

MEG & PLS PIPELINE:

SOFTWARE FOR MEG DATA ANALYSIS AND PLS STATISTICS

USER DOCUMENTATION

VERSION: 2.02B

MAR. 17, 2015

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S1. REQUIRED SOFTWARE & TOOLBOXES:

FIELDTRIP: <http://fieldtrip.fcdonders.nl/>

- Extract FieldTrip to your desired location and select it in the Installation GUI (see below).

SPM8: <http://www.fil.ion.ucl.ac.uk/spm/>

- Extract SPM8 to your desired location and select it in the Installation GUI (see below).

AFNI-MATLAB: <http://afni.nimh.nih.gov/afni/matlab/>

- Extract AFNI-Matlab to your desired location and select it in the Installation GUI (see below).

AFNI: <http://afni.nimh.nih.gov/afni>

1. Extract the AFNI binaries folder to your desired install location.
2. Add the AFNI path to your **shell file** (i.e. your `.bashrc`, `.tcshrc`, or `.cshrc` file).
3. Log out and back in to apply your settings.

Example: If your AFNI binaries were extracted to: `/usr/local/afni_bin`

- If using `.bashrc`, add the line: `export PATH=$PATH:/usr/local/afni_bin`
- If using `.tcshrc`, add the line: `setenv PATH "${PATH}:/usr/local/afni_bin"`

Important: AFNI must be added properly to your shell file.

- AFNI commands must be callable from the Linux terminal.
- Note: Shell files for each user are normally located within their home directory.

S2. CONTACT INFO & GOOGLE GROUP:

CONTACT INFORMATION:

- **Name:** Michael Cheung & Natasa Kovacevic
Emails: mcheun45@gmail.com & mcheung@research.baycrest.org
Google Groups Link: <https://groups.google.com/d/forum/megpls>

GOOGLE-GROUPS FORUM:

- ❖ To keep up-to-date with [MEG]PLS, a Google-Groups forum has been created. [Download links](#), [announcements](#), [updates](#), and [patch-notes](#) will be posted here.
- ❖ Please post any [questions and bug-reports](#) in the forum. We'll do our best to check it frequently and answer any questions regarding the pipeline and its usage. Posts in this forum can be seen by other members allowing others to view and participate in discussions.
- ❖ To join the group, simply follow the link above and send a join-request. If you do not have a gmail account, you can also contact me directly via the email above.

S3. PIPELINE INSTALLATION & SETUP:

SYSTEM REQUIREMENTS:

1. Operating System: Linux (Tested on Fedora17).
2. Matlab 2009b or above.
3. FieldTrip (Version 2014/09/22 or newer)
4. SPM8 (with latest Feb. 2013 updates)
5. AFNI (Last tested with version: AFNI_2011_12_21_1014)
6. AFNI-Matlab

Recommended: Your monitor should be capable of displaying at least **1400 x 1050 pixels**.

- GUI windows may be truncated or appear distorted if adjusted.

INSTALLING THE [MEG]PLS PIPELINE:

1. Unzip the package and move the "**MEGPLS_PIPELINE**" folder into desired install directory.
2. Start Matlab and navigate into the [MEG]PLS pipeline folder.
3. Start the pipeline by running the "**Launcher.m**" function.
4. Open the installation window by clicking the "**Toolbox Paths & Installation**" button.
5. Finalize the installation by selecting the required paths and clicking "**Save Settings**".

Important: You must have write permissions to the FieldTrip toolbox selected in the Installer.

- If you are working on a server and do not want the primary FieldTrip install modified, it is recommended to extract a copy of FieldTrip into your own directory and select that instead.

For proper installation, make sure to use the Installation GUI:

- Required [compatibility fixes](#) will be installed (See FIXES_README.txt for more details).
- Specified folders will be scanned for key functions to ensure correct toolboxes have been added.

You do not need to run the setup GUI again unless you wish to update toolboxes.

- Once saved, a file called "**ToolboxPaths.mat**" will be created inside the pipeline directory.
- Whenever the pipeline is called, it will read this file and add all required paths automatically.

What if I've updated my toolboxes and want to change or reset my paths?

- Simply delete the "**ToolboxPaths.mat**" file and go through the Installation GUI again.

TOOLBOXES & FUNCTIONS INCLUDED IN [MEG]PLS:

- NK PLS Functions & View4D Viewers: Natasa Kovacevic
<http://www.rotman-baycrest.on.ca/index.php?section=101> (see articles for PLS citations).
- PLScmd Toolbox (Baycrest) & View4D Viewers (Natasa Kovacevic):
<http://www.rotman-baycrest.on.ca/index.php?section=345> (see link above for PLS citations).
- Matlab File Exchange functions:
uipickfiles (D. Schwarz), rdir (G. Brown), clickablelegend (A. Deoras), parforprogress (W. Goeji).

S4. PIPELINE DESIGN & OVERVIEW:

PIPELINE DESIGN:

- ❖ [MEG]PLS is organized around a few primary GUI modules:
 1. MRI Preprocessor
 2. MEG Preprocessor
 3. MEG Cleaning Modules
 4. Builder
 5. Driver
 6. Viewers

- ❖ The Preprocessing and Cleaning modules read and import MRI and MEG data into the pipeline. They also perform basic MRI processing (coregistration and reslicing) and MEG signal preprocessing (epoching, filtering, etc). The cleaning modules can be used to perform ICA artifact removal or remove bad channels and/or trials from the MEG data.

- ❖ Once the MRI and MEG data have been preprocessed, they are passed onto the Builder module. The Builder is used to configure settings and select the input data for sensor and source analysis. These input parameters and settings are stored into a MATLAB .mat file.

- ❖ The Driver module reads the Builder .mat file and serves as the "central hub" to initiate different types of analyses. The Driver is also responsible for configuring and running PLS analyses. Finally, the various Viewer modules are used to visualize results.

MRI & MEG PREPROCESSING:

- MRI processing: Coregistration, reslicing, and segmentation.
- MEG preprocessing: Epoching, filtering, baseline correction, detrending, artifact removal, etc.
- Bad channel & trial removal
- ICA artifact removal

SENSOR ANALYSIS:

- Time-domain (ERP) analysis: Both single subject & group-average analysis
- Global mean field power (GFP) computation
- Frequency & Time-Frequency analysis: Both single subject & group-average analysis

SOURCE ANALYSIS:

- MRI segmentation: Can segment for brain, gray matter, etc.
- Headmodel & Leadfield computation
- Source reconstruction & normalisation

STATISTICAL ANALYSIS:

- PLS datamat generation
- PLS multivariate statistics

S5. CITATIONS, COPYRIGHT & LICENSING:

CITING [MEG]PLS:

- **When using [MEG]PLS for scientific publications, please cite it as follows:**

[Placeholder: Paper currently in submission]

Michael J. Cheung, Natasa Kovacevic, Bratislav Mistic, Zainab Fatima, Anthony R. McIntosh.
[MEG]PLS: A pipeline for meg data analysis and pls statistics.

- [MEG]PLS relies on the following toolboxes, which should also be cited as follows:
McIntosh, A. and Lobaugh, N. (2004). Partial least squares analysis of neuroimaging data: applications and advances. *NeuroImage*, 23:S250-S263.

Kovacevic, N., Abdi, H., Beaton, D., and McIntosh, A. R. (2013). Revisiting pls resampling: Comparing significance versus reliability across range of simulations. In *New Perspectives in Partial Least Squares and Related Methods*, pages 159-170. Springer.

Oostenveld, R., Fries, P., Maris, E., and Schoffelen, J. M. (2011). Fieldtrip: open source software for advanced analysis of meg, eeg, and invasive electrophysiological data. *Computational intelligence and neuroscience*, 2011:1.

Cox, R. W. (1996). Afni: software for analysis and visualization of functional magnetic resonance neuroimages. *Comput Biomed Res*, 29(3):162-173.

Friston K. J., Ashburner, J. T., Kiebel, S. J., Nichols, T. E., and Penny, W. D. (2011). Statistical parametric mapping: The analysis of functional brain images. *Academic Press*.

COPYRIGHT & LICENSE INFO:

The MEG & PLS Pipeline ([MEG]PLS) is software for MEG data analysis and PLS statistics.

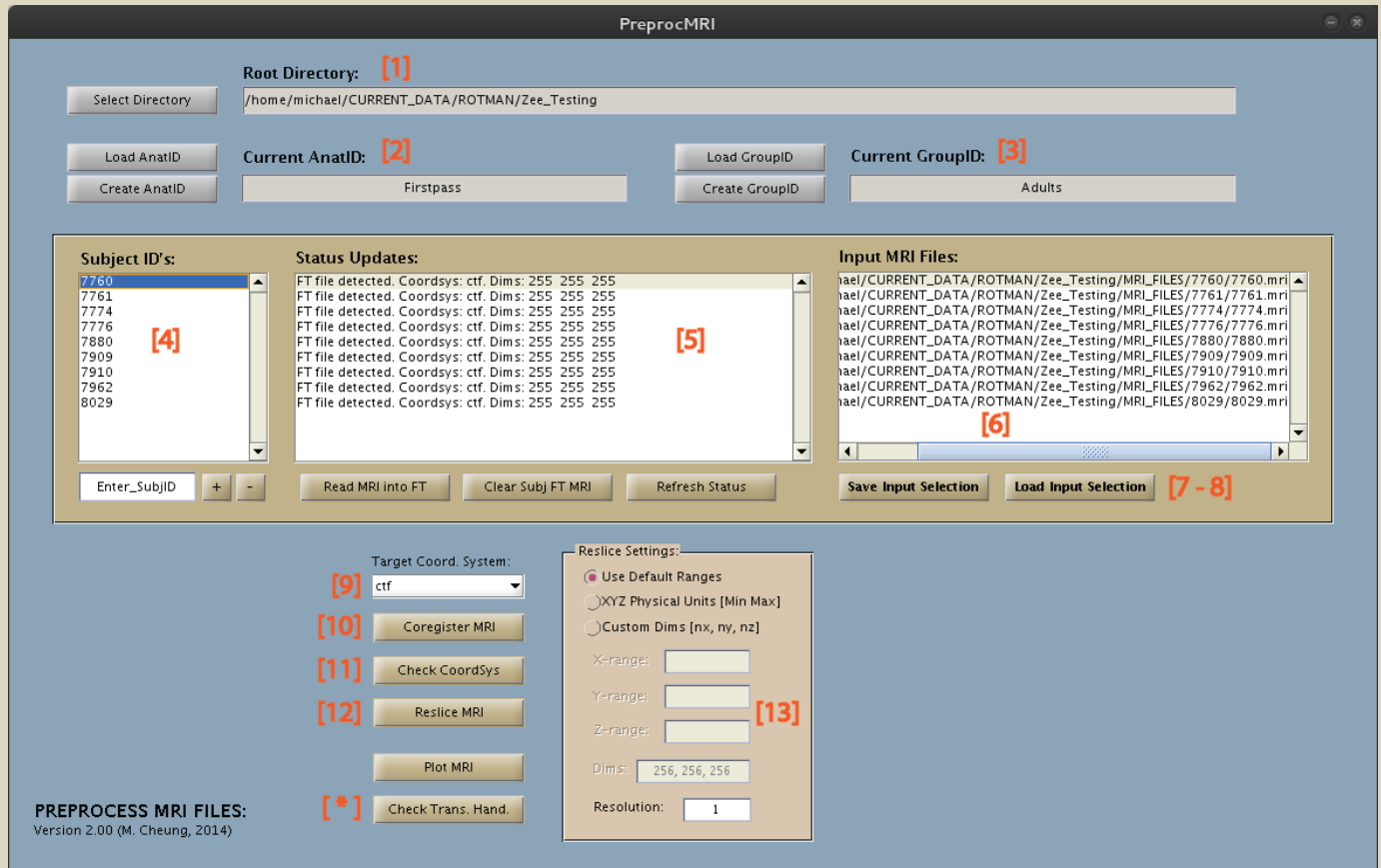
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Baycrest Centre for Geriatric Care ("Baycrest")

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The MEG & PLS Pipeline depends on other toolboxes and functions to do much of the actual data analysis. For convenience, the release includes some functions from these toolboxes that are **not** under the [MEG]PLS license, but remain under their respective licenses and are copyrighted by their respective authors. For more information, see the license files or individual functions. Unauthorised copying and distribution of functions that are not explicitly covered by the GPL is not allowed!

A1. MRI PREPROCESSING GUI:



WHAT DOES THE MRI PREPROCESSOR DO?

- Reads input MRI data into the pipeline (whether it be raw or ".mri" files).
- Performs coregistration and reslicing on the MRI data.

OVERVIEW OF MRI PREPROCESSING (Detailed steps below):

1. Specify Group-ID's and Subject-ID's.
2. Select input MRI files for each subject.
3. Coregister MRI files and check coregistration.
4. Reslice coregistered MRI files.

INPUT & OUTPUT STRUCTURE:

- ❖ Input MRI files are read into the pipeline via the FieldTrip "ft_read_mri" function. For a list of supported MRI formats, see: "help ft_read_mri".
- ❖ Output preprocessed MRI files are saved as **FieldTrip .mat files** in:
`../RootDirectory / AnatID_YourAnatID / GroupID_YourGroupID / SubjectID_PreprocMRI.mat`

A2. SELECTING INPUT MRI FILES:

[1] Root Directory:

Directory that the [Current Anatomy-ID](#) folder (and preprocessed files) will be placed in (see below).

Note: The [same](#) root directory should also be selected for [Data-ID & Analysis-ID](#) folders later on.

[2] Current Anatomy ID:

Each session or stream of MRI preprocessing is organized under a different [Anatomy-ID folder](#).

This allows you to separate and keep track of different sets of preprocessed MRI data.

Preprocessed MRI files will be output into this folder.

[3] Current Group ID:

Name-ID for the current group of subjects being preprocessed.

Ex: You may have an "Adult" group and a "Child" group.

[4] Subject ID's:

Name-ID's for each subject being preprocessed.

[5] Status Updates:

Displays status updates and instructions for each subject.

Info displayed includes: [Input file status](#), [coordinate system](#), and [volume dimensions](#).

[6] Input MRI Files:

Displays the input MRI file loaded in for each subject.

[7] Save Input Selection:

Saves input parameters for the current [AnatID](#) and [GroupID](#) being preprocessed.

Subject ID's and selected input MRI files will be saved into a [.mat](#) (inside the [AnatID](#) folder).

[8] Load Input Selection:

Imports Subject ID's and respective input MRI files from a selected ["PreprocInputMRI"](#) [.mat](#) file.

PREPARING MRI FILES FOR THE PIPELINE:

❖ Loose MRI files (i.e. DICOM or IMA) should be stored in folders organized by Subject-ID's. Otherwise, MRI files should contain the [Subject-ID](#) somewhere in the filename.

❖ Files should be organized and named in a consistent manner.
Recommended organization for easy selection: [Subjects within Groups](#).

If MRI files are in a raw "loose" format such as DICOM or IMA:

Ex: `../DataFolder/GroupID/SubjectID/Loose.DICOM or .IMA files`

If MRI files are already converted to ".mri" format:

Ex: `../DataFolder/GroupID/SubjectID.mri`

READING MRI DATA INTO FT:

1. Select your desired [Root Directory](#) folder, where output will be placed.
 2. Create or load an [Anatomy-ID](#).
 3. Create or load a [Group-ID](#).
 4. Add [Subject-ID's](#) by entering their ID's into the textbox and pushing the "+" button.
 5. To add an MRI file for a subject, select it from the list and click "[Read MRI into FT](#)".
 6. Repeat [Step 5](#) to load input MRI files into the pipeline for each subject.
 7. Once finished, click the "[Save Input Selection](#)" button to save the current input parameters.
- ❖ **Note:** For loose files such as DICOM or IMA, select the first image and the rest will be added. The folder will be scanned for other loose image files, which will be compiled for the subject.
- ❖ **Important:** If you wish to start over for a given subject, click the "[Clear Subj FT MRI](#)" button. Otherwise, remnants from previous preprocessing steps will remain.

IMPORTING INPUT PARAMETERS:

1. Click the "[Load Input Selection](#)" button.
2. Navigate to the folder of the [Anatomy-ID](#) you wish to load from.
3. Select the "[PreprocInputMRI](#)" .mat file within.

A3. MRI COREGISTRATION:

[9] Target Coordinate System:

Coordinate system that you wish to coregister your MRI images to (Set to CTF by default).

[10] Coregister MRI:

Runs the FieldTrip coregistration function for the currently selected subject file.

[11] Check Coordinate System:

Opens a display that allows users to check the coordinate system for the selected subject file.

[*] Check Trans. Handedness:

Checks whether the [transformation-matrix](#) is [left / right-handed](#) for the selected file (see below).

WHAT DOES COREGISTRATION DO?

- Coregistration aligns the anatomical MRI image to the coordinate system of the MEG data.
- This is normally done by specifying the location of external fiducials or anatomical landmarks.

COREGISTRATION INSTRUCTIONS:

1. Click the "Coregister MRI" button to open coregistration window (calls "ft_volumerealign").
 2. For CTF, use "L", "R", and "N" keys to place left, right, and nasion fiducials, respectively.
Note: Push "F" if you do not see the fiducials showing up as circles as you place them.
 3. Use the "Z" key to place a marker on any **positive Z-coordinate** (usually near the top of head).
 4. Press "Q" to save your coregistration and exit.
 5. Check your coregistration (see below).
- ❖ **Important:** To manually determine what is **left or right** in the coregistration window, see below. If you are not sure, you may also rely on the **additional Z-point** (see below for placement).
 - ❖ **Note:** The above steps assume we are coregistering to CTF datasets. For Neuromag and other formats that require it, landmarks can be specified using the "A", "P", and "Z" keys.
 - ❖ Each time you click and change the crosshair location in the coregistration GUI, the MATLAB command window will display the current location in **[X, Y, Z] physical units** (usually "mm").

Why are my images oriented oddly in the coregistration window?

- By default, FieldTrip functions will plot data without applying the transformation matrix. Therefore, orientation of the plotted image will depend on the coordinate system of the MRI. Once the image has been coregistered and resliced, it will be displayed as expected.

What does the additional Z-point during coregistration do?

- FieldTrip will use the **additional Z-point** along with the header information in the MRI to detect if the left & right fiducials were placed correctly. If a flip is detected, it will automatically reverse the left and right fiducial labels and display a warning in the MATLAB window.

How do I know where to place the Z-point?

- To determine which direction the positive Z-axis is in, you can use the following methods:
 - A. **Method 1:** Click the "Check Coordsys" button to open up a new GUI window. In the new display, you can see which direction the **+z-axis** is moving towards.
 - B. **Method 2:** Plot the MRI by clicking the "Plot MRI" button. In the new plot, click around and observe the change in **[X, Y, Z] coordinates**.

DETERMINING LEFT & RIGHT MANUALLY:

- ❖ Summarized from the FieldTrip documentation:
http://fieldtrip.fcdonders.nl/faq/what_is_the_plotting_convention_for_anatomical_mris
- ❖ If the **XYZ coordinate system** is **right-handed**, and the **transformation matrix** is also **right-handed**, then **left-is-left and right-is-right** (neurological); see below to check handedness.
- ❖ If the **XYZ coordinate system** is **right-handed**, but the **transformation matrix** is **left-handed**, then **right-is-left and left-is-right** (radiological); see below to check handedness.

CHECKING HANDEDNESS:

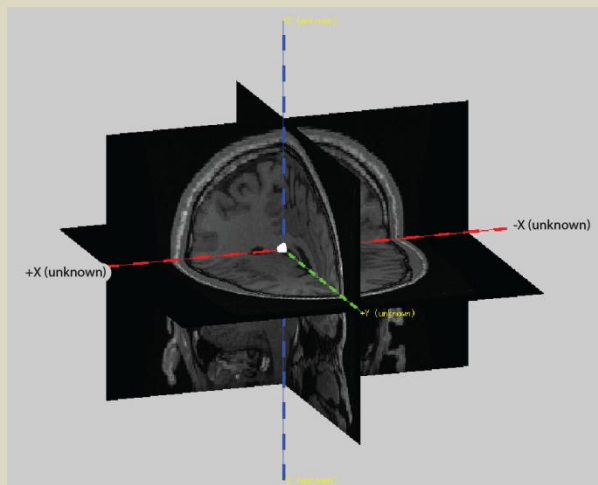
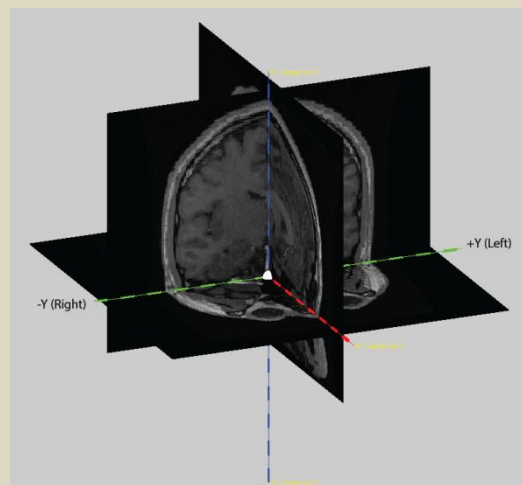
- To check the handedness of the **transformation matrix**:
Simply click the "Check Trans. Hand." button (see [*]).
- To check the handedness of the **XYZ coordinate system**:
 - A. **Method 1:** Click the "Check Coordsys" button (can use even if file not coregistered).
Look at the axis going along the **left / right plane** and see which direction is **positive**.
If the positive direction of the axis is going towards right, than it is right-handed.
 - B. **Method 2:** Alternatively, you can plot the MRI by clicking the "Plot MRI" button.
In the new plot, click around and observe the change in **[X, Y, Z] coordinates**.

Example 1 (see FIGURE A):

1. Click the "Check Trans. Hand" button: We see the transformation-matrix is **right-handed**.
Now we want to check the handedness of the XYZ coordinate system.
2. Click the "Determine Coordsys" button, and look at the **axis along the left / right plane**.
The axis going towards the **left side of the head is +X** (positive direction of the axis).
Therefore, the XYZ coordinate system is **left-handed**.
3. Therefore, the MRI file in the viewer is in **radiological** view.
Left-is-right and right-is-left when looking towards the front of the face.

Example 2 (see FIGURE B): Be careful of odd orientations such as CTF's ALS.

1. For CTF, the **X-axis and Y-axis are swapped** (ALS-orientation).
We know that CTF-space is a right-handed coordinate system.
2. Click the "Determine Coordsys" button, and look at the **axis along the left / right plane**.
The axis going towards the **right side of the head is +Y** (positive direction of the axis).
Warning: Don't be fooled by the "Left" label! Focus on the **direction** of the left/right plane.
3. Therefore, the MRI file in the viewer is in **neurological** view.

FIGURE A:**FIGURE B:**

CHECKING YOUR COREGISTRATION:

1. Push the "Check Coordsys" button to open a new GUI window.
2. Ensure that the images are labelled correctly and no odd flipping has occurred.
3. Check the orientation displayed in MATLAB command window (CTF should be ALS-orientation).

Orientation Legend:

- CTF & 4D/BTi: ALS
- Neuromag, NIFTI & Freesurfer: RAS
- Analyze: LAS (by default).

A4. RESLICING MRI FILES:

[12] Reslice MRI:

Runs the FieldTrip reslice function for the currently selected subject file.

[13] Reslice Settings Panel:

Controls the [dimensions and resolution](#) of the reslice operation.

WHY DO WE NEED TO RESLICE?

- After coregistration, we have information on how to align the MRI image into the coordinate space of the MEG data (in the form of a transformation matrix).
- Reslicing applies this transformation matrix to the actual anatomical data of the MRI file.

DEFAULT RESLICE:

1. Select the option for "Use Default Ranges" in the settings panel.
2. Push the "Reslice MRI" button (make sure desired subject is highlighted).
3. **Check the results** in the new plot window that opens.
4. If any of the brain is cut off, click "Revert" and perform a [custom reslice](#) instead (see below).

CUSTOM RESLICE:

1. Select the option to use "XYZ Physical Units" (recommended).
2. Acquire X, Y, and Z-ranges by using the "Plot MRI" function (see below for an easy method).
3. Push the "Reslice MRI" button once desired X, Y, and Z-ranges have been specified.
4. Check the results in the new plot window that opens.
5. If any of the brain is cut off, click "Revert" and adjust the ranges as needed.

Recommended: Use "XYZ Physical Units" instead of "Custom Dims".

- Manually specifying X, Y, and Z-range will give you greater control over how the image is sliced.

Important: Always check your resliced images!

- The entire brain needs to fit inside the image in order for all "inside-brain" [dipoles](#) to be included for the leadfield computation. If any of the brain is missing, adjust the XYZ-ranges.

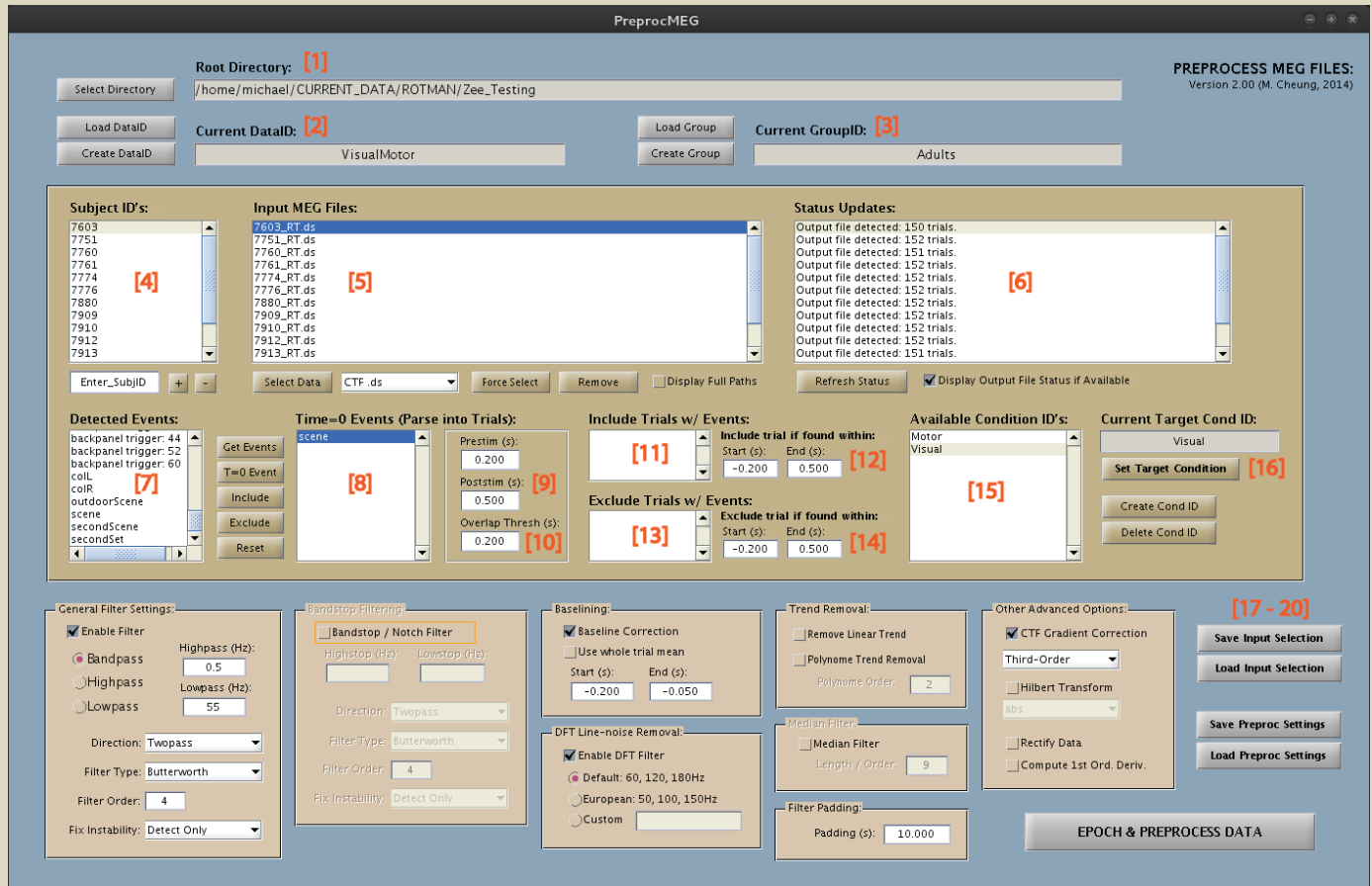
"ONE-SIZE-FITS-MOST" METHOD FOR DEFINING CUSTOM RESLICE RANGE:

1. Click the "Plot MRI" button, and place the crosshair approximately in the center of the brain.
2. Make note of the [X, Y, Z] location coordinates for the crosshair.
3. To get the lower-bounds of the XYZ-ranges, do: [X, Y, Z] - 127
4. To get the upper-bounds of the XYZ-ranges, do: [X, Y, Z] + 127
5. This will result in a [255, 255, 255] box with the brain centered within.

Example:

- a) Say the coordinates of a crosshair placed in the center of the brain is approximately: [0, 0, 40].
- b) Using the method above: X-range = [-127, 127], Y-range = [-127, 127], Z-range = [-87, 167].

B1. MEG PREPROCESSING GUI:



WHAT DOES THE MEG PREPROCESSOR DO?

- Read input MEG data into the pipeline (continuous or epoched).
- Epoch & preprocess MEG data: Filtering, baselining, detrending, etc.

OVERVIEW OF MEG PREPROCESSING (Detailed steps below):

1. Specify Group-ID's and Subject-ID's.
2. Select input MEG data files for each subject, and specify Target Condition-ID.
3. Configure event & preprocessing parameters (see below if data has already been epoched).
4. Preprocess and read data into [MEG]PLS. Repeat Steps 2-5 for other Condition-ID's.

INPUT & OUTPUT STRUCTURE:

- ❖ Input MEG files are read by FieldTrip into the pipeline via the "`ft_preprocessing`" function. For a list of supported MEG data formats, see: "`help ft_read_header`".
- ❖ Output preprocessed MEG files are saved as **FieldTrip .mat files** in:
`../RootDir/DataID_YourID/GroupID_YourID/TargetConditionID/SubjectID_PreprocMEG.mat`

B2. SELECTING INPUT MEG FILES:

[1] Root Directory:

Directory that the [Current Data-ID](#) folder (and preprocessed MEG files) will be placed in (see below).

Note: The [same](#) root directory should also be selected for [Anat-ID & Analysis-ID](#) folders.

[2] Current Data ID:

❖ Each session or stream of MEG preprocessing is organized under a different [Data-ID folder](#). This allows you to separate and keep track of different sets of preprocessed MEG data. Preprocessed MEG files will be output into this folder.

❖ **Note:** Within a given Data-ID, all preprocessing settings will be [locked](#) after configuration to prevent improper mixing of different preprocessing settings within a given analysis.

❖ **Important:** If your MEG sessions were run across multiple blocks, each block should be organized under a separate Data-ID. Each block will be run independently (due to differing gradiometer info), and then averaged after source analysis & normalisation (see [Section F2](#)).

[3] Current Group ID:

Name-ID for the current group of subjects being preprocessed.

Ex: You may have an "Adult" group and a "Child" group.

[4] Subject ID's:

Name-ID's for each subject being preprocessed.

[5] Input MEG Files:

Displays the input MEG files loaded in for each subject.

[6] Status Updates:

Displays status updates and instructions for each subject.

Info displayed includes: [Input file status](#), [header & event info](#), and [# of trials detected](#).

PREPARING MEG FILES FOR THE PIPELINE:

❖ Each input MEG file **must** contain its [Subject-ID](#) somewhere in the filename. The Subject-ID should be separated from the rest of the filename by [underscores](#). Files should be organized and named using a consistent system.

❖ For raw data, recommended organization for easy selection: [Subjects within Groups](#).
Ex: `../DataFolder / GroupID / SubjectID_name.ds`

For epoched data, recommended organization is: [Subjects within Conditions within Groups](#).
Ex: `../DataFolder / GroupID / ConditionID / SubjectID_name.ds`

What if I already have NIFTI or AFNI files and only want to run PLS?

- Skip this MEG preprocessing section and follow the instructions in [Section D4](#) below.

SELECTING INPUT MEG DATA:

1. Select the [Root Directory](#) for output (*Should be the same one chosen in MRI preprocessing*).
2. Create or load a [Data-ID](#).
3. Create or load a [Group-ID](#).
4. Add [Subject-ID's](#) by entering their ID's into the textbox and pushing the "+" button.
5. In the dropdown box, select the [file-type](#) of the MEG data you wish to load.
6. Click the ["Select Data"](#) button to open up an interface for file selection.
7. Select input MEG datasets in left panel for each subject and click add.

- ❖ **Note:** Selected datasets will **automatically be paired** to their respective Subject-ID's.
The name of each selected dataset will be scanned and matched to its respective Subject ID.

What if some MEG datasets failed to be paired?

- Check dataset name: Subject-ID should be separated from the rest of the name by underscores.
- Make sure you are not trying to add multiple datasets sharing the *same* Subject-ID.

Manually adding a dataset for a subject:

1. Select the desired [Subject-ID](#) in the listbox and push the ["Force Select"](#) button.
2. In the new window, specify the dataset you wish to manually add for the selected subject.

B3. EPOCHING & PREPROCESSING:

[7] Detected Events:

Displays all available events and triggers detected within the selected MEG datasets.

[8] Target Time = 0 Events:

Events to epoch the data by (data will be epoched with these events as time = 0).

[9] Pre-stimulus and Post-stimulus Time:

Amount of pre-stimulus and post-stimulus time relative to the selected T=0 events.

[10] Overlap Threshold:

Amount of time (in seconds) permitted for parsed trials to overlap. If the overlap threshold is exceeded, both overlapping trials will be excluded.

[11] Included Events:

After the data is parsed into trials, each trial can be searched for ["Included Events"](#).
If **any** "Included Event" is found [within the specified search-time](#) (see below), the trial will be **kept**.
This allows for more complex trial definitions (see example section below).

[12] Search Time-Range for Included Events:

Time (relative to T=0 events) that parsed trials will be searched for ["Included Events"](#).

[13] Excluded Events:

After the data is parsed into trials, each trial can be searched for "Excluded Events". If **any** "Excluded Event" is found **within the specified search-time**, the trial will be **removed**. This allows for more complex trial definitions (see example section below).
Note: The search for "Excluded Events" takes place after the search for "Included Events".

[14] Search Time-Range for Excluded Events::

Time (relative to T=0 events) that parsed trials will be searched for "Excluded Events".

[15] Available Condition ID's:

List of [Condition-ID folders](#) available for selection.
Note: Use the "Create Cond-ID" button to create a new Condition-ID.

[16] Current Target Condition ID:

Target Condition-ID that the current input MEG data will be epoched & preprocessed as. All the current event settings & preprocessing parameters will be applied as this Condition-ID.

[17] Save Input Selection:

Saves input and epoch parameters for the current [Data-ID](#), [Group-ID](#), and [Target Condition-ID](#). Input parameters will be saved into a "PreprocInputMEG" .mat file (within the Data-ID folder).

[18] Load Input Selection:

Imports input and epoch parameters from a selected "PreprocInputMEG" .mat file.

[19] Save Preprocessing Settings:

Saves preprocessing settings and **locks** them for the current [Data-ID](#). The settings will be saved into a "PreprocSettings" .mat file (within the Data-ID folder).

[20] Load Preprocessing Settings:

Imports preprocessing settings from a selected "PreprocSettings" .mat file.

HOW EPOCHING IN [MEG]PLS WORKS:

1. First, the dataset is parsed into trials based on the specified [T=0 Event\(s\)](#). Trial length is based on the amount of pre-stimulus and post-stimulus time specified.
2. Next, each trial is checked for [overlap](#) with other trials. If any overlap exceeds the specified threshold, both overlapping trials are rejected.
3. If specified, the remaining trials are searched for "Included Events". Any trial that contains [one or more](#) of these events within the specified search time will be **kept**.
4. Finally, the remaining trials are searched for "Excluded Events". Any trial that contains [one or more](#) of these events within the specified search time will be **rejected**.

NOTE: [MEG]PLS can also read data that has already been epoched.

- If your data has already been epoched, see [Subsection 2](#) below.

SUBSECTION 1: READING IN CONTINUOUS DATA:

1. Select the input datasets you wish to epoch & preprocess (see [Section B2](#)).
2. Set the [Target Condition-ID](#) that you wish to epoch and preprocess for:
Select the desired Condition-ID from the listbox and click "[Set Target CondID](#)".
If the Condition-ID does not exist, create it by pushing the "[Create Cond ID](#)" button.
3. Detect events and triggers available for selection by clicking the "[Get Events](#)" button.
Select [Target T=0 Event\(s\)](#) for epoching: Highlight desired events and click "[T=0 Event](#)".
4. Specify the amount of [pre-stimulus](#) and [post-stimulus](#) time (relative to the T=0 events).
If desired, change the [threshold](#) of time trials are allowed to overlap.
5. If desired, specify "[Included Events](#)": Highlight desired event(s) and click the "[Include](#)" button.
Set the [time-range](#) (relative to T=0 events) to search for the included events.
6. If desired, specify "[Excluded Events](#)": Highlight desired event(s) and click the "[Exclude](#)" button.
Set the [time-range](#) (relative to T=0 events) to search for excluded events.
7. If you have not done so yet, configure and save your desired [preprocessing settings](#) (see below).
Once ready, push the "[Epoch and Preprocess Data](#)" button to begin.
8. **Repeat Steps 1-7** as needed for each Condition-ID you wish to load into the pipeline.

SUBSECTION 2: READING IN EPOCHED DATA:

1. Create your [Data-ID](#) and specify the [Group-ID](#).
2. If you have not done so, configure and save [preprocessing settings](#) for the Data-ID.
3. Add and set the [Target Condition-ID](#) that the data will be read into the pipeline as.
4. Select the epoched MEG datasets you wish to read in (see [Section B2](#)).
5. Specify your pre-stimulus and post-stimulus time, and overlap threshold.
6. If desired, specify events to include and/or exclude.
7. Push the "[Epoch & Preprocess Data](#)" button to read datasets in.
8. **Repeat Steps 3-7** for each [Condition-ID](#) you wish to load into the pipeline.

MULTI-STAGE EPOCHING:

- [MEG]PLS also allows users to epoch the data [sequentially](#) in [multiple steps](#).
Useful for more complex trial definitions, where you [successively isolate](#) for trials of interest.
1. Follow the steps in [Subsection 1](#) above for the initial epoching & preprocessing of the data.
 2. Next, create a **new Data-ID** for the next stage.
 3. In the dropdown-box next to the "Select Data" button, change it to: "[FieldTrip .mat](#)".
 4. Select the [PreprocMEG .mat](#) files from the Data-ID folder you created in [Step 1](#).
 5. Follow the instructions again in [Subsection 1](#), but this time, do **NOT** select for T=0 events.
We've already epoched the data into trials, we just need to include / exclude desired trials now.
 6. **Repeat Steps 2-5** until datasets only contain trials of interest.

EXAMPLE TRIAL DEFINITIONS:

❖ **Sample Situation:**

Let's say our data contains the following events: **Stim**, **CorrectL**, **CorrectR**, **IncorrectL**, **IncorrectR**. Following each **Stim** event is a **left and right response** (each of which can be correct or incorrect).

Example 1: Epoch data using "Stim" (T=0 event), but only keep trials containing "**CorrectL**".

1. Select and add "Stim" as the T=0 event.
2. Select and add "CorrectL" as an included event.

Example 2: Same as Example 1, but only keep trials containing **both** "**CorrectL**" and "**CorrectR**".

1. Select and add "Stim" as the T=0 event.
2. Select and add "CorrectL" and "CorrectR" as included events.
Any trial that contains "CorrectL" **and/or** "CorrectR" will be kept.
3. Select and add "IncorrectL" and "IncorrectR" as excluded events.
This will ensure only trials with **both** "CorrectL" and "CorrectR" are kept.
Trials that contain one but not the other will be excluded.

Example 3: Same as Example 2, but done using **multi-stage epoching**.

1. In the first stage, add "Stim" as the T=0 event, and "CorrectL" as an included event.
This will epoch the data and keep any trial that contains "CorrectL".
2. In the second stage of epoching, select "CorrectR" as an included event.
This will further isolate for any "CorrectL" trial that also contains "CorrectR".

PREPROCESSING SETTINGS:

- ❖ These GUI panels contain all available options for the FieldTrip "**ft_preprocessing**" function. For more details on each setting, see the function help info: "**help ft_preprocessing**". Once you are finished configuring the settings, click the "**Save Preproc Settings**" button.
- ❖ **WARNING:** Saving will **lock** all preprocessing settings in for the current Data-ID. This prevents improper mixing of settings within a given stream of analysis. If you wish to preprocess the data differently afterwards, you will need to create a new Data-ID.
- ❖ **Note:** The defaults set in the **preprocessing settings** panels are commonly-used parameters. If you are unsure of what settings to use, the default settings are a safe choice.

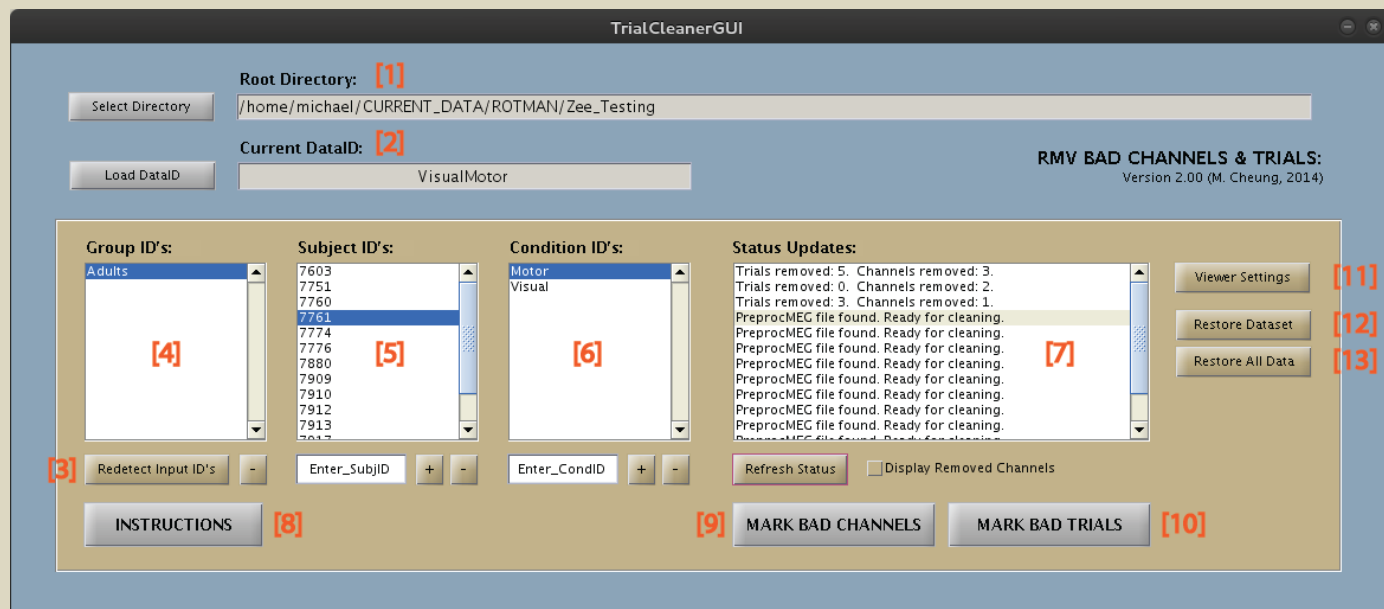
IMPORTANT: Demeaning vs. Detrending

- For ERP analysis, you generally want to demean using a baseline, and avoid detrending. See thread: <http://mailman.science.ru.nl/pipermail/fieldtrip/2013-January/006037.html>

LOADING OR IMPORTING SETTINGS:

1. Click "**Load Input Selection**" or "**Load Preproc Settings**" depending on what you want to load.
2. Navigate to the folder of the **Data-ID** you wish to load input parameters or settings from.
3. Select the appropriate **.mat** file within.

C1. REMOVING BAD CHANNELS & TRIALS (OPTIONAL):



WHAT DOES THE TRIAL & CHANNEL REMOVER DO?

- This GUI module allows users to manually identify and remove bad channels and/or trials.

INPUT & OUTPUT STRUCTURE:

- ❖ Upon loading a Data-ID, input files from MEG preprocessing will automatically be detected . All "PreprocInputMEG" .mat files within the loaded Data-ID will be scanned to acquire datasets.
- ❖ Preprocessed MEG files from the MEG preprocessing module will be overwritten.
Note: Backups of the original files will automatically be created allowing users to easily restore.

[1] Root Directory:

Directory that your Data-ID folder (and preprocessed MEG files) have been placed in.

[2] Current Data ID:

This is the Data-ID currently loaded for bad channel & trial removal.

Upon loading a Data-ID, all "PreprocInputMEG" .mat files within will be scanned to acquire datasets. Group, Subject and Condition-ID's found in these .mat files will automatically be added into the GUI.

[3] Redetect Input ID's:

Rescans "PreprocInputMEG" .mat files within the current Data-ID for Group, Subj and Cond ID's.

[4] Group ID's:

Name-ID's for each of your groups being analyzed.

Note: The GUI will display subjects and statuses for the currently selected Group & Condition-ID.

[5] Subject ID's:

Name-ID's of each subject for the currently selected Group-ID.

[6] Condition ID's:

Name-ID's for conditions within the current Data-ID.

[7] Status Updates:

Displays status updates and instructions for each dataset.

Info displayed includes: [File status](#), [trials removed](#), and [channels removed](#).

[8] Instructions:

Opens up a new window with instructions on how to use the ICA cleaner.

[9] Mark Bad Channels:

Opens a channel viewer for the selected dataset (to adjust the viewer settings, see below).

Displays the data for each channel (all trials at once).

[10] Mark Bad Trials:

Opens a trial viewer for the selected dataset (to adjust the viewer settings, see below).

Displays the data for each trial (all channels at once).

[11] Viewer Settings:

Opens a MATLAB .m file containing all available settings for the "[ft_rejectvisual](#)" viewer function.

Simply edit or add desired settings and save the file to apply these settings to the viewer.

Warning: Do **NOT** edit sections marked with "[DO NOT EDIT](#)". These are handled by the GUI.

[12] Restore Dataset:

Undo trial and channel removal for the selected dataset (restores the original backup file).

[13] Restore All Data:

Undo trial and channel removal for all current datasets (restores all original backup files).

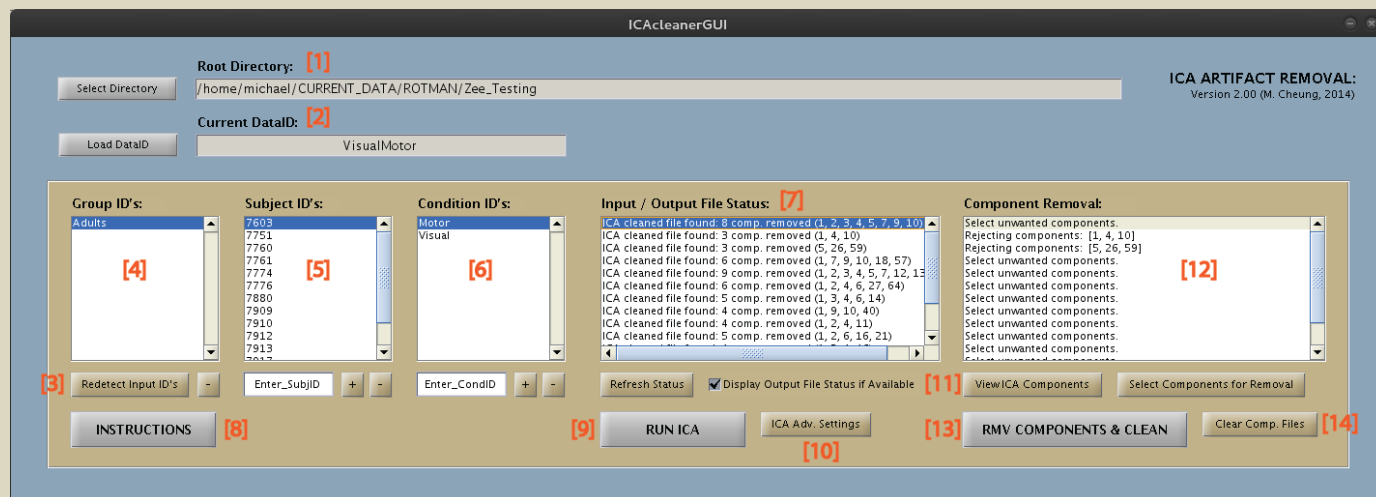
REMOVING BAD CHANNELS & TRIALS:

1. Select the [Root Directory](#) containing your Data-ID.
2. Load the [Data-ID](#) to clean (Group, Subject and Condition-ID's will automatically be added).
3. Add or remove Group, Subject and Condition-ID datasets as desired.
4. Select a dataset and click "[Mark Bad Channels](#)" to view and remove channels.
5. Select a dataset and click "[Mark Bad Trials](#)" to view and remove trials.
6. [Repeat Steps 4-5](#) for each Group, Subject and Condition-ID dataset of interest.

Note: If you wish to undo the removal, use the "[Restore](#)" buttons.

- For more information, push the "[Instructions](#)" button in the GUI panel.

C2. ICA ARTIFACT REMOVAL (OPTIONAL):



WHAT DOES THE ICA CLEANER DO?

- This GUI module allows users to utilize ICA for artifact identification and removal.
- Runs ICA decomposition on preprocessed MEG data from the MEG Preprocessor.
- Allows users to visually inspect and select unwanted components.
- Removes unwanted components and reconstructs the data.

INPUT & OUTPUT STRUCTURE:

- ❖ Upon loading a Data-ID, input files from MEG preprocessing will automatically be detected . All "PreprocInputMEG" .mat files within the loaded Data-ID will be scanned to acquire datasets.
- ❖ Output ICA-cleaned MEG files will be saved in a new "DataID-ICAclean" folder:
`../ RootDir / DataID-ICAclean_YourID / GroupID_YourID / TargetConditionID / SubjectID_PreprocMEG.mat`

[1] Root Directory:

Directory that your Data-ID folder (and preprocessed MEG files) have been placed in.

[2] Current Data ID:

This is the Data-ID currently loaded for bad channel & trial removal.

Upon loading a Data-ID, all "PreprocInputMEG" .mat files within will be scanned to acquire datasets. Group, Subject and Condition-ID's found in these .mat files will automatically be added into the GUI.

[3] Redetect Input ID's:

Rescans "PreprocInputMEG" .mat files within the current Data-ID for Group, Subj and Cond ID's.

[4] Group ID's:

Name-ID's for each of your groups being analyzed.

Note: The GUI will display subjects and statuses for the currently selected Group & Condition-ID.

[5] Subject ID's:

Name-ID's of each subject for the currently selected Group-ID.

[6] Condition ID's:

Name-ID's for conditions within the current Data-ID.

[7] Input / Output File Status:

Displays status updates and instructions for each dataset.

Info displayed includes: [File status](#), [ICA status](#), and [components removed](#).

[8] Instructions:

Opens up a new window with instructions on how to use the ICA cleaner.

[9] Run ICA:

Runs ICA decomposition for **all** Group, Subject and Condition-ID datasets currently loaded.

Desired changes to any ICA settings should be made prior to pushing this (see below).

[10] ICA Settings Button:

Opens a MATLAB .m file containing all available settings for the ["ft_componentanalysis"](#) function.

Simply edit or add desired settings and save the file to apply these settings to ICA runs.

Warning: Do **NOT** edit sections marked with ["DO NOT EDIT"](#). These are handled by the GUI.

[11] View Components:

Opens up an ICA component viewer for the dataset currently selected in the listboxes.

See the "Instructions" panel for information on how to use the component viewer.

[12] Component Removal List:

Displays the components selected for removal for each dataset.

Click the ["Select Components for Removal"](#) button to select unwanted components.

[13] Remove Components & Clean:

Removes the components selected in the ["Component Removal"](#) list and reconstructs the data.

Output files are stored as ["PreprocMEG"](#) .mat files in a new ["DataID-ICAclean"](#) folder.

[14] Clear Component Files:

Can be used to remove component files from the ICA decomposition step after cleaning is finished.

Note: [ICA unmixing information](#) will be kept, allowing these files to be recreated quickly if needed.

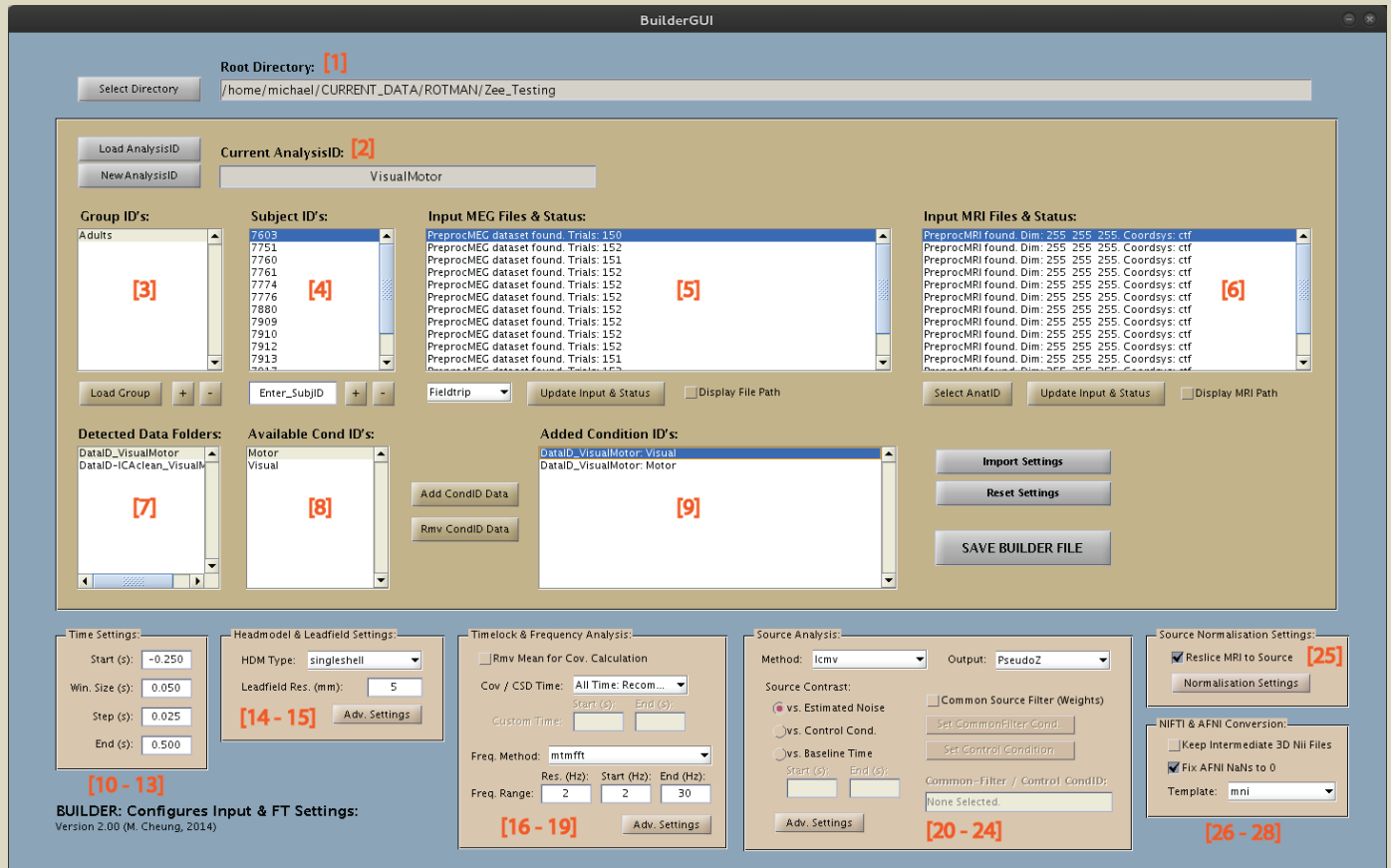
RUNNING ICA FOR ARTIFACT REMOVAL:

- **IMPORTANT:** The cleaner the data, the better the ICA decomposition will be. If the data contains a lot of correlated noise, components may not separate "cleanly". It is recommended that you remove bad trials & channels containing [extreme system or muscle-artifacts](#) **prior** to ICA.
 1. Select the [Root Directory](#) containing your Data-ID.
 2. Load the [Data-ID](#) to clean (Group, Subject and Condition-ID's will automatically be added).
 3. Add or remove Group, Subject and Condition-ID datasets as desired.
 4. Push the ["Run ICA"](#) button to begin the ICA decomposition.

5. Select a dataset and click the "View Components" button.
6. Identify unwanted components that contain obvious artifacts.
7. Click "Select Components" and highlight the unwanted components.
8. **Repeat Steps 5-7** for each Group, Subject and Condition-ID dataset that you wish to clean.
9. Once ready, push the "Rmv Components & Clean" button.

Note: For more information, push the "Instructions" button in the GUI panel.

D1. BUILDER GUI



WHAT DOES THE BUILDER MODULE DO?

- Selects preprocessed MRI and MEG datasets for sensor and source analysis.
- Configures all parameters and settings for the source analysis stream (and also sensor analysis).
- Loads all settings into a **Builder .mat file** that is then passed to the Driver.

OVERVIEW OF BUILDER USAGE:

1. Import or manually load Group and Subject-ID's.
2. Specify the **Anat-ID folder** to load input MRI files from.
3. Select and add **Condition-ID's** from **Data-ID folders** of interest.
4. Configure general settings for each analysis section.
5. **Optional:** Configure advanced settings for each analysis section (see below).
6. Push "**Save Builder File**" to finalize input files and parameters for analysis.

INPUT & OUTPUT STRUCTURE:

- ❖ Preprocessed MEG and MRI files created in the previous modules will be selected in the Builder.
Important: **Anat-ID** and **Data-ID folders** must be in the **same** Root Directory for the Builder.

- ❖ The Builder will output a **Builder .mat file**, which is read by the Driver module. This .mat file contains the input files and settings for the sensor and source analysis stream.

D2. LOADING GROUPS & SUBJECTS:

[1] Root Directory:

Directory that the **Current Analysis-ID** folder (and output analysis files) will be placed in (see below).

Note: This folder should also contain your input **Anat-ID** and **Data-ID folders**.

[2] Analysis ID:

- ❖ Each session or stream of analysis is organized under a different **Analysis-ID folder**.

This allows you to separate and keep track of different sets of analyses.

The **Builder .mat file** and **output analysis files** will be placed inside this folder.

- ❖ **Important:** If your MEG sessions were run across **multiple blocks**, each block should be analyzed under a separate **Analysis-ID**. Each block will be run independently (due to differing gradiometer info), and then averaged after source analysis and normalisation (See **Section F2**).

[3] Group ID's:

Name-ID's for each of your groups being analyzed.

Note: The GUI will display subjects and statuses for the currently selected Group & Condition-ID.

[4] Subject ID's:

Name-ID's of each subject for the currently selected Group-ID.

SELECTING GROUP AND SUBJECT-ID'S:

- ❖ Group-ID's and Subject-ID's can be loaded in two ways:
 - a) Import info from **"PreproInput" .mat** files saved during MRI & MEG preprocessing.
 - b) Manually specify Group ID's and Subject ID's from scratch.

Note: A combination of both methods may be used.

A. To **import** Group-ID's and their respective Subject-ID's:

1. Push the **"Load Group"** button below the Group-ID list.
2. Navigate to the **Data-ID** or **Anat-ID folder** of the data you wish to load.
3. Select a **"PreproInput" .mat** file for the **Group-ID** of interest.
4. **Repeat Steps 1-3** until all groups and subjects are loaded.

B. To **manually specify** Group-ID's and Subject-ID's:

1. To add a Group-ID, push the "+" button underneath the Group-ID list.
2. Select the newly created Group-ID in the list.
3. Add Subject-ID's for the selected group via the textbox and the "+" button for subjects.

D3. SELECTING INPUT MRI & MEG FILES:

[5] Input MEG Files & Status:

Displays [input MEG file or status](#) of each subject for the currently selected [Group & Condition-ID](#). By default, the status will be shown. To view the input file path, check the ["Show Paths"](#) box.

[6] Input MRI Files & Status:

Displays [input MRI file or status](#) of each subject for the currently selected [Group & Condition-ID](#). By default, the status will be shown. To view the input file path, check the ["Show Paths"](#) box.

[7] Detected Data Folders:

Displays [Data-ID](#) or [Analysis-ID folders](#) detected within the current Root Directory. The folder selected in this list will be scanned for [Condition-ID's](#) available for selection. These will then be displayed in the ["Available Condition IDs"](#) list.

[8] Available Condition ID's:

Displays [Condition-ID's](#) for selection within the Data-ID or Analysis-ID folder selected above.

[9] Added Condition ID's:

Displays the [Condition-ID's](#) that have been selected for analysis.

Note: The GUI will display subjects and statuses for the currently selected [Group & Condition-ID](#).

SELECTING INPUT MRI FILES:

1. Click ["Select AnatID"](#) to open a list [Anat-ID folders](#) within the current Root Directory.
2. Select the [Anat-ID](#) containing the preprocessed MRI files that you wish to load.
3. MRI files for the current [Group & Subject-ID's](#) will be selected from this Anat-ID folder.
4. Check the [MRI status](#) box to ensure an MRI file has been found for each group and subject.

SELECTING INPUT MEG DATASETS:

1. In the ["Detected Data Folders"](#) listbox, select the folder that contains your target MEG data. The ["Available Cond ID's"](#) list will now display all [Condition-ID's](#) within the selected folder.
2. Add Condition-ID's by selecting them and pushing the ["Add CondID Data"](#) button. Preprocessed MEG files for the added Condition-ID will be loaded for all [Group & Subject-ID's](#).
3. Check the [MEG status](#) box to ensure a MEG file has been found for each group and subject.
Note: Status box changes depending on the currently highlighted [Group & Condition-ID](#).

D4. LOADING CUSTOM NIFTI & AFNI FILES FOR PLS:

IMPORTANT:

- This section is for users who wish to load **custom** NIFTI / AFNI files into the pipeline for PLS.
- This means you are **bypassing** all sections regarding preprocessing and source analysis.

PREPARING CUSTOM NIFTI & AFNI FILES FOR INPUT:

- ❖ Your custom NIFTI & AFNI files **must** be named and organized in a specific way. Otherwise, the Builder will not be able to locate the files when Condition ID's are added.
- ❖ **NIFTI files** must be organized and named as follows:
Template: .. / AnalysisID_YourID / NORM_SOURCE_Nifti4D / GroupID_YourID / ConditionID / SubjID_Nifti4D.nii
Example: .. / AnalysisID_Run1 / NORM_SOURCE_Nifti4D / GroupID_Adults / Task1 / S01_Nifti4D.nii
- ❖ **AFNI files** must be organized and named as follows:
Template: .. / AnalysisID_YourID / NORM_SOURCE_Afni4D / GroupID_YourID / CondID / SubjID_Afni4D+tlrc.BRIK
Example: .. / AnalysisID_Run1 / NORM_SOURCE_Afni4D / GroupID_Adults / Task1 / S01_Afni4D+tlrc.BRIK

LOADING NIFTI & AFNI FILES INTO THE PIPELINE:

1. Change the filetype dropdown box below "Input MEG Files & Status" to **NIFTI or AFNI**. This will update the "**Detected Data Folders**" list to display available **Analysis-ID** folders.
2. Select the **Analysis-ID** folder that contains your input NIFTI / AFNI files. Then select and add your desired **Condition-ID's** like before (see [Section D3](#)).
3. Check the **MEG status** box to ensure a file has been found for each group and subject. If any are missing, ensure your files are named and organized as stated above.

D5. CONFIGURING ANALYSIS SETTINGS:

GENERAL AND ADVANCED SETTINGS:

- ❖ General settings can be found within the immediate GUI panels of the Builder module. These are the settings most **commonly accessed** for analysis (see below for basic descriptions). **Note:** The defaults set in the general GUI panels are commonly-used configurations.
- ❖ For power-users, more options can be accessed through "**Adv. Settings**" buttons (see below). These will open **MATLAB .m files** containing all available settings for each FieldTrip and SPM function called in that section. Settings edited in these files will be loaded into the **Builder .mat** and applied to analyses, allowing users to easily access and apply their desired settings.

CONFIGURING ADVANCED SETTINGS:

1. Click the "Adv. Settings" button belonging to the section you wish to access.
2. Edit or add your desired FieldTrip and/or SPM settings and save the file once finished.
3. Finish configuring the [Builder](#) and click "Save Builder File" to apply all settings.

IMPORTANT: Do not edit or remove sections marked under "DO NOT EDIT".

- These settings are handled by [MEG]PLS, and altering them may result in errors.

NOTE: All [settings .m](#) files are **automatically managed** for each individual [Data-ID](#) or [Analysis-ID](#).

- Therefore, you do not need to worry about making separate copies of these settings files.
Ex: Editing settings for one Analysis-ID will **NOT** affect or change settings in another Analysis-ID.

GENERAL TIME-WINDOW SETTINGS:

[10] **Start:** Start time of the analysis.

[11] **End:** End time of the analysis.

[12] **Window Size:** Size of each time-window in the sliding-window analysis.

[13] **Step Size:** Increment of time that the sliding-window will move up by.

GENERAL HEADMODEL & LEADFIELD SETTINGS:

[14] **Headmodel Type:** Method for headmodel computation (singleshell recommended).

[15] **Leadfield Resolution:** Resolution (in mm) of the leadfield grid.

GENERAL TIMELOCK & FREQUENCY ANALYSIS SETTINGS:

[16] **Remove Mean for Cov.:** Do **NOT** turn this on if you already baselined during MEG preprocessing.

[17] **Cov. / CSD Time:** Time-window of data used for COV / CSD matrix calculation.

[18] **Frequency Method:** Type of frequency or time-frequency analysis (see "[help ft_freqanalysis](#)").

[19] **Frequency Range Settings:** Start (Hz), end (Hz), and resolution (Hz) settings for frequency analysis.

GENERAL SOURCE ANALYSIS SETTINGS:

[20] **Method:** Source-localization method.

- LCMV (vector by default), SAM (scalar), and DICS are commonly used beamformer methods. Non-adaptive methods such as MNE and LORETA are also available.

[21] **Output:** Type of output statistic used for contrasts (see [\[22-24\]](#)).

1. **Pseudo-Z:** Signal over noise ratio (Only available if contrasting against Est. Noise).
2. **Pseudo-T:** (Active Power - Control or Baseline Power) / Projected Noise
3. **Pseudo-F:** (Active Power / Control or Baseline Power)

[22] Contrast vs. Estimated Noise:

- Contrasts source power against estimated noise (results in **Pseudo-Z output**).
- **Common-filter (or common-weights)** can be applied to the conditions being run. Otherwise, weights will be computed separately for each condition.

[23] Contrast vs. Control Condition:

- Contrasts power of the active condition against a control condition (**Pseudo-T/F output**).
- **Common-filter** will automatically be computed across active & control conditions.
Note: Can only be used if active & control datasets share the same gradiometer information.

[24] Contrast vs. Baseline Time:

- Contrasts power from active time against power from a baseline time (**Pseudo-T/F output**).
- **Common filter** will automatically be computed across active & baseline times.

GENERAL NORMALISATION SETTINGS:**[25] Reslice MRI Files to Source Images:**

- Reslices MRI files to the resolution of their respective source images prior to normalisation.
- ***It is highly recommended that you leave this ON.*** If turned off, each source image will be resliced to the resolution and dimensions of its MRI instead. This will greatly increase the amount of time and memory required for normalisation and PLS.

GENERAL NIFTI & AFNI SETTINGS:**[26] Keep Intermediate 3D Nii Files:**

- Retains intermediate 3D-NIFTI files created during the generation of 4D-NIFTI files. In most situations, these files can be removed to save hard drive space.

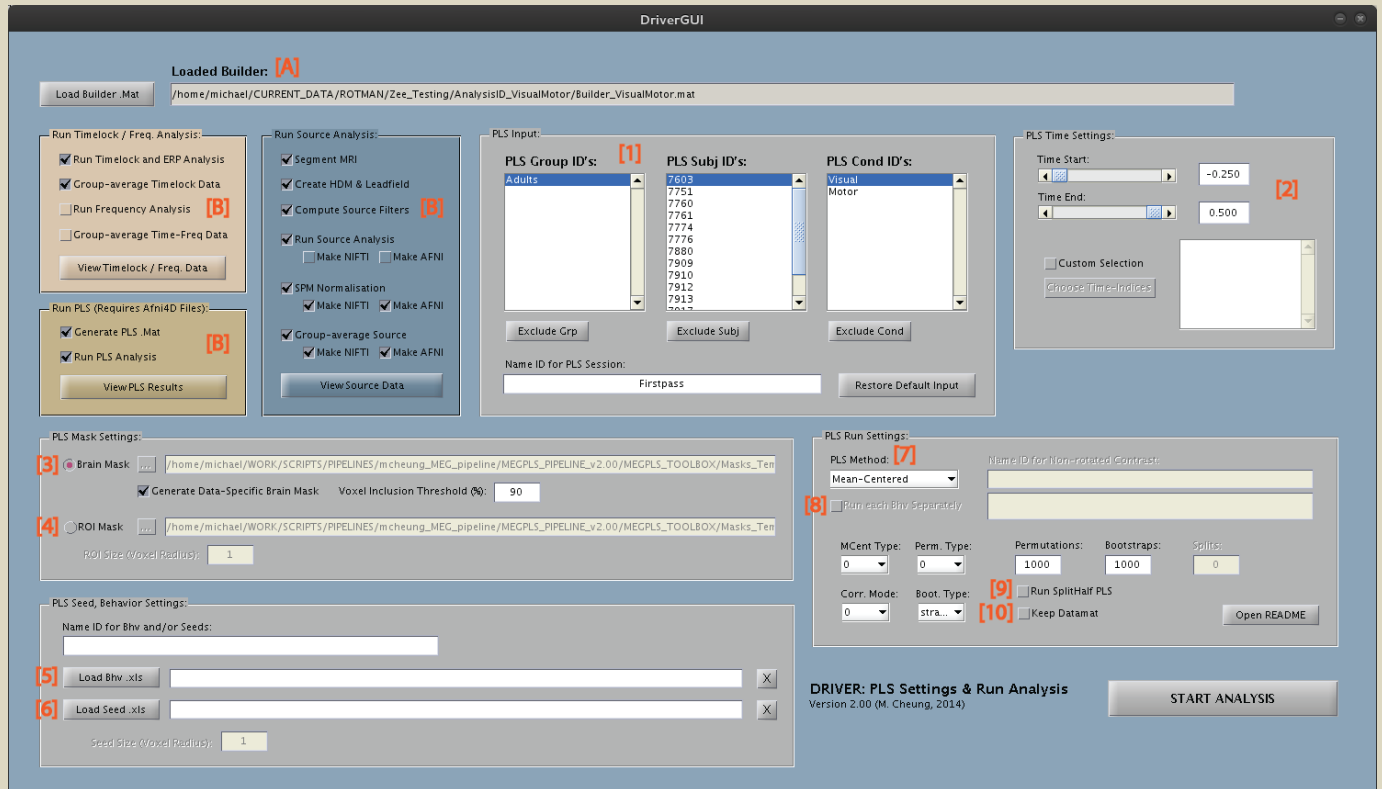
[27] Fix AFNI NaNs to 0:

- Converts NaN values to 0 in AFNI files.
Recommended: Leave this **ON** (required for input into PLS and for AFNI file viewers).

[28] Template:

- Template that source images were normalised to (for AFNI file association).
Recommended: If NIFTI files originate from [MEG]PLS, keep the template set to MNI.

E1. DRIVER GUI



WHAT DOES THE DRIVER MODULE DO?

- The Driver module acts as the **central hub** and initiates different analyses for [MEG]PLS.
- Reads information stored in **Builder .mat** files to initiate **sensor and source analyses**.
- **PLS runs are also configured and run from the Driver.** This allows users to successively run different types of PLS analyses without needing to go back to the Builder.

[A] Load Builder .mat File:

Selects and loads a **Builder .mat** file (input parameters and settings will be read from this file).

[B] Panels for Analysis Selection:

These panels determine which types of analyses are run from the Driver module. Enable / disable the respective checkbox to run that particular analysis.

OVERVIEW OF DRIVER USAGE:

1. Load the **Builder .mat** file output by the Builder module.
2. Activate the checkboxes for the types of analyses you wish to run.

Note: Analyses within each analysis panel will be **run sequentially** from top-to-bottom. For the source analysis stream: Segment MRI -> HDM & Leadfield -> Source Filters, etc.

IMPORTANT: You may start from any stage of an analysis stream so long as the preceding requirements have been computed (Ex: If you have already computed headmodels & leadfields in a previous run, you may proceed directly to source-filter computation and beyond).

3. If running PLS, configure settings and input parameters as needed (see below).
4. Once ready, initiate the analysis by pushing the ["Start Analysis"](#) button.

WARNING: When you [re-run](#) an analysis section, any existing files will be overwritten.

- However, to be safe, it is recommended folders within the Analysis-ID folder are removed first.

IMPORTANT: "ERRORLOG" and "DIARY" FILES.

- ❖ Errors detected during analyses will be written out into ["ErrorLog" files](#). If any errors are detected, these "ErrorLog" files will [automatically open](#) after the analysis. Make sure to **CHECK** these files if they are opened.
- ❖ [Diary files](#) will also be written out during analyses. These files log a history of the MATLAB command window for reference in case of errors.

PARALLEL COMPUTING SUPPORT:

- ❖ [MEG]PLS has been coded to utilize the MATLAB Parallel Computing Toolbox (PCT). Opening a MATLAB worker pool will greatly increase the speed of analyses.
- ❖ If the PCT is available, you will be asked whether you want to open a worker pool.
Important: Once analysis is finished, make sure to close your pool: ["matlabpool close"](#).

LONG-TERM STORAGE OF DATA:

- ❖ Once you are finished with the data analysis, you can save space by removing the certain folders in each [Analysis-ID](#). These folders are not required for further runs of PLS, and [don't need to be kept for long-term storage](#). If needed, they can be easily recreated via the Builder .mat file.

- ❖ **Recommended: Folders you can remove for long-term storage:**

These folders require large amounts of HDD space, and can easily be remade if needed:

[SEG_MRI]	[HDMLEAD_*] folders
[SOURCE_FILTER]	[SOURCE_*] folders
[SOURCE_RASorient_Nifti4D]	[SOURCE_RASorient_Afni4D]
[MRI_RASorient_Nifti]	[MRI_RASorient_Afni]

- ❖ **Recommended: Files & folders to keep for long-term storage.**

[Builder.mat]	[SETTINGS]	[NiftiAfni4D_TimeLegend.txt]
[NORM_MRI]	[NORM_MRI_Afni]	[PLS_*] result folders
[NORM_SOURCE]	[NORM_SOURCE_Afni4D]	

- ❖ **Optional: Not required for further PLS runs, but can be kept if desired.**

[TIMELOCK_*] folders	[FREQ_*] folders
[NORM_MRI_Nifti]	[NORM_SOURCE_Nifti4D]

E2. CONFIGURING PLS SETTINGS:

PLS DATAMAT SETTINGS:

[1] PLS Input Settings:

- Controls the [Group ID's](#), [Subject ID's](#), and [Condition ID's](#) being input for PLS analysis.
- These panels also display the order in which datasets are stacked in the PLS datamat. Data is stacked as: *Subjects within Conditions within Groups*.

[2] PLS Time Settings:

- Controls the [time-window\(s\)](#) of data that will be input into the datamat for PLS analysis.
- Time can be modified by moving the sliders, or by directly editing the textboxes.
- You can also manually select specific time-indices to include by doing the following:
 1. Check the "[Custom Select](#)" checkbox.
 2. Click "[Choose Time-Indices](#)", and select your desired time-windows from the list.

[3] Brain Mask Settings: Mask for whole-brain data prior to PLS.

- a) **Data-Specific Brain Mask:** Generates a brain mask for PLS based on the input datasets. Only voxels shared by a certain % of the input datasets will be included in the mask.
Recommended: If you have more than 8 subjects, keep this on.
- b) **Voxel Inclusion Threshold:** Determines which voxels are kept for [Data-Specific Brain Mask](#). Voxels must be shared by this % of the input datasets to be included in the PLS mask.
Ex: If 90%, for any given voxel, 90% of the input data must share it for it to be included.
- c) **Brain Mask File:** Selects a pre-computed mask file (by default, [T1.nii MNI template](#) is provided). You can change the mask to one of your own choosing as long as it is in AFNI .BRIK format.

[4] ROI Mask Settings: Mask for ROI data prior to PLS.

- a) **ROI Mask File:** Contains ROI-coordinates for generating an ROI mask for PLS.
To view or modify the ROI points being used for the mask, open the following file:
[../ Pipeline_Directory / MEGPLS_TOOLBOX / Masks_Templates / area_coords_RAI.xls](#)

Note: Full brain masks are recommended for most analyses.

ROI masks are normally used if the full datasets are too large to load into a PLS datamat.

- b) **ROI Size:** This controls the size of each ROI by modifying its radius in voxels. By default, voxel radius is set to 1 (meaning each ROI is composed of 9 voxels).

[5] Behavioural .xls File:

- Loads an excel spreadsheet containing your behavioural data for Behavioural PLS.
- To input your own behaviour data, [copy and modify](#) the template below (instructions within):
[../ Pipeline_Directory / MEGPLS_TOOLBOX / Behavior_Templates / Behavior_Data.xls](#)

[6] Seed PLS Settings:

- ❖ Loads an excel spreadsheet containing your seed-regions of interest for Behavioural PLS.
Note: Data for each seed will automatically be extracted and loaded into the BehavMat for PLS.
- ❖ If specifying seeds in **IJK coordinates** (ex: [acquired from the AFNI-viewer](#)), copy and modify:
[../Pipeline_Directory / MEGPLS_TOOLBOX / Behavior_Templates / SeedCoords_IJK.xls](#)
- If specifying seeds in **XYZ coordinates** (ex: [in LPI or RAI-orientation](#)), copy and modify:
[../Pipeline_Directory / MEGPLS_TOOLBOX / Behavior_Templates / SeedCoords_XYZ.xls](#)
- ❖ **Seed Size:** Determines the size of each seed by modifying its radius in voxels.
By default, voxel radius is set to 1 (meaning each seed is composed of 9 voxels).
The data for each seed is acquired by extracting and averaging the voxel data.

PLS RUN SETTINGS:**[7] Method:** Type of PLS being run.

1. **Mean-Centered:** Data-driven PLS where contrasts are derived from the data.
What contrast patterns between groups / tasks account for the most covariance in the data?
2. **Non-Rotated:** Hypothesis-driven PLS where user supplies the contrasts.
Are these contrast patterns significantly expressed within the input data?
3. **Behavioural:** Analyze correlations between behavioural measures and all space-time.
How do different areas in the brain correlate with certain behavioural measures?
How do different areas in the brain correlate with activity in seed regions of interest?
4. **Multi-Block:** Combination of both Mean-Centered and Behavioural PLS.

[8] Run Each Bhv Separately (Behavioural-PLS only):

- ❖ If turned **ON:** Each behavioural measure and/or seed-region will be run independently.
In other words, a separate PLS run will be done for each behaviour and/or seed-region.
- ❖ If turned **OFF:** All behavioural measures and/or seed-regions will be run at once.
Input data will be correlated with all behaviours and seeds simultaneously.

[9] Run Splithalf PLS:

- ❖ **Split-Half PLS** tests the reliability of the brain patterns and the contrasts separately.
How reliable is the contrast pattern given the brain data?
How reliable are the brain patterns given the contrast?
- ❖ Along with the usual **p-value**, Split-Half PLS will also output "**ucorr**" & "**vcorr**" probabilities.
ucorr: Reliability of the brain patterns (Probability of relating brain patterns given the design).
vcorr: Reliability of the design (Probability of relating the design given the brain patterns).

- ❖ For each split, the subject pool will be randomly separated into two halves. The design is projected on each half to test the reliability of the brain patterns. The brain patterns are projected on each half to test the reliability of the design.

WARNING: Split-Half PLS is very computationally heavy.

- As such, test your data with a regular PLS run prior to turning on Split-Half testing! Recommended that you **DO NOT** exceed more than 100 splits and 100 permutations.

[10] Keep Datamat:

If this box is checked, the input PLS datamat will be kept after the PLS run.

Recommended: Keep this **OFF** to save hard drive space.

[11] PLS Settings README button.

Opens a [README documentation](#) with descriptions on various PLS settings.

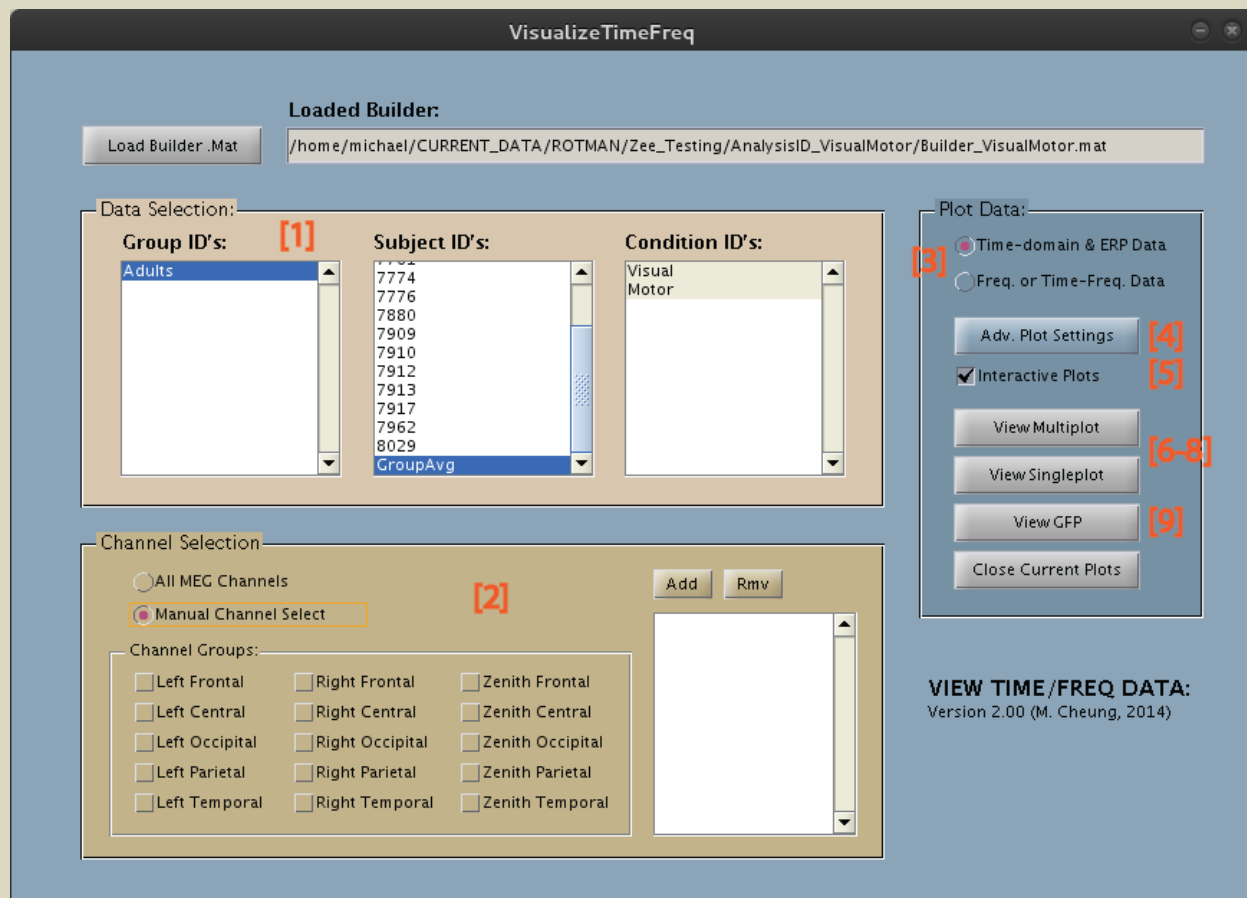
If you are unsure of what a setting does, click this button for more information.

GENERAL FLOW OF PLS ANALYSIS:

- ❖ In most situations, you can start off by running a data-driven **Mean-Centered PLS**. This will output the contrasts between groups / tasks that account for the most covariance.
- ❖ If the LV's from the Mean-Centered PLS are too broad or you don't see a specific contrast pattern that you are interested in, then you can run different types of **Non-Rotated PLS**.

IMPORTANT: For more info on PLS output and [interpretation of results](#), see [Sections W1 & W2](#).

V1. VIEWING SENSOR ANALYSIS RESULTS:



[1] Dataset Selection Panel:

Select the dataset(s) to plot by highlighting desired Group, Subject and Condition datasets to view. Multiple datasets can be selected at once for [time-domain results](#) and ["mtmfft" frequency data](#).

Note: For other frequency analysis methods, only one dataset can be plotted at a time.

[2] Channel Selection Panel:

Selects which channels in the data will be plotted (by default, all available channels are selected).

Note: To manually specify specific channels, use the ["Add"](#) & ["Rmv"](#) buttons in the panel.

[3] Data-Type Selection:

Selects whether you want to view results from time-domain analysis or frequency-domain analysis.

[4] Configuring Advanced Plot Settings:

Opens a .m file containing settings for the ["ft_multiplot"](#) and ["ft_singleplot"](#) viewer functions. Simply edit or add desired settings and save the file to apply these settings to the viewer.

Warning: Do **NOT** edit sections marked with ["DO NOT EDIT"](#). These are handled by the GUI.

[5] Interactive Plots:

Enables [sub-plots](#) to be opened from [multiplots](#), [singleplots](#), and [topoplots](#) (see [\[6-8\]](#)).
Disable this to prevent accidental opening of subplots (ex: If you wish to interact with legends).
Note: It is useful to disable this if you wish to interact with the singleplot legends.

[6] Multiplots (Figure A):

Displays time or frequency data for **all** selected channels in a full layout (see [Figure A](#)).
[Singleplots](#) of desired channels can be opened by drawing selection boxes around the data.

[7] Singleplots (Figure B):

Displays time or frequency data averaged across **specific** selected channels (see [Figure B](#)).
[Topoplots](#) can be opened by drawing a selection box around the desired data.
Note: Data can be hidden / shown by clicking corresponding labels in the legend [\[*\]](#).

[*] Clickable Legends (Figure B):

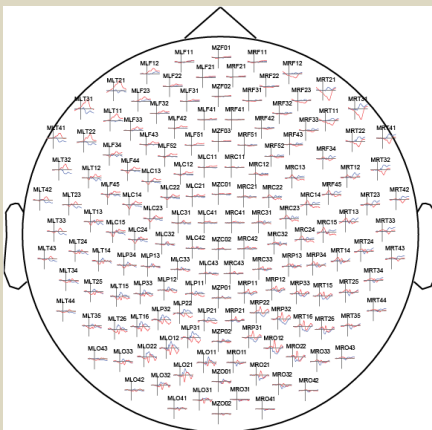
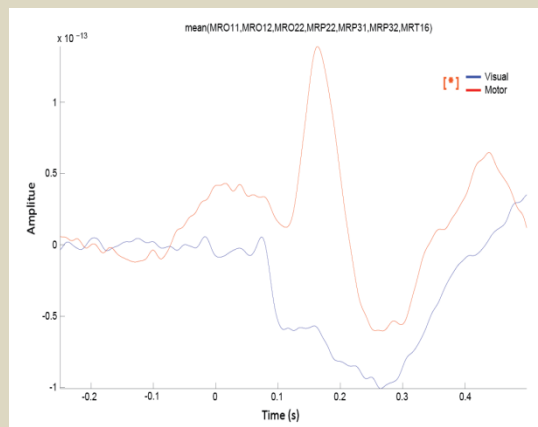
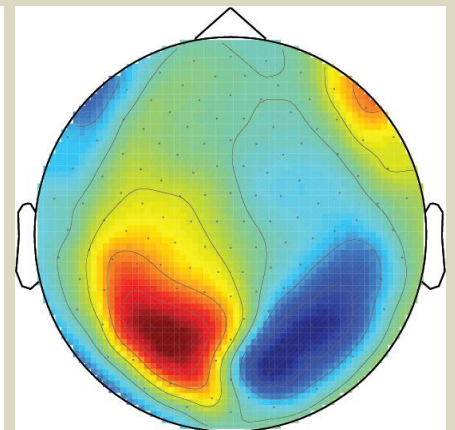
For [singleplots](#), datasets can be shown / hidden by clicking the corresponding labels in the legend.

[8] Topoplots (Figure C):

Displays a topographic view of the data from the selected channels (see [Figure C](#)).
[Singleplots](#) of the channel data can be viewed by drawing a selection box around the desired areas.

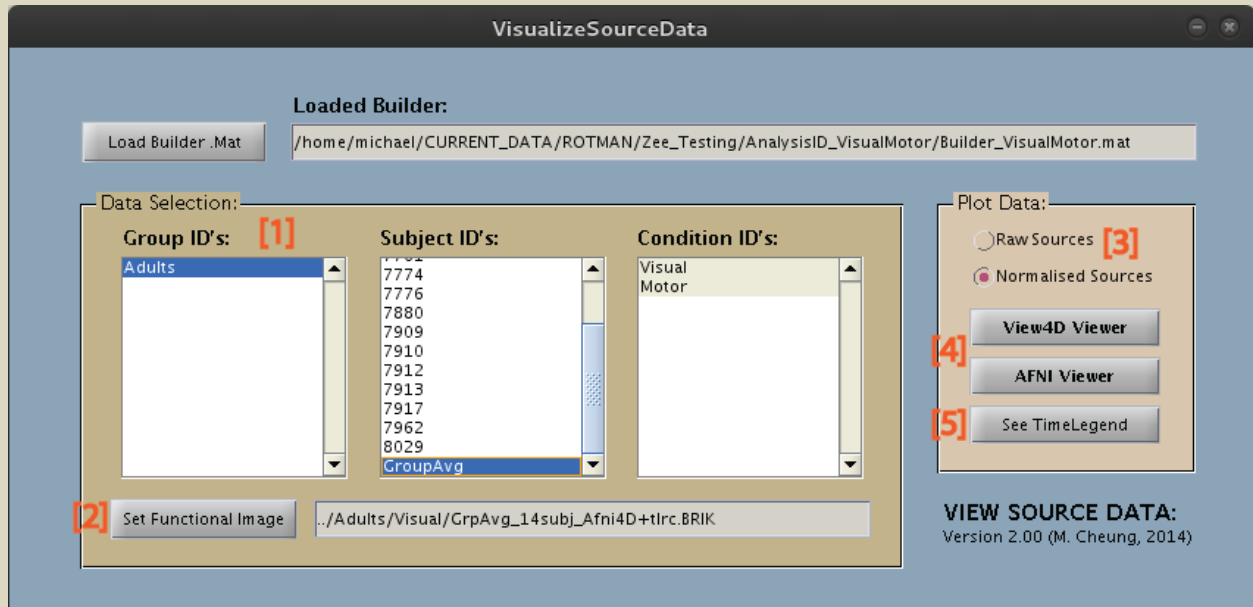
[9] Global Field Power Plots:

Displays global mean field power results for the selected datasets.

FIGURE A:**FIGURE B:****FIGURE C:****USING THE GUI:**

1. Load the [Builder .mat](#) file of the Analysis-ID you wish to view.
2. Select the Group, Subject and Condition-ID dataset(s) you wish to plot.
3. Configure your desired channel settings.
4. If desired, change advanced plot settings.
5. Specify the type of data you wish to view (time-domain or frequency-domain data).
6. Begin plotting by pushing the "View ..." buttons.

V2. VIEWING SOURCE DATA:



[1] Dataset Selection Panel:

Used to select the dataset that will act as the [functional overlay image](#). Also selects [additional dataset\(s\)](#) to be included in the View4D [voxel time-series plots](#) (see below).

[2] Set Functional Image:

Sets the currently selected dataset as the functional overlay image. This is the functional dataset that will be displayed in the viewer's axial, coronal and sagittal views.

[3] Data-Type Selection:

Selects whether to view [normalised sources](#) or [raw sources](#) (in subject-specific space). **Recommended:** Normalised sources are normally viewed.

[4] View4D & AFNI Viewers:

Opens the corresponding viewer for the current data selection. **Note:** Usage instructions for View4D and AFNI-viewers can be found in [Sections V5 & V6](#).

[5] Time Legend File:

Opens a text file that contains the [time-index information](#) for the source image selected. Allows you to relate time-indices seen in the viewers to the actual time-windows they represent.

USING THE GUI:

1. Load a **Builder .mat file** if one has not been loaded yet.
 2. Select the Group, Subj and Cond-ID of the dataset you wish to set as the **functional overlay**.
 3. Push the "**Set Functional Image**" button to lock the dataset in.
 4. **Optional:** Highlight **additional dataset(s)** to be included in the **View4D voxel time-series plot**.
 5. Select the type of data you wish to view (normalised or raw source data).
 6. Initialize your desired viewer (see **Sections V5 & V6** for more information).
- **Note:** When initiating the AFNI-viewer from the GUI, different **AFNI environmental variables** will automatically be configured for convenience.

ADDITIONAL DATASET SELECTION:

- ❖ After a dataset has been set as the functional overlay, additional subjects & conditions can be highlighted from the list. Data from these datasets will be included in the **voxel time-series** plot found in the View4D-viewer (see **Section V5** for more information).
- ❖ **Note:** For the AFNI-viewer, additional dataset selection will have no effect (only data from the functional overlay will be shown).

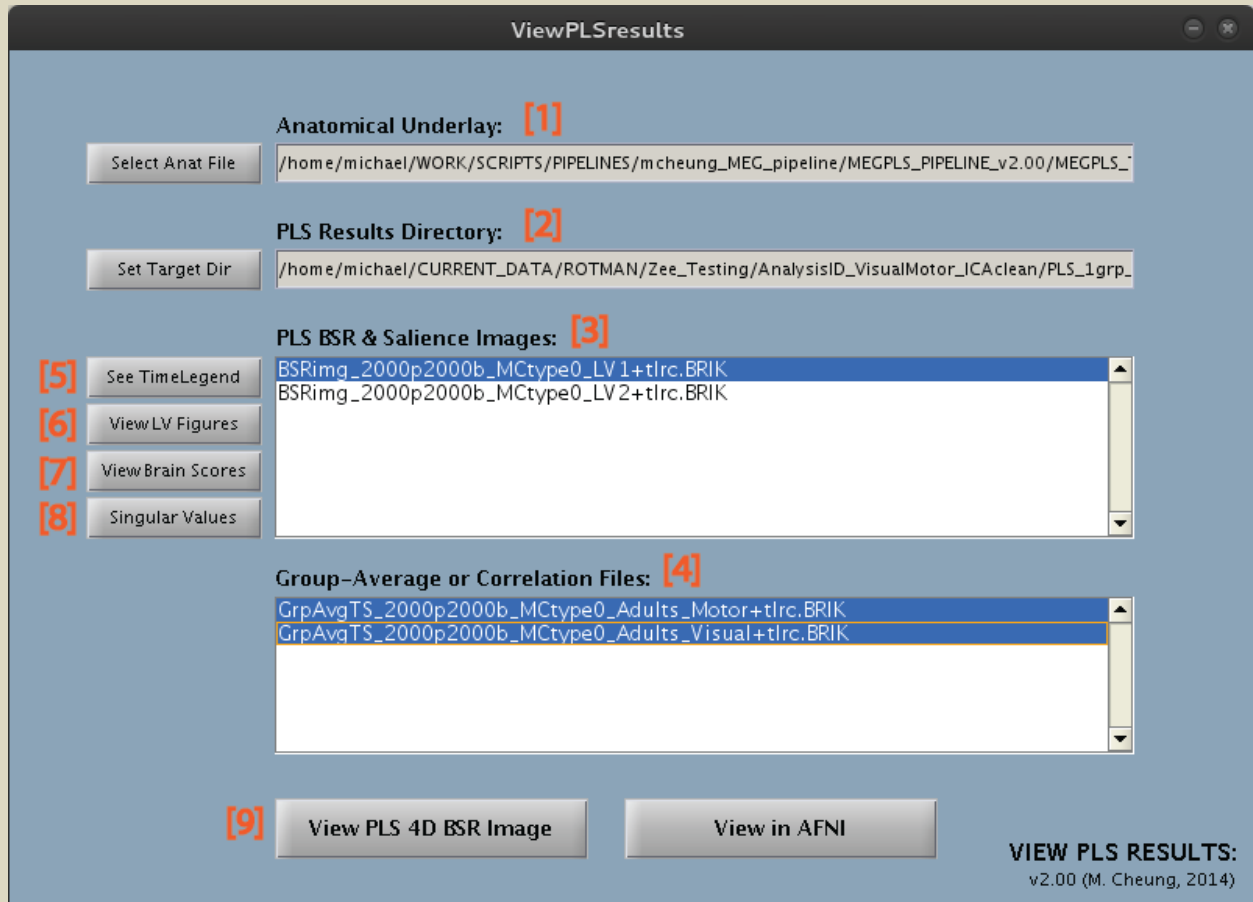
ANATOMICAL UNDERLAY INFO:

- ❖ The anatomical underlay will automatically be selected depending on the functional overlay file:
For **normalised sources** and **group-averaged data**, an MNI-template will be used.
For **raw sources** (in subject-space), the subject's corresponding MRI file will be used.
- ❖ **Note:** Do not worry about resampling or reslicing underlay files. The selected underlay will automatically be resampled to the same dimensions & orientation as the functional image.

VIEWERS AVAILABLE:

1. **View4D-viewer** (see **Section V5**):
 - This viewer has the ability to create brain-montages **across time**.
 - Also actively displays voxel time-series data for any selected voxel in the crosshair.
 - Anatomical underlay must have the same dimensions & orientation as the overlay image.
2. **AFNI Viewer** (see **Section V6**):
 - AFNI **clustering** and **atlas** functionality is useful for identifying ROI's from View4D.
 - Higher resolution anatomical underlay can be used (better images for papers).

V3. VIEWING PLS RESULTS:



[1] Anatomical Underlay:

- ❖ **AFNI or NIFTI file** that will serve as the **anatomical underlay image** displayed in the viewers. If desired, you may select your own underlay so long as it is in AFNI / NIFTI format.
- ❖ By default, an **MNI-template** is provided and selected ("**template_ch2+tlrc.BRIK**"). This default underlay can be used with any functional image in MNI or RAS-coordinate space.
- ❖ **Important:** Do not worry about **resampling or reslicing** the underlay files. The selected file will automatically be resampled to the same dimensions & orientation as the functional PLS image.

[2] Target PLS Directory:

Directory that contains the PLS results files that you wish to view.

PLS results are organized as: `../RootDirectory/AnalysisID_YourID/PLS_*/PLS-method/PLS result files`

[3] PLS Bootstrap-ratio & Saliency Images:

Displays [Bootstrap-ratio \(BSRing\)](#) and [Saliency \(SALimg\)](#) files within the selected target directory. The file currently selected in the list will be the [functional overlay image](#) displayed in the viewers.

Note: For interpretation and more information, see [Sections W1 & W2](#).

[4] Group-Average / Correlation Files:

Displays and selects data to be included in the [View4D voxel time-series plots](#) (see [Section V5](#)).

[Group-average](#) data files are automatically generated for [non-behavioural](#) PLS runs.

[Correlation](#) data files are automatically generated for [behavioural](#) PLS runs.

[5] Time Legend File:

Opens a text file that contains the [time-index information](#) for the current PLS image files.

Allows you to relate time-indices seen in the viewers to the actual time-windows they represent.

[6] View Latent Variable (LV) Figures:

Opens figures that display the contrasts or designs of [Latent-Variables](#) from the PLS run.

LV figures are saved in [".fig" format](#) for easy modification if desired.

Note: For interpretation and more information, see [Sections W1 & W2](#).

[7] View Brain Scores:

Plots brain score figures for the selected LV (contribution of each individual to the LV).

Figures are saved in [".fig" format](#) for easy modification if desired.

Note: For interpretation and more information, see [Sections W1 & W2](#).

[8] View Singular Values:

Plots singular values from the PLS run (measure of the total covariance each LV accounts for).

LV figures are saved in [".fig" format](#) for easy modification if desired.

Note: For interpretation and more information, see [Sections W1 & W2](#).

[9] View4D & AFNI Viewers:

Opens the corresponding viewer for the current data selection.

Note: Usage instructions for View4D and AFNI-viewers can be found in [Sections V5 & V6](#).

USING THE GUI:

1. **Optional:** If desired, change the [anatomical underlay](#) (a default MNI-template is provided).
2. Change the Target PLS Directory to the folder containing the PLS result files you wish to view.
3. View the [latent-variables](#) by pushing the ["Open LV Figure"](#) button.
4. Select the BSR image for an LV that you wish to view.
5. Highlight desired [group-average / correlation](#) files (hold "ctrl" to select multiple files).
6. Initialize the desired viewer (see [Sections V5 & V6](#) for more information).

- **Note:** When initiating the AFNI-viewer from the GUI, different [AFNI environmental variables](#) will automatically be configured for convenience.

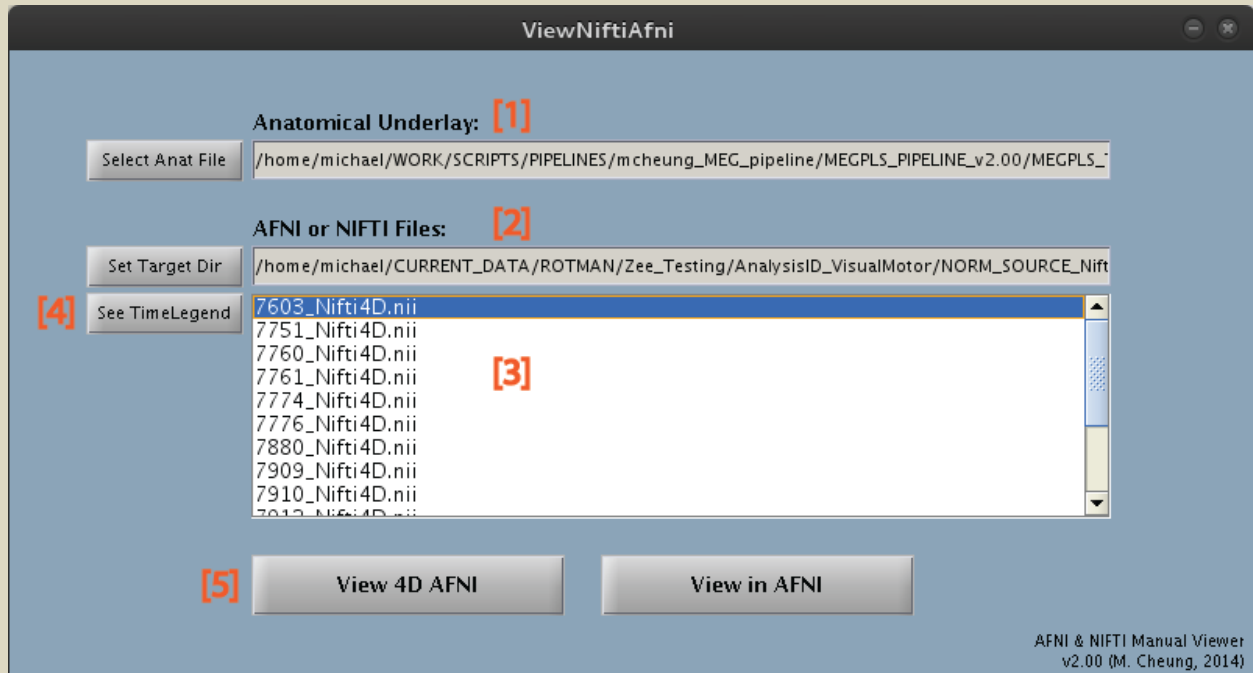
VIEWERS AVAILABLE:

1. **View4D-viewer** (see [Section V5](#)):
 - This viewer has the ability to create brain-montages [across time](#).
 - Also actively displays voxel time-series data for any selected voxel in the crosshair.
 - Anatomical underlay must have the same dimensions & orientation as the overlay image.

2. **AFNI Viewer** (see [Section V6](#)):
 - AFNI [clustering](#) and [atlas](#) functionality is useful for identifying ROI's from View4D.
 - Higher resolution anatomical underlay can be used (better images for papers).

IMPORTANT: For more info on PLS output and [interpretation of results](#), see [Sections W1 & W2](#).

V4. CUSTOM NIFTI / AFNI FILE VIEWER:



IMPORTANT: This viewer is for **custom** NIFTI & AFNI files created outside of [MEG]PLS.

- For files generated by [MEG]PLS, use the viewers above (see [Sections V1, V2, and V3](#)).

[1] Anatomical Underlay:

- ❖ **AFNI or NIFTI file** that will serve as the **anatomical underlay image** displayed in the viewers. By default, an **MNI template** is provided and selected ("template_ch2+tlrc.BRIK"). This default underlay can be used with any functional image in MNI or RAS coordinate-space.
- ❖ **Important:** Do not worry about **resampling or reslicing** the underlay files. The selected file will automatically be resampled to the same dimensions & orientation as the functional image.

[2] Target File Directory:

Directory that contains the NIFTI or AFNI files that you wish to view.

[3] Functional Image List:

Displays NIFTI and/or AFNI files found within the selected target directory. The file currently selected in the list will be the **functional overlay image** plotted in the viewers.

[4] Time Legend File:

If available, opens a text file that contains the **time-index information** for the file selected.

Note: Files created externally outside of the pipeline will not have time legends generated.

[5] View4D & AFNI Viewers:

Opens corresponding viewer for currently selected data.

Note: Usage instructions for View4D and AFNI-viewers can be found in [Sections V5 & V6](#).

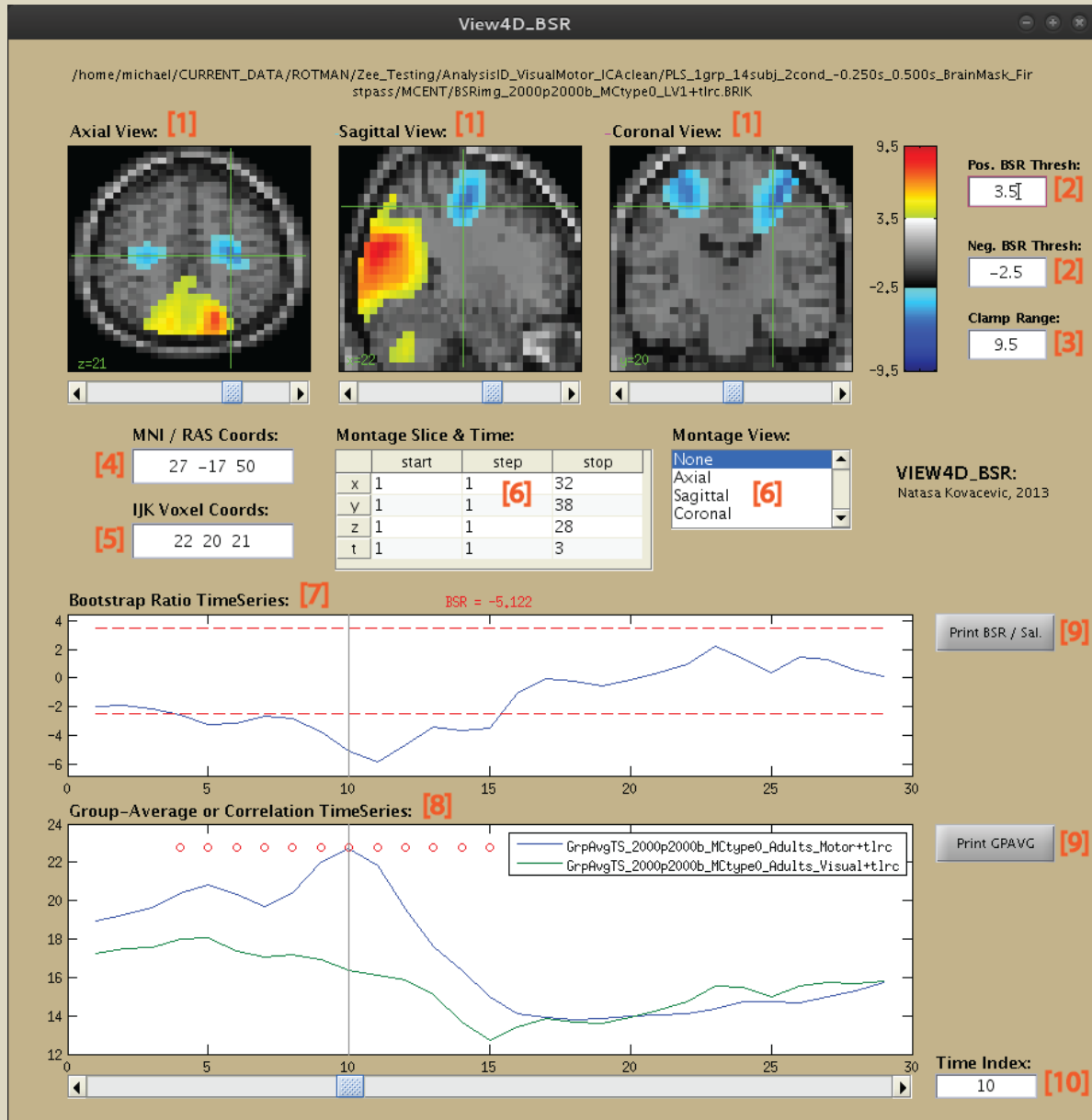
USING THE GUI:

1. **Optional:** If desired, change the [anatomical underlay](#) (a default MNI-template is provided).
 2. Specify the [target file directory](#) containing the custom AFNI / NIFTI files you wish to view.
 3. Select the file you wish to view from the [functional image](#) list.
 4. Initialize the desired viewer (see [Sections V5 & V6](#) for more information).
- **Note:** When initiating the AFNI-viewer from the GUI, different [AFNI environmental variables](#) will automatically be configured for convenience.

TWO TYPES OF VIEWERS AVAILABLE:

1. **View4D-viewer** (see [Section V5](#)):
 - This viewer has the ability to create brain-montages [across time](#).
 - Also actively displays voxel time-series data for any selected voxel in the crosshair.
 - Anatomical underlay must have the same dimensions & orientation as the overlay image.
2. **AFNI-viewer** (see [Section V6](#)):
 - AFNI clustering and atlas functionality is useful for identifying ROI's from View4D.
 - Higher resolution anatomical underlay can be used (better images for papers).

V5. USING VIEW4D VIEWERS:



[1] Axial, Sagittal, and Coronal Views:

The anatomical underlay and functional overlay images will be plotted here. Clicking will change the location of the crosshair and image slices being viewed.
Note: Click once to "pick-up" the crosshair, and click again to place it.

[2] Positive & Negative Threshold:

Adjusts the upper and lower **threshold** for which functional data is displayed. Thresholds are represented in the voxel time-series plots by **red-dotted lines**.
Note: For BSR images, voxels with **values >2.5 or <-2.5** are reliably contributing to the LV.

[3] Clamp Range:

Applies an upper and lower limit to values in the functional data for display purposes.

Ex: If the clamp range is 10, any value that exceeds -10 or 10 will be clamped back to -10 or 10.

Note: Adjusting the clamp range allows you to control the scaling of the colour bar.

[4] MNI / RAS Coordinates:

Displays the [MNI XYZ-coordinates \(in mm\)](#) of the voxel selected in the crosshairs.

Note: To jump to these coordinates in the [AFNI-viewer](#), use the "Jump to MNI" option in AFNI.

[5] IJK Voxel Coordinates:

Displays the [IJK-indices](#) of the voxel selected in the crosshairs.

Recommended: If jumping to coordinates in the AFNI-viewer, use MNI instead (see [Section V6](#)).

[6] Montage Panel:

Allows users to configure and create montages across XYZ-dimensions and time (see below).

[7] Functional Data Time-series Plot:

Plots functional data over time for the currently selected voxel.

For PLS results, this would display bootstrap-ratio or salience over time for the selected voxel.

[8] Group-Average / Correlation Time-series Plot (only for PLS results):

For [Non-behavioural PLS runs](#), displays [group-average amplitudes](#) over time for the selected voxel.

For [Behavioural PLS runs](#), displays [correlations](#) over time for the selected voxel.

[9] Print Time-series Data:

Outputs the time-series data for the selected voxel into the MATLAB command window.

[10] Time-Index Settings:

Changes the [current time-index](#) being viewed in the axial, sagittal and coronal views.

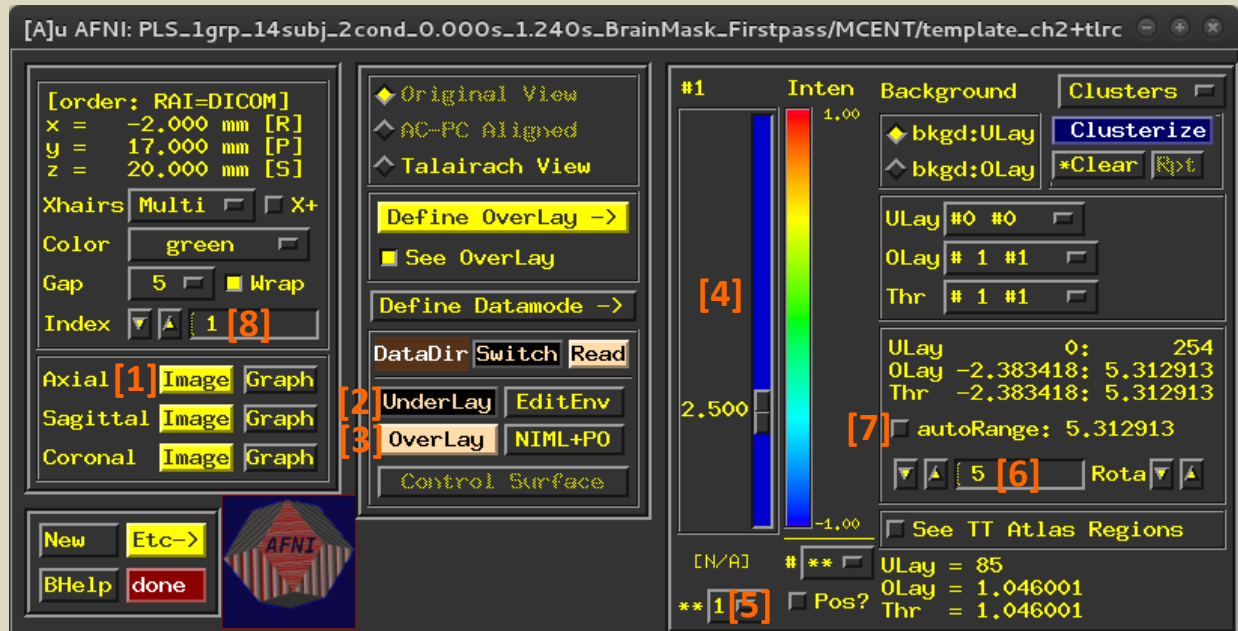
Note: See time legend files to match time-indices with their respective time-windows.

HOW TO CREATE A MONTAGE:

1. In the "[Montage Slice & Time](#)" table, configure the dimensions & time you want to slice across.
2. In the "[Montage View](#)" list, click the view you wish to slice the montage across.

Note: You can have multiple montage windows opened at the same time.

V6. USING THE AFNI VIEWER:



NOTE: You can initialize the AFNI-viewer through the [MEG]PLS GUI for convenience.

- Certain settings and environmental variables will automatically be configured for you.

[1] Axial, Sagittal, and Coronal Views:

Pushing the "Image" buttons here will open or close their respective orthogonal view.

[2] Underlay Button:

Pushing this button will allow you to select a different [anatomical underlay](#) file.

Note: If needed, use this to change to the [resampled version](#) of the underlay (see below).

[3] Overlay Button:

Pushing this button will allow you to select a different [functional image](#) file.

[4] Viewer Threshold Slider:

This slider adjusts the positive and negative thresholds of the functional data being viewed.

[5] Power for Threshold Slider:

Adjusts the power-of-ten factor for the threshold slider.

Increasing this allows you to adjust the threshold to higher values.

[6] Colour Scale Adjustment:

Adjusts the functional range of the colour-scale (similar to clamping range in the View4D-viewers).

[7] Colour Scale Auto-range:

Sets colour-scale to an automatically determined range (Uncheck if you wish to adjust manually).

Recommended: Keep this **OFF** and adjust the colour scaling yourself.

[8] Index Value:

For files generated in [MEG]PLS, this index represents the [current time-index](#) of the data.

Click the [up and down arrows](#) to change the current time-index of data being viewed.

Note: See time legend files to match time-indices with their respective time-windows.

USING ATLAS FUNCTIONALITY:

1. In any of the three AFNI view windows, right-click and select the ["Where Am I"](#) option.
2. In the new window, atlas information is displayed for the crosshair's location.

❖ **Note:** You do not have to close the "Where Am I" window to select a new location. Simply move the crosshair and the atlas information will update accordingly.

USING CLUSTERING FUNCTIONALITY:

1. To the right of the AFNI threshold slider, click the ["Clusterize" button](#).
2. In the new window, set clustering parameters and click ["Set"](#) to begin. The "Clusterize" button will now have an asterisk (*) next to it.
3. To view the [cluster report](#) for the current clustering operation, push the ["Rpt" button](#). In the new window, push the ["Jump" buttons](#) to view respective clusters.
Note: The ["Flash" button](#) can be used to identify the clusters after "Jump".
4. To clear the cluster report, push the ["Clear" button](#) underneath "Clusterize".

JUMPING TO MNI / RAS COORDINATES:

1. Acquire [MNI-coordinates](#) of interest (i.e. from the View4D-viewer).
2. In any of the three AFNI view windows, right-click and select ["Jump to MNI"](#).
3. Enter the MNI-coordinates into the new window and click ["Set"](#).

❖ **Important:** Be careful to use "Jump to MNI" instead of "Jump to XYZ"! The "Jump to XYZ" option will use [RAI-coordinates](#) instead of MNI (which are in RAS-space).

JUMPING TO IJK COORDINATES:

- ❖ **Important:** Before using ["Jump to IJK"](#), the [anatomical underlay must be the same resolution as the functional overlay](#). By default, a higher-resolution anatomical underlay is selected.
- ❖ However, if AFNI is initiated from the [MEG]PLS GUI, a [resampled version](#) of the selected underlay is [automatically generated](#). Before using "Jump to IJK", simply select the resampled file first by pushing the "Underlay" button in AFNI.

- ❖ **Warning:** If IJK-indices were acquired [outside of the AFNI-viewer](#), you will also need to subtract 1 from the IJK-indices prior to input (AFNI reads indices starting from 0 rather than 1).
1. Acquire your [IJK-indices](#) of interest (ex: from the View4D-viewer).
 2. In the AFNI-viewer, click "[Underlay](#)" and change the underlay to the "[_resampled](#)" version.
 3. In any of the three AFNI view windows, right-click and select "[Jump to IJK](#)".
 4. Enter the IJK-coordinates into the new window and click "[Set](#)".

HOW TO CREATE AN AFNI MONTAGE:

1. Open the AFNI view you wish to create the montage across (ex: Axial view window).
 2. At the bottom of the window, click the "[Mont](#)" button.
 3. Configure your montage settings and click "[Draw](#)" once ready.
- ❖ **Note:** The AFNI viewer cannot create montages across time. The View4D-viewers are recommended for montage-over-time and voxel time-series functionality.

VIEWING VOXEL TIME-SERIES IN AFNI:

1. Change the underlay to the [same file](#) as the functional overlay!
2. In the main AFNI panel, click one of the "[Graph](#)" buttons.
3. This will open a new window with 9 time-series plots: the voxel in the crosshair (center plot) and the 8 adjacent voxels around it.

W1. PLS RESULTS & OUTPUT VARIABLES:

OUTPUT FILE FROM PLS ANALYSES:

1. PLS result .mat file containing all information from the PLS run.
2. Latent-Variable (LV) figures showing the pattern or effect of each LV.
3. Bootstrap-ratio images (BSRing) for each LV (in AFNI .BRIK format).
4. Saliency images (SALimg) for each LV (in AFNI .BRIK format).
5. Group-average (GrpAvgTS) / Correlation (CorrTS) time-series files (for View4D-viewer).
6. Time legend file for PLS images.
7. Backup .mat files logging the Builder & Driver settings used for the analysis.

LATENT VARIABLES (LV):

- ❖ Latent variables reflect relationships (i.e. between patterns of brain activity and experimental effects) that account for a portion of the total covariance in the data. For a given PLS run, each consecutive LV explains a progressively smaller portion of the total covariance until all covariance in the data has been explained.
- ❖ Depending on the PLS method, an LV may be represented as a contrast between demographic groups and/or experimental tasks, or in the case of Behavioural PLS, as correlations between groups & conditions with behavioural measures and/or data from specific seed regions.
- ❖ Through permutation testing, each LV will have a p-value that allows us to tell whether the effect is significant or not. For convenience, we only output LV figures and AFNI image files for LV patterns that have a p-value below 0.1.
- ❖ **FIGURE B:** The LV in this figure displays a contrast between the visual and motor tasks. Combined with BSR and saliency images, we can interpret data from this LV (see below).

BOOTSTRAP-RATIOS (BSR):

- ❖ For each LV, a bootstrap-ratio (BSR) is computed for each voxel through bootstrapping. The BSR is a measure of how reliably each voxel is contributing to a given LV effect.
- ❖ It is calculated by: Saliency / Standard-Error (of the bootstrapped distribution). Large absolute BSR values mean that the voxel is resilient to subject changes & bootstrapping.
- ❖ In general, voxels with a BSR >2.5 or <-2.5 are reliably contributing to the LV.
 - Regions with BSR >2.5 (red) are reliably contributing to the current direction of the LV effect.
 - Regions with BSR <-2.5 (blue) are reliably contributing to the inverse direction of the LV.
- ❖ **FIGURE A:** Looking at the sample LV and BSR images:
 - Regions in red are brain areas that have greater activation in the visual task versus motor.
 - Regions in blue are brain areas that have greater activation in the motor task versus visual.

SALIENCE VALUES:

- ❖ For each LV, **saliency values** are computed for **each voxel**.
Saliency is a measure of **contribution (or weighting)** of a voxel to a given LV effect.
In other words, saliency measures **how much** the voxel contributes to a given LV.
- ❖ Saliencies can be positive or negative, depending on the direction of contribution:
 - **Positive saliencies** are a measure of contribution to the **current direction** of the LV effect.
 - **Negative saliencies** are a measure of contribution to the **inverse direction** of the LV effect.

SHOULD I FOCUS ON BSR OR SALIENCE?

- ❖ Start by viewing BSR images for LV's of interest (in conjunction with their respective LV figures). The BSR images will allow us to see which regions contribute reliably to the LV pattern. Once regions of interest have been identified, it may be useful to view their saliencies to see how much contribution and weighting those voxels have.
- ❖ Ex: A voxel with lower saliency may be contributing less, but if it has a high BSR, it means the contribution is reliable and resilient to subject changes. Conversely, a voxel may have a high saliency (high weighting), but not be reliable (low BSR).

HOW DOES PERMUTATION & BOOTSTRAP TESTING IN PLS WORK?

- **Permutation testing** is used to acquire **p-values** for each LV (significance testing). PLS will be repeated for each permutation resulting in a distribution of singular values for the LV's. If the singular value from each permutation exceeds the value of the original more than 95% of the time ($p\text{-value} < 0.5$), that LV is considered significant.
- For each bootstrap, subjects are randomly resampled and PLS is repeated, resulting in a distribution from which we can estimate standard error. From this, we can compute BSR's (see above), which can be used to identify stable voxels (similar to z-score).

BRAIN SCORES:

- ❖ For each LV, **brain scores** are computed for **each input dataset** loaded into PLS.
Brain scores are an index of how strongly each dataset **expresses** an LV effect.
- ❖ Plotting brain scores will allow you to see how each individual / task dataset expresses the LV.
This is useful if you are trying to determine whether there are any **outlier subjects** in your data.
- ❖ **Note:** The difference between **contribution & expression**. Each dataset **contributes equally** to the derivation of the LV, but they may differ in the level of expression of the LV pattern.

SINGULAR VALUES:

- For each LV output from a PLS run, a **singular value** will be computed.
A singular value represents the **"chunk" of total covariance** in the data that the LV accounts for.
Singular values can be used as a **measure of effect size** for the LV.

MAIN PLS RESULT .MAT FIELDS:

- | | |
|-----------------------------------|--|
| ▪ PLSresult.method | Type of PLS analysis |
| ▪ PLSresult.num_cond | # conditions in PLS datamat |
| ▪ PLSresult.num_subj | # subjects in PLS datamat |
| ▪ PLSresult.num_groups | # groups input into PLS run |
| ▪ PLSresult.v | Latent variables (column for each LV) |
| ▪ PLSresult.u | Saliency values (column for each LV) |
| ▪ PLSresult.s | Singular values |
| ▪ PLSresult.perm_result.sprob | p-values for each LV |
| ▪ PLSresult.perm_result.num_perm | # permutations |
| ▪ PLSresult.perm_splithalf | Split-half reliability testing if used |
| ▪ PLSresult.boot_result.compare_u | Bootstrap-ratios (column for each LV) |
| ▪ PLSresult.boot_result.num_boot | # bootstraps |

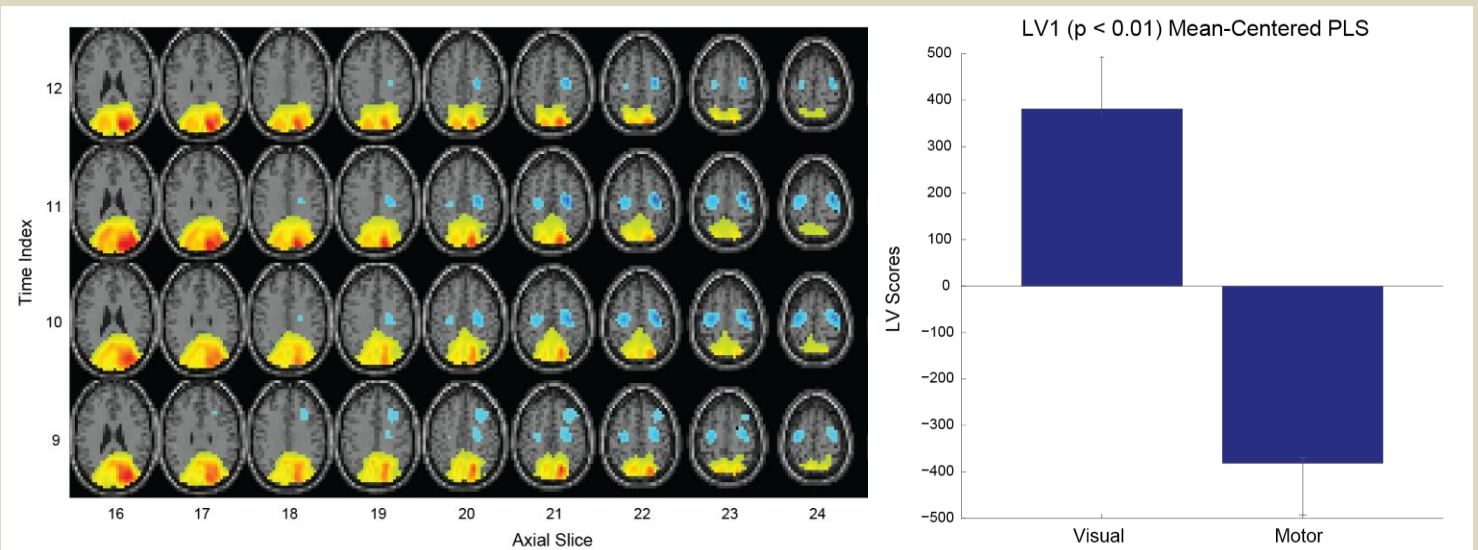
W2. INTERPRETATION OF SAMPLE PLS RESULTS:

SAMPLE RESULTS:

- ❖ To demonstrate, below are sample PLS results from a simple visual vs. motor task experiment. Trials for the visual condition were time-locked to the display of an image. Trials for the motor condition were time-locked to a button press in response to the visual stimulus.
- ❖ **FIGURE A:** Displays a montage across time (y-axis) and axial slices (x-axis) of bootstrap-ratios for LV1. The montage image was thresholded for BSR's above 2.5 and below -2.5.
- ❖ **FIGURE B:** Displays the contrast pattern reflected in LV1.

FIGURE A: AXIAL MONTAGE OF LV1 BSRimg:

FIGURE B: LV1 CONTRAST PATTERN



INTERPRETATION OF SAMPLE RESULTS:

- ❖ The first thing we want to do is look over the output LV's from the PLS run, and determine which ones are significant and display the effects we are interested in. In **Figure A**, we see that LV1 displays a significant contrast between the visual and motor tasks.
- ❖ However, the LV by itself only tells us that this effect is expressed within the data and is significant. Next, we want to look at the BSR images in order to see which regions are reliably contributing to the pattern displayed in LV1. For that, refer to **Figure B** above.
- ❖ Any area in **RED** represents voxels with **BSR's above 2.5**. This means that all voxels in these regions are **reliably contributing** to the pattern in LV1 (**visual > motor**). Therefore, any voxel in **red (BSR > 2.5)** shows greater activation in the **visual task** versus the **motor task**.

We can see that voxels in the **visual cortex are red**. This means that there is greater activation in the visual cortex during the visual task in comparison to the motor task.

- ❖ Any area in **BLUE** represents voxels with BSR's **below -2.5**. This means that all voxels in these regions are **reliably contributing** to the **INVERSE** of the pattern in LV1 (**motor > visual**). Therefore, any voxel in **blue (BSR < -2.5)** shows greater activation in the **motor task** versus visual.

We can see that voxels in the **motor cortex are blue**. This means that there is greater activation in the motor cortex during the motor task in comparison to visual.