PSYCHOPHYSIOLOGY TOOLBOX GRAPHICAL USER INTERFACE

Version 0.9.6

by

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Foreward

This utility is meant as a graphical user interface (GUI) to many of the most frequently used functions in the Psychophysiology Toolbox, which was written by Dr. Edward Bernat at the University of Minnesota. The functions in the `gui` directory within the toolbox are my own creations and maintenance responsibility; everything else is authored and maintained by Dr. Bernat.

It is imperative to note that many of the functions available in the toolbox are *not* included in this GUI yet. For example, the `clear_cache` and `score_HR` functions have not yet had a GUI front-end written for them yet. For that reason, it is important to peruse the documentation directory for the toolbox to ensure you know all of the functions that are available for you to use in reducing your data.

Finally, my goal in writing this GUI was to make script building easier; hence, one of the primary objectives in using this GUI is (paradoxically) to wean people off of using it. To accomplish this, each function has the option to write out its own script so that repeating actions is a matter of re-executing the script. As a user's confidence builds, s/he can modify these scripts at will to accomplish different things with the toolbox. In the end, the user may be so comfortable in scripting the operation of the toolbox that using this GUI would be more of an encumbrance than an assistance, at which point I would consider my work to be done.

Contents

Conventions, features and known limitations

CONVENTIONS

In this documentation, I've adopted certain typographical conventions to ease reading and comprehension. Items in **bold** refer to variable names, example inputs, or options in a drop-down box. Items in *italics* refer to GUI window components. Items deserving special attention are underlined.

FEATURES

Retention of inputted values. To allow the user to perform the same operations over and over again (or with only minor changes between iterations), each function window will save the parameters that you initially input to it.

Script output. To retain operations performed in the GUI, facilitate automated data processing, and reduce the learning curve for operating the psychophysiology toolbox, this GUI will output scripts to the **default_script_dir**.

Chaining of data import and modification functions. In the Import Data function, other functions (i.e., Epoch Data, Rereference Data, Filter Builder, and Add Stim functions) can be called to work each file into a final form, without having to mess with transitional files.

KNOWN LIMITATIONS

Only tested on Matlab 6.5 under Linux. Because I have developed this GUI under version 6.5 of Matlab under Linux, and I haven't tested it out on any other platforms or Matlab versions to see if it runs, I will only guarantee that this runs under Matlab 6.5 on Linux. However, if this GUI fails under any other versions of Matlab (e.g., 7.0) on other operating systems (e.g., Windows), I'd appreciate as detailed a report as possible about the failure (including any data files you were running it on, the errors that Matlab spit out at you in the command prompt, and – of course – the Matlab version and OS on which you're using it).

Only point-and-click buttons. Because I have limited reason to add KeypressFcn's to each button in each function, currently you can only click buttons with actual mouse clicks, not ENTER key presses. This will likely be changed in a future version.

Nonsensical tab-through order in some functions. In some windows, the tab-through order for different GUI elements makes no sense. This is because certain functions break the Tab Order editor in Matlab's GUI editor. This will likely be changed in a future version.

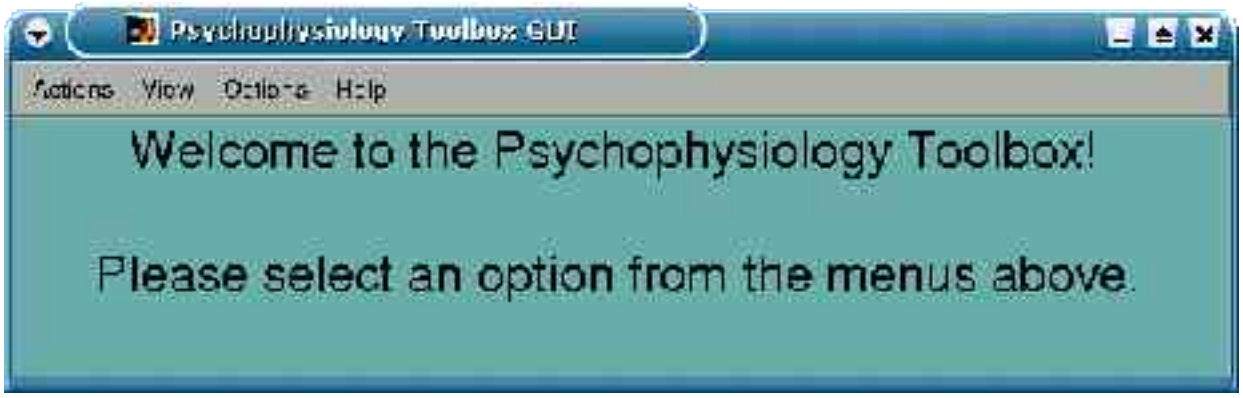
Data file structure

The basic variable in which all information relevant to operation of this toolbox is named **erp** for epoched files, or **cnt** for continuous files. Each of these has a number of subfields, which are detailed below and which may be useful for defining logical expressions that may define triggers to average together or statistical groups to form. Unless otherwise specified, in each subfield, each row represents an individual waveform (whether this be a single trial or a single average).

erp

.data	Each waveform is held here. Each column is a separate data point.
.elec	This number identifies from which electrode this waveform comes.
.sweep	This number identifies the sweep number within a trial.
.subnum	This number identifies from which subject this waveform comes.
.ttype	This number identifies the trigger number associated with this waveform.
.correct	This number reveals whether the subject responded correctly on this trial.
.accept	This number identifies whether this is a valid waveform.
.rt	This number gives the subject's reaction time to this waveform's stimulus.
.response	This number identifies the subject's response to this waveform's stimulus.
.subs	
.name	This string gives each subject's unique identifier. The row number of each entry in this subfield corresponds to a unique value for **erp.elec**.
.elecnames	This string gives each electrode's unique identifier. The row number of each entry in this subfield corresponds to a unique value for **erp.elec**.
.samplerate	This number specifies how many samples per second are in each waveform in **erp.data**.
.tbin	This number specifies the column in **erp.data** corresponding to the location of the trigger.
.domain	This string details whether components will be extracted in 'time', 'freq'uency, or 'TFT' (time-frequency) domains.
.stim	This subfield contains a number of additional subfields that allow a researcher to detail other relevant characteristics of the stimuli represented by each waveform.
.stimkeys	This subfield contains a number of additional subfields that provide human-readable keys for the **erp.stim** subfields, allowing a researcher to keep the values of each **erp.stim** subfield straight.

The main toolbox window

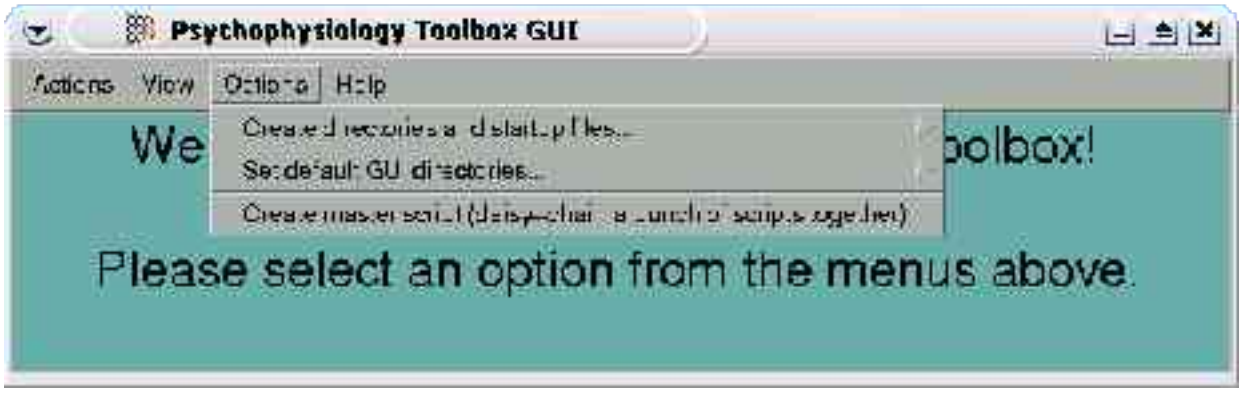


Once the toolbox is loaded with the psychophysiology_toolbox_startup script in the main toolbox directory, typing `Main` at the Matlab command prompt will bring up this window. As you can see, this is a pretty minimalist window. Only the Actions and Options menus have functions associated with them at this time.

Actions. You will be able to execute all of the major functions that the toolbox provides through this menu.

Options. In this menu, you can generate files and directories necessary to run the toolbox, as well as set default directories for use in the GUI.

Set defaults

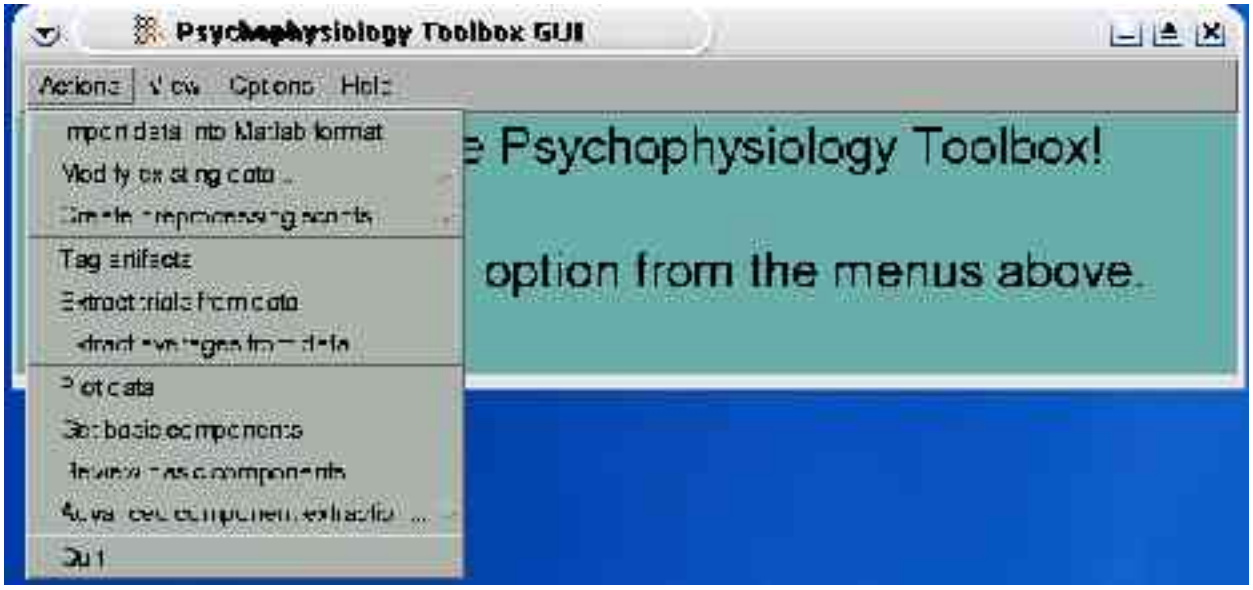


Clicking on the Options menu will bring up the following menu entries. Of primary concern here are the first two options in the menu.

Create directories and startup files... The subentries in this menu entry will allow you to create directories and startup files necessary to run the toolbox from a given location. *Create components directories* will create the directories needed for *Advanced component extraction* functions. *Create toolbox startup.m file* will generate a **startup.m** file (in a directory you select) that will start the toolbox and its GUI for you.

Set default GUI directories... The subentries in this menu entry will allow you to set default *Load data* (which sets the **default_load_dir** environment variable), *Save data* (which sets the **default_save_dir** environment variable), and *Save script* (which sets the **default_script_dir** environment variable) directories to save time in working with the toolbox. You'll definitely want to set the *Save script* directory, as otherwise, you'll simply save scripts in the directory from which you launched Matlab.

Actions



Once you click on the Actions menu, you will find the following menu, which lists all of the functions provided by the GUI. With the exception of the Quit function, which will close the main toolbox, all of the functions will be documented below. Nearly all of the functions have the following options:

Verbosity level. Enter the level of output you'd like the data import function to return in the Matlab window. A larger number means more information about the data import process will be returned. The default is **1**.

Generate script. This option allows you to select whether you want a script that will allow you to rerun the data import function using the parameters you've selected. If this option is on, the script will be saved in the default script directory that you set in the Options menu of the main toolbox window. The text box underneath this option allows you to set the filename to use for the script. You may use the Browse button to find a filename to overwrite, or type a filename in the text box. The default is **on**.

Import data


Import Data
Select the format of the data you want to import.
eeg (Neuroscan ecoched file)
Scale to microvolts
Verbosity level
1
Data byte length
Generate script
16 bit (NL <= 4.1)
import_data_
Browse
Epoch data
Event reference data
Filter data
Add stim
THEN
Choose filename to load data from.
Browse...
Choose filename to save data to (OPTIONAL)
Browse...
Import Data File
OR
Choose data to add a trial to
(if data file directory not desired)
Browse...
Choose data save directory
(default directory not desired)
Browse...
Text to append to filenames (OPTIONAL)
_filtered_stims
Import Directory of Data

If you're starting from scratch, this is likely the first function you'll want to call. It will allow you to import data from other data acquisition formats into Matlab format, which will let you perform all kinds of subsequent operations on it with the toolbox. After selecting the data import options in the first panel, use either the second panel to import data from a single file or the third panel to import all data in a directory of a given format.

FIRST PANEL

Data format bar. Use this drop-down menu to select the format of the data you want to import. Currently supported formats include **.cnt** (Neuroscan continuous file), **.eeg** (Neuroscan epoched file), **.avg** (Neuroscan epoched and averaged file), **.bdf** (BioSemi continuous file), or . **edf** (European Data Format continuous file). The default is **.eeg**.

Scale to microvolts. This option allows you to convert the data from meaningless A-D (analog to digital) units into physiologically meaningful microvolts. This is generally a good idea for epoched files; however, scaling data in continuous files (i.e., **.cnt**, **.bdf**, and **.edf** files) to microvolts eats up a lot of memory. The default is **off**.

Data byte length. Use this drop-down menu to select whether your data was recorded in 16-bit (i.e., if you used Neuroscan's Acquire program version 4.2 or below to acquire the data) or 32-bit (i.e., if you used Neuroscan's Acquire program version 4.3 or above or BioSemi software to acquire the data). The default is **int16**.

Verbosity level, Generate script. See p. 5.

Epoch data. Clicking on this button will allow you to epoch each file during the import process. If you click this button on, the Epoch Data window will pop up, allowing you to set the parameters for the epoching function. See pages 10-11 for more details.

Rereference data. Clicking on this button will allow you to rereference each file during the import process. If you click this button on, the Rereference Data window will pop up, allowing you to set the parameters for the rereferencing function. See page 12 for more details.

Filter data. Clicking on this button will allow you to filter the data in each file during the import process. If you click this button on, the Filter Builder window will pop up, allowing you to set the parameters for the various filter functions. See pages 22-24 for more details.

Add .stim. Clicking on this button will allow you to add **.stim** subfields in each file during the import process. If you click this button on, the Add Stim window will pop up, allowing you to detail the operations necessary to build each **.stim** subfield. See pages 18-21 for more details.

SECOND PANEL

Load data filename. You may either type a filename into this box (complete with path to the file) or use the *Browse* button to find one. When the value in this box is updated, it will be copied to the Save data filename box, with the file extension in this box replaced by .mat in the

Save data filename box.

Save data filename. If you would like to change the filename to which data will be saved, do it here (or use the *Browse* box to locate an alternative file). However, doing this is not recommended.

Import data file. This button will import the file with the filename given in the *Load data filename* into the *Save data filename*. It will then write out a script that will repeat this action into the default script directory, if the *Generate script* option is on. Epoched files will be written out as **.mat** files, and continuous files will be written out as **.xxx.mat** files, where **.xxx** is the extension of the continuous file that was imported.

THIRD PANEL

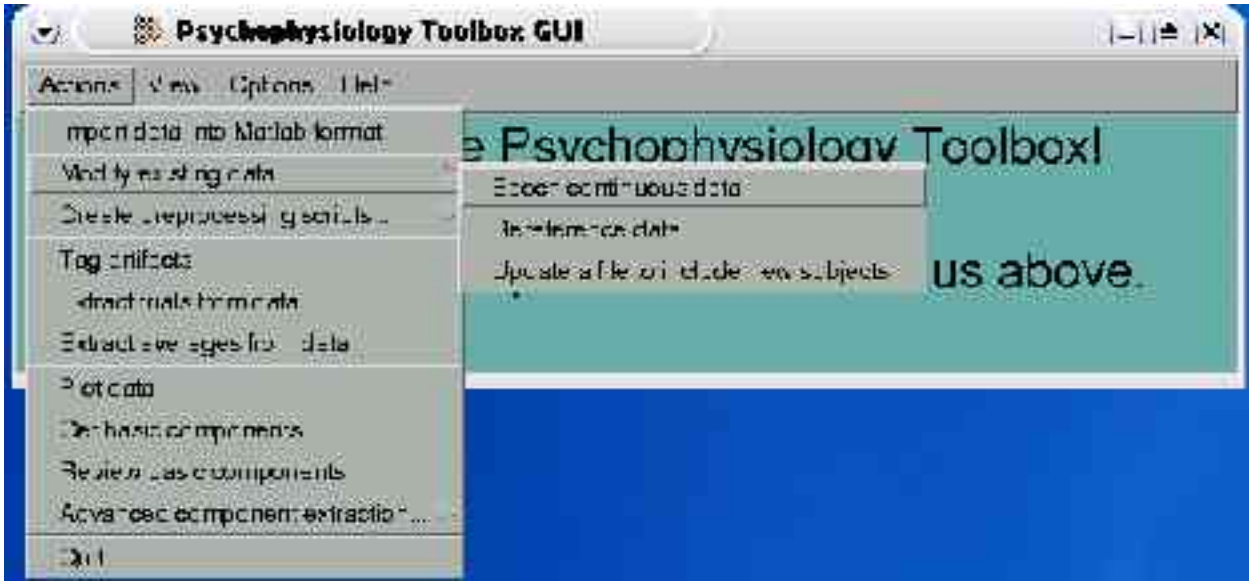
Data load directory. Type in a complete directory path that contains data of the given format, or use the *Browse* button to locate a directory. The default is the default load directory specified through the main toolbox window.

Data save directory. Type in a complete directory path to which you want to save all the imported data files, or use the *Browse* button to locate a directory. The default is the default save directory specified through the main toolbox window.

Text to append to filenames. Type in an extension that should be appended to each filename that describes the operations that were performed on it as it was imported (e.g., **_epoched_rereferenced_filtered_stims**). The default is empty.

Import directory of data. This button will import all data files of the given format in the *Data load directory* and save the resultant files in the *Data save directory*. It will then write out a script that will repeat this action into the default script directory, if the *Generate script* option is on. Epoched files will be written out as **.mat** files, and continuous files will be written out as **. xxx.mat** files, where **.xxx** is the extension of the continuous files that were imported.

Modify data



In this submenu, you can perform a number of operations that will allow you to modify data that you've already imported into Matlab format.

Epoch continuous data. This function carves out specified pieces of a continuous file to permit event-related analyses. You can specify which triggers (which mark particular events in the continuous record) should be extracted. You can also scale data to microvolts.

Rereference data. This function rereferences a set of electrodes (or creates wholly new electrodes from ones existing in the data file) by using a linear derivation file (.ldr) file.

Update a file to include new subjects. This function either updates one file with cases in another file or combines a number of files together into one master file.

Epoch continuous data

This function will epoch continuous files that have been imported into Matlab format. The

second and third panels behave exactly like their counterparts in the Import Data function (pp. 7-8), except that they write out scripts to epoch data instead of import it, so they will not be discussed here. Therefore, only the options in the first panel will be detailed here.

FIRST PANEL

Data format. This drop-down menu allows you to select the type of file (i.e., **.cnt**, **.bdf**, or **.ed**f) that was imported into Matlab format that you want to epoch. The default is **.cnt**.

Trigger numbers to extract. The trigger numbers to be extracted may be entered in this box. You may enter a comma-separated list of individual trigger numbers (e.g., **1,7,11,77**), ranges of trigger numbers, with the first and last trigger number to extract separated by a colon (e.g., **1:255**), or a mixture of the two (e.g., **3,33,100:199,207,214,215:230**). The default is **0**.

Epoch to extract. Define the beginning and end of the window for each epoch (relative to each trigger to include) in these text boxes. Epochs of the given width will then be extracted for each and every trigger falling in the range specified in *Trigger numbers to extract*. The default is **-500** ms to **1000** ms.

Verbosity level, Generate script. See p. 5. The default script name is **epoch_data_script**.

Rereference data

This function will allow you to reference all electrodes to a new reference electrode or create new electrodes from your original recordings, using a linear derivation file (.ldr) to specify how the electrodes should be recombined. There is only one unique option here (see pp. 7-8 for use of the second and third panels, and p. 5 for *Verbosity* and *Generate script* option usage – the default script name is **rereference_data_script**), which is detailed below.

LDR file. Enter the full path to a linear derivation file to use for the rereferencing, or use the Browse button to locate one.

Update a file to include new subjects

As you run a study, you'll likely want to update your main data files without having to reprocess data from all subjects. Instead, you'll just want to add data from new subjects into the main file. If you've got data from all of your new subjects combined into one big file, you can use the simple *Update ERP* function in the third panel. If not, you'll have to use the *Combine Files* function defined by the first and second panels.

FIRST PANEL

Resampling rate. Enter the number of samples per second to which you want to resample your data. The default is blank, which means that your data will retain its original sample rate.

Verbosity level, Generate script. See p. 5. The default script name is **update_data_script**.

SECOND PANEL

Trials to extract. The large list box holds a list of logical expressions that define trial types to extract (e.g. **erp.accept==1**). To add an expression, type it in the skinny text box, then click the *Add* button. To remove an entry, click on it in the list box and click *Remove*. The expressions in this list will be executed in order, from top to bottom, so you may want to use the *Move Up* or *Move Down* buttons to adjust the positions of each list entry. To use these buttons, click on an entry in the list box, then click *Move Up* to move it up one position or *Move Down* to move it down one position.

Files to combine. The large list box holds a list of files to be combined together. To add a file, either type its full path name into the skinny text box, or click the *Browse* button to locate it, then click the *Add* button. To remove a file from the list, highlight it in the list box and click *Remove*. You can also highlight a file in the list box and click the *Move Up* or *Move Down* button to move it up or down in the processing list.

Save data filename. Type the full path name of the filename to which you want to save the combined files, or click the *Browse* button to locate one.

Combine files. Click this button to combine files with the parameters above.

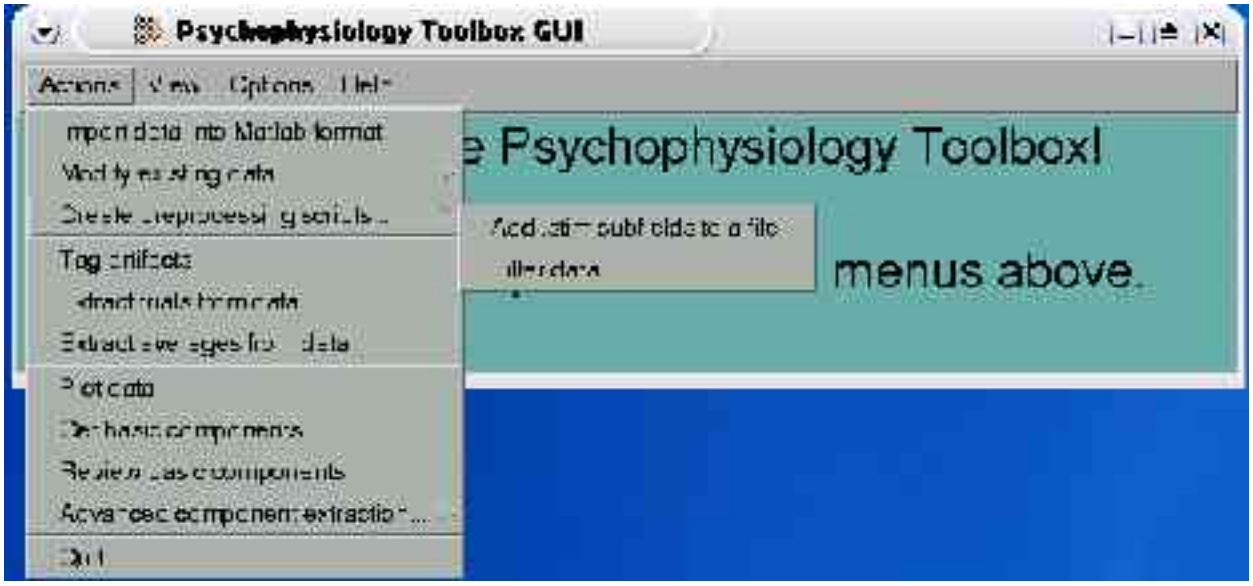
THIRD PANEL

Choose master file. Type the full path name of the filename that has the majority of cases (or at least to which you want to save the combined file to), or click the *Browse* button to locate one.

Choose append file. Type the full path name of the filename that has the additional cases you want to append to the master file, or click the *Browse* button to locate one.

Update ERP. Click this button to update the master file with cases in the append file.

Create preprocessing scripts

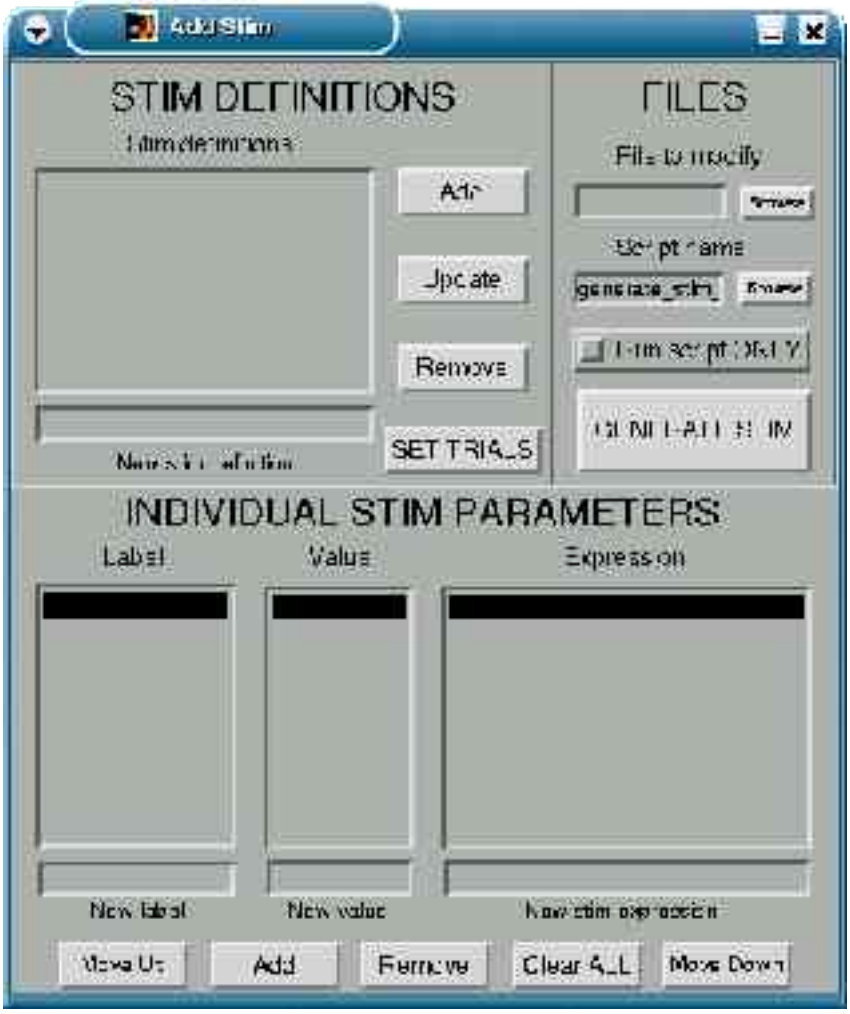


In this submenu, you can create scripts from an exemplar file that can be used in subsequent data processing. These functions will be summarized below.

Add .stim fields to a file. With this option, you can build a script that will add a number of **.stim** fields to an existing file. The values of these **.stim** fields consist of numbers or single characters that provide a more descriptive label for a given trigger number (or that summarize a range of trigger numbers). **.stim** fields are particularly useful when creating average waveforms.

Filter data. With this option, you can build a script that will perform a number of filtering operations in succession on an existing file. Thus far, currently supported filters include low and high pass filters, bandpass and pseudo-notch filters, contour following (which mimics an analog integrator), rectification, inversion, and deletion.

Add .stim subfields to a file



This function allows you to add **.stim** fields to an existing erp file. For each .stim definition in the *Stim definition* list, the subfields **.name** (corresponding to the *Expression* list), **.value** (corresponding to the *Value* list), and **.description** (corresponding to the *Label* list) will be written. Below, the different panels involved in executing this function successfully will be described.

STIM DEFINITIONS

In this panel, you can define the names of the individual .stim fields to be written. For example, if **valence** and **content** are the entries in *Stim definition* box, the fields **erp.stim.valence** and **erp.stim.content** would be written out, with individual values defined in the INDIVIDUAL STIM PARAMETERS panel.

To add another .stim definition, type its name into the *New stim definition* box, then click the *Add* button. To remove a .stim definition from the list, click on it to highlight it and click the

Remove button. To update a .stim definition (N.B.: This should be done automatically for you every time you press the *Add*, *Remove*, or *Clear ALL* buttons in the INDIVIDUAL STIM PARAMETERS panel), click the *Update* button. Click the *SET TRIALS* button to bring up a window that will allow you to define trial numbers within a certain combination of **erp** subfields (described on pages 20-21).

INDIVIDUAL STIM PARAMETERS

To add a value for a given .stim definition, the *New label*, *New value*, and *New stim expression* text boxes must all be not empty. Once these text boxes have some text in them, you can click the *Add* button to add a value.

To remove a given value, click on the appropriate entry in either the *Label*, *Value*, or *Expression* list box (the corresponding entries in the other two list boxes will be selected automatically) and click *Remove*. If you want to start over with a current .stim definition and clear all currently defined values for it, highlight that definition in the STIM DEFINITIONS panel and click the *Clear ALL* button in the INDIVIDUAL STIM PARAMETERS panel.

Label. This list box displays the descriptive, human-readable labels that have been entered for each value of the current .stim definition.

Value. This list box displays the actual values for each entry of the current .stim definition.

Expression. This list box displays the logical expressions that define the trials to be given the highlighted value in the current .stim definition.

FILES

File to modify. Type the full path name to the prototypical file you want to modify with the script that this function will output, or click the *Browse* button to locate one. This must be a real file, as it will be used to test the .stim subfields you've requested before the script is written. Changes made to this file will not be saved, as it is only a test file to ensure that the filters that are applied will actually work.

Script name. Type the filename for the script you want to generate. The default value is **generate_stim_script**.

Run script ONLY. If this option is on, a script will not be generated. Instead, an existing script will be run, the full path name of which is given in the *Script name* text box.

GENERATE SCRIPT. Click this button to generate the script that will create the **.stim** fields you've requested. Be warned that this step will fail if you've made an error in specifying the **. stim** fields, or if you haven't used a proper prototypical file in *File to modify*.

This window allows you to define trial number vectors in the *Trial definitions* window for combinations of *erp subfields*. Each instance of a unique combination of values for the variables in *erp subfields* will receive a sequential number.

TRIAL DEFINITIONS

Trial definitions. This list box displays the names of the trial number vectors to create. To add a new trial definition, type the desired name of the trial number vector (e.g., **trials_elec_content**) in *New trial definition*, then click the *Add* button. To update a trial number definition after making changes in the CHUNK TRIALS BY panel (N.B.: This should be done automatically for you every time you press the *Add*, *Remove*, or *Clear ALL* buttons in the CHUNK TRIALS BY panel), click the *Update* button. To remove a trial number definition, click on it in the *Trial definitions* box, then click the *Remove* button.

When you have created all the trial number definitions you want, click the *Done* button to return to the "Add Stim" window.

CHUNK TRIALS BY

erp subfields. This list box displays the names of the erp subfields that will be used in generating unique trigger numbers. For multi-subject files, you'll want to have at least **erp.subnum** and **erp.elec** included in this list; for single-subject files, only **erp.elec** should be absolutely necessary. The default value is **erp.elec**.

To add a new subfield to use in a given trial number definition, type it into the *New erp subfield* text box and click the *Add* button. To remove an erp subfield from the current trial number definition, click on it in the *erp subfields* list box, then click the *Remove* button. To remove all erp subfields from the current trial number definition, click the *Clear ALL* button.

Filter data

With this function, you can define a number of filters to apply successively to a prototypical data file. Each filter will require you to specify the electrodes and subjects to which it should be applied, with additional parameters that will be requested for certain other filters. To select a certain filter, click on the line appropriate to it in any of the list boxes (all the other lines will be highlighted automatically). If a selected filter does not require inputs to certain list boxes, those input boxes will be grayed out automatically.

INDIVIDUAL FILTER PARAMETERS

Use electrodes: This list box displays the electrodes that will be filtered for each filter. To add an electrode to the currently highlighted filter definition, type an electrode to use (e.g., **FZ**) in the *New electrode* text box (do not surround it with single quotes; the program will do this for you automatically), then click the *Add* button underneath the *New electrode* box. To remove the last electrode specified in the currently highlighted filter definition, click the *Remove* button underneath the *New electrode* box. The default is **ALL**.

Use subjects: This list box displays the subjects to which each filter will be applied. To add a subject to the currently highlighted filter definition, type a subject name (e.g., **s01**) in the *New subject* text box (do not surround it with single quotes; the program will do this for you automatically), then click the *Add* button underneath the *New subject* box. To remove the last subject specified in the currently highlighted filter definition, click the *Remove* button underneath the *New subject* box. The default is **ALL**.

Type. This list box displays the individual filters that will be applied. The following filters are available:

- **highpass** (include all frequencies above the frequency specified)
- **lowpass** (include all frequencies below the frequency specified)
- **bandpass** (include all frequencies within the frequency range specified
- **stopband** (like a notch filter; a narrower, more precise version of the bandpass)
- **sprIIR** (smooths data using an infinite-impulse recursive filter with a -3 dB time

constant)
- **rectify** (makes all waveform values range from 0 to +infinity)
- **invert** (flips the sign of all waveform values)
- **delete** (deletes all waveform values)

The first four of these require additional input into the *Filter freqs* and *Filter order* list boxes. The **sprIIR** filter requires additional input into the *High/low pass?* and *Time constant* list boxes. The last three filters require no additional input. To add a filter definition, fill in all the required input boxes, then click the *Add* button. To remove a filter definition, click the appropriate line of any non-grayed out list box and click the *Remove* button. To clear an entire filter definition, click the appropriate line of any non-grayed out list box and click the *Clear ALL* button. Because filters are processed sequentially, you can also move a filter definition up or down in the processing order by clicking on the appropriate line of any non-grayed out list box and then clicking *Move Up* or *Move Down*, respectively.

Additional input required for **highpass**, **lowpass**, **bandpass**, **stopband** filters:

Filter freqs. This list box displays the frequencies on which each filter will operate. If only one box is available for input underneath the *Filter freqs* box (i.e., for **highpass** or **lowpass** filters), only that box must be filled in for the filter definition to continue. Otherwise (i.e., for **bandpass** and **stopband** filters, both boxes must be filled in to provide a valid filter definition.

Filter order. This list box displays the powers to which each filter will be raised. It is suggested that you use a default of 3 in the *New filter order* box for filters requiring this option.

Additional input required for **sprIIR** filters:

High/low pass? This list box displays whether the given **sprIIR** filter should use a highpass (**hp**) or lowpass (**lp**) filter to help smooth the data. The default in the *New pass* drop-down box is **lp**.

Time constant. This list box displays the time it will take for half of the signal at one point to decay out of the smoothing filter. FYI, a time constant of 35 ms replicates a Coulbourn integrator's time constant of 80 ms fairly well.

MISC

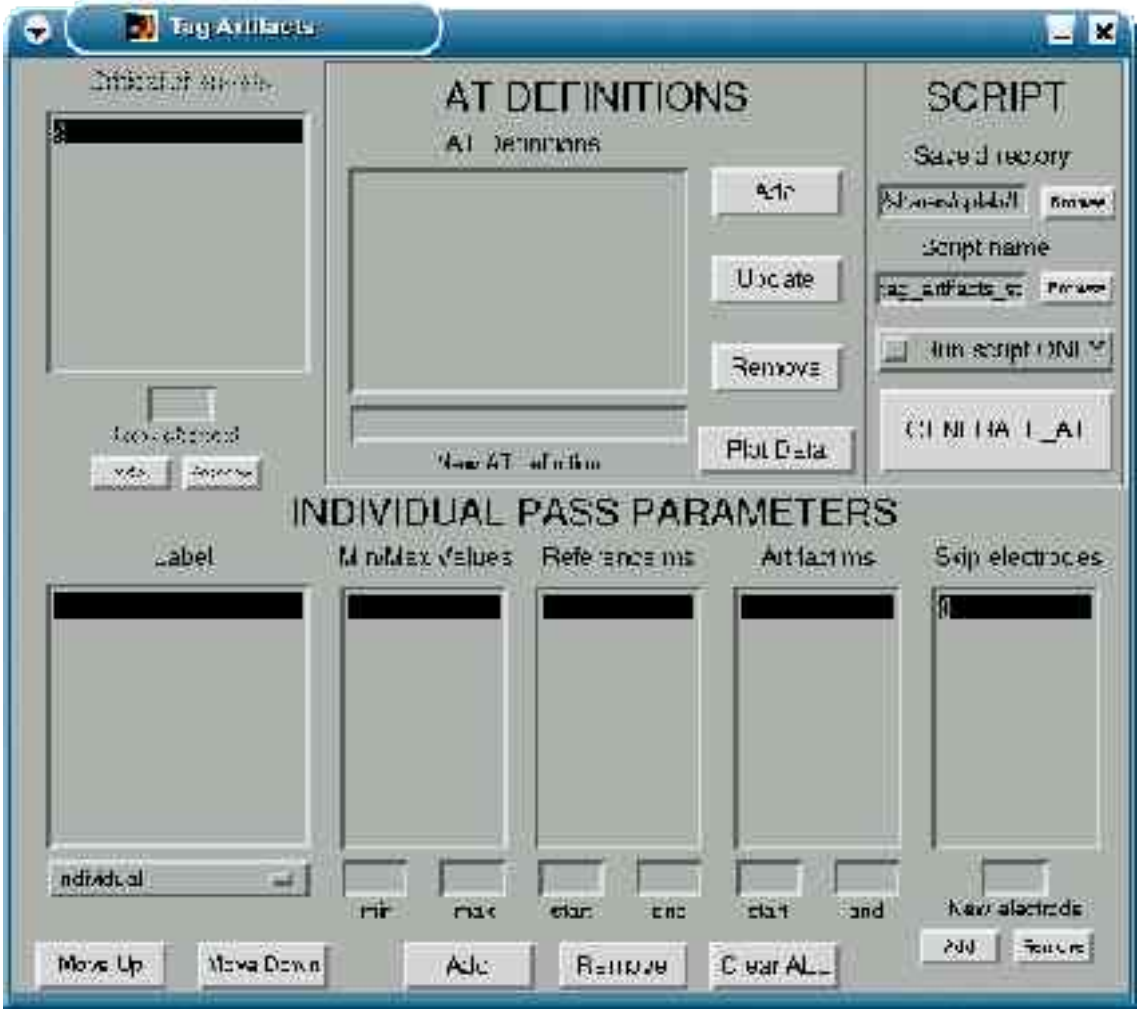
File to modify. See p. 18. Changes made to this file will not be saved, as it is only a test file to ensure that the filters that are applied will actually work. Hence, you can use any file you want without fearing that it will be altered.

Verbosity level, Generate script. See p. 5. The default script name is **filter_builder_script**.

CREATE FILTERS. Click this button to generate a filter script incorporating the various filter

definitions you've specified. Be warned that this step will fail if you've made an error in specifying any filter, or if you haven't used a proper prototypical file in *File to modify*.

Tag artifacts



With this function, you can create a script that features any number of artifact tagging (AT) definitions, each of which contains any number of passes to help you eliminate all artifacts in your data before processing it further.

AT DEFINITIONS

In this panel, you can add, update, or remove entire AT definitions, which are displayed in the *AT Definitions* list box. Of all the AT definitions you may create, only one AT definition may be used to clean up data! To add an AT definition, type a name for it (e.g., **AT1000_individual**) in the *New AT definition* text box, then click the *Add* button in this panel. To remove an AT definition, click on it in the *AT Definitions* list box, then click the *Remove* button in this panel. To update a highlighted AT definition (N.B.: This should be done automatically for you every time you press the *Add*, *Remove*, or *Clear ALL* buttons in the INDIVIDUAL PASS PARAMETERS panel), click the *Update* button in this panel.

To plot your data to ensure that the current AT definition removes all artifacts from your data, click the *Plot Data* button. This will bring up the "Plot Data" window, which is described in greater detail on pages 32-34.

INDIVIDUAL PASS PARAMETERS

The list boxes in this panel specify individual passes to apply sequentially to the data in the highlighted AT definition. To add a new pass, click whether you want to use an *individual* or *CRITchannel* artifact tagging strategy under the *Label* list box; fill in the *min* and *max* text boxes under the *Min/Max Values* list box, the *start* and *end* text boxes under the *Reference ms* list box, and the *start* and *end* text boxes under the *Artifact ms* list box; then click the *Add* button in this panel. To remove an AT pass, click on the appropriate line in one of the non-grayed out list boxes in this panel, and click the *Remove* button in this panel. To clear all AT passes in a given AT definition, click the *Clear ALL* button in this panel.

Because AT passes are executed sequentially, you may wish to alter the order in which a certain AT pass is applied. To move an AT pass up or down in the list, click on the appropriate line in one of the non-grayed out list boxes in this panel, and click the *Move Up* button or *Move Down* button, respectively.

Label. This list box displays whether each AT pass of a given definition should be applied to each channel *individual*ly, or whether instead it should be applied to every channel only if certain critical channels (*CRITchannel*s) would be tagged as artifactual. Click the drop-down box below the *Label* list box to select which of these options you want for this AT pass.

Critical channels. If you select *CRITchannel* from the drop-down box below the *Label* list box, this box will become active, allowing you to enter which channels should be used as the critical channels for artifact tagging. To add a new critical channel for this AT pass, enter an electrode into the *New channel* text box (e.g., **VEOG**) and click the *Add* button underneath the *New channel* text box. To remove the most recently entered critical channel for the currently highlighted AT pass, click the *Remove* button underneath the *New channel* text box.

Min/Max Values. This list box displays the minimum and maximum values that would be considered non-artifactual in a given AT pass. Put another way, these numbers represent the range of acceptable values in a given window. Enter the smallest non-artifactual value in the *min* text box, and the largest non-artifactual value in the *max* box underneath the *Min/Max Values* list box.

Reference ms. This list box displays the minimum and maximum milliseconds that should be used as the baseline for a given AT pass to subtract from the values in the window defined in the *Artifact ms* to determine whether an artifact is present in the data. Enter the earliest time point to be considered as part of this window in the *start* text box, and the latest time point for the window in the *end* box underneath the *Reference ms* list box.

Artifact ms. This list box displays the minimum and maximum milliseconds that should be used as the window in which to check for artifacts for a given AT pass. Enter the earliest time

point to be considered as part of this window in the *start* text box, and the latest time point for the window in the *end* box underneath the *Artifact ms* list box.

Skip electrodes. This list box displays the electrodes to skip in each AT pass for a given AT definition. These electrodes should be qualitatively different than the other electrodes in some way (for example, the HEOG and VEOG electrodes will have routinely larger waveform amplitudes than every other electrode). To add an electrode to the highlighted AT pass, enter an electrode (e.g., **HEOG**) into the *New electrode* text box (do not surround it with single quotes), then click the *Add* button underneath the *New electrode* text box. To remove the most recently added electrode in a given AT pass, click the *Remove* button underneath the *New electrode* text box.

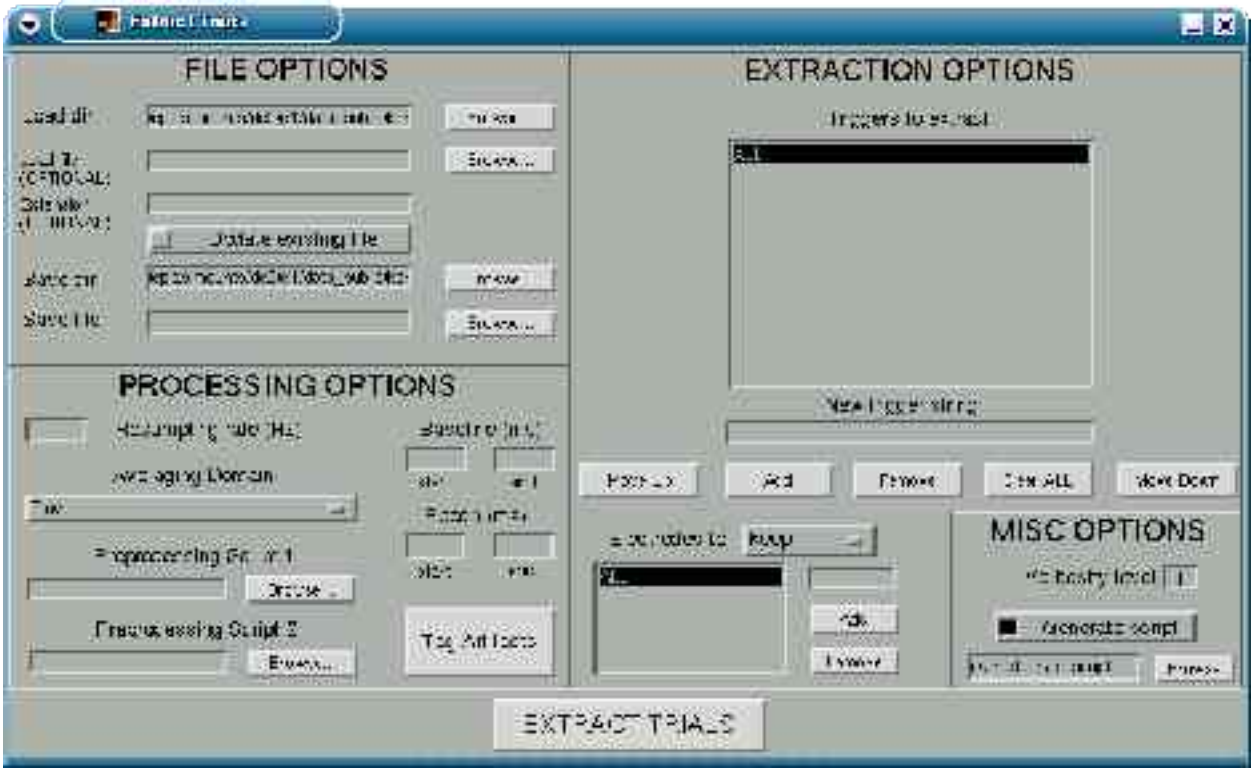
SCRIPT

Script directory. Type a full path name to the directory to which you want to save the script, or use the *Browse* button to search for one.

Script name, Run script ONLY. See p. 19. The default script name is **tag_artifacts_script**.

GENERATE_AT. Click this button to generate the AT definition script. The currently highlighted AT definition will be the one assigned to the **AT** environment variable that will define artifacts in subsequent processing.

Extract trials from data



In this window, you can set parameters that allow you to extract individual trials from a file or directory of files. Once you have set all the parameters in the panels listed below, click the *EXTRACT TRIALS* button to perform the data extraction.

FILE OPTIONS

Load dir. Type the full path name of the directory from which files (or a single file) should be loaded, or click the *Browse* button to search for one. The default value is the **default_load_dir**.

Load file. If you want to extract data from a single file, type its filename here, or click the *Browse* button to find one. If you want to extract data from all files in the *Load dir* directory, leave this field blank. The default is to leave this blank.

Extension. If there is a suffix that should be appended to locate the files you want to extract, add it here. The default is to leave this blank.

Update existing file. If you've already generated an average file that has a goodly amount of data in it, you may not want to have to spend the processing time necessary to regenerate the whole thing if you just want to add a few subjects to it. Click this box to add only those subjects that would be new to the file you specify in the next two boxes. The default setting is off.

Save dir. Type the full path name of the directory to which the extracted trials should be saved, of click the *Browse* button to search for one. The default value is the **default_save_dir**.

Save file. Type a filename to which you want to save that describe the trials you've extracted, or click the *Browse* button to find one.

PROCESSING OPTIONS

Resampling rate. If you want to resample your data to have a different number of samples per second, enter the number of samples per sample you want to use here. The default is to leave this blank.

Averaging domain. Click on this drop-down menu to select the domain in which you want to extract components during later toolbox work. The **Time** option will allow you to get components later that are defined in the time domain (e.g., P3, N400, LP). The **Frequency (amplitude)** option allows you to get components that are defined in the frequency domain (e.g., alpha, beta, gamma bands), with the original amplitude metric. However, it's more common to use the **Frequency (power)** option, as it essentially rectifies the frequency components to make them most comparable. You may also create time-frequency decompositions by selecting the **TFT** option. The default value is **Time**.

Preprocessing Script 1 (or 2). In each of these text boxes (if desired), enter the full path name of a preprocessing script to execute (perhaps generated by the “Add Stim” or “Filter Builder” windows?), or use the *Browse* button to find one.

Baseline (ms). If you would like to baseline correct your data, enter values that define the baseline to use in milliseconds. Baseline correction will subtract from every data point the mean amplitude of the waveform in the baseline window you define, thereby correcting any offset from zero present in your data. Enter the earliest time point to be considered as part of this window in the *start* text box, and the latest time point in the *end* box.

Epoch (ms). Enter values that define the epoch window you want to extract for each trial. Enter the earliest time point in the *start* box and the latest time point in the *end* box.

Tag Artifacts. Click this button to allow you to create an artifact tagging script, or to run an artifact tagging script. For more information on this window, see pages 24-26.

EXTRACTION OPTIONS

Triggers to extract. This list box displays logical expressions corresponding to the triggers you want to extract (e.g., **erp.ttype>0 & erp.ttype<256**). The default value is **ALL**.

To enter a new trigger extraction logical expression, type it in the *New trigger string* text box, then click the large *Add* button. To remove a logical expression, click on it in the *Triggers to extract* list box and click the large *Remove* button. To clear all trigger extraction logical

expressions, click the *Clear ALL* button. To move a logical expression up or down in the processing list, click on it in the *Triggers to extract* box and click the *Move Up* button or *Move Down* button, respectively.

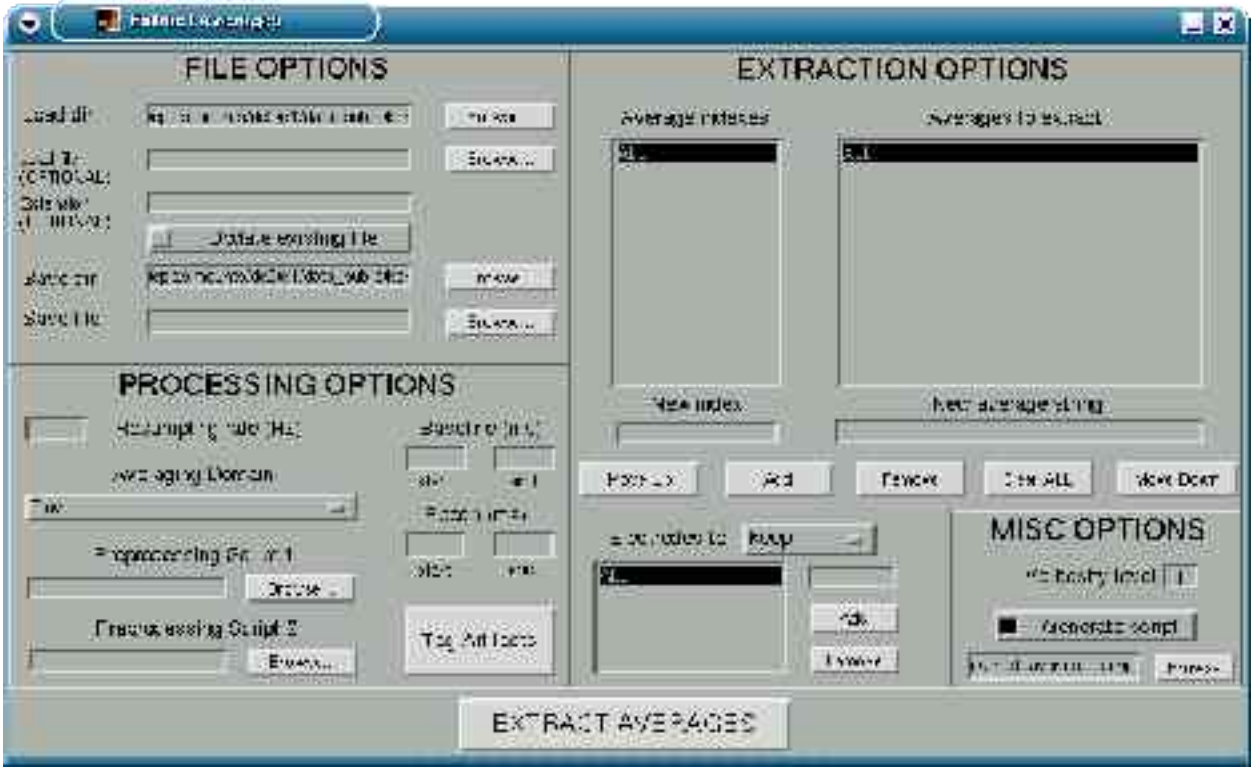
Electrodes to keep/skip. This drop-down box allows you to specify whether you want to keep or skip the data for the electrodes listed in the box below. The default is **keep**.

The list box below the drop-down menu lists the electrodes to be kept or skipped in the extraction. To add an electrode, type an electrode name (e.g., **P3**) into the skinny text box next to the list box (do not surround it with single quotes; the program will do this for you automatically), then click on the small *Add* button. To remove an electrode from the list box, click on it, then click on the small *Remove* button. The default value is **ALL**.

MISC OPTIONS

Verbosity level, Generate script. See p. 5. The default script name is **extract_trials_script**.

Extract averages from data



This window is nearly identical to the **Extract trials from data** window (pages 26-28), except that instead of a single *Triggers to extract* list box, there are now two list boxes that allow you to define the averages you want to create: *Average indexes* and *Averages to extract*. This function will also write an **erp.stim.catcodes** vector in the *Save file* that reflects the average definitions that you will define in these two list boxes. **erp.stim.catcodes.name** is created by the values you input to the *Average indexes* field, and **erp.stim.catcodes.text** is created by the values you input into the *Averages to extract* field.

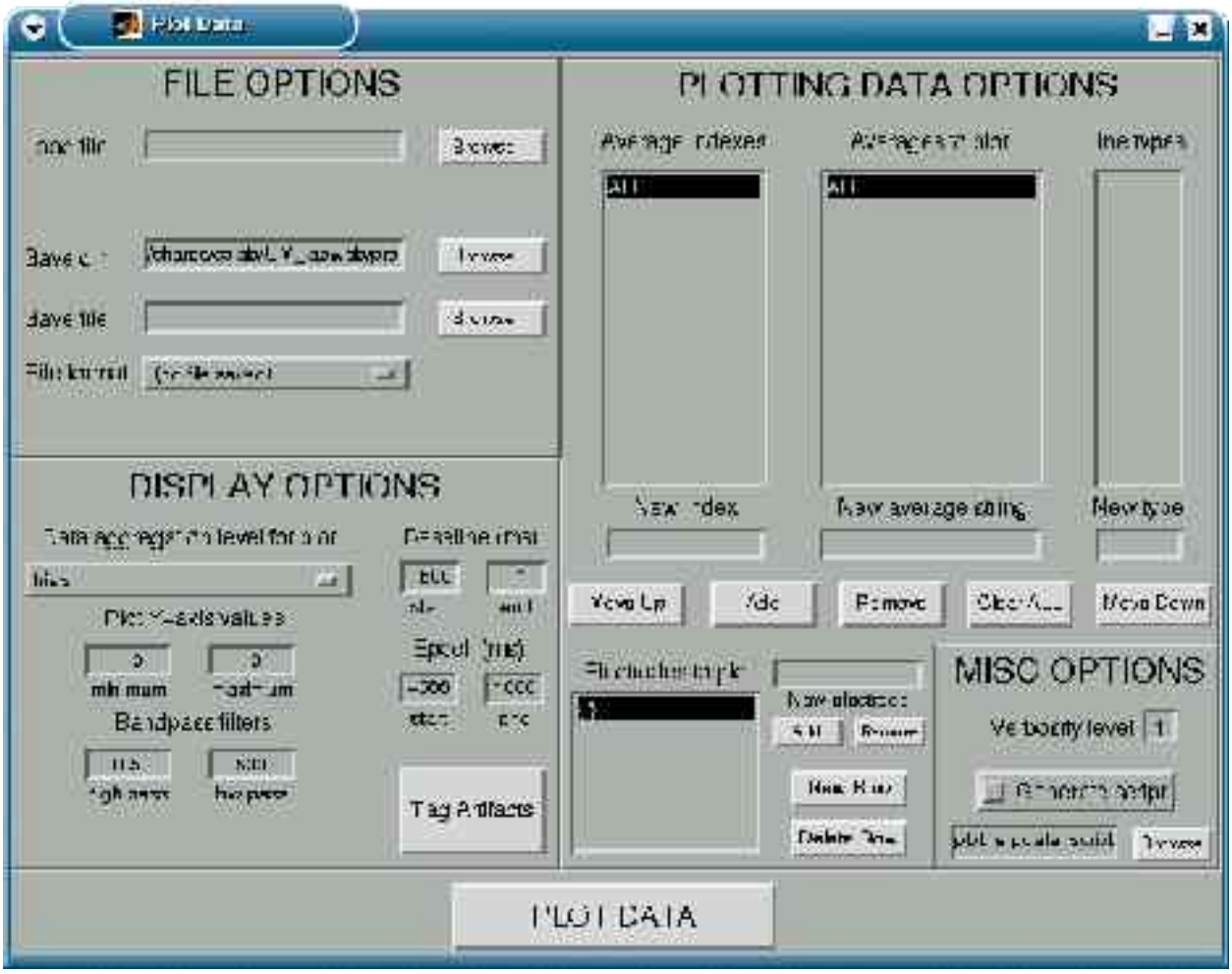
To enter a new average, type either a number (e.g., **137**) or a single character (e.g., **v**) that will serve as the identifier for the new average in the *New index* box, and type a logical expression that will define all trials to be included in that average (e.g., **erp.ttype>0&erp.ttype<10**), then click the *Add* button. Make sure to be consistent in using only numbers or single characters as *Average indexes* vectors, as the **erp.stim.catcodes.name** field must be a numeric or character vector.

To remove an average from the list boxes, click the line in either list box that corresponds to the average to be removed (the program will highlight the line in the other list box automatically), then click the *Remove* button. To clear all average definitions from the list boxes, click the *Clear ALL* button. To move an average up or down in the processing list, click the line in either list box that corresponds to that average, then click the *Move Up* button or *Move Down* button, respectively.

Average indexes. This list box displays the indexes of the averages to be created. Entries in this list must be either all numbers or all single characters. The default value is **ALL**.

Averages to extract. This list box displays the logical expressions corresponding to the trials that should comprise each average waveform. Each line in this list box should correspond to a logical expression that defines all trial types that should be included in a given average (e.g., **erp.ttype==21 | erp.ttype==121 | erp.ttype==221**). The default value is **ALL**.

Plot data



This window will allow you to plot data from a matrix of electrodes (defined in *Electrodes to plot*), with each electrode's plot starting at the *start* value in *Epoch (ms)* and ending at the *end* value. The individual lines that will be plotted are defined by each line in the *Average indexes*, *Averages to plot*, and *Line types* list boxes. Once you have set all the parameters in the panels listed below, click the *PLOT DATA* button to plot your data.

FILE OPTIONS

Load file. Enter the full path name to a filename that contains data you want to plot, or click the *Browse* button to find one.

Save dir. Enter the full path name to a directory to which you want to save the plots generated by this function, or click the *Browse* button to search for one.

Save file. Enter a file name to describe the plots generated by this function, or click the

Browse button to find one. The default value is the **default_save_dir**.

File format. Click on this drop-down box to select a file format to use in saving the plots from this function. The default is no file format, which will result in having no plots saved.

DISPLAY OPTIONS

Data aggregation level for plot. Click on this drop-down box to select a level of aggregation for the plots. You can choose from **trials** (which plots each individual trial within a category), **mean** (which plots the mean of each data point of all trials within a category), or **median** (which plots the median of each data point of all trials within a category). The default value is **trials**.

Plot Y-axis values. The minimum and maximum values for the vertical axis of each plot are defined here. Enter the smallest value to plot in the *minimum* text box and the largest value to plot in the *maximum* text box. The default values are -10 and 10, respectively.

Bandpass filters. The range of frequencies (in samples per second, or Hz) to be displayed in each plot is defined here. Enter the lowest frequency to display in the *high pass* box and the highest frequency to display in the *low pass* box. The default values are 0.5 and 500, respectively.

Baseline (ms), Epoch (ms), Tag Artifacts. See p. 28. In this case, the values in *Epoch (ms)* define the window to be plotted, while those in *Baseline (ms)* define the window to use for baseline correcting the plotted data.

PLOTTING DATA OPTIONS

To define a new average, the text boxes *New index* and *New average string* must not be empty. The box *New type* may be empty; however, if it is, you will have no control over the format and coloring of the line that will be plotted.

Once there is text in the *New index* and *New average string* text boxes, click the large *Add* button. To remove a line that would be plotted, click on the appropriate entry in either the *New index* or *New average string* list box (the entry in the other box will be highlighted automatically), then click the large *Remove* button. To clear all lines that would be plotted, click the *Clear ALL* button. If you would like to have the highlighted line drawn earlier or later in the plotting process, click the *Move Up* button or *Move Down* button, respectively.

Average indexes. This list box displays the descriptive labels for each line that will be plotted. To add a new descriptive label for a line to plot (e.g., **Aware: Correct**), type it in the *New index* text box.

Averages to plot. This list box displays the logical expressions that define the waveforms to be plotted. As each entry in this list box defines a single line, the logical expression entered into the *New average string* box should be complete enough to define all trials that should be included in a given line. To add a new line's logical expression (e.g.,

erp.stim.aware==1&erp.correct==1), type it in the *New average string* text box.

Line types. This list box displays the style in which each individual line will be plotted. Each style is a concatenation of "line style" and "color style" attributes.

There are four "line styles":
- **-** draws a solid line (e.g., _____)
- **--** draws a dashed line (e.g., ---------)
- **:** draws a dotted line (e.g., ...)
- **.-** draws a dot-dash line (e.g., ._._._)

And there are eight "color styles":
- **r** = red
- **g** = green
- **b** = blue
- **c** = cyan
- **m** = magenta
- **y** = yellow
- **k** = black
- **w** = white

To enter a new line style (e.g., **r-** for a red solid line, or **k.-** for a black dash-dot line), type it into the *New type* box.

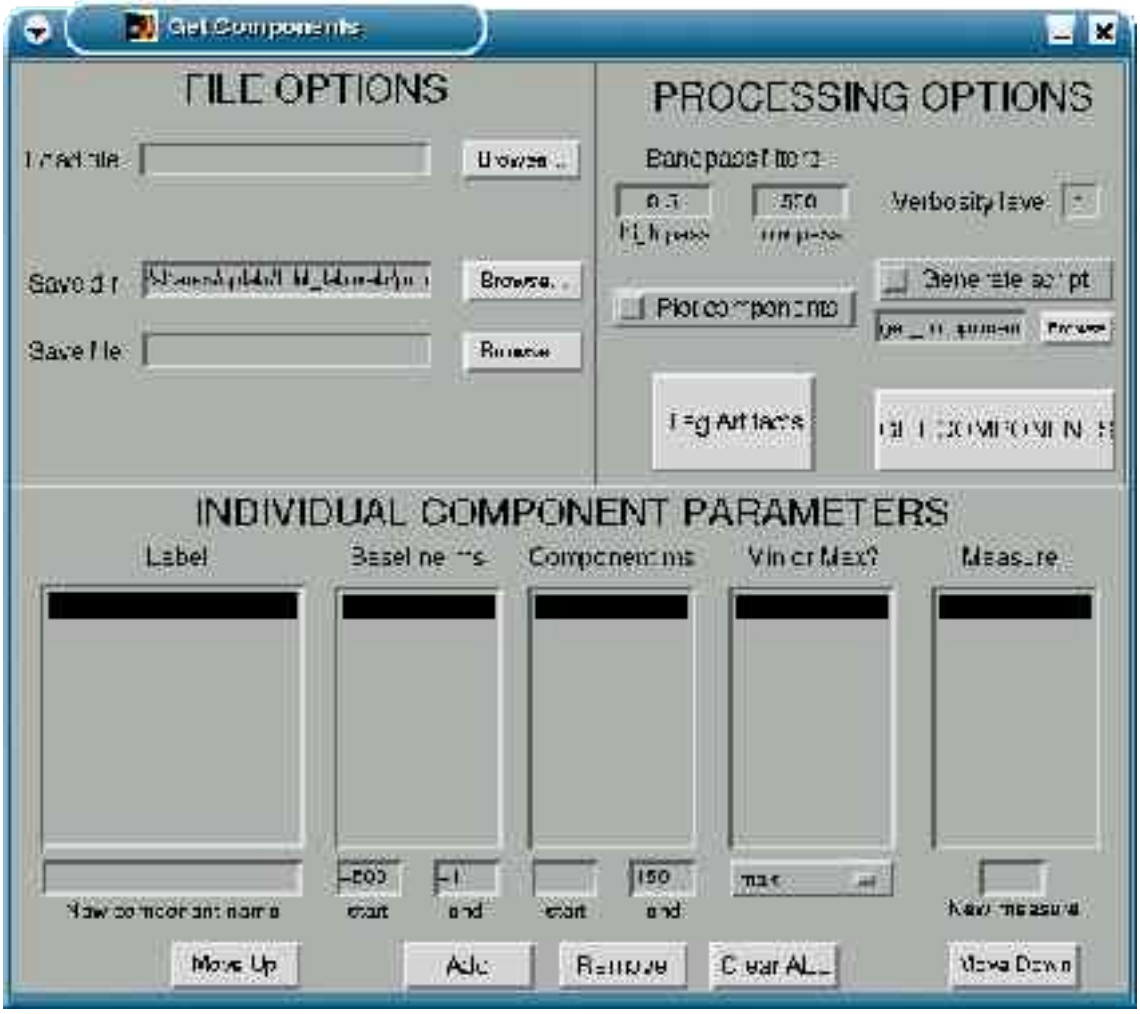
Electrodes to plot. This list creates a matrix of electrodes to plot. Electrodes should be entered in the order in which you want to see them displayed, as the plot window will be laid out precisely as you specify in this list box.

To add a new electrode to the current row (e.g., **C4**), type it in the *New electrode* text box (do not enclose it in single quotes; the program will do this automatically for you), then click the small *Add* button immediately below. To remove the most recently added electrode from the current row, click the small *Remove* button immediately below the *New electrode* text box. To add a new row of electrodes to plot, click the *Add Row* button. To delete an existing row of electrodes, highlight that row in the list box, then click the *Delete Row* button.

MISC OPTIONS

Verbosity level, Generate script. See p. 5. The default script name is **plot_erpdata_script**.

Get/Review basic components



This window allows you to get any number of basic components whose characteristics you define manually. Note that time-based components are defined in terms of milliseconds. You can also choose whether you'd like to review the components that were picked automatically (particularly useful for things like SCR that need hand-scoring!) by selecting whether you'd like to *Plot components* or not. By default, *Plot components* is off if you select *Get basic components* from the main window. In contrast, *Plot components* defaults to on if you select *Review basic components* from the main window. Otherwise, there's no difference between those two menu entries in the main *Actions* menu.

FILE OPTIONS

Load file. Type in the full pathname of a file from which to load the source data, or click the *Browse* button to find one.

Save dir. Type in the full pathname of a directory into which to save component scores, or

click the *Browse* button to locate one. The default value is the **default_save_dir**.

Save file. Type in the filename to which you want to save component scores (both a **.mat** and a tab-delimited **.dat** file will be saved), or click on the *Browse* button to find one.

INDIVIDUAL COMPONENT PARAMETERS

This panel displays information about the components you've defined. To define a new component, *New component name*, *start* and *end* underneath *Baseline ms*, and *start* and *end* underneath *Component ms* must not be empty. Once these fields are filled, however, you may add a component by clicking the *Add* button. To remove a component, click on the line appropriate to it in the *Label*, *Baseline ms*, *Component ms*, *Min or Max?*, or *Measure* list boxes (the corresponding lines in the other list boxes will be highlighted automatically), then click the *Remove* button. To remove all component definitions, click the *Clear ALL* button. If you'd like to have a component output before or after other components, click on its corresponding line and click the *Move Up* button or the *Move Down* button, respectively.

Label. This list box displays the descriptive names you've assigned to each component. To name a new component (e.g., **FZ**), type the name into the *New component name* text box (do not enclose the name in single quotes; the program will do this for you automatically).

Baseline ms. This list box displays the windows to use as the component baselines to subtract from the peaks obtained in the windows defined in *Component ms*. To define a new time-based baseline window, type the earliest millisecond for the window in the *start* text box under *Baseline ms*, and the latest millisecond in the *end* text box under *Baseline ms*. The defaults are **-500** and **-1**, respectively. If you would prefer not to baseline correct the new component, enter **0**s in the *start* and *end* boxes.

For frequency-based components, **0**s should be entered in the *start* and *end* boxes, as frequency-based components (or activity bands) should not be baseline corrected.

Component ms. This list box displays the windows in which to search for component measures. To define a new time-based component window, type the earliest millisecond for the window in the *start* text box underneath *Component ms*, and the latest millisecond in the *end* text box under *Component ms.* The defaults are **1** and **150**, respectively.

To define a new frequency-based component window, type the lower frequency in the component band in the *start* box, and type the higher frequency in the *end* box.

Min or Max? This list box displays whether the minimum activity in a window should be taken as the peak for each component, or whether instead the maximum activity in the window should be the peak. Click this drop-down box to select whether the **min**imum or **max**imum activity should be the peak for a new component. The default is **max**.

Measure. This list box displays the component measures that will be extracted for each component. There are four measures that can be extracted:

- **d** = median activity in the component window
- **m** = mean activity in the component window
- **p** = peak activity in the component window
- **l** = latency of the peak activity in the component window

To add measures for a new component, type them in succession in the *New measure* text box (e.g., **dlp** for median, peak latency, and peak measures; or **m** for mean). The default is blank, which is equivalent to typing **mpl**.

PROCESSING OPTIONS

Bandpass filters. If desired, you can have an additional bandpass filter roll over your data before picking components. To enter a new bandpass specification, type the lowest frequency to include in the *high pass* text box, and the highest frequency to include in the *low pass* text box. The defaults are **0.5** and **500**, respectively. If you'd like to leave your data alone before picking components, leave both the *high pass* and *low pass* boxes blank.

Plot components. If you would like to view plots of the components you've picked, and possibly adjust component scores by hand, click this option on. If not, click it off.

You can navigate through the plotted components with the following controls:

Mouse buttons:

Left	Accept current component and go forward to the next one
Middle	Go back one component
Right	Modify current component's location in time

Number pad keys:

7 = go forward 5 trials	8 = raise amplitude axes	9 = go forward 1 component
4 = reduce time display	5 = reset axes	6 = increase time display
1 = go back 5 trials	2 = lower amplitude axes	3 = go back 1 component

Keys:

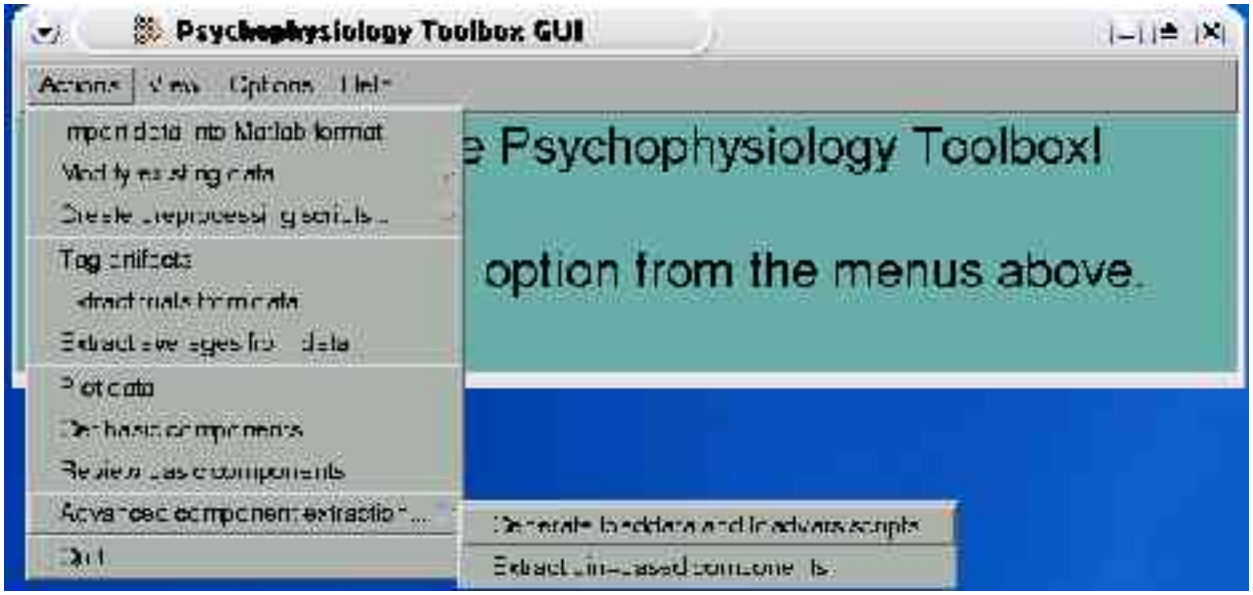
r = reject (time and amplitude -9)	x = exit review without saving
z = zero response (time and amplitude 0)	s = save .mat and .dat data files

Tag Artifacts. See pages 25-27.

Verbosity level, Generate script. See p. 5.

GET COMPONENTS. Once you've defined all the components you want to get, click this button to run the extraction function, which will save .mat and .dat formatted files with the component scores in them.

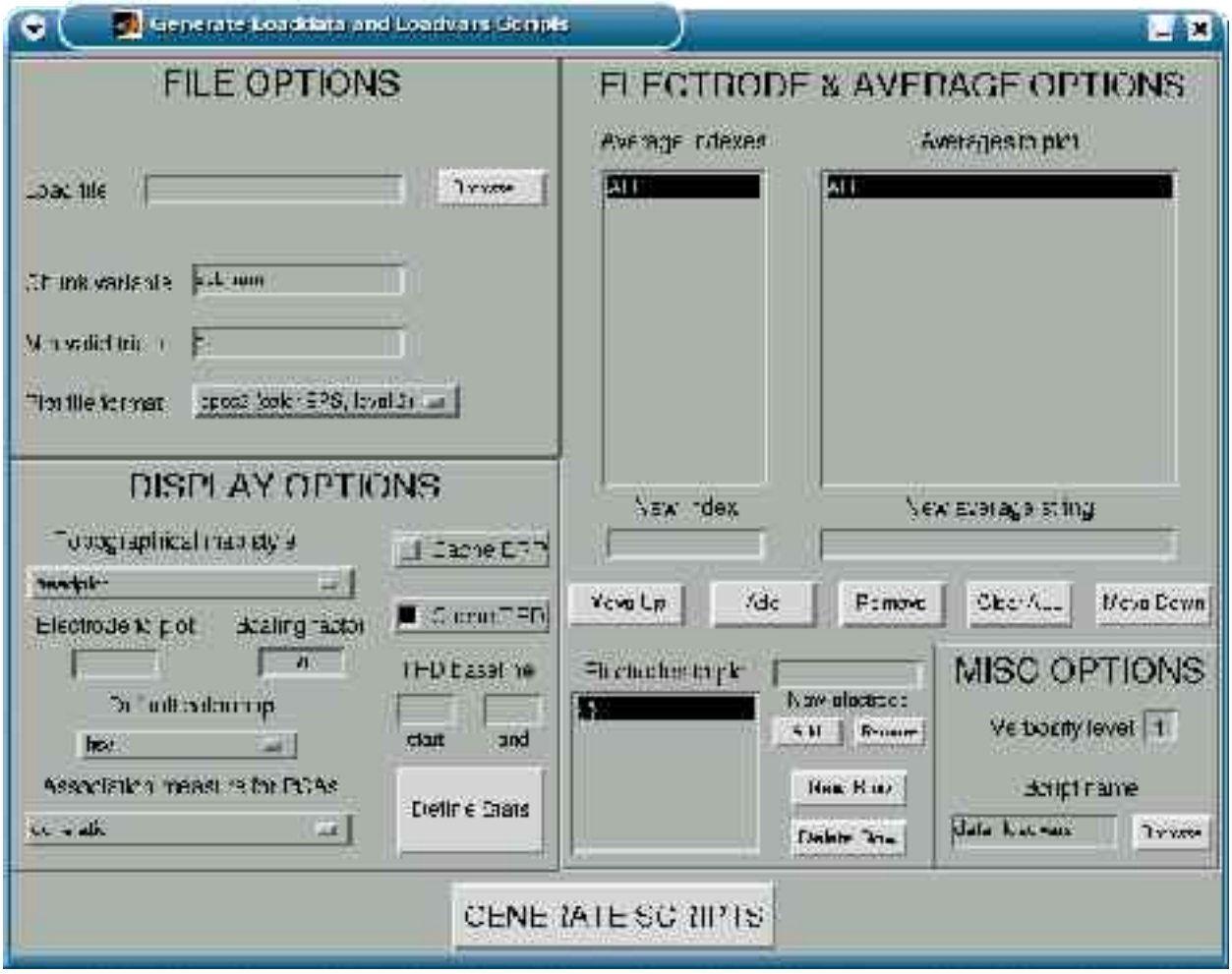
Advanced component extraction



In this submenu, you can either *Generate loaddata and loadvars scripts* that will be used to *Extract bin-based components*, or you can just *Extract bin-based components*, using pre-existing **_loaddata** and **_loadvars** scripts. These two functions require the most savvy with the toolbox to use profitably, but then again, they wouldn't be under an “advanced” section if they didn't, right?

Keep in mind that all functions here operate on bins, rather than milliseconds. Hence, the windows you specify are dependent on the sampling rate of the current data file.

Generate loaddata and loadvars scripts



This window will allow you to set all the parameters necessary to create **_loaddata** and **_loadvars** scripts that can be used to conduct advanced component extractions. Keep in mind that all functions here operate on bins, rather than milliseconds. Hence, the windows you specify are dependent on the sampling rate of the current data file.

FILE OPTIONS

Load file. Type the full path name of a file from which to load data (and for which **_loaddata** and **_loadvars** scripts will be created) in this text box, or click the *Browse* button to find one.

Chunk variable. This text box gives the **erp** subfield by which to chunk components. It is recommended that you keep this at the default value of **subnum**, unless you have a <u>really</u> compelling reason to do otherwise.

Min valid trials. This text box sets the minimum number of trials required to define a valid average. The larger the number set here, the higher the probability that certain averages will be set to missing. The default value is **1**.

Plot file format. This drop-down box sets the file format to use when writing out plots. Further details about each file format may be obtained by clicking on the drop-down box. The default value is **epsc2**.

DISPLAY OPTIONS

Topographical map style. This drop-down box sets whether to plot head maps as interpolated **headplot**s or as rectangular **box/grid plot**s. If most or all of your electrodes are scalp electrodes, use the **headplot** option. If most or all of your electrodes are peripheral electrodes, use the **box/grid plot** option. The default option is **headplot**.

Electrode to plot. If this box is blank, the average waveforms that will be plotted will involve the mean of all electrodes in the data file. If this text box has an electrode in it (e.g., **CZ**), the average waveforms that will be plotted will involve the data for only that electrode. The default value is blank.

Scaling factor. This text box sets the number of standard deviations from the mean activity in the epoch window are used as the anchor points in the topographical color maps. The default value is **.8** SD.

Default colormap. This drop-down box sets the default colormap to be used in all plots, if no colormap is specified. The following options are available:

- **hsv** = the standard "blue is more negative, red is more positive" colormap
- **gray** = the standard "black is greater, white is smaller) colormap
- **jet** = a variant of the **hsv** option
- **bone** = a variant of the **gray** option, with some blue tint added to the white to mimic X-rays
- **spring**, **summer**, **autumn**, **winter** = seasonal color palettes
- **cool**, **hot** = palettes of only more muted or more striking colors
- **colorcube**, **prism**, **flag** = colormaps with abrupt shifts between relatively few colors
- **copper**, **pink**, **white** = colormaps with various shades of one basic color

The default option is **hsv**.

Association measure for PCAs. This drop-down box allows you to select whether you would like to use a **correlation** (standardized covariance), **covariance** (unstandardized covariance), **SSCP** (covariance with variances on the diagonal), **data**, or **data scaled** association matrix for PCA-based analyses. The default option is **correlation**.

Cache ERP. If this option is selected, the data files resulting from non-TFD analyses will be cached in **dir_data_cache**. Otherwise, these files will not be cached. The default is off.

Cache TFD. If this option is selected, the data files resulting from time-frequency decomposition (TFD) analyses will be cached in **dir_output_data**. Otherwise, these files will not be cached. The default is on.

TFD baseline. If you want to specify a custom baseline for TFD analyses, enter the earliest bin to use (relative to each trigger) in the window in the *start* text box, and the latest bin to use (relative to each trigger) in the *end* text box. If you leave these boxes blank, the entire epoch will be used as the baseline. The default values are blank.

Define Stats. This button will bring up a window that will allow you to define statistical comparisons to perform on different groups. This window's operation is detailed on pages 41-42.

ELECTRODE & AVERAGE OPTIONS.

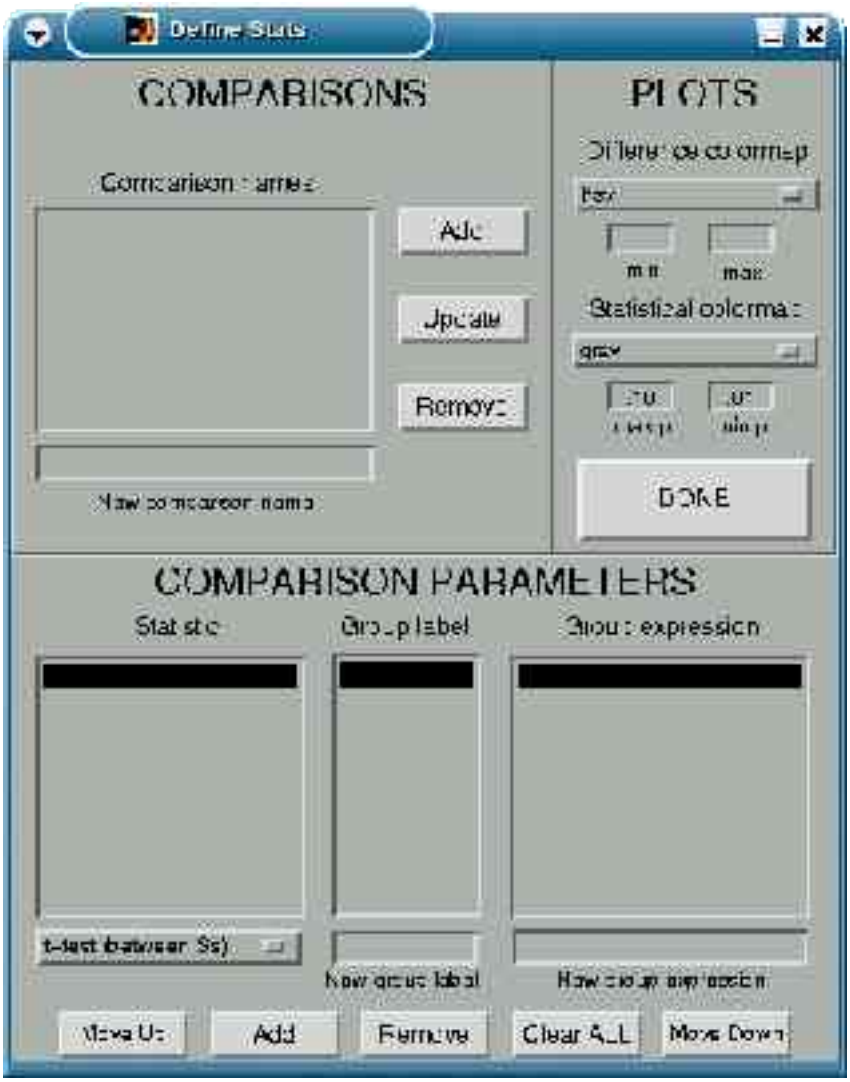
Average indexes, Averages to plot. If your *Load file* does not contain the averages you want, you can use these listboxes to generate them, as detailed on pages 32-33. Otherwise, leave these list boxes blank.

Electrodes to plot. See page 33 for details on how to define this list box. The precise order of electrodes is extremely important for **box/grid plot**s, as it is in the "Plot Data" function. However. it is far less important for **headplot**s, as electrode positions will be assigned automatically, based on matches between each electrode's name and its presumed topography in standard electrode naming systems. However, you must be sure to include all electrodes that you want plotted in this list box, even if you're using the **headplot**, as you want to interpolate as little as possible.

MISC OPTIONS

Verbosity level, Script name. See p. 5. The default script name is the filename in *Load file* with **_loadvars** appended to the end of it. A script with the filename and **_loaddata** will also be written out.

You should change this name only if you want to *Extract bin-based components* from a file that is altered beyond creating additional averages in this script. To create such a file, modify the **_loaddata** script to create a data set that meets your needs (e.g., that selects only certain subjects or certain trial types from a huge, central data file).



In this window, you can define any number of statistical comparisons to be performed on components picked in *Extract bin-based components*. Each comparison consists of one statistic and two (or more, in the case of ANOVAs and Kruskal-Wallis analyses) groups to compare. You may also tweak the appearances of all group and statistical difference plots.

COMPARISONS

Comparison names. This list box displays the descriptive labels for each comparison that you want to conduct. To aid in plotting, these labels should include only alphanumeric characters or underscores. To add a new comparison, type a descriptive name into the *New comparison name* text box, then click the *Add* button in this panel. To update a highlighted comparison (N.B.: This should be done automatically for you every time you press the *Add*, *Remove*, or *Clear ALL* buttons in the COMPARISON PARAMETERS panel), click the *Update* button. To remove a highlighted comparison, click the *Remove* button in this panel.

COMPARISON PARAMETERS

This panel provides details for a single statistical comparison to be performed. To add a group to the comparison, the *New group label* and *New group expression* text boxes must be filled. Once these fields are filled, however, you may add a group by clicking the *Add* button in this panel. To remove a group, click on the appropriate line in either the *Group label* or *Group expression* list boxes (the program will highlight the corresponding line in the other list box automatically), then click the *Remove* button in this panel. To clear all group definitions from the current comparison, click the *Clear ALL* button.

Because groups are plotted in the order in which they appear in the list boxes, you may wish to rearrange their positions once they are defined. To move a group up or down in the list boxes, click on the appropriate line in either list box, then click the *Move Up* button or the *Move Down* button, respectively.

Statistic. This list box displays the current statistic that will be computed for this comparison. The list box will display the name of the statistic, but it will not display whether the statistic is computed between- or within-subjects. Click on the drop-down box below the *Statistic* list box to select a statistic. There are currently seven statistics that can be computed:

- **t-test (between subjects)** – parametric, two-group test
- **Wilcoxon (between subjects)** – non-parametric, two-group test
- **ANOVA (between subjects)** – parametric, multi-group test
- **Kruskal-Wallis (between subjects)** – non-parametric, multi-group test
- **correlation** – parametric, two-variable test
- **t-test (within-subjects)**
- **Wilcoxon (within-subjects)**

Group label. This list box displays the descriptive labels for each group. To add a new group's descriptive label, type the name in the *New group label* text box.

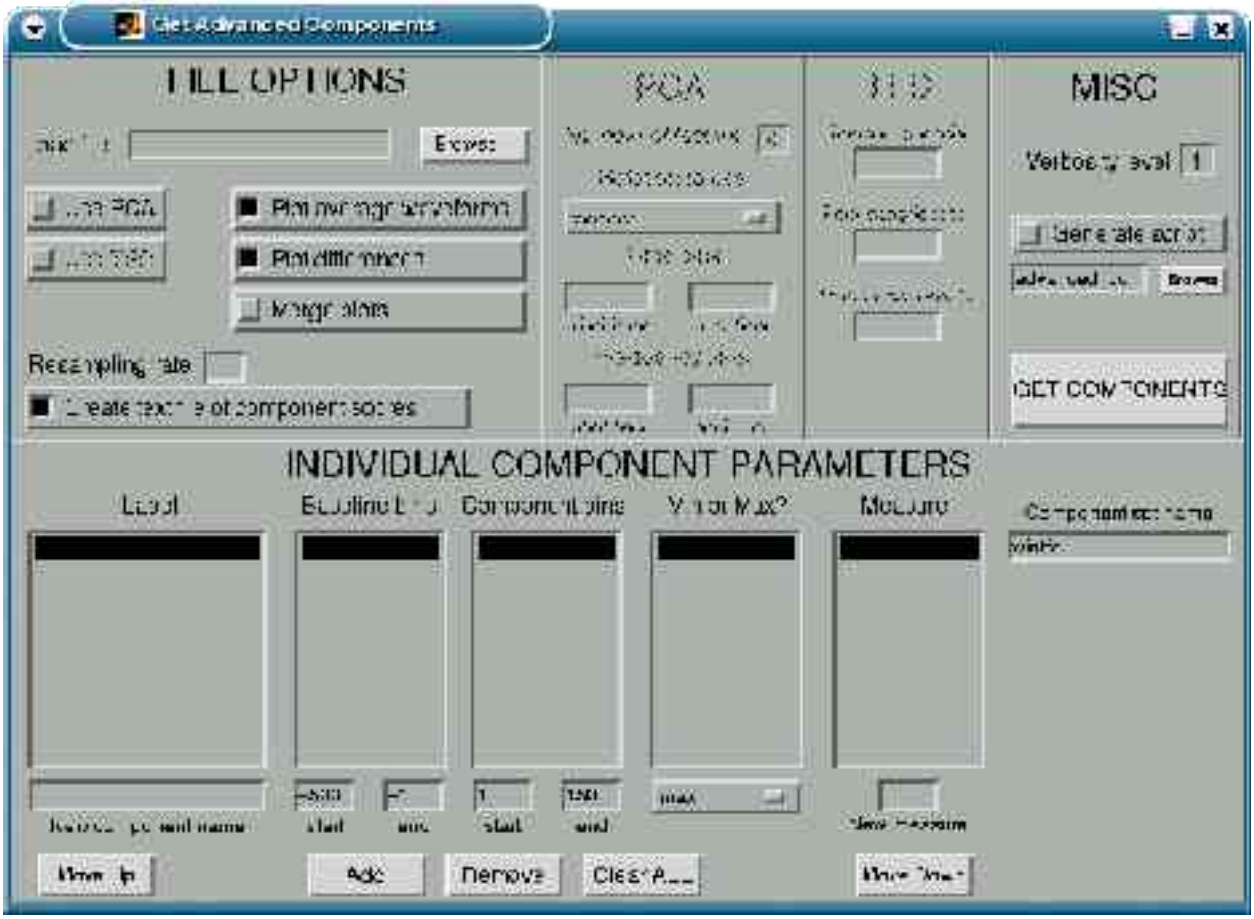
Group expression. This list box displays the logical expressions that define each group. To add a new group's logical expression, type the name in the *New group expression* text box.

PLOTS

Difference colormap. For details on the colormaps that may be selected, see page 39. The default value is **hsv**. If the *min* and *max* text boxes underneath the drop-down box are empty, data in each plot will be scaled automatically to accommodate the minimum and maximum waveform values in the plot. However, you may also set the range of values you want plotted on the vertical axis. Type the smallest value to plot in the *min* text box, and type the largest value to plot in the *max* text box.

Statistical colormap. For details on the colormaps that may be selected, see page 39. The default value is **gray**. You may also specify a range of p-values to plot. Type the largest p-value to plot in the *max p* text box, and the smallest p-value to plot in the *min p* text box. The default values are **.10** and **.01**, respectively.

Extract bin-based components



With this function, you can pick components from predetermined windows using predefined time or frequency windows, predefined time-frequency decomposition (TFD) windows, time or frequency components derived from principal components analysis (PCA; aka single-value decomposition or SVD), or PCA/SVD-derived TFD components. Options that are not valid for the current combination of options will be grayed out. You may also select to plot average waveforms, pre-defined group differences, and merge individual plots into a single .pdf file (not available on Windows platforms!).

FILE OPTIONS

Load file. This text box should contain one of three things:

- the full path name of a file for which **_loaddata** and/or **_loadvars** scripts have been written
- the filename of a file for which **_loaddata** and/or **_loadvars** scripts have been written
- a string that defines a unique set of **_loaddata** and/or **_loadvars** scripts

You may type any of these three in the text box, or click the *Browse* button to locate a file.

Use PCA. If this option is selected, components will be selected algorithmically, using PCA

analyses to decompose the aggregate waveform in your data into separate components. The PCA options will also be enabled. Otherwise, components will be selected using predefined windows, and the PCA options will be grayed out. The default is **off**.

Use TFD. If this option is selected, components will be selected using a combination of time and frequency, rather than selected using only time or frequency information to define components. The TFD options will also be enabled. Otherwise, components will be selected using only time or frequency information, and the TFD options will be grayed out. The default is **off**.

Resampling rate. If this text box is left blank, data will not be resampled. Otherwise, data will be resampled to have the number of samples per second you type into this box. The default is blank.

Create text file of component scores. If this option is selected, an ASCII data file of component scores will be written out, along with the Matlab-formatted data file. The default is **on**.

Plot average waveforms. If this option is selected, average waveforms displaying each component that is extracted will be plotted. The default is **on**.

Plot differences. If this option is selected, group differences and statistics that are defined in the **_loadvars** script for this *Load file* will be plotted. The default is **on**.

Merge plots. If this option is selected and you're not running Matlab on the Windows operating system, the various plots that are created will be merged into a single .pdf file. The default is **off**.

PCA (enabled only if *Use PCA* is selected)

Number of factors. In this text box, you must specify the number of factors to extract in the PCA analysis. The default is **0** (which allows you to specify the number of factors to use after inspecting the scree plot); however, this doesn't work quite right yet. It's best to specify a theoretically meaningful and small number of factors (e.g., **3**), look at the plots, then modify this number as needed in subsequent runs.

Rotation to use. This drop-down box specifies whether a **varimax** (orthogonal) or **promax** (oblique) rotation should be used, or whether **none** of these rotations should be used (leaving the factors unrotated). The default is **varimax**.

Time bins. The name of these text boxes is deceptive. It refers to either the epoch range of time bins from which components should be extracted or the range of frequencies from which components should be extracted. For time components, type the earliest time bin to use in the *start time* box, and type the latest time bin to use in the *end time* box. For frequency components, type the lowest frequency to use in the *start time* box, and type the highest frequency to use in the *end time* box.

Frequency bins (enabled only if *Use TFD* is enabled). When both *Use PCA* and *Use TFD*

are enabled, you should enter the time bins to use in the *Time bins* text boxes above, and the frequency bins to use in these *Frequency bins* text boxes. Type the lowest frequency to use in the *start freq* box, and type the highest frequency to use in the *end freq* box.

TFD (enabled only if *Use TFD* is selected)

Time sample rate.

Freq sample rate.

Frequency weight. Type in a numerical weight to use to emphasize high-frequency activity in selecting components.

MISC

Verbosity level, Generate script. See p. 5. The default script name is **advanced_components_script**.

INDIVIDUAL COMPONENT PARAMETERS (enabled only if *Use PCA* is not selected)

See pages 35-36 for details on how to specify components using this collection of list boxes and text boxes. In this function, there is also an additional *Component set name* that must be specified. To specify a descriptive *Component set name* (e.g., **componentsp1n1p3lp** for a components set with P1, N1, P3, and LP components), type it into the *Component set name* box. The default is **components**.

Create master script

With this function, you can create a master script that will run a number of scripts successively to create a completely automated data processing routine.

Scripts to combine. This list box displays the scripts that are to be combined into a master script. To add a new script to the list, type its full path name into the text box underneath the list box (or click the *Browse* button to find one), then click the *Add* button. To remove a highlighted script from the list, click the *Remove* button. Because scripts will be processed in the order that they appear in the list box, you may wish to move them up or down once they have been added. To move a highlighted script up or down the list, click the *Move Up* button or the *Move Down* button, respectively.

Choose master script name. This text box gives the name of the master script to be generated. To change this name, type the new name in the text box, or click the *Browse* button to find one. The default is **master_script**.

Create Master Script. Click this button to generate the master script detailed in *Scripts to combine* in the **default_script_dir**.