analyses, the color green represents activation moving out of the ROIs and blue represents activation moving towards the ROIs.

- Select the surface wanted to visualize the data.
- Under *Portions* menu select the sections of the cortex desired to visualize the data. As a default they come all selected.
- The menu *Cortex Options* gives the option to either visualize 'inflated', 'white matter' or 'grey matter' when the cortex surface is selected.
- The *Cortical Atlas* menu gives the option to select how ROIs should be laid on the cortex surface :
    - bg- background- ROIs are shown on the background of the cortex.
    - fg- foreground- ROIs are shown on the same level as the cortex.
    - top- ROIs are shown on the top of the cortex.

- The background color of the plot and its width and height can also be specified using its respective boxes.

Cortical Activity

- This section is used to set up visualization of cortical activity on the Cortex surface.
- Click on the 'Show Activation' in order to show activation on the surface cortex.

Regions

- Click on the button Regions. This button opens a menu which allows the selection of ROIs for visualization on the chosen surface.
- Under the *Primary* menu 3 buttons can be selected::
    - *All:* Selects all ROIs for visualization
    - *L*: only selects ROIs on the left hemisphere for visualization
    - *R:* only selects ROIs on the right hemisphere for visualization

- Specific ROIs can also be selected by using the *Primary* menu. More than one ROI can be selected by pressing Ctrl while clicking the desired ROIs.
- Under the *Connections* menu specific pairs of ROIS can be selected. More than one pair can select by pressing Ctrl and clicking on the desired pairs. Arrows between pair show the direction of activation.
- Under *Labels* click in the box *Show Labels*. Abbreviations for ROIs will be added To the plot. *Font Size* and *Color* for the labels can also be specified.
- The *Filter* menu gives 3 boxes:
    - *Exclusive*: when two or more ROIs are selected, this will show outgoing and incoming activation only among those ROIs.
    - *Between Hemis:* when two or more ROIs are selected, only the connections which are between hemispheres will be shown.
    - *Inbound:* Only activation going towards the selected ROIs will be displayed.
    - *Outbound:* Only activation going away from the selected ROIs will be displayed.

Method

- Click on the button *Method.* This section gives the option of inputting a threshold where only activation above the threshold is shown or to visualize the data with activation under the P value.
- *GCI*: Specify that time points are significant if the Granger Causality Index is above a certain value. 0 is the baseline GCI, but numbers around 0.25 generally work in practice. However, once you have run significance testing use P values.
- *P Value*: Timepoints can be evaluated on how unusual they are from the null hypothesis tests.
- On the MATLAB *Command Window* the Granger weigh between ROIs is shown. In order to make the visualization more clear user should be aware of those values. The connections that have low weight in relation to most of the other connections can be deleted from the

visualization by selecting the box *absolute value below* and by adding a number to the space next to it. ei;5

- The option 'prob. same below': The `prob. same below` option only works when there are p values for a primary and comparison condition. It will run a binomial test based on the number of timepoints that show significant GCi values in each condition to determine whether this number is significantly different in the two conditions ($p < 0.05$).

Time

The *Time* section gives the option to select the time period for the visualization.

- Select the start and ending time by inputting the milliseconds in *Window*. Then, modify *Duration* and *Interval* appropriately.

Arrow

- Click on the icon 'Arrow' and then select the box *Show Arrows* in order to add arrows to the surface. These arrows will show the directional Granger interactions between ROIs in the time window previously selected.
- The first drop, *Terminal Wedge,* down menu allows the selection of different kinds of arrows.
- The second drop, *Green-Blue Gradient,* down gives a selection of possible colors for the arrows.
- You can also select the scale of the arrow by inputting a number and pressing *Enter*
- Click on the button *Weight* if you would like to see the weight between the pair of ROIs connected by the arrows.
- Click on *Borders* in order to have the arrows outlined.

Bubbles

- The *Bubbles* menu gives the option to display bubble on the visualization plot that shows the accumulative activation in each ROI. Click on the bubble icon.
- Select the *Outgoing* button in order to see activation living the ROIs.
- Select the *Incoming* button to see activation moving towards the ROIs. Both options can be selected simultaneously.
- The scaling can also be modified by typing the direct scaling for the bubbles on the box next to *Scaling,* and pressing *Enter*
- The button *Label Weights* allows the visualization of granger weight of each ROI.
- Click the box '*Don't show primary regions'* in order to only display circles on the ROIs that are influenced by the selected ROIS, thus there will be no circles on top of selected ROIs
- *Borders:* Checking this box will draw borders around the circles.
- Using this dropdown menu, *Circle overlaid,* you can select how to display the circles.
- Selecting *Asterisk* will indicate comparative significance in circles/labels.

Comparing Data between 2 different conditions

*Please note that this comparison analyses are only possible when condition share the same set of ROIs

- On *Dataset* load the first condition as explained on the **Dataset** section.
- Under *Compare* load the second condition.
- On *Surface*, select the surface desired to visualization of the data.
- Go to *Region* and select the pairs you would like to see under the menu *Connections.*
- Click on *Methods*, and under *the* first drop down menu select the comparison you would like to do.
- Select the box *prob. same bellow* to see....
- Under time select the start and ending time by inputting the milliseconds in *Window*. Then, modify *Duration* and *Interval* appropriately.
- In both Cortex and Circle surfaces, the causality shown will be equal to the difference between conditions. Different pairs of ROIs will be displayed with a different set of colors.

Time course

- The *Timecourses* menu allows visualization of Granger causality index per time. In order to have a clear visualization, specific pairs of ROIs should be selected first on the *Regions* menu.
- This menu has several box which can be combined to generate different visualizations:
    - *Show Timecourse:* opens the plot with the Granger causality index per time graph.
    - *Fill*: fills with color any space that is above the threshold line.
    - *Tips Only:* shows only data equal or above the threshold line.
    - *Plot P value:* Change the legend to p values as well as the nature of some of the functions.
    - *Flip Y Dir:* Switches the direction of the Y coordinate from higher to lower values.
    - *Reflections*. It shows you the selected data in a backward direction as well as chosen direction. (Better visualized if the box *Tips Only* is selected.)
    - *Signif. Spikes:* Draw vertical lines where timepoints are significant
    - *Log Scale:* Makes the graph a log scale instead a linear scale
    - *Right Y Axes:* Switches the Y coordinate from the left to the right side of the graph
    - *[ ] Plots*: Allows you to input the number of plots to be generated, which can be useful when viewing a lot of connections.
    - *Legend:* This menu allows user to choose where lengent should be positioned within the picture.
    - *Y Bounds:* The minimum and maximum for the plot
    - *Background:* This menu allows user to choose the background color for the graph.
    - *Width:* The approximate width of the plot
    - *Height:* The approximate height of the plot
    - *Font:* What font to render the names in. Some journals require specific fonts. Be careful, this list is generated from your computer but not all fonts listed may render corrected in Matlab.