

ERP PCA Toolkit 2.68

Tutorial

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Thanks to Tim Curran for being a patient, long-suffering beta-tester, to Scott Miller for his extensive, helpful editing of the Tutorial document, to Dennis Molfese for his unstinting support for the development of the 2.00 version of the Toolkit, and Don Tucker for first suggesting to me that it might make some sort of mad sense to visualize the ERP PCAs by multiplying the factor loadings by the factor scores.

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About the ERP PCA (EP) Toolkit

Uses

The EP Toolkit is a collection of software tools for enhancing analysis of ERP data. It runs in MATLAB and is meant to be an adjunct to the various ERP software suites currently used by researchers. The Toolkit contains functions for improved artifact correction, trial averaging, file editing, data viewing, factor analysis, and inferential analysis. The EP Toolkit has three major goals:

- 1) Facilitating multivariate decomposition of ERP data in order to better characterize their components. This is done by:
 - a) providing automated routines for conducting principal components analysis (PCA), including the two-step sequential PCA procedure.
 - b) providing a range of rotation options, including facilitated access to EEGLAB's independent components analysis (ICA) Infomax rotation.
 - c) translating PCA results back into voltage space so that they can be transparently evaluated as ERP waveforms and exported into various file formats for additional analysis.
- 2) Facilitating analysis of noisy data, including data from developmental and clinical research populations. This is made possible by:
 - a) multivariate techniques for automated removal of blink, saccade, and motion artifacts from session data using the Multiple Algorithm Artifact Correction (MAAC) procedure (Dien, in preparation).
 - b) implementation of robust ANOVA statistics that are more resistant to noisy data than conventional ANOVA statistics.
 - c) use of trimmed means for trial averages and robust ANOVAs for inferential analyses.
 - d) provision of quality control (QC) measures that allow for easier detection of problematic data files.
- 3) Supporting analysis of multi-modal data and combined analysis techniques. This is made possible by:
 - a) application of fMRI artifact correction procedures.
 - b) provision of ERP, spectral, and time-frequency measures.
 - c) support for eye-tracking data (not yet documented).

The EP Toolkit is freely available under the GNU General Public License version 3. It is intended to be a research tool only and must not be used in clinical practice.

Citation

When used for a publication, please provide credit in the methods section and let me know that you have used it. I am hoping to eventually get some grant funding to support

continued development of this toolbox. This in turn would benefit you the user. The appropriate citation is:

Dien, J. (2010). The ERP PCA Toolkit: An open source program for advanced statistical analysis of event-related potential data. *Journal of Neuroscience Methods* 187(1), 138-145.

Website

You can always download the latest version of the EP Toolkit from the following address: <http://sourceforge.net/projects/erppcatoolkit/>

Mailing List

If you wish to be informed of new releases, please be sure to sign up for the mailing list: <https://lists.sourceforge.net/lists/listinfo/erppcatoolkit-support>

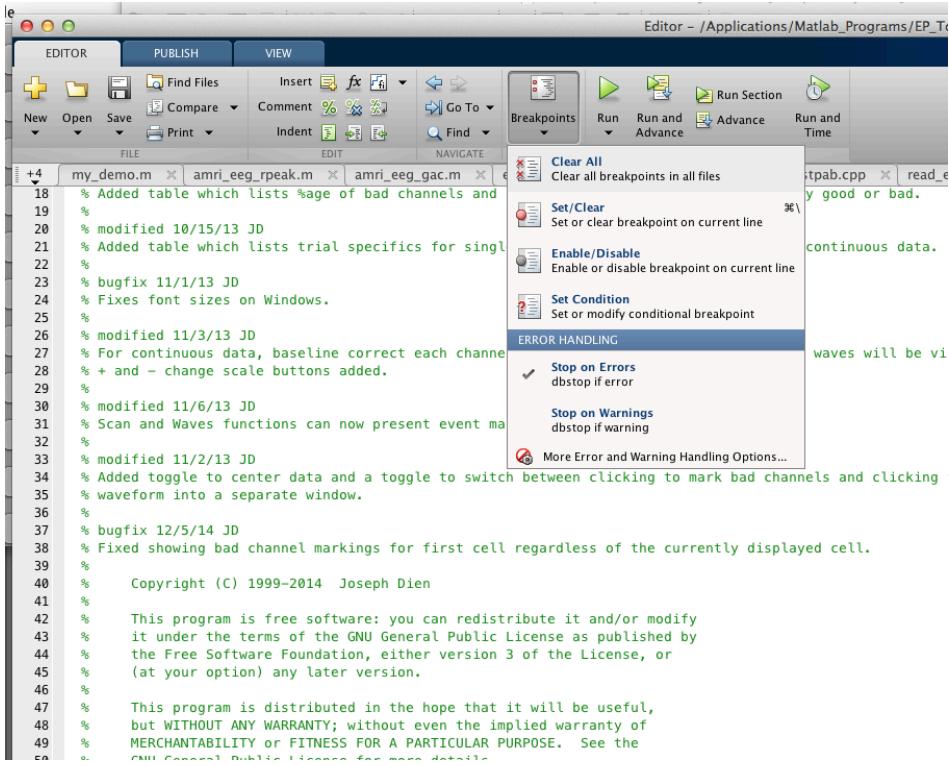
Suggestions and Bug Reports

Please feel free to send me suggestions or bug reports at: jdien07@mac.com.

When sending a bug report, please include the output you get from typing the command `ver` in the Matlab command window, the messages the EP toolkit generates when first starting it up, a copy of the file that you are trying to use, a screenshot with the settings you used, and an exact description of the problem and any error messages.

To get a screenshot, on the Mac simultaneously press command, control, shift, and 4 (yeah, it's a bit tricky). The cursor will turn into a crosshairs. Use it to select the part of the screen you wish to include in the snapshot (it will generate a gray selection region as you click and drag). Paste the resulting picture into the e-mail. On a Windows computer, click on the window you wish to make a picture of (only it will be in the picture), then press alt and prtscrn. Then paste the resulting screenshot into your e-mail.

It will be especially helpful if you can turn on the Stop on Errors setting and trigger the error again. At this point Matlab will be in a troubleshooting mode, denoted by a K>> prompt in the command window. Then type `save test;` This will have the effect of saving the Matlab session to a file named test.mat. If you are on a Windows computer, it may label it a microsoft access table but don't worry about it. What's going on is that Matlab produces data files that have .mat as the suffix. Windows computers think that any file that has .mat as a suffix is a microsoft access table shortcut and labels them that way but they're really not. Anyway, if you send me the file it'll be particularly helpful to me. The files will often be too large for e-mail. Internet services like Dropbox and Box and Google Drive can be used.



Please do not assume that I will be familiar with the problem that you have run into. Most bugs are triggered by a specific combination of circumstances and it is likely that I have never seen it before myself, otherwise I would already have fixed it. Also, please keep in mind that although I try hard to fix problems that arise, I literally have to do this work on my spare time as I do not have grant support and my time is limited.

Getting Started with Principal Components Analysis

You may find Dien and Frishkoff (2005) to be a useful introduction to the topic of applying PCA to ERP datasets. Dien (2012) provides a more advanced treatment, focusing on the different choices one must make as one progresses through a PCA of ERP data. Dien, Khoe, & Mangun (2007) provide a detailed consideration of ICA and how it contrasts with PCA rotations.

System Requirements

This package has been tested for use on an Intel Macintosh under OS X 10.12.4 using version 9.2 (2017a) of MATLAB. The toolbox has also been used somewhat in Windows 7 with MATLAB 7.11 (2010b) but has not been fully tested so caveat emptor. I would be happy to help users troubleshoot platform incompatibilities if they are willing to work through them with me. I don't support anything earlier than Matlab 2016a as I

just don't have the time to juggle all the myriad differences between the versions.

I mostly work with EGI files and so the Toolkit has mostly been tested with them, although it has received some use with other file formats. I would be happy to work with users to better support the existing list of file formats or to add new ones. The Toolkit functions also need significant amounts of RAM. I would suggest a minimum of 2GB and preferably at least 4GB, depending on the size of the datafiles. Also, the faster the computer the better as the algorithms it implements are quite computationally intensive.

Supported File Types

The EP Toolkit currently reads EGI Simple Binary (EGI .raw) including the epoch-marked variant for session files only, EGI EGIS (BESA .raw), EGI Matlab, EGI MFF, EEGLAB set/study including the Widmann variant, ERPlab erp, Neuroscan average, text, Biosemi BDF, Neuromag FIFF, BrainVision EEG/DAT/SEG, and EP Toolkit format files. The EP Toolkit can read some subject and trial data (like accuracy and reaction time and condition) from information encoded in the trigger channel of BrainVision files. An example E-Prime file (AP2-LD-Assoc-CB1.es2) is included in the Documentation directory. There is an attempt to support reading .EDF files but it needs to be tested and an initial attempt failed. I would be happy to complete this implementation if someone with access to .EDF files could help me work out the remaining issues. It currently can write out EGI Simple Binary (EGI .raw), EGI EGIS (BESA .raw), EEGLAB set/study, ERPlab erp, text, Neuromag FIFF, and EP Toolkit format files. The support for both reading and writing FIFF files is currently limited as it is a very complex file format.

Credits

Thanks to Dennis Molfese for helping support the development of the 2.0 version of the Toolkit.

Also, credit should be given to the algorithms used for the rotations:

VMAX - Varimax

Kaiser, H. F. (1959). Computer program for varimax rotation in factor analysis. *Educational and Psychological Measurement, 19*(3), 413-420.

PMAX - Promax

Hendrickson, A. E. & White, P. O. (1964). Promax: A quick method for rotation to oblique simple structure. *The British Journal of Statistical Psychology, 17*, 65-70.

IMAX - ICA Infomax

Delorme, A. & Makeig, S. (2004). EEGLAB: An open source toolbox for analysis of single-trial EEG dynamics including independent component analysis. *Journal of Neuroscience Methods, 134*, 9-21.

Gradient Projection method used for the following rotations:

QMAX - Quartimax

QMIN - Quartimin

OMIN - Oblimin (gamma=0 tends to be recommended)

CRFE - Crawford-Ferguson family

MINE - minimum entropy

IPSC - Bentler's invariant pattern simplicity criterion

TIIC - Comrey's tandem II criterion

GMIN - Geomin

MMER - McCammon minimum entropy ratio

Jennrich, R. I. (2001). A simple general procedure for orthogonal rotation.

Psychometrika, 66, 289–306.

Jennrich, R. I. (2002). A simple general method for oblique rotation. *Psychometrika*,

67(1), 7-20.

Also, credit for the rotational criteria themselves:

VMAX - Varimax

Kaiser, H. F. (1958). The varimax criterion for analytic rotation in factor analysis.

Psychometrika, 23, 187-200.

PMAX - Promax

Hendrickson, A. E. & White, P. O. (1964). Promax: A quick method for rotation to oblique simple structure. *The British Journal of Statistical Psychology*, 17, 65-70.

IMAX - ICA Infomax

Bell, A. J. & Sejnowski, T. J. (1995). An information-maximisation approach to blind separation and blind deconvolution. *Neural Computation*, 7(6), 1129-1159.

QMAX - Quartimax

Carroll, J. B. (1953). Ananalytical solution for approximating simple structure in factor analysis. *Psychometrika*, 18, 23-38.

QMIN - Quartimin

Carroll, J. B. (1953). Ananalytical solution for approximating simple structure in factor analysis. *Psychometrika*, 18, 23-38.

OMIN - Oblimin

Carroll, J. B. (1957). Biquartimin Criterion for Rotation to Oblique Simple Structure in Factor Analysis. *Science*, 126(3283), 1114-1115.

CRFE - Crawford-Ferguson family

Crawford, C. B. & Ferguson, G. A. (1970). A general rotation criterion and its use in orthogonal rotation. *Psychometrika*, 35, 321-332.

MINE - minimum entropy

Jennrich, R. I. (2004). Rotation to simple loadings using component loss functions: The

orthogonal case. *Psychometrika*, 69, 257-273.

IPSC - Bentler's invariant pattern simplicity criterion

Bentler, P. M. (1977). Factor simplicity index and transformations. *Psychometrika*, 42, 277-295.

TIIC - Comrey's tandem II criterion

Comrey, A. L. (1967). Tandem criteria for analytic rotation in factor analysis. *Psychometrika*, 32, 277-295.

GMIN - Geomin

Yates, A. (1987). *Multivariate exploratory data analysis: A perspective on exploratory factor analysis*. Albany, New York: State University of New York Press.

MMER - McCammon minimum entropy ratio

McCammon, R. B. (1966). Principal components analysis and its application in large-scale correlation studies. *Journal of Geology*, 74, 721-733.

Example Datasets

Two example datasets are available for testing the EP Toolkit and are used in the tutorial (in a separate file entitled tutorial.zip). The first example dataset was kindly provided by Dennis Molfese's lab, which supported the development of the 2.0 version upgrade. This example dataset consists of ten children from a larger study of speech perception. The ERPs reflect the perception of the phonemes "da" and "ga", which vary in the point of articulation, and which in turn are divided into a normal version (da9+ and ga11) and an unrealistic version (da7+ and ga13). Collection of ERP data from such young children (2-4 years old) can be quite challenging as they are very distractible and will move constantly. These data are therefore filled with movement artifacts. An additional feature of the data is that the lower VEOG channels were not placed below the eyes as very young children do not tolerate them well. The data were collected using an EGI 129-channel Geodesic Net.

The second dataset is a continuous file collected by myself and my colleagues (Dimitrios Donavos and Luiz Pessoa) during a combined EEG/fMRI pilot session. The format is EGI's new mff format. In addition to the EEG data, it contains an EKG channel for helping correct the ballistocardiogram artifact. The task itself is a simple oddball with rare and frequent X's and O's. Due to an equipment issue, no response information is available. The data were collected using an EGI 257-channel Hydrocel Net.

Set Up

Installation

In order to run the EP Toolkit, you will need to install the following programs:

- (1) MATLAB
- (2) EP Toolkit
- (3) EEGLAB
- (4) FieldTrip
- (5) Satimage osax (for Macs only).

All of these are freely available online except for MATLAB, which has affordable options for student and academic licensing.

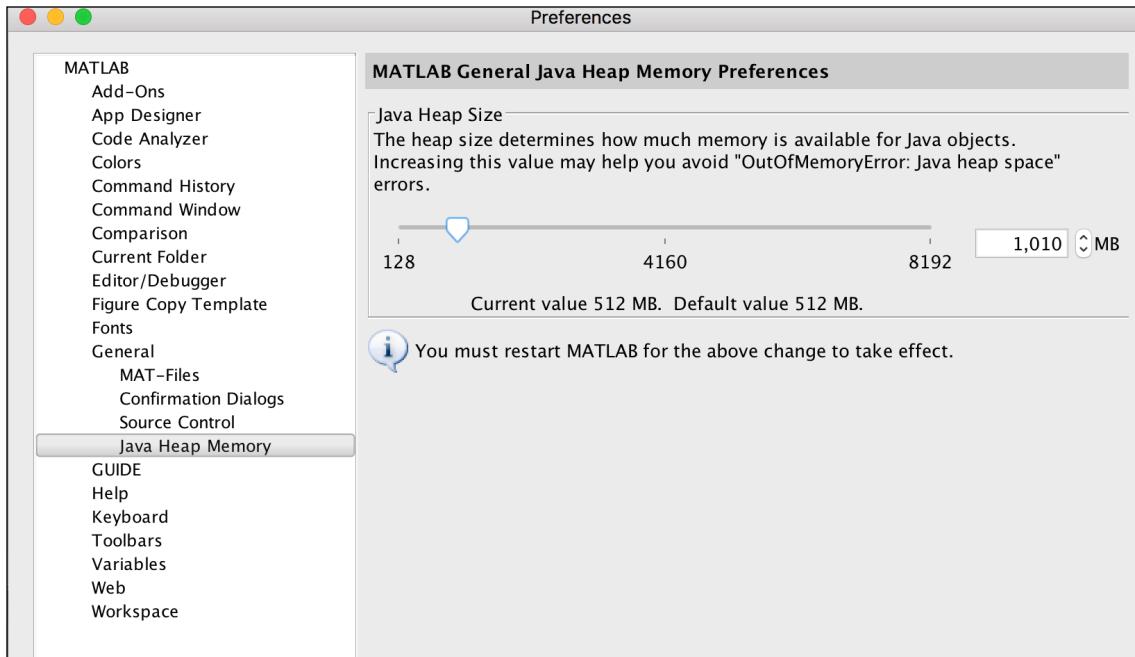
1. Install MATLAB

MATLAB may be purchased directly from The Mathworks, Inc. (www.mathworks.com), but check with your academic institution first as it may already have a volume license or reduced pricing. Only the core MATLAB program is needed to run most of the EP Toolkit, so it is not necessary to purchase any MATLAB add-ons from Mathworks. One exception is the Statistics Toolbox, which is required for the sampleTest functions. For those who intend to use EEGLAB extensively, it will also run on the core MATLAB program, but the EEGLAB authors recommend that you purchase the Signal Processing Toolbox and Statistics Toolbox to improve the efficiency of some EEGLAB functions. The Signal Processing Toolkit is also needed for the fMRIb EEGlab plug-in (for correcting fMRI artifacts) but not for the AMRI fMRI artifact correction routines. The Signal Processing Toolkit also enhances a number of the FieldTrip functions used by the EP Toolkit, such as spectral decomposition. These add-ons are already included in the current student version of MATLAB.

Follow the instructions that come with MATLAB to install it.

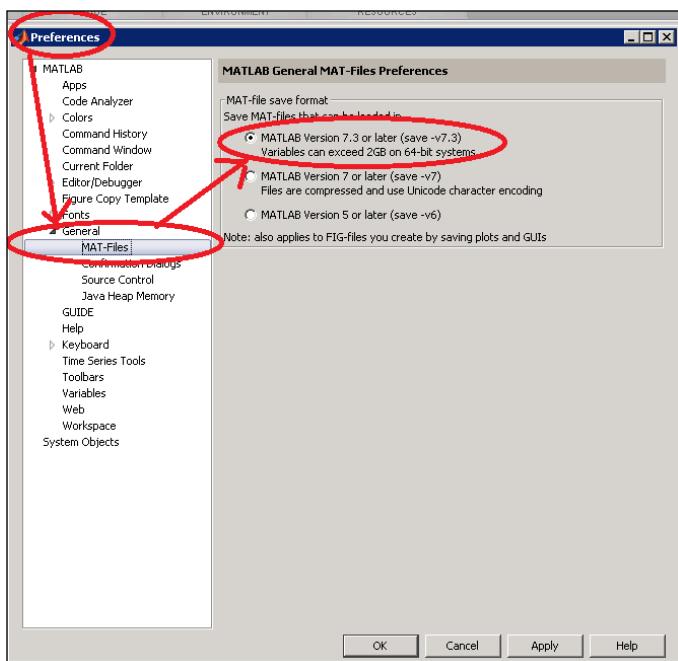
At this point, I recommend creating a single folder on your computer to contain the EP Toolkit, EEGLAB, and FieldTrip, as well as any other MATLAB programs you may wish to run on your computer. For example, on my Mac, I have created a folder within the Documents folder named *Matlab_Programs*. Simply create the new folder, name it, and make sure it is placed where you want it. This keeps the programs organized and provides a common path within MATLAB for accessing applications. Note that I used an underscore rather than a space in the name of the folder as the presence of spaces can confuse Matlab if the programmer of Matlab software is not careful.

By default, the Java environment that Matlab runs in does not set aside enough memory to run large datasets. Go to the Matlab preferences and move the slider up as shown:



which tells it to set aside 1GB of memory, up from the default of 256MB. Note that this setting is for what is called the heap space, which is a sort of a workspace that Matlab uses for whatever it is working on at the moment. This is aside from the more general memory storage represented by the Matlab workspace. Matlab can and will use more memory than the heap space (and virtual memory stored in available disk space as well) for general memory storage so it is not necessary for the heap space to be more than this to take full advantage of your installed RAM. You do, however, want to make sure that both your operating system and Matlab is 64-bit to make full use of your available memory space.

You should also make sure that the Matlab preferences are set to use the current version of .mat files. If it is set to use a legacy version then it may not be able to handle large datasets.



If the preferences are set to an older version, you may end up getting an error message like the following:

```
The name of the experiment is:
The pre-stimulus period of the data is: 0 msec
Warning: Variable 'EPdata' cannot be saved to a MAT-file whose version is older than 7.3.
To save this variable, use the -v7.3 switch.
Skipping...
> In ep_saveEPdataset at 95
In ep at 2634
>> ver
```

2. Install EP Toolkit

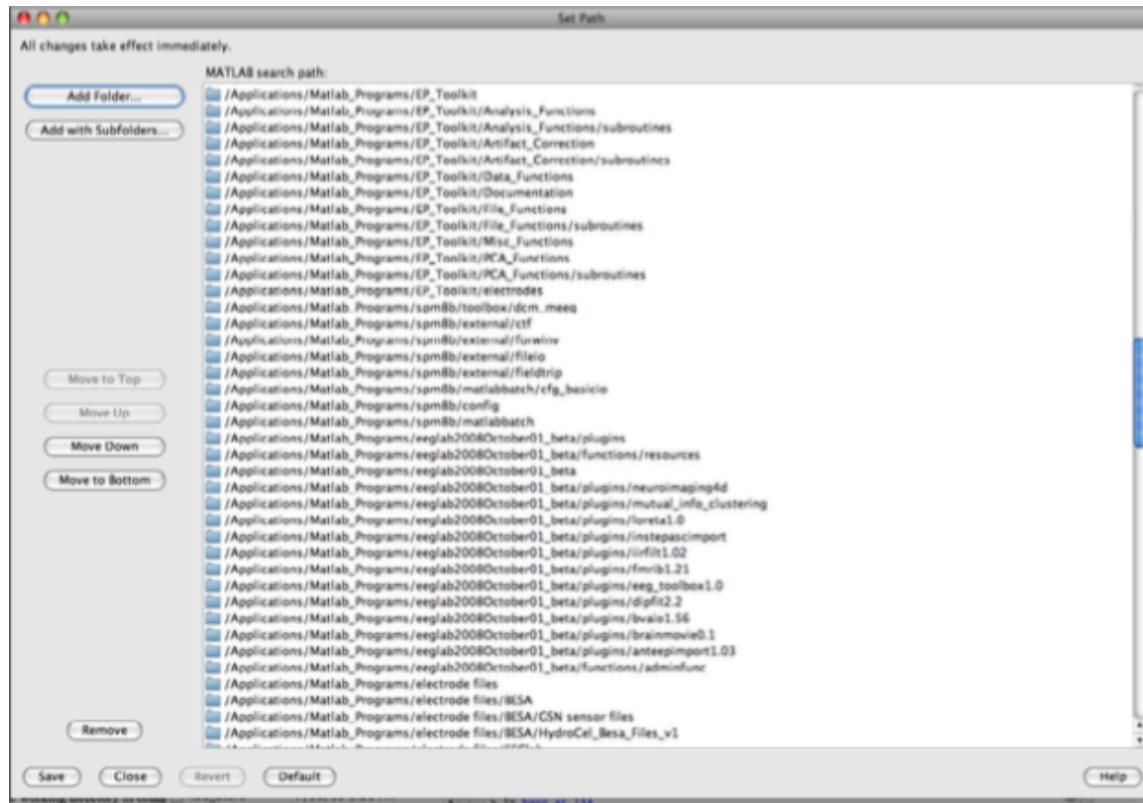
If you haven't already done so, download the latest version of the EP Toolkit from the project website listed above, and unzip the file. This will produce a folder named *EP_Toolkit* with several files and folders inside of it. On non-Mac platforms you will find a number of files starting with "_" which contain Mac-specific information and can be ignored.

Put this *EP_Toolkit* folder into the desired directory. On my computer, I place it in the *Matlab_Programs* folder that I created and placed in the *Documents* folder.

Now open MATLAB and add this folder to the MATLAB path. To do this, click on the Set Path button on the Home tab of the main Matlab window.



In the window that then appears, click on the "Add with Subfolders" button. A browser window will open. Navigate to the EP_Toolkit folder (e.g. on my Mac, I click on *Documents*, then *Matlab Programs*, then *EP_Toolkit*). With the EP_Toolkit folder selected, click the “Open” button. The path list for the Toolkit should end up looking like this, with several lines, one for each subdirectory in the Toolkit folder:



Now save these changes by clicking “Save” at the bottom of the Set Path window. Many new users of MATLAB forget this critical step. If you close the window without saving, MATLAB will discard the path changes the next time you quit the program and you will have to repeat the process.

3. Install EEGLAB

You will also need Delorme and Makeig's excellent EEGLAB toolbox (<http://scen.ucsd.edu/eeglab/index.html>) if you wish to run the InfoMax rotation (ICA) and to make use of their 2D and 3D plotting functions for visualizing the data. They recommend using the latest "stable" version. As of "eeglab14_0_0b" this worked fine.

1. Download the compressed EEGLAB distribution below into an eeglab directory/folder	
<small>What version should I download? If you do not have Matlab, download the compiled version. If you are just starting with EEGLAB, download the stable version (EEGLAB 9 or 10). If you are planning to do extensive multi-subject analysis, download the development version (EEGLAB 11).</small>	
EEGLAB v11 most current (32MB) Download link	<small>EEGLAB most current. For developers and advanced users only (tutorial demo STUDY, separately available in downloads below). This version is also recommended if you are actively working with EEGLAB studies. Use the latest generated development version in the FTP folder. The current version contains the most recent developments and bug fixes. Instead of downloading the ZIP, it is also possible to use SVN (SubVersion). See the download wiki page for more information. Revision details are available on the EEGLAB wiki.</small>
EEGLAB v10 stable (32MB) Download link	<small>EEGLABv10. This version is still supported. Use the latest generated EEGLAB version 10 in the FTP folder (latest is at the bottom). The latest changes made to this version are detailed here. Older EEGLAB versions are available here.</small>
EEGLAB compiled (162MB) Download link	<small>EEGLAB compiled version for windows OS 32-bit. This version does not require Matlab. If you have access to Matlab though, we recommend the version above. More information about the compiled version of EEGLAB is available here.</small>

After downloading and unzipping EEGLAB, move the folder to the desired directory (e.g. Matlab_Programs folder). Then open MATLAB and add the EEGLAB folder to the path. Do so by first adding just the root directory (without the subdirectories) using the Add Folder... button rather than the "Add with Subfolders" button in the "Add Path..." window. Then type "eeglab" in the command window. EEGlab will add appropriate subdirectories to the path. **Go back to the "Set Path" window and save the new additions to the path!**

If you install the binary version of EEGLAB's *runica* (<http://sccn.ucsd.edu/wiki/Binica>) it may run the ICA routine faster but probably not. The problem is that the current binary code only uses one core whereas the current version of MATLAB uses all available cores. With modern computers, which are all multi-core these days, my experience is that it's not worth using. Unfortunately, it is at present only available for Linux, FreeBSD, and OS X. Results are not exactly the same as the current MATLAB version but seem to be quite close (in a test run the largest divergence in the FacPat results was .01). If someone can adapt it for multi-core computers then it would be quite a bit faster.

To install the binary version of *runica* (called *binica*), follow the instructions on the website above. Here is an example of how to do it on a Mac. Download the correct version for your operating system. Unzip the file, and place the resulting folder (e.g. *binica_osx_fat*) in the desired directory (e.g., Matlab_Programs). Then open MATLAB and add the new folder (with subfolders) to the path. Inside this new folder is a file named *ica_osx*. Open an OSX Finder window to locate *ica_osx*, and write down the full path to this file. Do a web search if you are uncertain how to view the full path on your version of OSX. Then open MATLAB and use the File menu to open the *functions/sigprocfunc/icadefs.m* file, which can be found in the EEGLAB folder. Edit the line after "ICABINARY =" so that it specifies the full path to the *ica_osx* file, as in:
ICABINARY = '/Documents/Matlab_Programs/binica_osx_fat/ica_osx'.

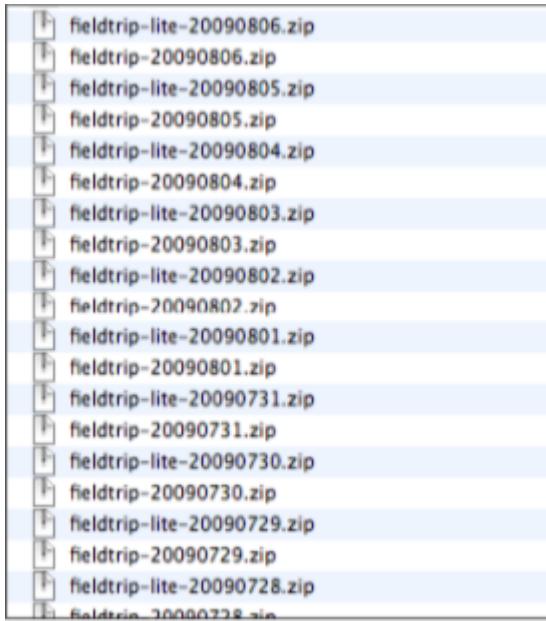
There cannot be any spaces in the path (e.g., "Macintosh HD") to either the binary ICA file or to the working directory in order for it to work. Use the File menu to save this change. Each time you download an update to EEGLAB, you will need to remember to edit this line again.

EEGlab downloads with this line set as "*ICABINARY = fullfile(eeglab_p, 'functions', 'resources', 'ica_linux');*" which not only means that it will default to running the binary version but it will try to run the linux version, **which will**

then promptly crash if you are not on a linux computer. If this happens to you, change this line to "ICABINARY = [];"

4. Install FieldTrip

You will also need Robert Oostenveld's excellent FieldTrip toolbox (<http://www.ru.nl/fcdonders/fieldtrip/>) in order to be able to read in files and for CSD and spectral analyses and a simple dipole source analysis routine. Go to the website and register. They will email you an ftp site to download the file from. The site will contain a list that will look like the figure below, if sorted by date. The number is the date of the file (YYYY-MM-DD). Take the latest version (MAKE SURE IT REALLY IS THE LATEST VERSION! If you just take the top file and your computer is set to sort them in order of name, not date, then you will be taking the oldest one, not the newest one). There are two versions for each, the full FieldTrip and the Lite version. I use the full version for all my testing and cannot guarantee that the EP Toolkit will work properly with the Lite version.



Download the file, unzip it, place it in the desired directory (e.g. Matlab_Programs). Remember to add it to the MATLAB path too. Do so by first adding just the root directory (without the subdirectories) using the Add Folder... button rather than the "Add with Subfolders" button in the "Set Path" window. Then type "ft_defaults" in the command window. FieldTrip will add appropriate subdirectories to the path. It's no longer necessary to worry about what is in the "external" directory. **Go back to the "Set Path" window and save the new additions to the path!**

In order for the dipole analysis feature to work, it will also be necessary to have a copy of the gcc compiler installed on your computer. On the Mac (with OS X 10.7+), this can be done in a roundabout but simple way. First go to the app store and download the free

Xcode application. Then (if you're on Xcode 4.3+) start Xcode, go to Preferences, then to the Downloads section, then the Components tab. Choose to install the Command Line Tools. I'm not really certain how to install gcc on Windows but it should be available from the internet for free as it is the open source compiler (there are lots of hits on google for this topic).

5. Install Satimage osax

On a Mac, you may want to install *Satimage osax* to allow the EP Toolkit to automatically set the montage information in EGIS files. This function will not be available on other platforms, since the implementation relies on AppleScript. Download the software from this address

(http://www.satimage.fr/software/en/downloads/downloads_companion_osaxen.html).

No other programs listed at this address are needed, just *Satimage osax*. After downloading, quit out of all programs, and install the package. Installing creates a file named "Satimage.osax" in the "ScriptingAdditions" directory in your main Library directory. This makes the scripts available "for all users" on the computer; but the option to install for the "current user only" (i.e. in the Library directory under your home directory) should also work. If the "ScriptingAdditions" directory doesn't exist yet, just create it. Note that *Satimage osax* does not fully operate under OS X 10.6 or 10.7 but as of OS X 10.8 appears to be working again.

6. Add fMRI artifact correction routines

If you wish to perform fMRI artifact correction, install the fMRIb EEGLab plug-in, using the "File > Manage EEGLab Extensions > Data processing extensions" function. I made some fixes to it and they were accepted by EEGLab so make sure you have the 2.0 (or later) version installed. Afterwards, save the path again using Matlab's Set Path button.

An alternative fMRI artifact correction routine, which relies primarily on the ICA approach rather than the OBS template approach and does not require the Signal Processing Toolbox, can also be installed. To do so, go to the following website:

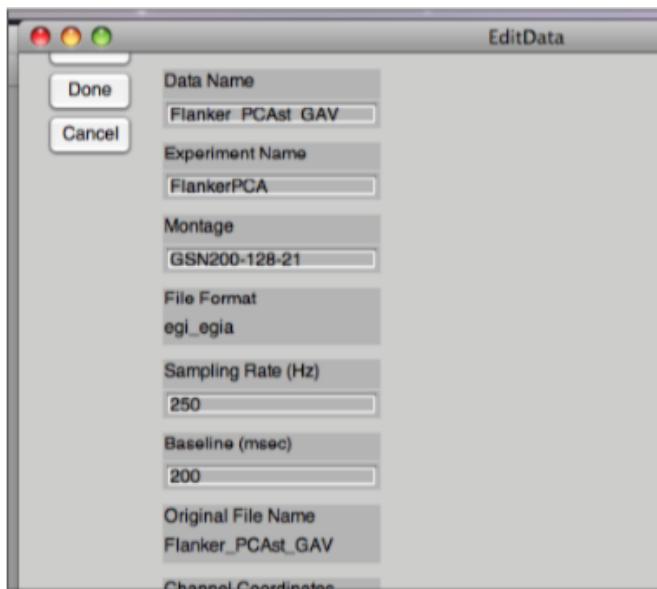
<http://amri.ninds.nih.gov/cgi-bin/software>

Create an account and then use the resulting password to download the available software. The current release (amri_eegfmri_toolbox.20130731.v0.1.4.tar) crashes if the final gradient artifact is too near the end. A fix for this is included in the externals directory of the EP Toolkit. Either substitute it for the original or make sure that the EP Toolkit is higher on the path list than the AMRI package. Also, the "mi" subdirectory is currently missing compiled mex files for Intel Macs. These mex files are also provided in the EP Toolkit's external directory.

Avoiding Common Problems

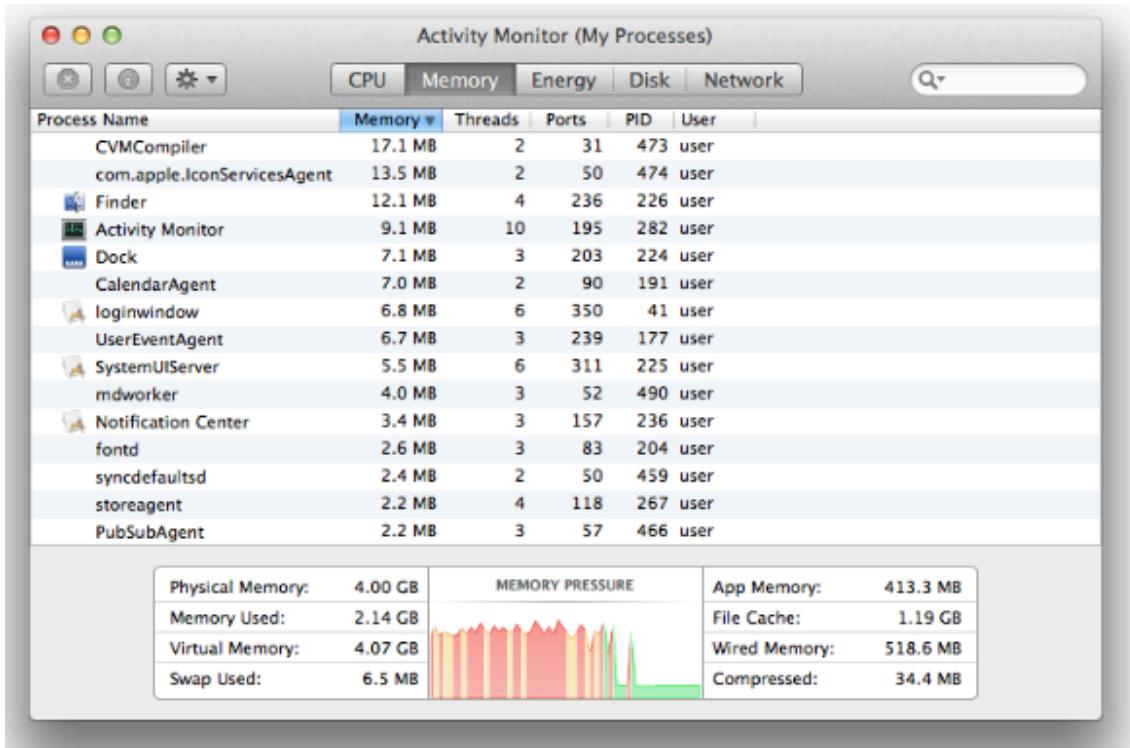
Monitor Resolution

On a Mac with a smaller monitor, make sure to set your Dock to appear on the right or left side of the screen. If it is set to be at the bottom and is abutting onto the EP Toolkit pane then it may throw off its contents, as in this picture. Note how the contents of the pane have been shifted upwards, resulting in some things disappearing off the screen. The Task Bar can cause the same problem on Windows machines.



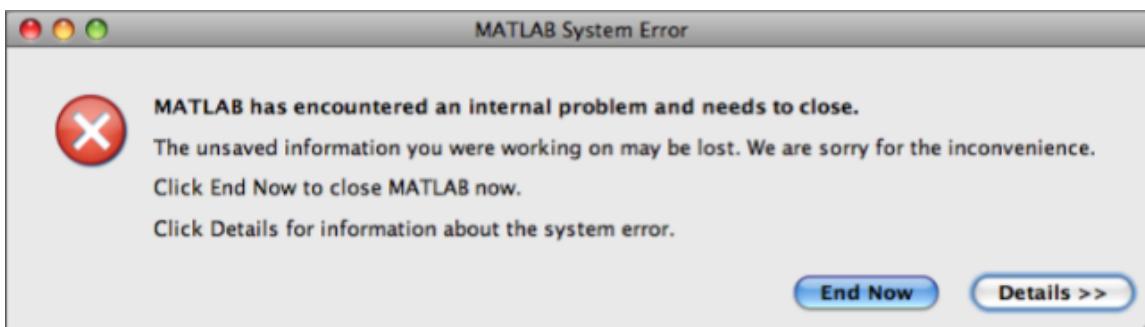
Memory Issues

On OS X, it is highly recommended that you use the Activity Monitor (Linux and Windows should have their own equivalent). Starting with OS X 10.9 (Mavericks), you'll need to keep the main window open on the Memory pane, where it'll show you an overall “memory pressure” graph, which you'll want to have in the green zone. Mavericks has improved memory management over previous versions of OS X so if the memory pressure gets too high, it will merely put Matlab on hold rather than crashing the computer. This problem can be exacerbated if you use Safari as your browser as it suffers from memory leaks that cause it to keep growing until it takes up all the RAM and the Mac crashes. Again, I find the Activity Monitor useful for keeping an eye on Safari's memory usage.



One reason you want to keep an eye on this is that MATLAB at least used to have very poor memory management. You can think of memory like a large room where objects are placed for later use. Objects are then removed when no longer needed. The problem is that when a new object is added, MATLAB cannot rearrange the existing objects to make efficient use of the floor space. If it tries to store a large object and there is no existing space large enough to accommodate it, then the program will crash. You will start getting alarming red messages about being OUT OF MEMORY in the command line and the EP Toolkit will stop working. When there is enough overall memory but it has simply been cut into too many small pieces to handle the new object (like a new data file), then this is called "memory fragmentation."

Examples of memory errors are:

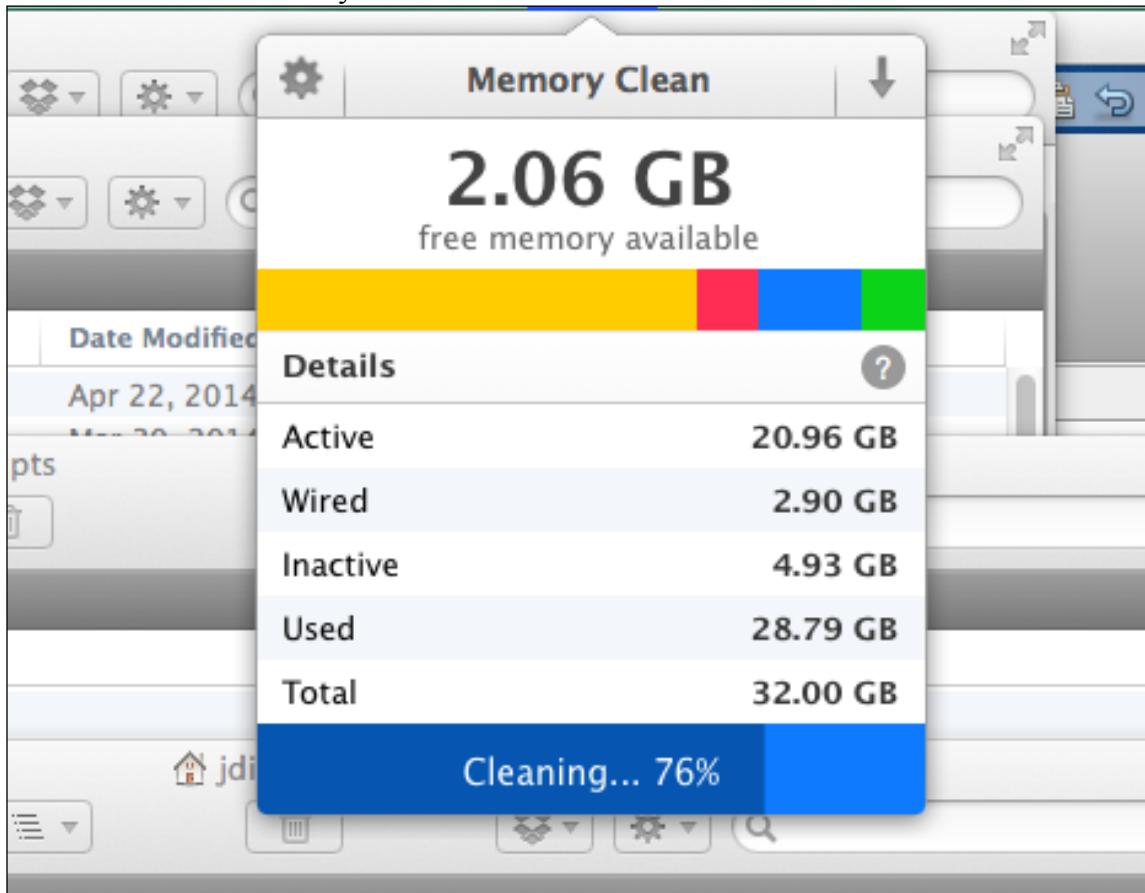


Or you may see the text:

```
??? Error using ==> zeros  
Out of memory. Type HELP MEMORY for your options.
```

Once memory fragmentation has occurred, the only way to deal with it is to quit out of MATLAB and then restart it. If you see the memory pressure gauge go red (in OS X 10.9), this is an indication that you may soon run into memory problems. Another symptom of memory fragmentation, short of an actual crash, is that MATLAB starts slowing down to a crawl. Again, the best solution is to just restart MATLAB at this point. The working set of data will still be present when you restart the Toolkit. It's also not a bad idea to set the Activity Monitor to show the floating window with CPU usage so you can have a better sense of what is going on when you're waiting for the Toolkit to finish a function.

For OS X, something that is very helpful is Memory Clean, a free utility available through the AppStore. It provides a running indicator how much free memory you have available and it can free up much of it if needed, although if you run it when memory is near zero it can lead to a system crash.



In principle, these memory issues should be greatly ameliorated by the advent of 64-bit

computing, which allows for the use of much more memory. On the Mac, this requires OS X 10.6 (Snow Leopard); and on the PC, a 64-bit version of Windows. This also requires MATLAB 2009b or later and a computer with 64-bit hardware (a recent computer) and lots of RAM. You will also need to remember to increase the Java heap size, as described in the Installation section. Indeed, I haven't had problems like this in some time. Perhaps it would still be a problem on a computer with less RAM (I currently run with 32GB).

Energy Saver Settings

An issue specific to OS X is that MATLAB does not register as an active program to the Energy Saver controls. Thus, if the Energy Saver is set to put the Mac to sleep after a certain amount of time, it will put it to sleep in the middle of an ongoing MATLAB run. Thus, if you are planning on running long MATLAB sessions, such as eyeblink correction runs, it would be best to at least temporarily set Energy Saver to Never Sleep.

File Preparation

EP Toolkit File Types

The EP Toolkit recognizes three types of files:

1. *continuous* - is a single stretch of unsegmented raw data recording. For many functions continuous data will be treated as a series of one second segments. The EP Toolkit has in-depth functionality for performing segmentation.
2. *single_trial* - is a segmented raw data recording.
3. *average* - is one or more subject averages. The Toolkit's PCA functions are designed to work on combined subject averages in which a single file contains an experiment's entire set of subject averages in the form of separate waveforms. If you have separate subject average files, you can use the "append" function on the subject pane of the Edit function to glue them together into a single combined subject average file or use the single file mode to merge them together with the Read function.

A full EP data file may have all of the following dimensions: channels, time points, cells, subjects, factors, and frequencies. This structure can be perused via the Edit function and the waveforms may be examined directly via the View function. It may also have a seventh dimension of channel relationships, as in coherence, for which the Edit and View functions do not provide separate controls.

The EP file format itself is described in the header of the `ep_readData.m` file. While it is really a .mat file, the suffix for EP files is .ept (to help distinguish it from normal .mat files). If using an EP file created previous to the implementation of the .ept suffix, you

may just rename the file from ".mat" to ".ept". Note that on the Mac, you should do so using Get Info via a right click or you may find that the renaming isn't working properly (the suffix can be invisible so you haven't actually changed the suffix when you thought you changed it).

As a side note, while it is true that various software packages can produce .mat files, such files are not useable by the EP Toolkit. The reason is that critical information like whether channels are the rows or the columns are not specified in such files and basic information like the sampling rate will be entirely missing. It's not worth the effort to add support to the Toolkit for them and it's not worth the effort you would have to make to manually add the missing information every time you wanted to use such a file.

Electrode Coordinates

Many EP Toolkit routines, especially the artifact correction function, require a file that provides the 3D electrode locations in order to locate the EOG channels and to determine which channels are neighboring. EEGLAB's .ced format is used for this purpose. The EP Toolkit already includes .ced files for the EGI montages and they will be automatically accessed as needed. To create a .ced file from an existing coordinate file in some other format type the following into the Matlab command window:

- 1) pop_chanedit([]);
- 2) click on Read Locations.
- 3) click on Save (as .ced)

The .ced file will be treated as the definitive statement on what channels should be in the data file and their proper ordering, except for the EGI EGIS and simple binary formats where all channels are always present and in the same fixed order. Except for these two formats, if the data file has channels that are not present in the .ced file, then they will be used but will not be utilized for operations that need electrode coordinates like bad channel replacement. If there are EEG channels in the .ced file that are not present in the data file, it will be assumed that the channels were bad channels and had been dropped (normal practice for Neuroscan files) and they will be added back in as zeroed out channels and they will be internally marked as being bad channels. If all the channel names in the file and in the CED file are different but there are the same number of channels, it will be assumed that they correspond and are in the same order and so the channel names and other information in the CED file will be used.

If you need to edit your own ced file, there should only be nine channel types listed in the final column of the ced file: EEG, REF, FID, MGM, MGA, MGP, ANS, ECG, and BAD. REF should indicate the reference channel(s) used during data collection, regardless of whether it has been subsequently rereferenced. It will be relabeled as EEG in the data file. FID stands for "fiducial" and indicates locations that are merely landmarks. They will not be included in the dataset. MGM, MGA, and MGP (MEG) is allowable but support is not fully implemented as it is intended for future development. ANS is for autonomic channels and will not be included in EEG operations. ECG is for

electroencephalogram data and will also not be included in EEG operations. It has a separate label so that the toolkit can identify it for ballistocardiogram (fMRI) artifact correction. BAD is for inactive channels that should be completely deleted (as opposed to channels that were bad for a particular subject but has meaningful data for other subjects and can be dealt with using channel replacement). Note that when editing a .ced file, you should not use the Notepad accessory if you are using Windows as it adds the wrong kind of line delimiter. Use Word or an equivalent word processor instead.

Reference Channels

Also, note that data files often have the reference site present only implicitly. Reference channels are by definition zero voltage and so to save disk space software (not the EP Toolkit) often leaves them out entirely. If the reference channels specified in the .ced file are missing from the data file, they will be added as explicit flat channels. Note also that for a mean mastoid reference, if both mastoid channels are missing then they cannot be reconstituted as only their average is zero; they should both have non-zero waveforms that are mirror images of each other that split the difference between the two sites (for more on reference issues, see Dien, 1998 and Dien, 2017). When using software that gives you an option as to whether to include them (such as Neuroscan's software), you should always choose to do so. BrainVision's PyCorder program gives the option to use a "no-reference" option. As far as I can tell after discussions with tech support, all this means is that the voltage numbers are not interpretable until the data are rereferenced. It also gives the option to choose more than one channel as being the reference (e.g., mastoids) but then it drops all these channels and their data are lost so it is best not to do so. Either choose one channel as reference or none and then rerefence as needed during analysis.

Net Station Files

If you are using Net Station, you will need to use the new mff file format, although importing it only works smoothly with continuous data (EGI needs to fix its mff API code) and you cannot export back to NetStation. I think you can still use Simple Binary, although it has numerous drawbacks. My understanding is that EGIS is no longer an option for NetStation as of version 5 unfortunately.

The EGIS session format cannot represent baseline period information and so that has to be input manually using the Edit function (to be described). EGIS average files can represent baseline period information but when Net Station saves them, it leaves it out. Also, it leaves out the subject number information. Both types of information will need to be added in using the Edit function. EGIS files are only accurate up to about two decimal places but that is normally sufficient. EGIS files, unlike Simple Binary, can support Trial Specific information but Net Station does not support this aspect of the file format. EGIS files also do not preserve the full event information the way Simple Binary files do but as Net Station does not import the event information in Simple Binary files, this is largely moot. **Note: NetStation 4 sometimes exports EGIS files with the data scaled about three times larger than they should be, causing most of the data to be dubbed bad data. If a data file is labeled as being excessively bad, verify data**

scaling against the original data file. Note also that NetStation 4 appears to have difficulty exporting multi-session EGIS average files. At least under some circumstances they instead output as EGIS session files which are then read in as a single subject by the EP Toolkit (since EGIS session files are by definition a single subject). Simple Binary (next) can be used as a substitute in such a case.

Simple Binary format has the drawback that it does not represent the baseline period information but the FieldTrip import routine (which I wrote) will try to guess what it is. You will therefore need to verify that it deduced it correctly (using the Edit function). More seriously, Simple Binary format does not represent the montage information (the information needed by NetStation to display the data). The Toolkit will ask you what it is when you import the file. On non-Mac computers you will need to wait for the Toolkit to ask you which montage is to be used even with EGIS files. If you are not using NetStation, the montage information is irrelevant. Note also that NetStation (as of 4.1.2) loses the trial-specific information when writing out continuous (non-segmented) simple binary files. Also note that the Simple Binary format is not designed to handle epochs of different sizes (although the epoch-marked variant can get around this limitation) so if you try to export such a file from NetStation, the file may be corrupted and cause errors when you try to read it. The easiest way to test for this is to just try to open the file using NetStation. It will fail to open if the file is corrupted in this manner.

Net Station can generate EGIS and Simple Binary files by either using the Save a Copy... command in the File Menu or the File Export tool. If using the former method make sure to deselect the option to apply viewer transformations.

Text files can also be used as a data export option from NetStation. A separate file will be generated for each segment (for single trial data) or each average (for averaged files). In this case, use the Single File mode to merge these files back together again. **Note: NetStation 4 sometimes exports text files with the data scaled several times larger than they should be, causing most of the data to be dubbed bad data. If a data file is labeled as being excessively bad, verify data scaling against the original data file.**

Another option for data exporting is Matlab file format. In this case, use the File Export Tool, not the Save as menu item. Choose the "cell array" option. Depending on the version of NetStation, this will have either a .mat or a .nsf file suffix. Note that the EP Toolkit does not support importing of event data due to problems in how NetStation exports them (if the "export good segments only" option is chosen, the bad segments are dropped only from the data, not the events, making it impossible to determine which events go with which data).

If you wish to skip the initial steps and go straight to PCA, you can just export an EGIS average file. Make sure that it is a combined subject average file. You can use the Combine Files Tool to generate such a file if you normally keep your subject average files separate. Combining the subject average files makes them easier to work with and is the default approach for Net Station as well. If you subsequently decide to drop a subject

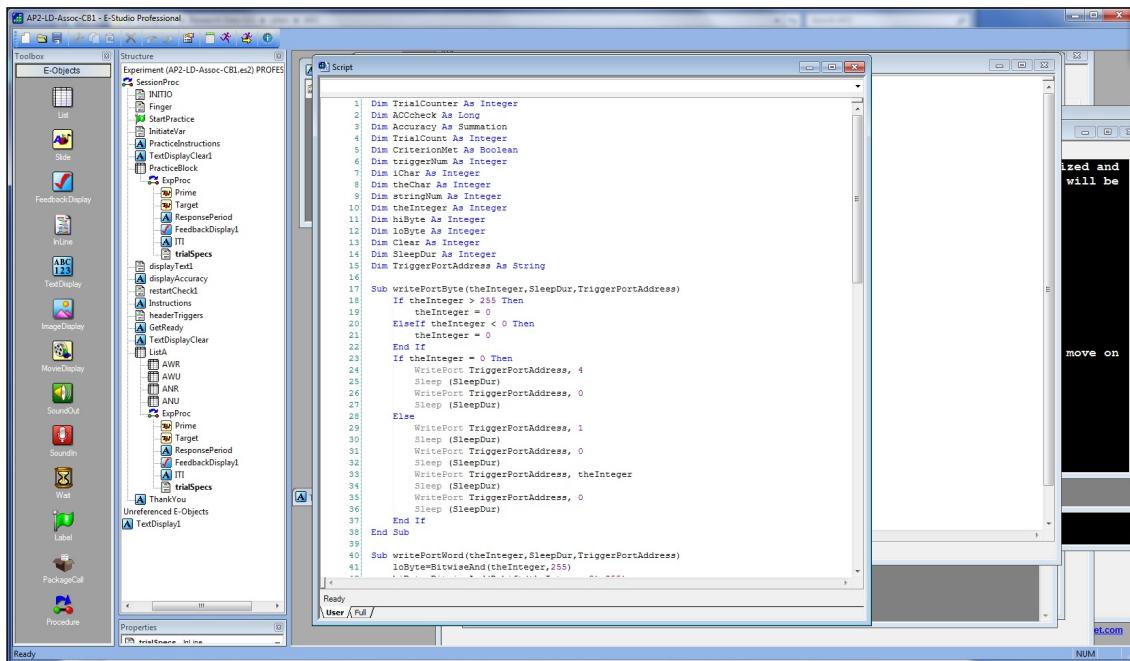
or add a subject, you can use EP's Edit function to do so.

You can also just export the raw data from NetStation (as simple binary or mff) and perform all the processing using the EP Toolkit. This is recommended as the Toolkit will retain a variety of information that will otherwise not be available.

BrainVision Files

In order to facilitate the use of BrainVision files, I've implemented a method for encoding subject and trial information in the trigger channel. This information is translated by the EP Toolkit and incorporated into the data file when read and can then be used for segmentation purposes. I've had some problems with consecutive repeats sometimes not being distinguished however (e.g., two ones in a row) even though all the numbers are supposed to be separated by zeros. The EP Toolkit will issue warnings when a header or trial specific information is not decoding properly (and in the latter case the trial will be dropped). This problem may be hardware dependent but in any case careful testing is required.

An example E-Prime file (AP2-LD-Assoc-CB1.es2) is included in the Documentation folder to demonstrate how to do so. To implement it, one must copy the code from the User tab of the Script window to provide the needed global variables and subroutines. Also the inline code objects named headerTriggers and trialSpecs. The trial information can take as much as a second to encode so to control the ITI the trialSpecs inline object is also set to time how long it took and to then pad the ITI out to the desired length. In order to run this E-Prime script, the file INIT_IO.txt will also need to be present in the same directory.



```
1 Dim TrialCounter As Integer
2 Dim ACCCheck As Long
3 Dim Accuracy As Summation
4 Dim TrialCount As Integer
5 Dim Criterion As Boolean
6 Dim iTriggerNum As Integer
7 Dim iChar As Integer
8 Dim theChar As Integer
9 Dim stringNum As Integer
10 Dim theInteger As Integer
11 Dim hiByte As Integer
12 Dim loByte As Integer
13 Dim Clear As Integer
14 Dim SleepDur As Integer
15 Dim TriggerPortAddress As String
16
17 Sub writePortByte(theInteger, SleepDur, TriggerPortAddress)
18     If theInteger > 255 Then
19         theInteger = 0
20     ElseIf theInteger < 0 Then
21         theInteger = 0
22     End If
23     If theInteger = 0 Then
24         WritePort TriggerPortAddress, 4
25         Sleep (SleepDur)
26         WritePort TriggerPortAddress, 0
27         Sleep (SleepDur)
28     Else
29         WritePort TriggerPortAddress, 1
30         Sleep (SleepDur)
31         WritePort TriggerPortAddress, 0
32         Sleep (SleepDur)
33         WritePort TriggerPortAddress, theInteger
34         Sleep (SleepDur)
35         WritePort TriggerPortAddress, 0
36         Sleep (SleepDur)
37     End If
38 End Sub
39
40 Sub writePortWord(theInteger, SleepDur, TriggerPortAddress)
41     loByte=BitwiseAnd(theInteger,255)
```

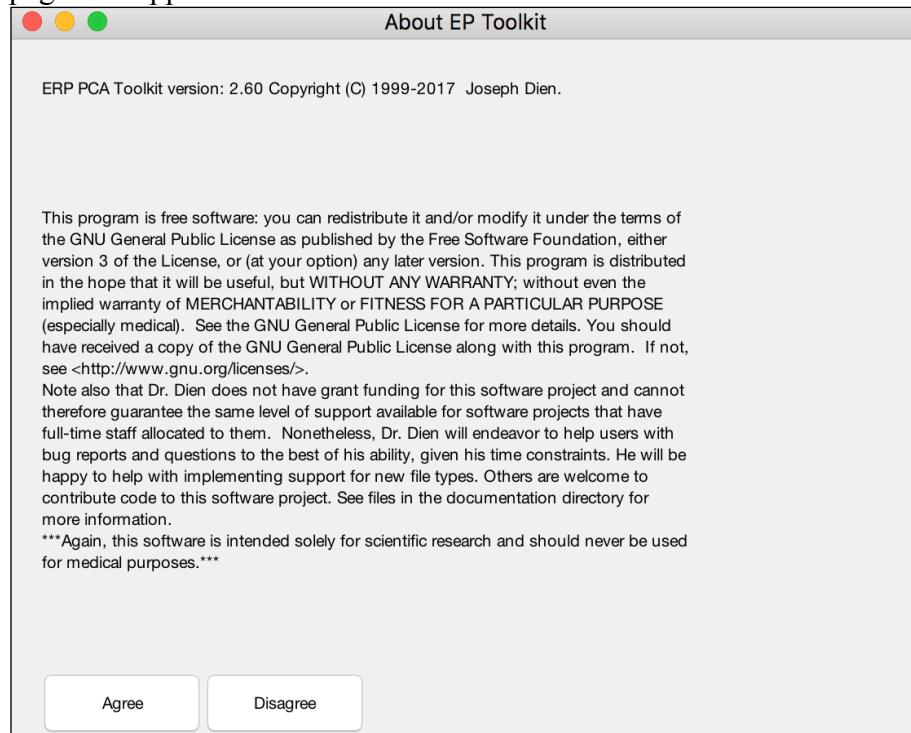
Other Formats

For average files other than EGI EGIS and EGI Simple binary formats, if the cell names all start with "Sub" and are followed by three numbers then the Toolkit will interpret this situation as meaning that this means that this suffix (Sub###) refers to subject numbers and will arrange the data accordingly. Any text following the three numbers will be interpreted as the actual cell name (e.g., "Sub001target" would be interpreted as the cell "target" for subject "Sub001"). This is a workaround for a limitation of the FieldTrip I/O code.

Running the Toolkit

Starting Up

To start the Toolkit, type ep at the command line of MATLAB. The following splash page will appear:



Read it and indicate whether you agree with the stipulations. If you disagree then the Toolkit will quit (sorry).

The Main Window should also appear, showing the Main Menu:



Note that some of the options will be grayed out until appropriate data have been loaded.

Preference file & EPwork directory

A working directory called EPwork will be placed in Matlab's default user directory. On a Mac, this is in the Documents/Matlab folder. Other operating systems have their own user locations. A permanent preference file called EPprefs will be placed inside the EPwork folder. If you already had an EPwork or EPpreferences folder installed from a prior version of the Toolkit, it will continue to use them.

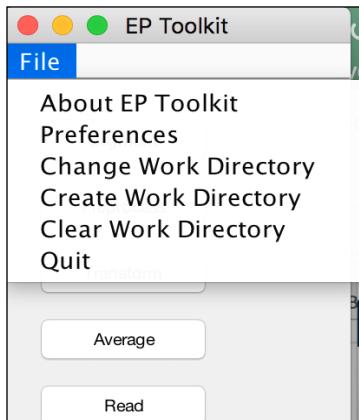
EPwork contains a working copy of each data file that you have loaded into the Toolkit. DO NOT modify the contents of the EPwork directory. It is meant for the internal workings of the Toolkit.

The EPwork working directory makes it possible for the Toolkit to maintain a working set of data. This set is listed on the Read, Edit, View, PCA, Window, and Save functions. You can add files or remove files from the working set using the Read function. The resulting data file from PCA is also added to the working set. When using these functions, you just select the data to be processed from this working set. When you are done, you must use the Save function to make a permanent copy of the file in the working set.

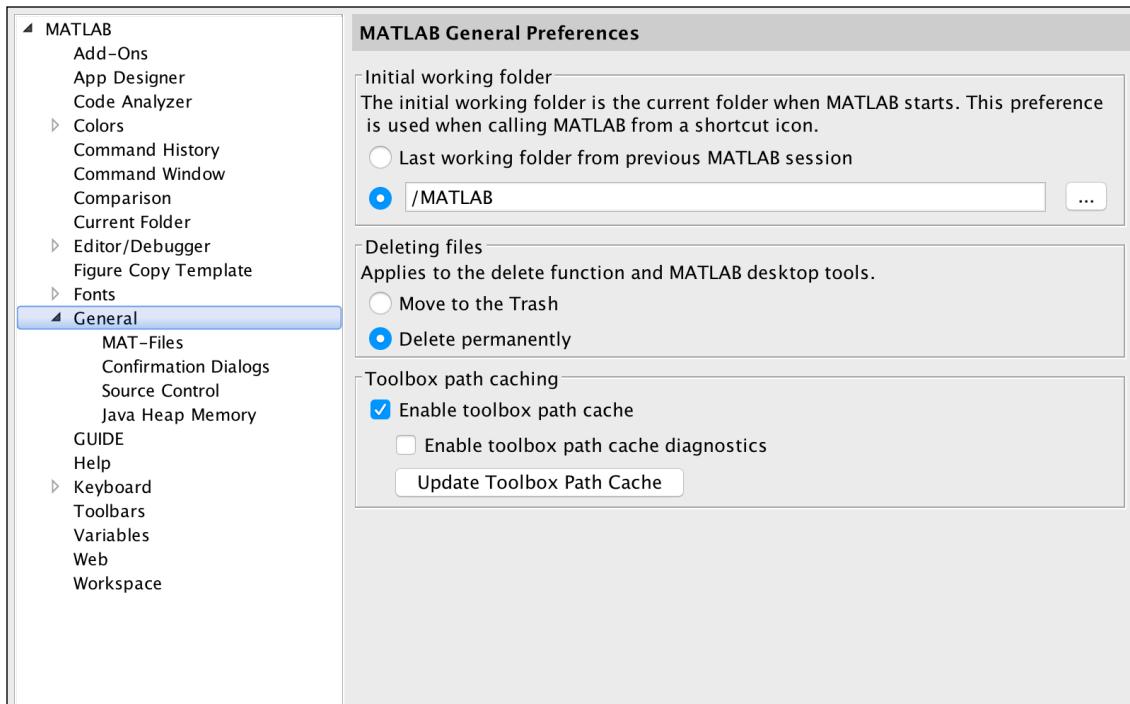
For the top four functions (prior to Read) the working set is not used. For these four functions (Segment, Preprocess, Transform, and Average) you will select the files to be

processed directly from the disk and the resulting files will be saved directly to the disk. Minor exceptions are when you need to manually construct a blink template and when providing an example template file for segmentation.

You can maintain multiple EPwork directories as long as they are located in different directories. When you start up the EP Toolkit, the EPwork directory in the current directory will be used if present. You can switch to a different EPwork directory using the Change Work Directory command in the File menu of the Toolkit and you can create a new one by using the Create Work Directory command.



Since EPwork contains a working copy of the files, it may take up a large amount of disk space so make sure that the disk has sufficient space to accommodate them. You can use the Clear Work Directory command to clear it out. The EPwork directory and its preferences file will remain. If your main disk does not have enough space, it is possible to specify a directory on a different disk as being your default Matlab directory.



Restarting

If the EP Toolkit is stopped in mid session (as by memory fragmentation), you can continue where you left off by restarting MATLAB (on a non-Mac, EPwork will need to be in the active directory when you type ep into the command line). If you have encountered some other type of error state (such as due to a bug in the Toolkit) it may be sufficient to just click on the close box of the Main Window and then type ep at the command line again. Sometimes MATLAB has been left in an odd state and you may need to type in ep a second time, as in the following:

```

Caught std::exception Exception message is:
St9bad_alloc
Unexpected error status flag encountered. Resetting to proper state.
>> ep
??? Error using ==> set
Invalid handle object.

Error in ==> ep at 1731
    set(EPmain.handles.view.view , 'enable','off');

>> ep

```

(The second time the initial splash window appeared as normal.)

Quitting

When you Quit out of the Toolkit, you will be asked if you wish to clear the working set. The EPwork directory and its preferences file will remain.

Toolkit Functions

Continuous Data File Example

For ERP analyses, the recommended order of operations is to first low-pass filter, then segment, then apply artifact correction. Low-pass filtering should be conducted first because filtering algorithms do not handle the edge of recordings well. Segmentation should then occur, followed by artifact correction. Artifact correction should occur afterwards because: 1) the ICA used to remove blinks benefits if the very noisy periods outside of the experiment blocks are first excluded (although one can also manually trim the files) and 2) the baseline correction that can then be applied to each epoch provides a lossless high-pass filter that further benefits the various artifact correction steps.

An exception is for ERP data collected inside an fMRI scanner as the gradient and the ballistocardiogram correction algorithms benefit from having intact data before and after each artifact. For such data, the fMRI correction option of Artifact Correction should be run first, followed by the low-pass filter, followed by segmentation, and then the rest of the artifact correction procedure.

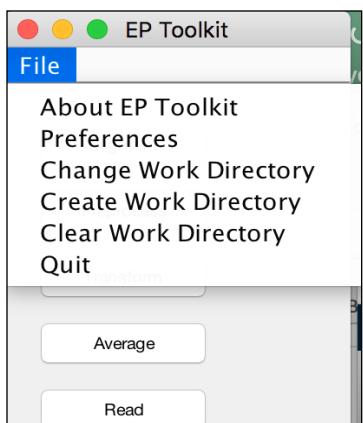
For traditional spectral analyses, segmentation should only be applied if the data are divided into epochs (as in time-frequency analyses). If the data are continuous in nature (as in over several minutes), then segmentation can be skipped entirely if each recording is one condition.

The following example uses one of the files included with this tutorial (see *Example Dataset* in the *About the ERP PCA (EP) Toolkit* section above for instructions on how to download these files). This tutorial dataset is the EEG-fMRI pilot data named EEG-fMRI.mff. Before the MRI noise can be removed, an initial unused portion with significant uncorrectable noise needs to be trimmed off or it will cause the entire dataset to be deemed uncorrectable by the Toolkit.

Read

Setting Preferences

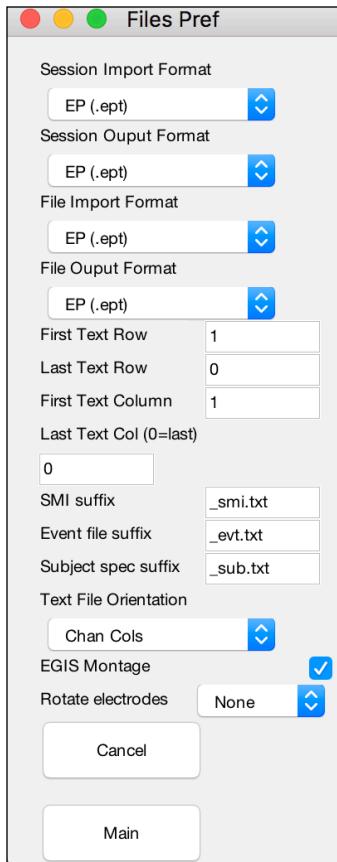
Before reading data, you might want to adjust the preferences. Choose Preferences from the File menu.



Then click on Files:



The following window should appear:



The Files preferences pane allows one to change the default settings for file operations. The first four change the default file type settings for the pop-up menus for read and write functions. The next four control whether any of the rows or columns should be ignored when reading in text data files. SMI suffix indicates the default name for SMI eye-tracker data files (a rather experimental feature that will not be further documented). Event file suffix specifies the suffix for event text files. Subject spec suffix specifies the suffix for subject text files. Text file orientation controls whether rows or columns of text data files are to be understood as being channels (as opposed to time points). EGIS montage controls whether montage information should be added to saved EGIS files (on a Mac). Rotate electrodes indicates whether the head orientation in files containing electrode information (i.e., eeglab and mff) should be rotated and by how much when reading them into EP Toolkit (to accommodate its convention of nose facing upwards). The rotate electrodes popupmenu also allows you to specify that the electrodes should be flipped L/R, which also needs to be done for mff files.

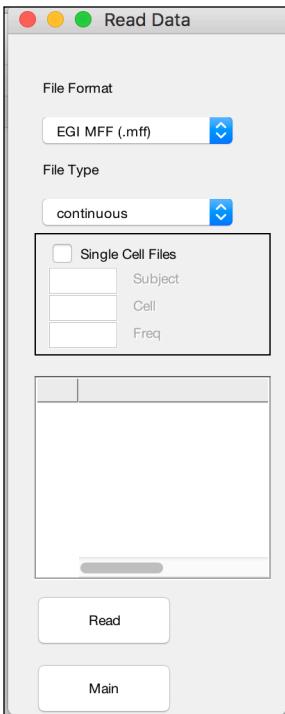
If any changes are made, then click Main, otherwise either Cancel or Main is fine.



Click Main to return to the Main Menu. Click Save to make any changes permanent (applying to future EP Toolkit sessions). Click Reset if you wish to return all the preference settings to the original default values.

Reading Data Files

First, click on Read button in the main menu. This function reads files into the EP Toolkit' working set for use with the Edit, View, PCA, Window, and Save functions. The working set is also used in a limited way for some other functions, as will be seen. The working set is a set of working copies of your files and so any changes you make will not be reflected in your original files until you Save your work to the disk.



To use, specify the file format. Make sure the file has the proper suffix (noted after the format name). If the file is not EP format, it will also be necessary to indicate what kind of file it is (File Type). The options are “continuous” (one long recording), “single_trial” (epoched but not averaged), “average” (averaged epoched data), “grand average” (average of subject averages), and factors (average data that has undergone PCA and is assumed to have a specific structure – provided strictly for legacy datasets analyzed using the 1.0 version of the EP Toolkit). It is possible to read in a batch of files by selecting multiple files in the dialog, once the Read button is pressed.

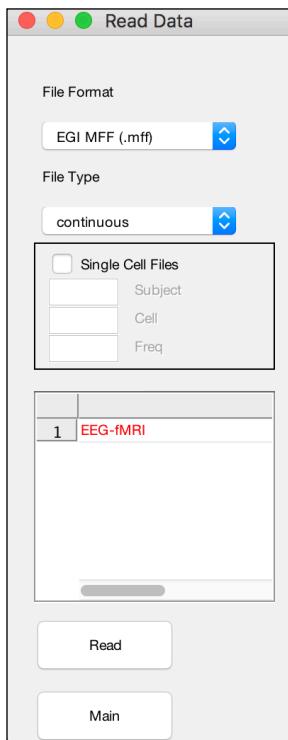
If the data take the form of separate files for each cell then it would be necessary to click on the Single Cell Files option and to specify in the Subject and Cell fields which characters in the file names correspond to the subject and cell labels (as in 4:6 and 7:9 for APP001TAR.txt for subject #001 in the TAR condition). Note that it will be necessary for each file to have an appropriate suffix in order to be recognized (listed along with the file format name). By default, the channels will be the columns.

It is possible to construct a separate text event file to contain the event information. By default, such a file would have the same root name as the data file but end in _evt.txt (e.g., test_evt.txt for test.bin). When any data file is read in, if a text event file is present in the same directory, then it will also be read in and its contents will replace the event information in the data file (if any). This functionality is especially helpful for file formats that do not accommodate event information (like text files) and for manually editing the event information. The file should be tab-delimited. The first row has header names. The first column contains the subject number and the second column contains the cell number for each event (for a continuous file, these will all be "1"). The Type,

Sample, Value, and Duration numbers follow FieldTrip conventions, wherein Type is a generic category name (e.g., "trigger") and Value is the more specific event information (e.g., "prime"). Sample is which sample (of the epoch for segmented data) and duration is its length in samples. Following EGI mff conventions, it is also possible to have "keys" associated with each event that contain more information. Each key has four fields: code (the label), data (the actual information), datatype (the type of variable, mostly ignored), and description (explanatory comments, mostly ignored). In the event file, keys are named code1, data1, datatype1, and description1 and so forth (see next figure).

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	cell	type	sample	value	duration	code1	data1	datatype1	description1	code2	data2	datatype2	description2	
2	1	1 Stimulus	S1 S51		1 stim	# Message:C char								
3	1	1 eye-tracker	90.9215	saccadeET	1 SMlevent	1 short		word	colleagues.	char				
4	1	1 eye-tracker	151.923	saccadeET	1 SMlevent	1 short		word	(AP)	char				
5	1	1 eye-tracker	178.918	saccadeET	1 SMlevent	1 short		word	INDIANAPOL	char				
6	1	1 eye-tracker	51.1445	fixationET	1 SMlevent	1 short		word	colleagues.	char				
7	1	1 eye-tracker	110.92	fixationET	1 SMlevent	1 short		word	(AP)	char				
8	1	1 eye-tracker	161.9178	fixationET	1 SMlevent	1 short		word	INDIANAPOL	char				
9	1	1 eye-tracker	192.9183	fixationET	1 SMlevent	1 short		word	Indiana	char				
10	1	2 eye-tracker	30.9215	saccadeET	1 SMlevent	1 short		word	colleagues.	char				
11	1	2 eye-tracker	91.923	saccadeET	1 SMlevent	1 short		word	(AP)	char				
12	1	2 eye-tracker	118.918	saccadeET	1 SMlevent	1 short		word	INDIANAPOL	char				
13	1	2 eye-tracker	213.9142	saccadeET	1 SMlevent	1 short		word	Indiana	char				
14	1	2 eye-tracker	50.92	fixationET	1 SMlevent	1 short		word	(AP)	char				
15	1	2 eye-tracker	101.9178	fixationET	1 SMlevent	1 short		word	INDIANAPOL	char				
16	1	2 eye-tracker	132.9183	fixationET	1 SMlevent	1 short		word	Indiana	char				
17	1	2 eye-tracker	224.9235	fixationET	1 SMlevent	1 short		word	State	char				
18	1	3 eye-tracker	40.923	saccadeET	1 SMlevent	1 short		word	(AP)	char				
19	1	3 eye-tracker	67.918	saccadeET	1 SMlevent	1 short		word	INDIANAPOL	char				
20	1	3 eye-tracker	162.9142	saccadeET	1 SMlevent	1 short		word	Indiana	char				

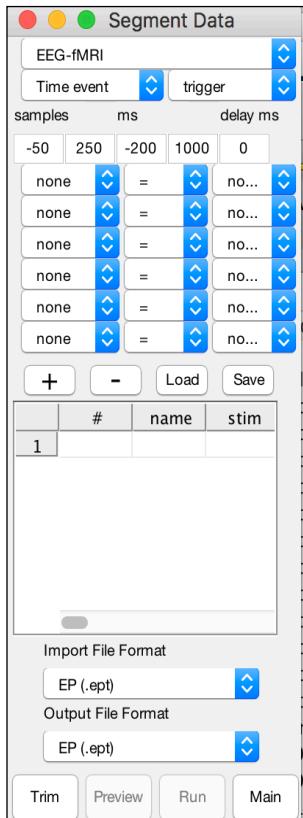
In any case, click on the Read button and then the EEG-fMRI.mff file in the tutorial folder. Keep an eye on the Matlab command window to monitor its progress. Once it is done, you should see:



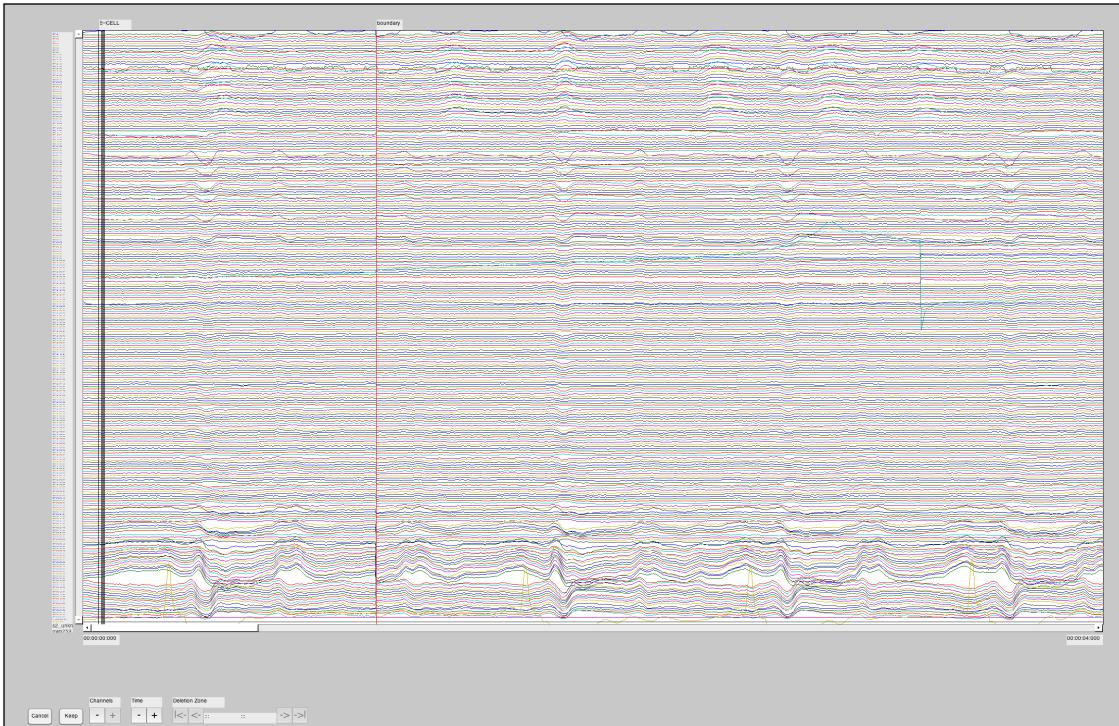
Next click on Main to get back to the main menu.

Trimming

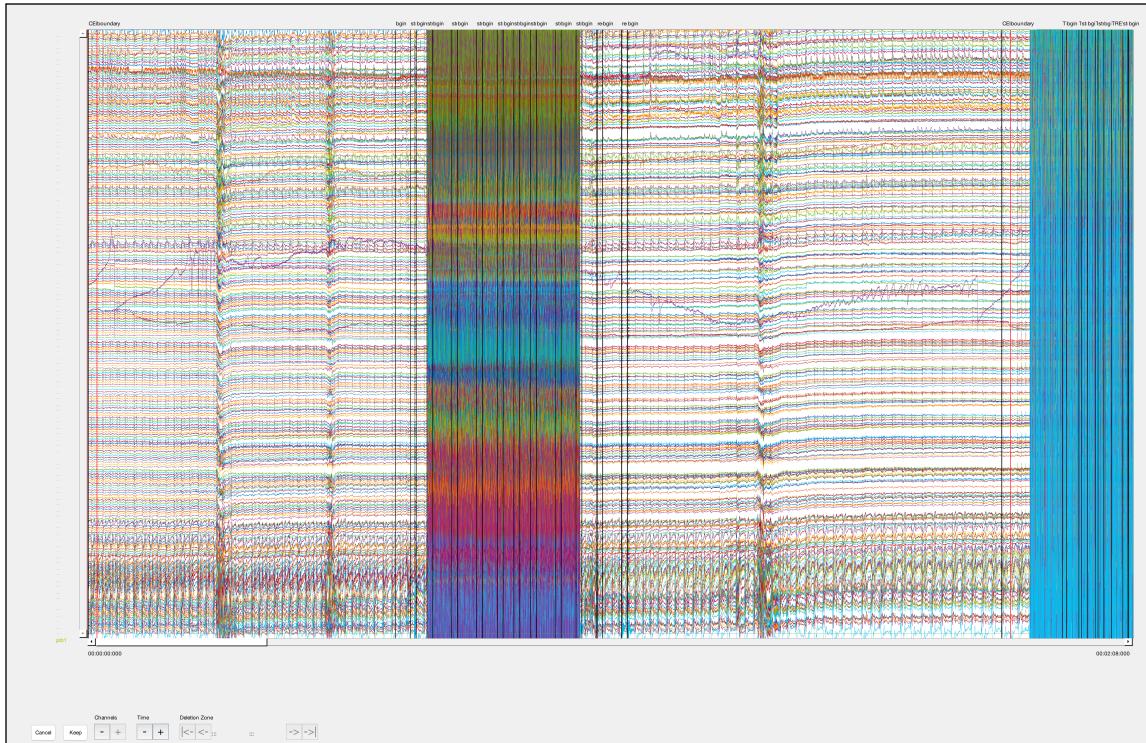
The next step is to trim the data to remove the unwanted initial period. Click on Segment to bring up the Segment pane.



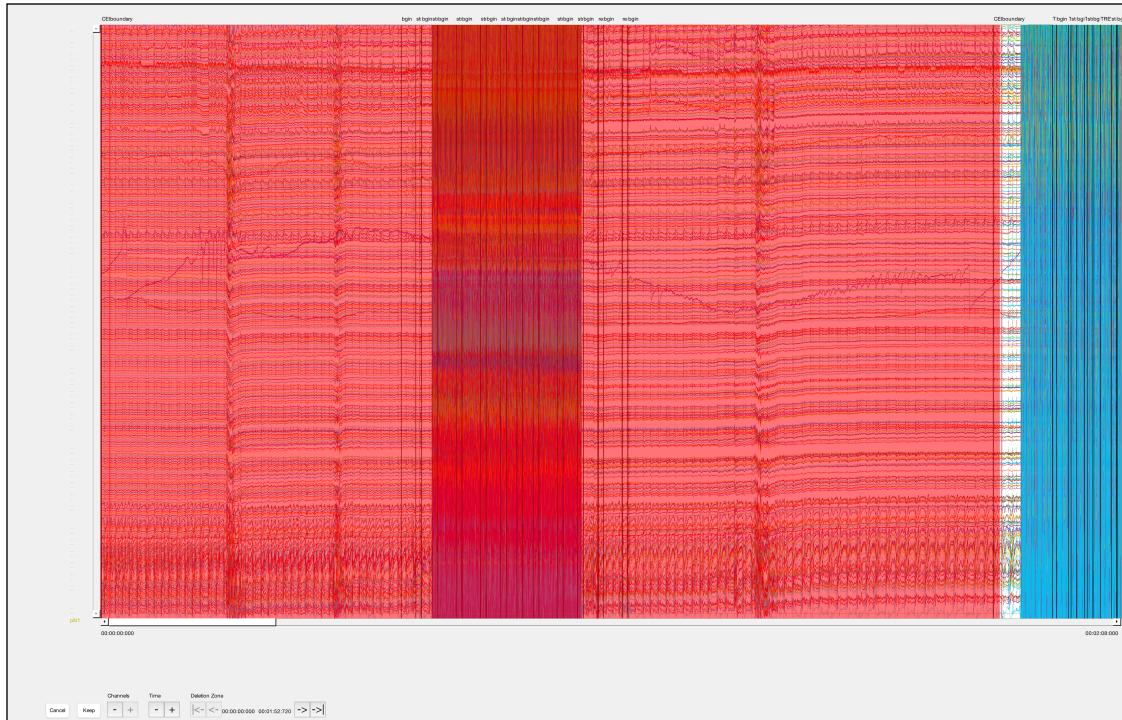
First select the EEG-fMRI in the first menu (which lists every continuous data file in the working set). If you press the Trim button a new window will open up with each channel occupying a separate line to facilitate a high-level view of the recordings. By default, four seconds of data will be displayed at a time and for all the channels. The - and + buttons below allow one to zoom in and zoom out the channels and the time points (menemonic for the buttons is to think in terms of showing less vs. more channels and time points). Events are shown along the top and marked across the channels with a black line. Discontinuities in the recording (boundary events) are marked with a red line. Moving around the data should be pretty quick and smooth with a decent computer (in my case a 6-core Xeon 3.33Ghz Mac Pro) but Matlab sometimes starts bogging down and will need to be restarted.



If the + Time button is pressed five times, it will be possible to see the entire period that needs to be trimmed away. The session was begun (resulting in a cluster of CELL events), then paused (resulting in a first red boundary event), then after a period the experiment script started (resulting in a series of bgn+ and stm+ events), then the experiment script was restarted (resulting in another cluster of CELL events) then paused again (producing a second red boundary event) and then finally the experiment proper starts. The TREV events were provided by a pulse from the scanner itself, indicating the onset of each pulse sequence. The TREV events were not being generated in the initial experiment start which is why this period could not be corrected by the fMRIb code. It therefore has to be manually trimmed away.



The CELL events are information that NetStation generates to facilitate its operations but is not needed by the EP Toolkit. It will therefore suffice to delete everything up to the third boundary event. The second boundary event can be found at about the 00:01:52 mark (one minute, 52 seconds). Drag the mouse from off the left side to somewhere before the second boundary. This will highlight this region in red. Then right-click within the red deletion zone and select the word “delete” to delete this portion of the recording.

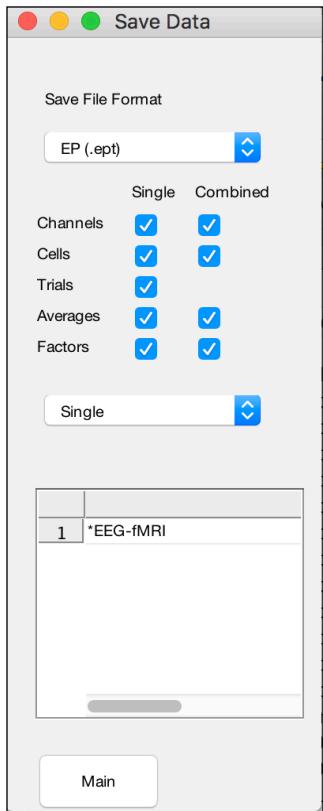


Next zoom in with the - button (less time points) so you can see both the start of the trimmed recording and the red boundary marker. Drag the mouse from off the left side of the screen up to the red boundary marker. This portion of the recording will be highlighted in red. Then click on the -> button to extend the right edge of the deletion zone to extend to the sample just prior to the next event, which in this case is the boundary event. Normally this means that the event would not be part of the deletion zone but boundary events are deleted if they end up at the edge of a recording. The -> button would extend the right edge by a single sample. Then right-click within the red deletion zone and select the word "delete" to delete this portion of the recording. Once done, click on the "keep" button to keep all the changes to the recording and click "cancel" to discard them. Then click on Main to return to the main menu.

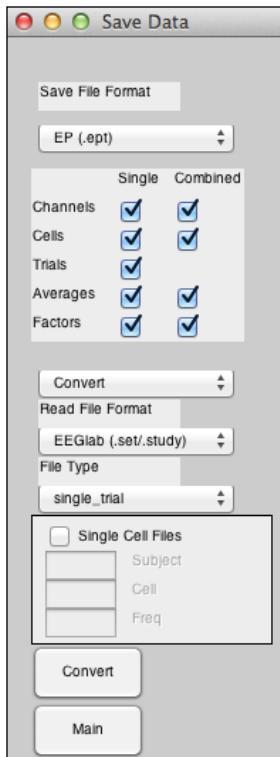
Save

The next step is to save the trimmed file to the disk. Changes made to the copy in the working set do not affect the original files. The Save function at the bottom of the main menu allows files in the working set to be saved permanently. Just specify the file format and which types of data are to be saved. By default, all adds to the data are saved (that is, all the ERP data plus all the combined channels, cells, subjects, and factors), although some adds may require separate files. Also, if one saves a factor file in EGIS average format then it will be necessary to save a separate file for each subject, in addition to the Grand Average Data. If not needed and one wished to avoid the clutter of all the subject average files, one could just deselect "Averaged Data." It would also be advisable to save a copy of the file in EP format as it will retain information that might otherwise be lost in

translation to other file formats. When ready, just click on the name of the dataset to be saved. The asterisk in front of the file name indicates it has unsaved changes. Indicate that the new file should be named: as EEG-fmri_trim.ept. It will ask you if you wish to change the name of the copy in the working set, to which you shouls say Yes.



If you wish to convert a batch of files directly from one format to another without first loading them in, then change the pop-up menu from "single" to "convert" and it will allow you to select a batch of files on disk and convert them for you without loading them into the working set.



Exporting to EEGLAB

One may often wish to save into the EEGLAB format. The .set file format is an option but incompatibilities between the way the two file formats are organized makes it difficult to provide full compatibility. For example, factor results cannot currently be saved to .set file format and likely never can (EEGLAB .set file format is predicated on the approach of keeping all the single trial data and then generating the averaged data on the fly).

Factor matrices are applied to the single trial data and are stored alongside the raw single trial data. There doesn't appear to be a way of having the factor matrices be applied to the averaged data.). If the .set file format is not working for you, then you may wish to try one of the EGI file formats.

EEGLAB calls the EGI simple binary format "EGI .RAW". However, it would be better to use the option "From other formats using FILE-IO" as it will then use the FieldTrip code (which makes an effort to deduce what the baseline period should be since this information is missing from this file format, if you are using the most recent version of FieldTrip rather than the one bundled with EEGLAB). You find the options under "File>Import Data". You can also import EGI EGIS format files using "File>Import Data>From other formats using FILE-IO". Remember that while this file format keeps track of the baseline period information it does not keep track of events so that information will be missing.

Exporting to Net Station

If you wish to export to NetStation 4, use either EGIS or Simple Binary formats. I

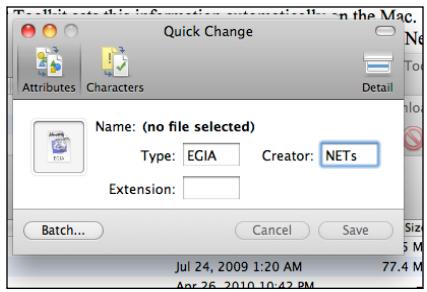
recommend using EGIS unless the file is very large (in which case the file format may not be able to accommodate the data and will generate an error message when you try to save it). The major reason for using EGIS average files instead of Simple Binary is that the latter does not represent the prestimulus period information. EGIS session files don't represent prestimulus period information either. The reason why this is important is that the lack of prestimulus information causes problems with a number of NetStation waveform tools, especially the Combine Files function. If you are using NetStation 5 then you will have to use Simple Binary despite its limitations. They are currently developing support for Matlab programs to save mff files, which hopefully will be ready soon.

EGIS files will need to have their file type and creator set. ERP PCA Toolkit functions should be able to do this under MATLAB 7+ and OS X 10.5+ should be able to do this automatically. If you get an error message saying it was unable to do so, then you will need to use a utility like Quick Change and use it to change the file type to "EGIA" and the Creator to "NETs" without the quotation marks.

In order to properly display the contents of an EGIS file, NetStation 4 needs the electrode formats. The EP Toolkit sets this information automatically on the Mac. However, the montage information from NetStation 4.3 differ from prior versions of NetStation. Since only version 4.3 includes Hydrocel net montages, this means that versions of NetStation prior to 4.3 cannot view such data sets. Also, depending on the version you have, NetStation may not give you the full list of possible electrode nets.

There are some incompatibilities in the montages between NetStation 4.3 and earlier versions for Hydrocel nets, with 4.3 unable to open montages from earlier versions and vice versa. Because of this problem, I've added an option under the Files preferences to not add the montage to EGIS files (montage information is not used for other types of files).

If the .sbin or .egis files were originally made on a non-Mac computer or if the file were subsequently moved to such a computer then the metadata normally added by Satimage osx will not be available. In this case, NetStation will not recognize the files. It will be necessary to manually add them. A good program for doing so is Quick Change (<http://www.everydaysoftware.net/quickchange/index.html>). Changing the Creator field to NETs allows the Mac to know that the file belongs to NetStation. Changing the Type field to EGIS for .egis files and eGLY for single_trial and average (segmented) .sbin files and UGLY for continuous (unsegmented) .sbin files allows NetStation to know which type of file it is. Just type in the fields and then drop the file on the box on the leftmost side or onto the program icon itself (including a Dock icon).

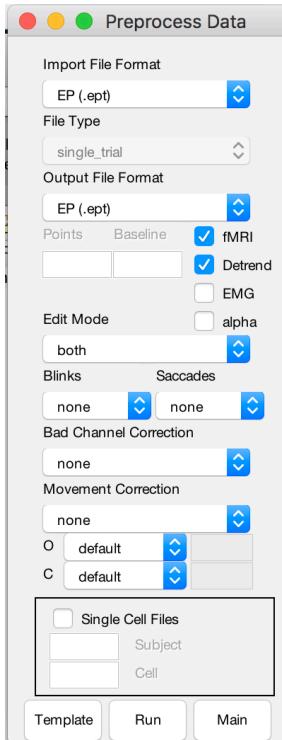


Note that NetStation (as of 4.1.2) does not seem to read in event data at all from such files. If you need the event information, you should use the Mark-up tool to add the events back in once the files are converted back to NetStation format.

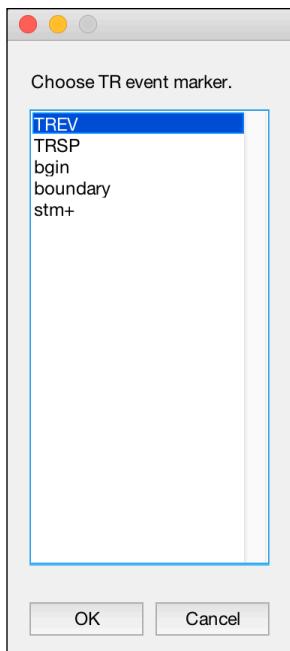
Click on Main to return to the main menu.

Removing fMRI Artifacts

The next step is to remove the MRI noise (which reaches tens of thousands of microvolts). Make sure you installed the MRI correction routines as described in the installation section. Click on the Preprocess button on the main menu. Click on the fMRI option to invoke the MRI artifact correction routines (further explained in the Preprocessing section) and Detrend to correct for overall drift. Turn off all the other options (which will be explained in the Preprocessing section). The controls should now look like the following.



Then click on Run and select the file. If checked and the fMRIb function is specified in the preferences, the EP Toolkit will ask for the TR event marker as it needs to know when each rep began in order to correct gradient artifacts. For this dataset choose TREV.



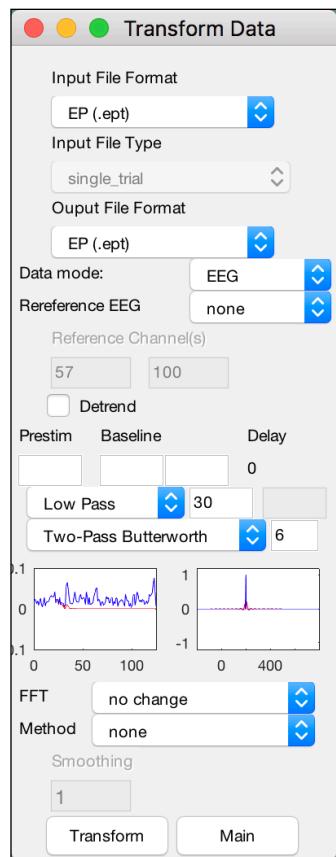
After this point the preprocessing will proceed without further input. It will need an ECG channel in order to correct ballistocardiogram artifacts (which EEG-fMRI does have). It will add 'qrs' events to each point that it detects a heartbeat. Watch Matlab's command

window to monitor its progress. Ignore the colorful Artifact Correction figure that pops up for now. When it is finished, the command window will show "Done." and the buttons at the bottom of the Preprocessing pane will stop being grayed out. A new file named EEG-fMRI_trim_bcg.ept will contain the corrected data. Click on Main to return to the main menu.

Transform

The next step is to low-pass filter the data. Click on Transform. The Transform function is used to rereference, baseline correct, filter, and/or convert to spectral measures.

Luck (2014) advises against filtering, only filtering for illustration figures, due to temporal smearing. However, I am generally uncomfortable with presenting figures that do not directly correspond to what is being analyzed. My suggestion is to use a two-pass filter (which preserves the peak latency) for conventional analyses and to use a one-pass filter (which preserves the onset latency) for sample-by-sample analyses. Clearly more systematic studies of this issue are required, however. In any case, set up the controls as follows.



The first setting is the file format, which in this case will be .ept (the EP Toolkit's native file format). Since this file format specifies the type of data, the next setting is not

necessary and is grayed out. The third setting is the file format of the resulting file and should also be .ept. In general, it is recommended to use the .ept format while using the EP Toolkit as other file formats will result in loss of EP Toolkit-specific information.

The Data mode setting indicates what type of channels should be transformed. For example, if ECG was selected then filtering would be applied to the ECG channel instead of the EEG channels.

The next control rereferences the data. If reference is set to Traditional then it will be referenced to the channels listed below it. If it is set to Average then those fields will be ignored and it will instead be referenced to the average of the entire dataset (Dien, 1998b). Alternatively, the data can be transformed to CSD (current source density) form (Perrin, Pernier, Bertrand, & Echallier, 1989), which is essentially a high-pass spatial filter which eliminates broadly distributed voltage fields in favor of sharply defined focal features. It has the benefit of being reference-independent and of allowing for a crude source localization but runs the risk of eliminating ERP components of interest that happen to be broadly distributed. Finally, it can be average-referenced using the PARE-correction, which corrects for the lack of electrode coverage on the underside of the head (Junghöfer, Elbert, Tucker, & Braun, 1999). For EGI high-density montages (which are designed to maximize head coverage) I'm not seeing a lot of difference from average reference and the EP Toolkit's implementation is quite slow and can take hours. You can use the Topos Rerefence right-click option to see kind of effect it has on your data. The PARE correction is influenced by the reference in effect prior to the correction so the EP Toolkit always applies an average reference first. We will not rerefence the data yet as doing so would risk spreading the effects of bad channels to other channels.

Detrend, as for the Preprocessing function, corrects for overall drift across the dataset (or epoch for segmented data) by fitting and removing a linear function to the channels. It is generally not recommended except for continuous data as applying it to segmented ERP data can result in attenuation of ERP components.

The prestimulus period is length of the epoch prior to the onset of the event to which the epoch was locked. The Prestim field allows one to label segmented data with the appropriate prestimulus time but has no other effect. There is no need for this setting until the data has been segmented. Note that some file formats, such as EGIS session, cannot represent the prestimulus period and so this information will be lost if they are used as the output format.

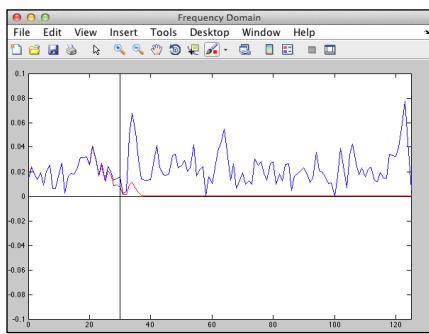
The Baseline period (often the same as the prestimulus period) is the part of the epoch that is used to estimate zero voltage. It need not be the same as the prestimulus period. The two fields specify the baseline period in ms (i.e., "-100" and "0" means the first 100 ms). We will return to this procedure after segmentation.

The Delay field is not a control. It indicates how much of a delay (in ms) is being caused by a given filter setting so that it can be corrected for when segmenting the data.

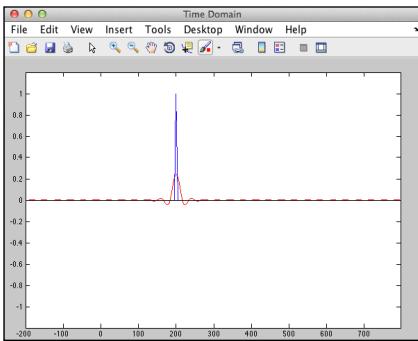
The next setting specifies the filter range. Low Pass means passing through frequencies below the setting. High pass means passing through frequencies above the setting. Band pass means passing through frequencies within a specified range. Band stop means stopping frequencies within the specified range. Notch means stopping only the specified frequency. Luck's book has a very nice chapter on filtering and its effects.

The next row sets the filtering parameters. The first aspect is “one-pass” vs. “two-pass” (also known as “causal” vs. “non-causal”). A one-pass filter starts from the front and goes to the back, with the result that the EEG activity can be smeared a bit towards the back, potentially artifactually delaying the latency of ERP components (the extent of this delay for the sample figure is indicated in the Delay field). A two-pass filter adds a second pass, starting from the back and proceeding to the front. This has the effect of undoing any changes to latency but at the cost of smearing effects towards the future, potentially artifactually advancing the onset latency of ERP components. The second pass also increases the strength of the filtering. The field following this menu specifies the order of the filtering, which is to say the strength of the filtering.

In general there is a trade-off between accuracy of filtering in the frequency-domain and in the temporal-domain. This can be seen in the two figures on the next row. The first generates some random data in blue and then illustrates the effect of the filter in red. The stronger the order, the steeper the roll-off (the shorter the transition zone between unfiltered and filtered) and the more complete the filtering, but the more smearing occurs in the temporal domain.



This effect on the temporal domain can be seen in the figure in the rightmost figure, which provides a spike in blue and shows in red what the data looks like after filtering. Both figures can be expanded by clicking on them. The frequency domain figure usually shows a vertical line indicating the location of the nominal filter settings. If the filter lines don't appear, close and open the expanded figure a few times.



Butterworth, FIR, and FIRLS are three filter types made available by Matlab. In general the Butterworth is the recommended filtering algorithm. Try playing the settings and see what effect they have on the figures.

Finally, one can convert the data into the frequency domain using FFT (fast Fourier transform). “no change” means staying with voltage measurements over time. The “Frequency” and “Time-Frequency” are for performing frequency domain analyses and will be explained in the Spectral Analysis section.

This step is also performed upon files on the disk rather than on the working set (which is why the preparatory functions of Segment, Preprocess, Transform, and Average, are listed above Read on the Main Menu).

For the tutorial, click on the Transform button and select the EEG-fMRI_trim_bcg.ept file. It will generate a new file named EEG-fMRI_trim_bcg_f.ept. The suffixes are “r” for rereferenced, “c” for CSD, “b” for baseline corrected, “f” for filtered, “s” for spectral frequency transform, and “w” for wavelet time-frequency transform (even if the wavelet algorithm wasn’t used for the transform).

Segmentation

First, switch to the Read pane to read in the new EEG-fMRI_trim_bcg_f.ept file by selecting the ept format, and then clicking on the Read button to select the file. It will take substantial time to read in since it is a large file. The reason the tutorial data needed to be loaded into the working set is that in order to segment it helps to have a representative continuous data file to serve as the template (to provide the types of events present in the experiment). Once at least one set of continuous data has been read into the working set, the Segment button will no longer be grayed out. Switch to the main menu by clicking on the Main button and then click on the Segment button to reveal the Segment Data function.

The Toolkit can perform segmentation of continuous data files into epochs. Click on the Segment button to switch to the Segment function. The top popup menu is the list of continuous and single-trial files in the working set. Select the dataset that will serve as the template for the segmenting specifications (i.e., EEG-fMRI_trim_bcg_f). The top

portion helps make it easier to construct the segmentation table in the lower half but can be bypassed directly in favor of typing the criteria directly into the segmentation table.

Each row of the segmentation table will define a condition. There is no limit to the number of conditions that may be defined. Each condition may have up to six criteria stipulated to define the condition. The criteria on a given row have an AND relationship to each other, so for a potential segment to be included in the condition it must pass all the stipulated criteria. In order to define criteria with an OR relationship, provide more than one row where the condition name is the same. A segment that meets either set of of stipulations will be included in the condition.

In the upper half of the pane, the “Time event” menu will then be populated with the event names in the template file. Both the contents of the Type field (the general event label) as well as the Value field (the specific event label) will be listed. Then select the event that will serve as the time-locking event, which in this case will be stm+.

Then set the epoch period. In this case, enter in -50 samples in the first box and 200 samples in the second box to specify a 1000 ms epoch starting 200 ms prior to the event. Since equipment issues resulted in no behavioral data being recorded, we'll just set the one criterion of cell #. If prior filtering resulted in a delay (as due to the use of a one-way low-pass Butterworth filter or EGI GSN300 and GSN400 amplifiers) then enter the delay into the "delay ms" field so that the epochs are offset accordingly.

The menus in the first column of the criterion line will be populated with the fields associated with the time-lock event. It will also contain the fields associated with Trial Specs (TRSP) events, if present. Trial Specs are special event structures that are used by some file formats that provides trial-specific information like reaction time. They are generated at the end of each trial and are associated with an epoch if the epoch includes the time point when the Trial Spec was generated. The criterion menu includes the fields included in any Trial Spec present in the data file but will only be considered for segmentation if a Trial Spec event fell within the defined epoch. If multiple Trial Specs are present in an epoch, only the first will be used. Fields derived from the Trial Specs will be prefixed with a “TS-“ to differentiate them from those derived from the time-lock event. Choose “cel#.”

If there is a trial-spec named TS-offset, the epoch will be delayed by that number in ms (negative for earlier), allowing for trial-level control of segmentation offsets.

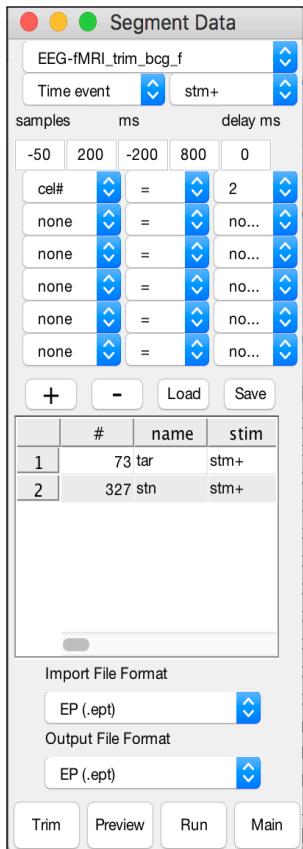
The second column provides a number of options for how the spec value might relate to the criterion value. Comparisons are evaluated numerically for numbers, otherwise alphabetically. For now, leave it at “=”. The third column menu will be populated with the values present in the template file. Set it to 1. Then click on the + button. This will take the settings you have chosen and insert it into the segmentation table. You can then edit the contents of the segmentation table as desired. For example, if the criterion value you wanted to choose wasn't in the menu, you can change it at this time. Change the

criterion value to 2 and click on + again. You should also add the names of the conditions to the segmentation table (second column). In this case they are "tar" and "stn" for target and standard respectively.

There is also a flexible segment option available for the case where one wishes to average together segments with different lengths (most likely TFT data). In this case one clicks on the "time event" popupmenu to change it to "flex event". As before one sets the event that the segments are locked to but now instead of specifying a set duration one specifies the event that ends the segment in the row below. In the line below one sets how many samples will be in the flexible segments. All the segments will be interpolated to yield segments the same length regardless of the original length. The default setting of 20 results in samples representing 5% increments of the original segment length. This procedure is likely meaningless in the time domain (except possibly for slow potentials) but can be useful for TFT data.

To delete the last condition in the segmentation table, click on the “-“ button. You may save the segmentation for later use by clicking on Save. To access this saved segmentation table, click on Load.

To verify that the criteria have been correctly specified, click on the Preview button. It will determine how many segments would be generated if the segmentation table was applied to the template file and provide the number in the # column. The button will not be enabled till all the conditions have a name (the second column of the segmentation table). Remember - only the contents of the segmentation table affect the actual segmentation. All the controls above the table are just for facilitating the construction of the table. One could actually bypass these controls entirely and just construct the segmentation manually by typing directly into the table. In any case, at this point, the function should look like:



The first column criteria columns also provide a “-follows-“ option. If this is chosen, it means that a time-lock event should only be used to generate a segment if it follows (at any distance in time) another event. When “-follows-“ is chosen, the third column menu is populated with the list of events present in the dataset. Once one chooses the event, the next row down will be populated to contain the fields for that event (but no Trial Spec fields). Thus, one might specify that only a resp (response) time-lock event that follows a stm+ event from Cell 1 would meet these criteria (i.e., -follows- = stm+; cel# = 1). If the first stm+ preceding the resp was instead from Cell 2 then it would not meet criteria. Or one could specify that a resp time-lock event immediately preceded by any another other event would meet criteria (i.e., -follows- ~= stm+; none = none). One could also string together two “-follows-“ criteria. In this case, the first “-follows-“ acts as before. The second “-follows-“ criterion specifies an event that is interposed between the “-follows-“ event and the time-locked event. Thus, one might specify the criteria that the resp time-lock event must follow first a stm+ event of cel#2 and then a stm+ event of cel#1, which is to say it must be a response in a target trial that followed a standard trial (i.e., -follows- = stm+; cel# = 2; -follows- = stm+; cel# = 1). Only two such “-follows-“ events may be specified. It is possible to specify unrelated criterions between the two “-follows-“ criteria. It will not affect the interaction between the two “-follows-“ criteria. A “-follows-“ criteria cannot be used in the sixth slot because there is not a further slot to complete the specification. A corresponding “-precedes-“ option is also available. It

operates in the same manner as -follows- but refers to events happening after the time-lock event.

If everything is ready, save the segmentation specs by click on Save. Set the file format of the data files to be read in and the file format to save the resulting single-trial data files and then press Run. It will ask you to indicate which files (on the disk drive, not in the working set) to segment. The copy of the data loaded into the working set will not be affected by the segmentation process. The Segment function will generate a new file with a _seg suffix (e.g., EEG-fMRI_trim_bcg_f_seg.ept).

It is also possible to apply the segmentation function to single-trial data that has already been segmented. In this case the existing segments will be reassigned to new conditions if they meet the stipulations or otherwise dropped. This can be a useful approach if, for example, one has a complicated dataset that can be potentially segmented in different ways, one wishes to run segmentation prior to Preprocessing (as recommended since baseline correction enhances the process), and one does not wish to rerun the Preprocessing function after each and every use of the Segment function.

For data with behavioral data (reaction time and accuracy), one should make sure to retain the error and the bad RT trials during segmentation as they will be handled during averaging.

Press Main to return to the starting menu when finished.

Artifact Correction

The next step would be to proceed with the normal artifact correction process using the Preprocessing pane. However, for didactic reasons we are going to now shift to the set of children's data in the ten EGIS files.

The Toolkit can automatically eliminate blink, saccade, movement, and alpha artifacts from session files as well as detecting and correcting bad data. It does so via the Multiple Algorithm Artifact Correction (MAAC) procedure, which applies an algorithm that is especially well-suited to the characteristics of each of the artifacts (Dien, in preparation).

It is recommended for the data to have already have been segmented into discrete trials if it is meant for ERP analysis as using the full continuous data takes more time and disk space than is needed. Also, my observation is that applying the artifact correction (especially the ICA-based eyeblink and saccade corrections) work best on baseline-corrected segments as it provides a loss-less high-pass filter. While Luck (2014) recommends not using baseline correction on the basis that it distorts the scalp topography if there is ERP activity in the baseline period, my opinion is that this is not actually correct. If there is ERP activity in the baseline period, all that happens is the total epoch's waveform is offset such that the baseline period averages to zero (so a negative blink artifact in the baseline period will become a positivity in the non-baseline

period). Although the timecourse is thus modified and the polarity flipped, the scalp topography of the effect remains the same (spatial ICA doesn't care about the polarity or which time points have the effect, just the relations between the channels) and the blink is still efficiently removed. I find that the ICA does, however, benefit from having the drifts in the recordings minimized by the baseline correction of the segments. Presumably at some point someone needs to put these competing views to the test.

Chunking

The artifact correction function reads in a session file and segments it into manageable chunks which are temporarily stored (since an ICA of an entire session file can often exceed the available RAM). Since the final chunk (the remainder) would often be too small for an effective ICA run, it is appended to the previous chunk and the total chunk is divided into two chunks that are smaller than the others but large enough to process. The chunking is not allowed to divide any trials in two. Then it processes each chunk individually and stores the result. Then it glues them back together into a new session file with a “_e” appended.

Note: If the data are large enough to be chunked and you have more than 2GB of RAM, you should go to the preferences menu and see if you can increase the chunking size without running into out of memory errors. About 100,000 per GB of available RAM seems to generally work well. Basically, if the preprocessing routine is chunking your data, try upping the preference setting and see if it'll still run. Unfortunately Matlab does not provide a way to adjust this setting automatically, at least on the Mac.

Default Procedures

Preprocessing parameters can be changed in the Preprocessing Preferences, but the default procedures of the Toolkit are as follows:

As you have already done for the tutorial, if the data was collected inside an MRI scanner, first run the data through Preprocessing as a continuous file with just the fMRI correction option chosen. An electrocardiogram channel (with the channel type designated as ECG) will be required to detect heart beats for ballistocardiogram artifact correction. The fMRI correction is invoked simply by checking the fMRI box. The option is determined by the Preference setting (see #19 below). Both options provide both MRI pulse sequence and ballistocardiogram artifact corrections. Then, whether or not fMRI correction was performed, either segment the data and run it through Preprocessing as single-trial data or just run it through as continuous data, depending on analysis needs. All steps are independent of referencing scheme. The full Multiple Algorithm Artifact Correction or MAAC procedure is presented elsewhere (Dien, in preparation).

- 1) *Prepare data* - The first step is to prepare the data by controlling for the wild DC shifts sometimes present. Baseline correction and/or detrending can address much of them. Detrending fits a linear trend line to a waveform that is then subtracted from it. For

segmented ERP data only baseline correction should be used as detrending can attenuate ERP components. Detrending can be useful for continuous data.

2) *Bad channel identification* - The first step is to check for any channels whose best absolute correlation with neighboring channels falls below .4 (across all the timepoints, irrespective of bad trials). In order to detect channels that went bad partway through the session, it will divide the session into five sections (if the badTrials setting is at the default of .20) and test for bad channels in each. If a channel is bad in at least one such section, it is considered to be globally bad and is excluded from further analyses.

Furthermore, if a channel has more than 20% (if the badTrials setting is at the default of .20) timepoints over +/-500 microvolts from the median in a section, it will also be marked bad.

If the session has more than ten percent bad channels then it will be considered a bad subject and it will not be further processed. A warning will be provided if any of the globally bad channels are neighbors. Additionally, flat channels are identified as being bad channels (unless it was identified as being the reference channel). Additionally, channels that correlate perfectly with a reference channel will be marked bad (this happens when a file with a flat bad channel is rereferenced). Channels that are shorted together (perfectly correlated) will generate a warning in the log but will not be touched. It will also identify time points that exceed a certain threshold (+/-1000 microvolts by default) that will be excluded from the saccade and blink correction steps as such extreme outliers can otherwise distort the results. The Edit Mode option controls whether this automatic routine is performed.

3) *Saccade correction* - The next step is to correct two artifacts associated with saccades: saccadic spike potentials or SPs (Blinn, 1955) and corneo-retinal dipoles or CRDs (Lins, Picton, Berg, & Scherg, 1993). SPs are produced each time the eyes initiate a saccade and are problematic because they resemble a P300 and they also mimic gamma band activity in spectral analyses (Yuval-Greenberg, Tomer, Keren, Nelken, & Deouell, 2008). First a blink detection is run (if the blink correction option has been chosen) to identify putative blink time points so they can be excluded from the SP correction process. To further complicate things, SPs can distort the blink detection procedure so prior to the blink detection a preliminary SP detection run is conducted just to exclude those time points from the blink detection run. Needless to say, these putative SP time points are not excluded from the SP correction process itself. Once the putative blink time points have been identified the actual SP correction procedure is conducted using a vector-filter algorithm. A SacPot event is recorded at each such point to facilitate analysis and segmentation of saccades. Also, a SacPot channel is added that describes the time course of the data that has been removed.

After this is done, then the CRD artifact is corrected using a regression algorithm. The CRD is a persistent voltage field that reflects the current gaze direction so it is not a saccade artifact so much as it is an eye position artifact. The CRD produces positivity in the direction of eye gaze. XEY and YEY channels are added to the data indicating the

gaze direction inferred from this procedure. This estimate is roughly accurate for horizontal gaze direction and less so for vertical. For continuous data, the putative eye movement activity can then be observed using the View Scan function.

The routines for all three artifacts (blink, SP, CRD) use templates to identify the artifacts. These templates can either be generated automatically or can be manually produced using the Template button on the Preprocessing pane. Automatic template generation requires four VEOG and two HEOG channels. Normally, the EP Toolkit is able to automatically determine which channels are the EOG channels (or the next closest EEG channels) if it is given the electrode coordinates information. If the automatic determination process is not working, it is also possible to set the EOG channels manually via the preferences settings. Just in general, it is best to check what channels are being used for the blink correction (reported by the preprocessing log) and confirm that they are the correct ones. If one of these channels is a bad channel, the EP Toolkit will first generate a best estimate of it via interpolation, which may take some time.

4) *Blink correction* - The next step is to perform the blink correction process. The artifact detection routine uses EEGLab's runica routine to decompose the data into basic scalp topography components. These components are then compared to a blink template which specifies the topography of a typical blink (that can be generated either automatically or via a manual template constructed via the Template button of the Preprocessing pane). Components which correlate highly (.9 by default) with this blink topography are deleted from the data. The removal of the blink topography will apply to blink recoveries as well (which have the inverse scalp topography and are caused by the amplifiers recovering from the sudden blink amplitudes). Event markers are added to indicate the following for each blink: blink_start, blink_peak, and blink_end. Also, a blink channel is added to describe the timecourse of the data that has been removed.

5) *Movement artifact removal* - Using an experimental approach (Dien, in preparation), movement artifacts can then be removed. Whereas ICA is highly effective at removing eye blinks, it is not suited for movement artifacts because they are typically highly variable between trials so ICA can't be applied to them at the level of a dataset (there may not even be enough ICA factors available to account for all of them, let alone the ERPs themselves, since there cannot be more factors than there are variables, which in this case is the number of channels). ICA can't be applied to isolated trials because it needs more observations (i.e., time points) than are available from a typical trial. In contrast, PCA (using the Promax rotation) works even with small numbers of observations and seems to provide adequate results for individual trials. For this reason, a temporal PCA (using the Promax rotation) is used to identify factors which account for activity with an amplitude difference between minimum and maximum values greater than 200 μ v and this activity is removed.

6) *EMG artifact removal* - Using a newly developed method (De Vos et al., 2010) based on blind source separation canonical correlation analysis (BSS-CCA), the toolkit will use code kindly made available by the developer to attempt to remove EMG activity.

Essentially it capitalizes on the characteristic of EMG that it is more discrete than EEG in both spatial and temporal domains by preferentially removing activity that is not correlated between adjacent time points across multiple channels. I have not had the opportunity to evaluate its efficacy so I cannot make a recommendation but it does seem like a promising approach. My impression is that it works best if the sampling rate is on the order of 1000 Hz so it will not be used with the tutorial datasets (which are 250 Hz). Note that EMG correction requires the Signal Processing Toolbox.

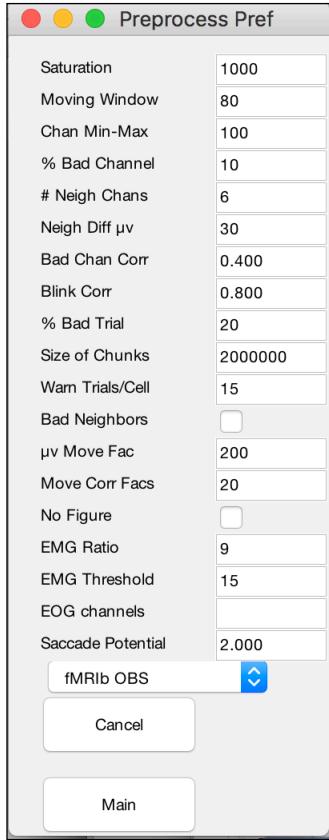
7) *Alpha Correction* - If a participant is sleepy or otherwise zoning out, alpha activity can arise that is so large that it swamps ERPs even after averaging. This experimental option removes some of the alpha activity using a spectral-spatial two-step PCA to remove the major activity in the alpha band. This is very experimental and I cannot guarantee that it won't remove part of the ERPs as well. It should not be used on data that will be analyzed using spectral measures. It can require a great deal of RAM and has a tendency to crash even my 32GB Mac unless I make sure to free up all the memory that I can first.

8) *Bad channel and trial identification* - Bad channels are then detected on a trialwise basis. They are defined as having a difference of more than 100 μ V from the minimum and the maximum values in that trial (so the trial contains substantial swings in the voltage). They are also declared bad when the maximum divergence from all the other channels is computed and even the least different is 30+ μ V (so all the other channels are quite different). Flat channels are also marked as being bad, unless they were identified as being a reference channel AND the channel is flat over the entire dataset. If more than 10% of the channels (including globally bad channels) are marked as bad then the entire trial is marked bad. If a channel is marked as bad on more than 20% of the good trials, then it is marked as globally bad. The Edit Mode option controls whether this automatic routine is used and/or manual editing marks from before the automatic preprocessing routine was set in motion.

9) *Bad channel replacement* - If the "replace" option was chosen, channels that were marked bad are replaced via interpolation from the good channels of the scalp voltage field (the entire scalp is interpolated and then the missing channel voltage is obtained from this interpolated scalp surface) and bad trials are zeroed out. The quality of interpolation for channels on the edge or with neighboring bad channels is likely to be reduced.

10) *Log file* - A log file is generated to summarize the results of the session. Also, a template file is generated that provides the scalp topographies of the templates used (whether automatic or manual) and of the overall data that were actually removed.

If you wish to change the Preprocessing preferences setting, go to the preferences as before. In particular, you may wish to change the Blink Corr setting to .8 since it will be more difficult to match up blink factors to the blink template without the lower VEOG channels.



- 1) *Saturation* is the voltage level at which the data should be considered to be bad and excluded from the blink and saccade correction steps.
- 2) *Moving Window* is the number of milliseconds over which the artifact correction routines average the data in a form of low pass filtering. The larger the number, the less sensitive it is to high frequency spikes.
- 3) *Chan Min-Max μv* is the maximum allowed change in voltage levels for a channel during a trial before it is deemed to be a bad channel for that trial.
- 4) *% Bad Channel* is the maximum percentage of channels allowed to be bad in a trial before it is deemed to be a bad trial.
- 5) *# Neigh Chans* is the number of channels considered to be a neighbor for purposes of the artifact correction algorithms. The electrode coordinates are then used to figure out which channels are to be used.
- 6) *Neigh Diff μv* is the maximum voltage difference allowed between a channel and its neighbors before it is deemed to be a bad channel.

- 7) *Bad Chan Corr* is the multiple-R regression criterion for determining whether a channel is a globally bad channel over the entire session.
- 8) *Blink Corr* is the correlation criterion for determining whether an ICA factor matches the blink template and should therefore be subtracted from the data.
- 9) *% Bad Trial* is the maximum number of trials a channel is allowed to be judged bad before it is deemed to be globally bad.
- 10) *Size of Chunks* is the number of time points that are read into each chunk (about 100,000 per GB of available RAM seems to generally work). If there is sufficient memory, it is best to process a datafile as a single chunk so be sure to set this number as high as is possible. Unfortunately, on the Mac it is not possible to have MATLAB set this parameter automatically so the user has to set this. If the data files are already being processed as a single chunk then raising this number will have no effect.
- 11) *Warn Trials/Cell* is the minimum number of good trials that is considered to be sufficient for a cell. Any cells dropping below this number will trigger a warning in the artifact correction log. There is no other effect of this setting.
- 12) *Bad Neighbors* is an option where if two neighboring channels are marked as being locally bad then the trial is also marked bad (because this typically means that a movement artifact of some sort is present, as opposed to isolated bad channels). This is a very stringent criterion and should not be used for developmental data.
- 13) *μ v Move Fac* is the maximum voltage difference (maximum-minimum) allowed by a factor by the movement artifact correction step. Factors exceeding this limit are deemed to reflect artifacts and are subtracted from the data.
- 14) *Move Corr Facs* is the number of factors to be retained by the movement artifact correction routine. A larger number results in a more accurate but slower process.
- 15) *No Figure* is an option to not provide a summary figure for the artifact correction process. While a very useful figure, it requires substantial memory and so dropping it can be helpful when encountering recalcitrant memory problems.
- 16) *EMG Ratio* is the minimum ratio of signal power to EMG noise to retain during EMG correction. In other words, factors smaller than this number are discarded as likely being EMG.
- 17) *EMG Threshold* is the Hz threshold considered to be the lower bound of possible EMG frequencies during EMG correction.
- 18) *EOG channels* are the EOG channels. If left blank, the Toolkit will try to automatically determine which are the EOG channels based on electrode coordinates. If

it fails to properly identify them, then fill in this field to specify them manually: [LUV RUV LLV RLV LH RH]. Specify missing EOG channels with a -1.

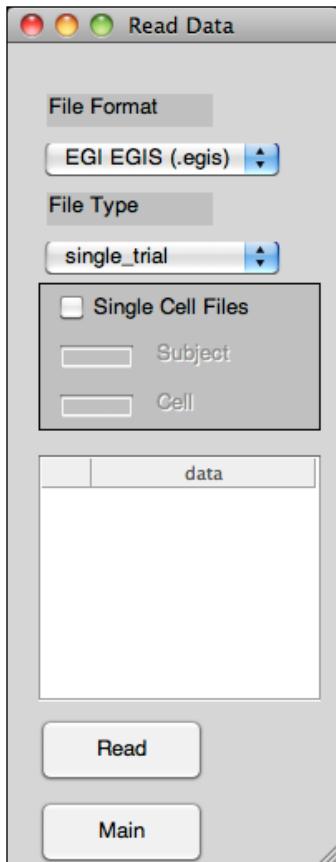
19) *Saccade Potential* is the minimum microvolt threshold for detecting saccadic spike potentials.

20) This pop-up menu is a list of available fMRI artifact correction routines. At present the two available are the fMRIb EEGlab plug-in which uses the Optimal Basis Set method (Niazy, Beckmann, Iannetti, Brady, & Smith, 2005) and the AMRI EEG fMRI Toolbox which uses an ICA-based method (Liu, de Zwart, van Gelderen, Kuo, & Duyn, 2012) for removing ballistocardiogram artifacts. They also both remove gradient artifacts. I've gotten better results with the OBS method in my initial efforts so I've made it the default but your mileage may vary so it would be best to try both. The two software packages have many options but I don't yet see any reason to implement a user interface to access them.

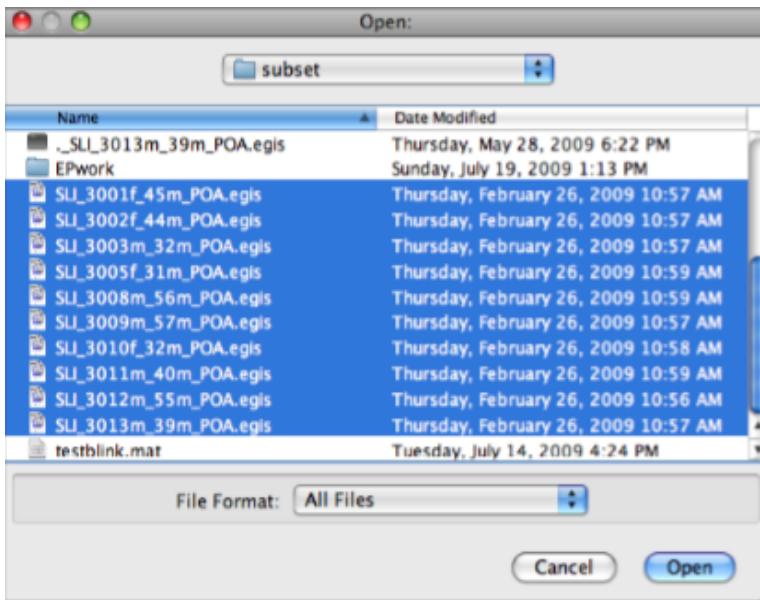
Manually Forming an Blink Template

While you may enjoy finishing the analysis process to see what the oddball effect can look like in an EEG-fMRI dataset (rather attenuated due to all the noise), for the purposes of this tutorial we will now shift to the second set of files. This dataset is very noisy and challenging for a different reason, insofar as it is a developmental dataset with very young children.

In this dataset, the lower VEOG channels were purposely not placed in the normal location (as very young children do not tolerate them well) and so it may be difficult to identify the blinks automatically (the lower and upper VEOG channels do not diverge from each other in the usual manner). The first step is therefore to generate a blink template manually. First click on Read in the Main Menu to load in the session files. This will bring up the Read Data Panel. Change the File Format to the appropriate type. The File Type should be "single_trial" since these are session files.



Then click on Read and choose all ten example files and then click on Open:



On a Mac, it may then ask you to identify the montage if the Satimage osax is not fully

working (as noted earlier). If so, choose "Adult GSN200 128-channel 2.1". On a non-Mac, it may ask you to identify the Electrode Coordinate file, which would be "GSN129.ced".

For each file, the MATLAB command line will say something like:

Read in 4 cells with a total of 180 trials.

Loading the ced file:

/Applications/Matlab_Programs/EP_Toolkit/electrodes/GSN129.ced

The following ced file channels are not represented in the data file:

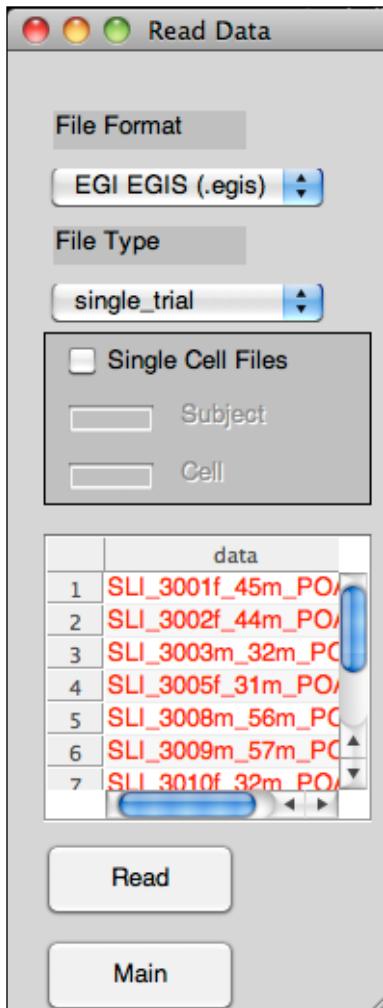
Cz

The name of the experiment is: _Éô _ÍÜ _ÊX _ÊX_ Sp_48_ _P ð_4~È_49"
O}d_ segm OÆ`ÿÿÿ O}d

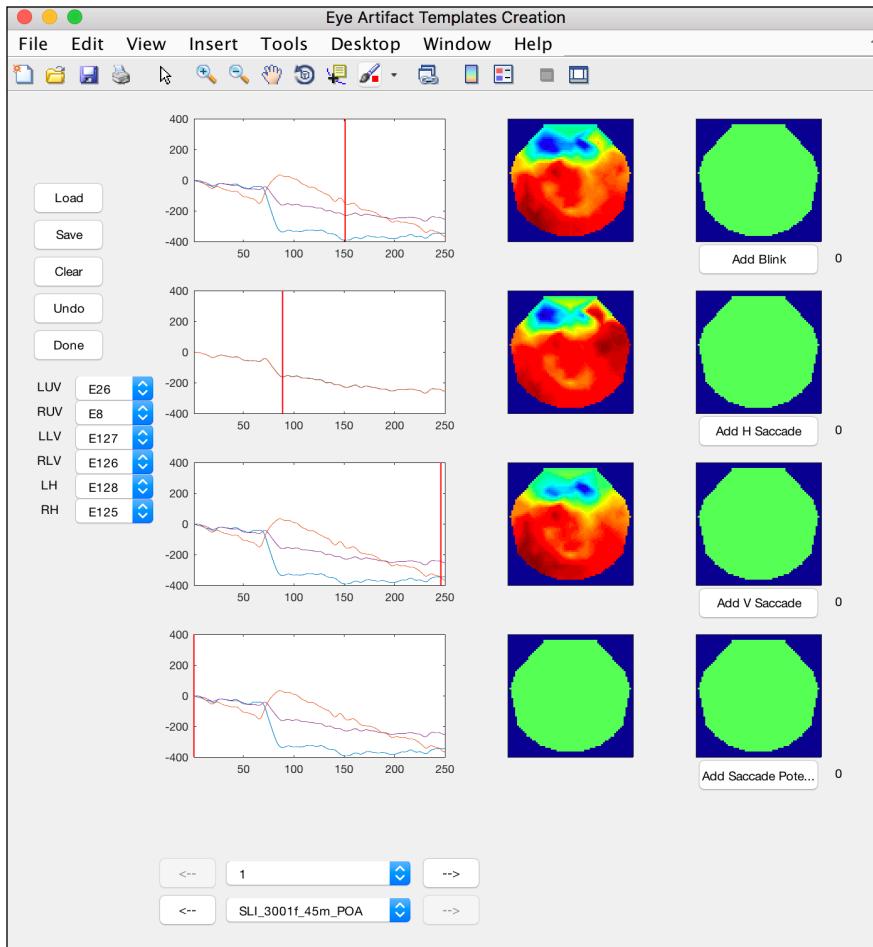
The pre-stimulus period of the data is: 0 msec.

Note that the data file format (egi_egis) is unable to specify the baseline period so it may be in error, in which case you will need to manually fix it using the Edit function.

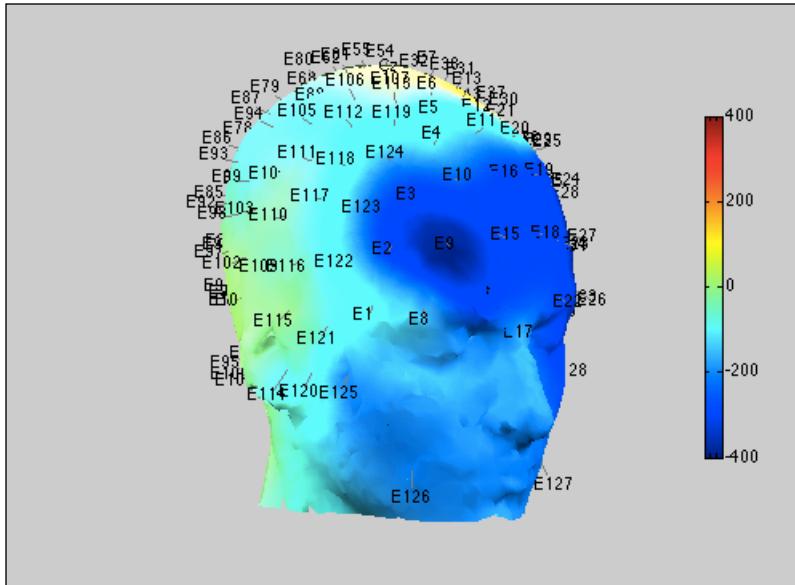
You can fix the baseline and experiment name information later on if you'd like. The files that you loaded in will now be listed in red. A copy of them have been loaded into the working directory (EPwork) but will not be taking up space in the computer memory. If you need to purge any from the set of work files, click on them and they will be immediately removed (the red is a reminder not to click on them unless you really want to delete your working copy of the file). Also, a star will be displayed in front of every file that contains unsaved changes (changes following the initial file import but not including anything that occurred during the import itself).



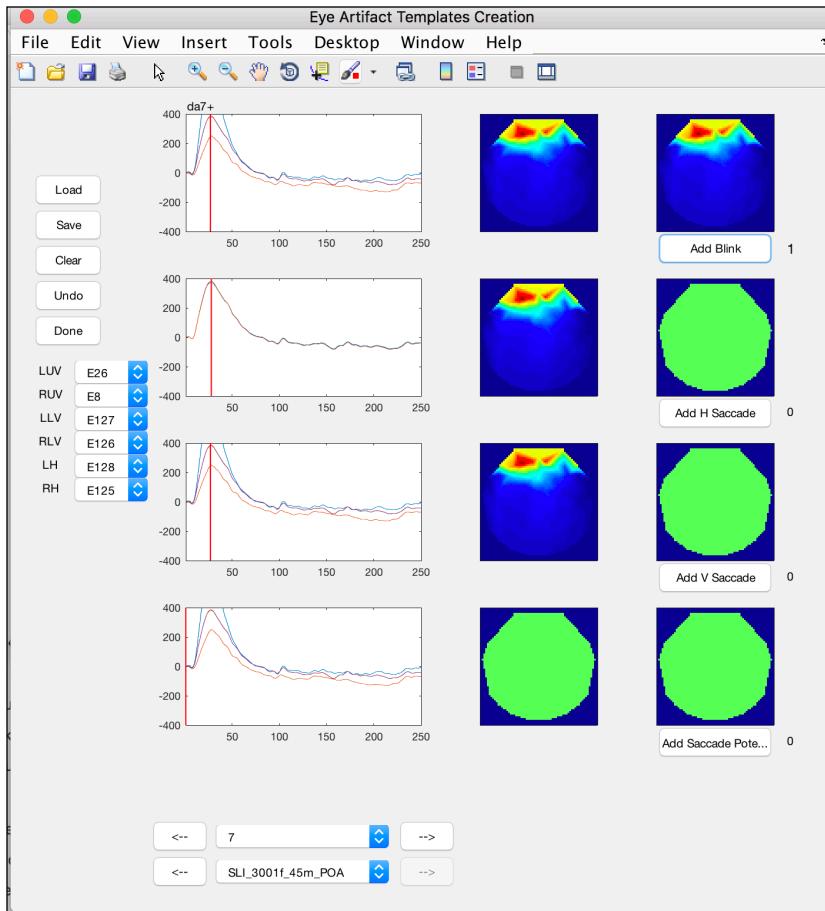
Now click on Main to go back to the Main Menu. Next, click on Preprocess. Click on Template to bring up the Template Creation Window. In the first row (blinks), it shows the VEOG waveforms of the first data file, one second epoch at a time. It also marks the time point with the maximum voltage (across all the channels, including the ones not plotted so it may not always be apparent why it's chosen the time point) with a red line. To the right of the waveforms is the scalp topography at that point of maximum voltage (across all the channels). To the right of that is the scalp topography of the new blink template. Since nothing has been added to it yet, it is a blank green. The second row (horizontal saccades) shows the two HEOG channels and the scalp topography at the point of maximal divergence between the two HEOG channels. The third row (vertical saccades) shows the VEOG channels and the scalp topography at the point of maximal divergence between just the VEOG channels.



One should first confirm that the correct channels have been automatically identified as EOG channels. The channels are listed on the left side of the window and can be manually changed if need be. These settings only affect which channels are used to automatically identify artifact candidates. One should also visually confirm electrode locations by clicking on any of the 2D plots. The electrodes were not mapped to the 3D head perfectly but close enough for visualization sake. The important thing is that there were not any major distortions, such as being rotated 90 degrees to the right.

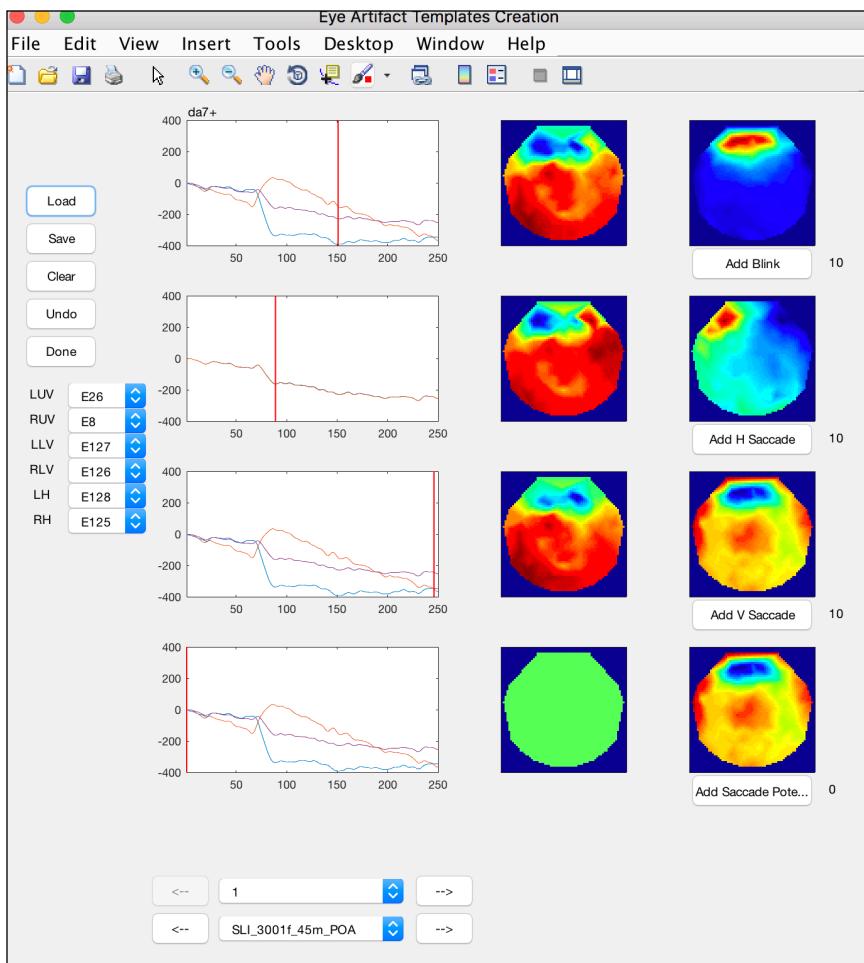


Clicking on right arrow or the pop-up menu below the waveforms brings one to the first blink (in the 7th one second epoch). It can be recognized as such because of the smooth, high amplitude bell-shaped curve which the scalp topography image shows to be tightly centered around the eyes. If the lower VEOG channels were correctly placed, they would be seen to be going negative even as the upper ones went positive. Click on the Add Blink button to add this blink to the template. The counter below the blink template image increases to one. If a mistake was made, one can Undo the last addition. One can also Clear the template formed thus far. If the red line is not at the right time point, you can drag it by left-clicking on it and then moving the cursor.



There is no hard and fast rule on how many blinks to use in a template but I find that having ten of them (two each from five subjects) tends to yield acceptable results. Using two each helps remind one to confirm that a putative blink really is a blink as blinks should be quite consistent across a session. Using blinks from multiple subjects helps ensure that the template is not overly specific to a single subject. The template doesn't have to be exact, though, since the eyeblink correction process only uses it to determine which ICA factors correspond to blinks and the match to an individual's blink does not need to be exact (the default setting in the preferences is to correlate .9).

Once the second blink has been added to the template (in the 25th epoch), click on the lower right arrow to bring up the next active dataset. The trial counter will be reset to one.

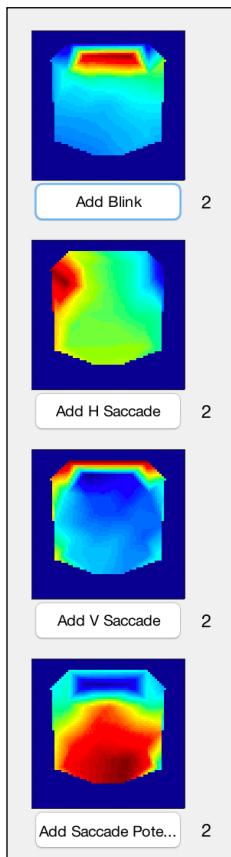


The second subject in the example dataset has no apparent blinks. Proceeding on to the rest of the session files, the blinks are reasonably consistent across the datasets, resulting in a blink template quite similar in appearance to the first blink found. Avoid examples of blinks that are noisy as they will degrade the effectiveness of the template.

If some of the subjects had the lower VEOG channel placed in the normal fashion (they aren't), it would be best to test them separately as their blinks would be different. One could add only the displaced lower VEOG blinks to the template and then use the "bothTemplate" option with the expectation that the manual template would catch the displaced VEOG blinks and the automatic template would catch the normally placed VEOG blinks. Alternatively, one could form a separate manual blink template for each subject and run them individually (usually not necessary).

Although this dataset is not well-suited for demonstrating saccades, manual templates are handled in much the same fashion. The corneo-retinal dipole (CRD) artifact has an asymmetric topography with the EOG channels in the direction of the saccade becoming more positive. If the gaze started at central fixation (where the CRD will be balanced across the EOG channels), the EOG waveforms should start diverging at about 200 msec

after the stimulus onset. The saccadic spike potential, on the other hand, takes the form of a sharp spike that is parietal positive and negative under the eyes at the onset of a saccade. This dataset does not appear to have saccadic spike potentials, either because of the task or because of the young sample. The following shows example blink and saccade templates from a different experiment. Note that the saccade polarity would be reversed for a saccade in the opposite direction. You can choose examples of saccades in either direction. The EP Toolkit will automatically reverse the polarity when adding it to the template. This template will be used to detect saccades in both directions. When looking for exemplars of horizontal CRDs, look for cases where both the horizontal and vertical channels diverge (the left and right VEOG channels should mirror the HEOG channels) and produce the characteristic asymmetric topography. When looking for exemplars of vertical CRDs, look for cases where the VEOG channels (upper and lower) diverge but the HEOG channels do not and the overall topography is symmetric. Remember that you can manually drag the red line to the desired time point (you may need to try a few times before it responds).



Once finished, click on Save and give the file a name. It will ask to do so twice, once for the blink template file and once for the saccade template file (if such a template has been constructed). One can also Load a template back for later inspection or to add more examples to it. Click on Done to go back to the Preprocess Data Window.

Once the template has been formed, it is no longer necessary to have the files in the working set. The preprocessing step operates directly upon the files on the disk (since reading in a large batch of files to the working set can take some time, it's more efficient to just read them in one at a time during the batch session rather than having to wait around). To avoid confusion, one may wish to purge the working set at this point. To do so, click on Main to return to the Main Menu and then click on Read. From the Read Window, one can purge the files by clicking on their names. Alternatively, one can choose Quit from the File menu of the Main pane, at which point it will ask if you want to clear the working set. Once done, return to the Preprocess Window (by clicking on Main and then click on Preprocess).

Setting the Preprocessing Controls

The next step is to provide the proper settings for the preprocessing. It is recommended to set the Output File Format to EP (.ept) since this is the native file format for the EP Toolkit program and will preserve information that might otherwise be lost should another file format be used. At the end of the process the data can be saved into a different format as needed.

The next field is the Points field. Oftentimes only a portion of the epoch is needed for the analysis. If so, it may be desirable to specify the timepoints in the Points field (will not segment continuous data). Not only would doing so save time and disk space, it would also avoid losing trials due to artifacts outside the parts of the epoch of interest. They should be described in terms of samples. Colon means that a range of numbers if being described. For example, "1:250" would indicate that the first 250 time points should be retained. If each sample is 4 ms (i.e., 250 Hz sampling rate), then these samples would correspond to the first second. If the field is left blank then by default the entire trial will be retained. The label of the field is initially grayed out to denote that this control is inactive but if timepoints are typed into the field then the label will no longer be grayed out.

The Baseline field specifies samples to use for baseline correction (ignoring the baseline field of the data file). If the baseline parameter is set, the function will baseline correct each trial using the time points specified (e.g., 1:25 means use the first twenty-five time points). This ensures that random swings in the baseline do not degrade the quality of the automatic artifact detection process. The use of this option is strongly recommended. Note, though, that the output data will then be baseline corrected. For this tutorial dataset, type in "1:25".

The next control indicates when to apply fMRI artifact correction routines for EEG collected inside an MRI scanner. Generally for ERP data it makes most sense to run this routine as a separate step on the continuous data, segment, and then run the rest of the artifact correction routine on the segmented data.

The next control indicates whether to detrend each trial. In general, this option is not

recommended for segmented ERP data as it may attenuate the ERP components but can be of use for continuous data prior to filtering and for segmented data that will be analyzed in the frequency domain.

The Edit Mode setting indicates whether the results of previously performed manual editing should be utilized to determine bad channels and trials, either in combination with or instead of the automatic routines. Manual scanning for bad data will be explained in a later section.

The next control sets whether the blink correction step should use a manually generated blink template ("fileTemplate"), an automatically generated template ("autoTemplate"), or both ("bothTemplate"). For the tutorial, use "fileTemplate" both because the data is so noisy that the automatic template may not be correctly generated and because the lower VEOG channels that the autoTemplate routine relies heavily upon were not used. There is also an "eyeTrack" option that is not yet documented.

Next to this is the Saccade Correction setting. It determines whether saccade correction (both saccadic spike potential and corneo-retinal dipole) will be carried out. This too allows for both manual and automatic templates, as well as an eye-track option that is not yet documented. This session did not provide any visible saccadic spike potentials and it did not provide pure horizontal or vertical corneo-retinal dipole exemplars so instead of trying to use a manual template it would be appropriate to use the autotemplate.

The Bad Channel Correction control indicates whether to "replace" bad channels (via interpolation) and to zero out bad trials, to "mark" the bad channels and bad trials with a flat line and a large spike (when saving to non ept file formats), or to do nothing except to record their existence in the log (and in the file if ept format). For the tutorial, choose "replace."

The Movement Correction control indicates whether to use the experimental PCA procedure to "fix" movement artifacts or not. For the tutorial, choose to use it (quite helpful for developmental datasets such as this).

The next set of controls is for indicating which, if any, of the channels are explicit reference channels, meaning that their voltage numbers are included in the data. The "O" line is for the original reference channel(s) during data collection. The "C" line is for the current reference channel(s), for cases where the data has been rereferenced.

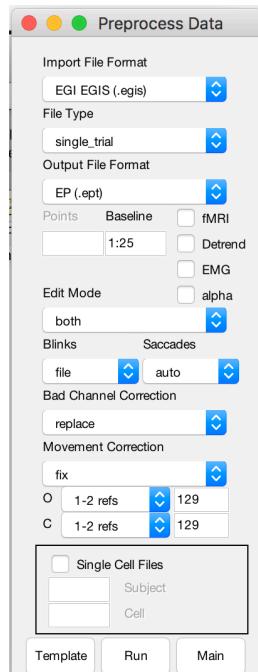
A single reference channel will by definition be a flat line of zeros. Usually, in order to save on disk space, such a channel is simply left out of the file and is considered to be present implicitly. Mean mastoids reference channels will have a mean of zero and will split the difference, becoming mirror images of each other. Sometimes one of them will be left out of the file as it is redundant with the other one but will still be considered to be present implicitly. If both mean mastoid channels are missing, then nothing can be done and they should be treated as being missing channels.

The reference channel(s) needs to be indicated when: 1) a single channel reference is explicitly present so that the EP Toolkit will know that it is flat because it is a reference channel rather than because it is a bad channel. 2) when mean mastoids reference is utilized and both channels are explicitly included because the ICA process used to extract eye blinks can be derailed by their presence (since they are mirror images of each other, they will have a perfect correlation of -1, which can end up causing computational problems). "ave ref" means average referenced. "1-2 refs" means one or two explicit reference channels. "default" means that the reference channels indicated by the CED file (when the data file was imported) should be used. These values provided by the CED may not be correct if they indicate the original reference electrode and the data were subsequently rereferenced to some other scheme.

In this tutorial dataset Cz was used as the recording reference and is present only implicitly; however, if the CED information is provided when the data is read in, it will automatically be added back into the dataset. For this reason, "1-2 refs" and "129" would be appropriate settings. Alternatively, for this and for all other EGI datasets, the reference channel is already provided by the CED file so it is sufficient to use "default" for such files as long as the CED file is used.

The Single Cell Files controls operate in the same fashion described under "Read Data".

When done selecting the proper settings, click on the Run button.

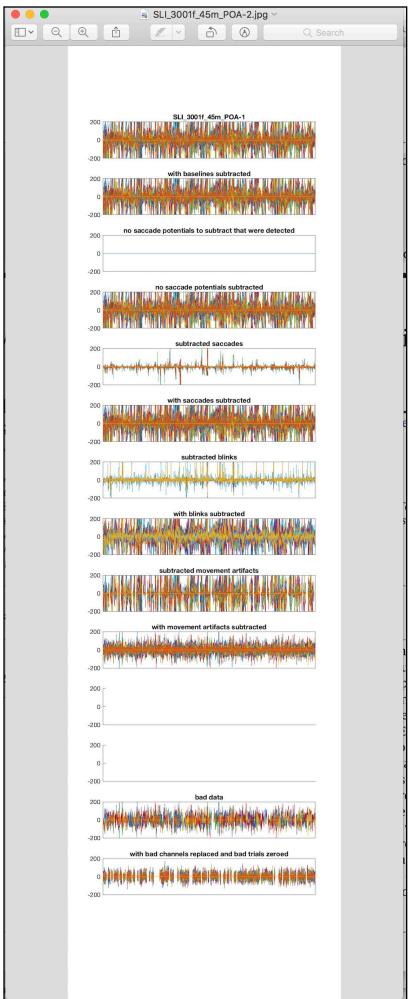


Processing can take anywhere from ten minutes to three hours per data file, depending on its size and the speed of the computer. The channel replacement can take up half the total

period. The tutorial files take 40 minutes each on a 3.33GHz 32GB 6-Core Intel Xeon OS X 10.9.4 Mac running MATLAB 2014a. It's best to just set up an entire batch and let it run overnight. Remember to set the computer to not sleep if it is a Mac.

During the artifact correction process, a new Artifact Correction figure will be presented illustrating the progression of the process. For each chunk (there will be multiple chunks if the size of the data file is larger than the maximum chunk size that you set earlier on in the preferences), it will chart the state of the data in a butterfly plot, which consists of all the trials laid end to end, with one line corresponding to each channel. Artifacts can be easily detected as high amplitude divergences from the central mass of lines. Several such plots are provided:

- 1) the original data
- 2) the data after baseline correction
- 3) the portion of the data identified as saccadic spike potentials. They should be small and distinct.
- 4) the data with the saccadic spike potentials subtracted.
- 5) the portion of the data identified as corneo-retinal dipole artifact. They may be quite large and continuous, depending on the nature of the experiment.
- 6) the data with the corneo-retinal dipole artifacts subtracted.
- 7) the portion of the data identified as blinks. They should be sharp spikes.
- 8) the data with the blinks subtracted.
- 9) the portion of the data identified as movement artifacts.
- 10) the data with the movement artifacts removed.
- 11) the portion of the data identified as EMG artifact.
- 12) the data with the EMG artifact removed.
- 13) the portion of the data identified as bad channels or bad trials.
- 14) the data with bad channels interpolated and bad trials zeroed out.



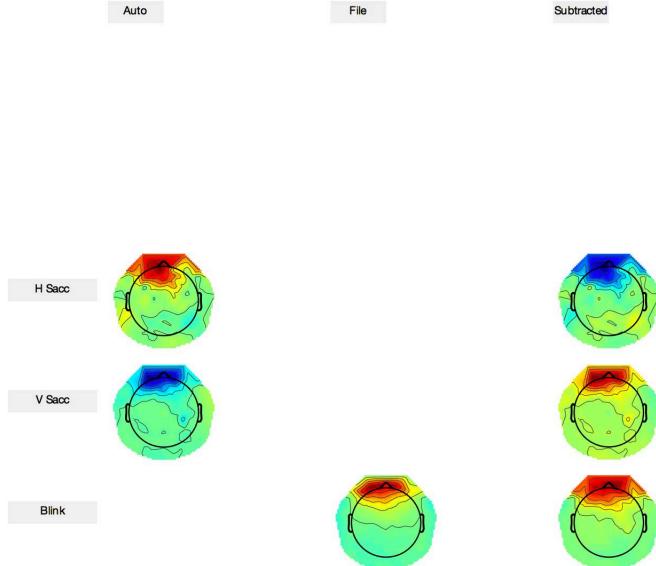
The subplots for options that were not chosen will not be included in the summary figure. If a combined subject average file is being preprocessed, then each subject will be laid end to end just like trials are for single-trial data, resulting in just a single summary figure.

The following files will be generated:

- 1) an eyeblink corrected file with a "_e" suffix added. A new regional channel will be added that contains the timecourse of the removed blink activity (upper VEOG-lower VEOG) and another for saccades (if these two types of corrections were made). This can be helpful for determining whether any residual blink activity might be responsible for apparent experimental effects. Also, blink start/peak/end events will be added to mark the maximum point of the blink if it exceeded 100 microvolts at the peak channel and is separated by at least 300 ms from the last blink peak. Saccade events will be added to mark the point at which the differential between the HEOG channels first exceeded 2 microvolts prior to the saccade peak.
- 2) a .jpg file of the butterfly plots. Each one should be examined, principally to determine if the blinks were in fact removed. If not, it may be necessary to rerun the file

using a customized blink template formed using blinks just from the one file.

3) a .jpg "templates" file of the artifact and template topographies. It is best to check this file to confirm that the algorithms did a reasonable job at characterizing the artifacts, especially when using automatically generated templates.



4) A file titled `Artifact_Correction_Log` containing the record of the preprocessing session. It is highly recommended that it be examined carefully for signs of problems.

For the first session file, the log file output is:

ARTIFACT CORRECTION SUMMARY

The blink channels are: LUVEOG(26) RUVEOG(8) LLVEOG(127) RLVEOG(126).

The saccade channels are: LHEOG(128) RHEOG(125).

Minimum number of good trials per cell to avoid warning message is: 15.

Moving average window for smoothing during bad channel detection: 80 ms.

Difference from minimum to maximum for bad channel: 100 μ V.

Percent of bad channels exceeded to declare bad trial, rounding down: 10%.

Number of electrodes considered to be neighbors: 6.

Minimum predictability from neighbors to not be considered globally bad: 0.4.

Maximum difference from most similar neighboring electrode to be considered bad: 30 μ V.

Blink template option is: fileTemplate.

Threshold correlation with blink template: 0.9.

Saccade Potential Threshold: 2.

Detrend data: OFF.

Percentage of good trials chan is bad to declare a channel globally bad: 20%.

Number of factors to retain when correcting movement artifacts: 20.

Maximum voltage difference allowed when correcting movement artifacts: 200.

Bad channels and trials: replace.

Samples used to baseline epochs: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
21 22 23 24 25.

Editing mode option is: both.

Working on: /Users/jdien/Documents/Matlab_Programs/tutorial/SLI_3001f_45m_POA.egis.

The channel 129 is marked as being the original reference.

The channel 129 is marked as being the current reference.

Baseline Correcting.

Warning: shorted channels: E125-E126; E125-E127; E126-E127; E126-E128; E127-E128;

Global bad channels: None

Starting preliminary saccade potential scan to exclude them from the preliminary blink detection routine.

No automatic template could be formed.

Something went wrong with the preliminary saccade potential run of file

/Users/jdien/Documents/Matlab_Programs/tutorial/SLI_3001f_45m_POA.egis. Skipping the operation.

Starting preliminary blink scan to identify which time points to exclude from the saccade and the saccade potential corrections.

13 blinks corrected.

Starting final saccade potential correction, excluding blink time points.

No automatic template could be formed.

Something went wrong with the saccade potential correction run of file

/Users/jdien/Documents/Matlab_Programs/tutorial/SLI_3001f_45m_POA.egis. Skipping the operation.

Starting saccade correction, interpolating blink time points.

12 blinks corrected.

159 trials corrected for movement activity.

There were 44 bad trials.

Originally there were 0 bad trials.

There were 44 bad trials due to too many bad channels.

There were 0 bad trials due to neighboring bad channels.

For good trials, there was an average of 5.7647 bad channels per trial.

The file took 14 minutes to process.

Done.

The header gives information about the settings used for the preprocessing run. Then each section after that provides a summary of each file processed. In this case, it is providing a warning that some pairs of channels appear to be shorted together as they are nearly identical. The EP Toolkit does not take any action when it detects possible shorts aside from issuing the warnings. They can help warn the experimenter that extra attention to the electrode applications may be needed. Such shorts reduce spatial resolution but should not invalidate results.

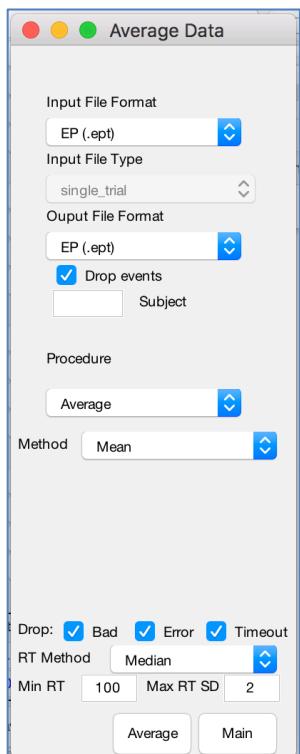
For maximum rigor, one could perform an initial artifact correction run with just blink and/or saccade correction where Bad Channel Correction and Movement Correction are set to None, followed by manual scanning and adjusting of edit marks, followed by another automatic artifact correction run with blink and saccade correction turned off and Bad Channel Correction and Movement Correction turned on.

What you do next depends on what kind of analysis you are planning on conducting. If you are planning on a spectral analysis then you should use the Transform function

followed by the Average function (next section). If you are planning on an ERP analysis then you should use the Average function followed by the Transform function. For the purposes of this tutorial, we will proceed with an ERP analysis.

Averaging

To perform the Average step, click on Main to return to the Main Menu. Next, click on Average.



Set the file formats and types to the appropriate values. It is recommended to use the EP .ept format. In the figure, File Type is grayed out because the .ept format includes the information about what type of file it is. The Drop Events control instructs the averaging procedure to drop the events contained in the session files in order to reduce the size of the resulting file. The box can be unchecked so that the distribution of the events can be inspected in the View function to determine whether there is the possibility of confounds.

The Subject box is normally left blank. It is intended for the case where a session is divided into multiple files (as in one for each block). If one includes the subject label in the file name (e.g., SLI_3011m_40m_POA.ept), then one indicates in the box which characters in the file name represent the subject label (e.g., 5:8 to denote 5th through 8th characters). When you select the entire batch of files to be averaged, the EP Toolkit will use this information to identify which files belong to a given session and will merge them

together.

The settings at the bottom of the pane control the handling of behavioral information. If the trial specs include a field named "RT" for reaction time data and "ACC" for accuracy data (where 0=error and 1=correct and 2=timeout) then the average function will compute the reaction time and accuracy data for the resulting averages. The checkboxes in the first line indicate whether bad trials, error trials, and timeout trials should be dropped from the averages. The RT method popupmenu indicates whether the mean, median, or trimmed mean (using the trimming parameter from the preferences) should be used for the reaction time data, independent of the method used for the EEG data (median is the default as it is more robust than the mean against outliers). The min RT field indicates that RTs smaller than this number should be dropped as being false start trials. The Max RT field indicates that RTs with a standard deviation larger than this figure (computed within cell) should be dropped as being an outlier. When computing cell accuracy, only error trials will be counted as errors. All other dropped trials will be excluded from the accuracy computation.

There are several possible procedures for the EEG averaging, each with associated methods:

1) Average - which is the standard averaging process. Single-trial files will be averaged into subject averages and subject averages will be averaged into grand averages. If multiple single-trial files are chosen, a single combined subject average file will be generated in which each of the separate subject averages are present. This is the recommended approach as it greatly facilitates analysis and is the method that works best for the EP Toolkit.

The averaging methods are:

a) mean - which is the conventional averaging procedure.
b) median - which uses the median instead of the mean.
c) trimmed mean - which uses the mean but first trims off the most extreme values at each time point. The default value (which can be changed under Preferences) is 25% so the highest and lowest 25% will be dropped. This results in a more robust estimate of the central tendency of the event related potentials. The trimmed mean is recommended over the median (Leonowicz, Karvanen, & Shishkin, 2005).

2) Latency-Lock - is averaging in which a trial spec such as reaction time is used to time-lock the averages. So although a stimulus event may have been used to generate the epochs, one can then use this option to realign the epochs in terms of the ms measure provided by the trial spec (usually reaction time). The new time-lock point will serve as the new time zero. One should also specify a range of values that will be accepted as latencies (e.g., 300-700 ms). If no range is specified, the procedure will default to 100 ms after the start of the epoch and 100 ms prior to the end of the epoch. Due to the need to accommodate latencies at the extremes of this range, the length of the resulting epoch will be equal to the length of the epoch before and after the latency range. For example,

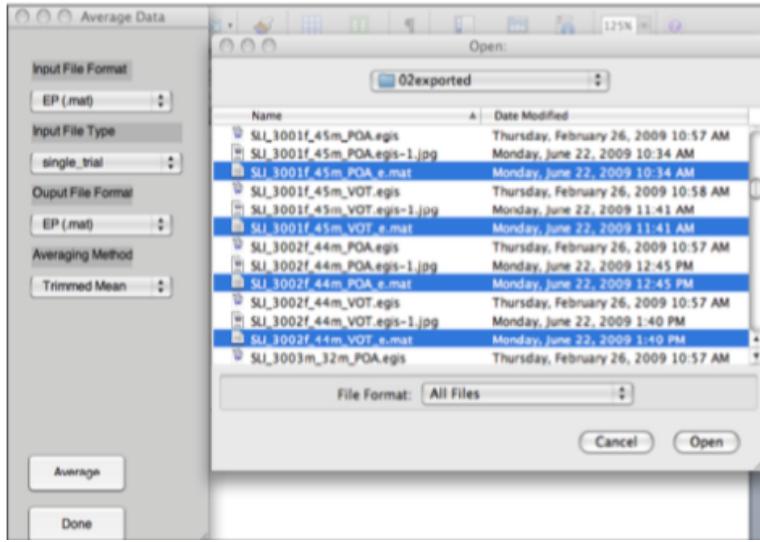
for a latency range of 300-700 and an epoch of -200-800 ms, the resulting epoch would be (-200-300) to (800-700) = -500 to +100 ms or 600 ms long. The new zero will be the latency lock event. When choosing this procedure, a menu with all the single-trial files in the working set will be presented as potential model files. A menu populated with all the trial specs present in the chosen model file is available below it. Thus, one could select the reaction time trial spec if it was so desired. The model file's sole purpose is to generate the list of possible trial spec names and is not otherwise used.

3) Jitter-Correct - is much like latency-lock except that one does not need to generate the latencies in a prior step. Instead, a rough peak-picking algorithm is employed in which the point of minimum or maximum voltage within the latency range is treated as the peak of the ERP component of interest. One must also specify the channel. This can be especially helpful when one is trying to measure the amplitude of an ERP component with a variable latency (like the P300) to control for the effects of jittering on the amplitude measure, but only if the signal-to-noise is good enough. A full list of the datasets in the working set is available under Channel Model. One chooses one of them and then a list of channels from this model file will populate a Channel menu below it. One should also specify whether the positive or negative peak in the window is to be used. Thus, one could specify that the averages are to be aligned according to the positive peak in Pz within the 200-500 ms range if one wished to jitter-correct the P300.

4) Frequency-coherence - generates a coherence measure, using either multi-taper (with the indicated frequency smoothing) or Hanning methods.

5) Time-Frequency-Coherence - does the same but producing a TFT equivalent (that is, with a timecourse as well), using the phase-lock wavelet method.

When ready, click on Average. Select the desired session files and they will be combined into a single combined subject average file (name it "tutorial" when it asks for the name) with separate averages for each subject. The files will be selected from those on the disk and not from those in the working set. This process will take a while. The command window will announce which file is being worked on. When it is finished, the Average and Main buttons will no longer be grayed out. If the session files were generated by the Toolkit's preprocessing step and are in EP format, then trials that were marked as bad will be dropped from the average. Likewise, uncorrected bad channels will be dropped. If the prestimulus duration information hasn't been added yet to the file (which it has not yet for the tutorial dataset) then a warning message that the covariance information needed for the MNE software won't be calculated correctly. This is not a problem unless one is planning on exporting the data to FIFF file format and submitting it to MGH's MNE software.



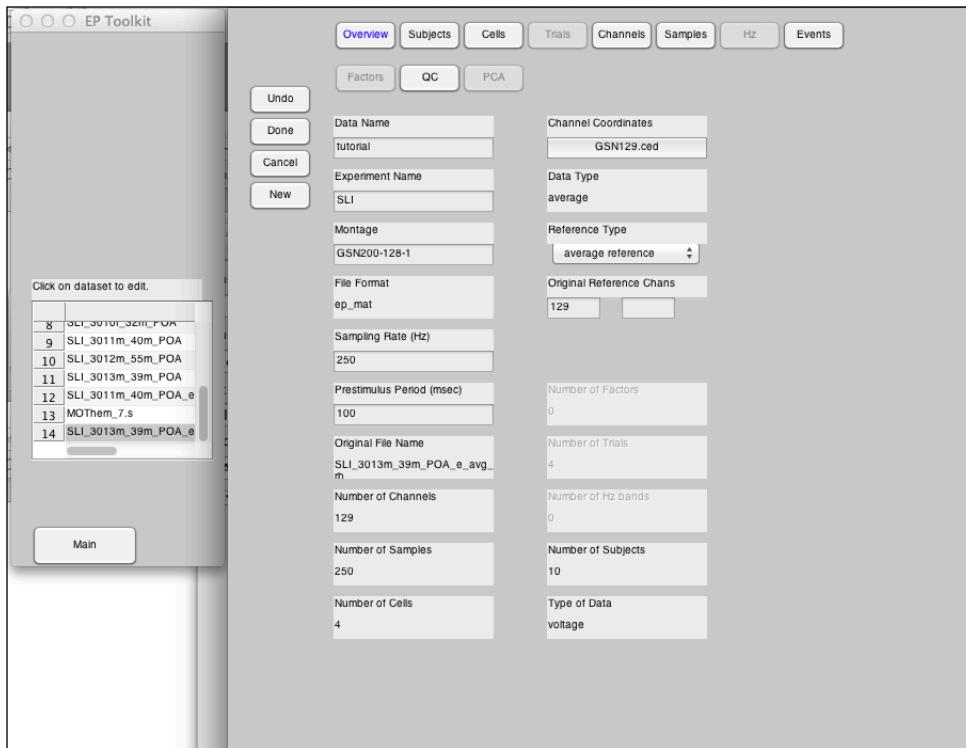
Click Main once it is no longer grayed out to get back to the Main Menu.

Now go back to the Transform panel to rereference the data to average reference, provide the information that the data have a 100 ms prestimulus period, and baseline correct using that 100 ms period. Note that specifying the prestimulus period will not by itself baseline correct the data. The prestimulus period is usually used for baseline correction but not necessarily. This setting is just to provide the information on the duration of the prestimulus period. Also set the low-pass filter to 30 Hz to reduce the noise level. Once you have run this function, it will generate a file with an _rbf suffix (standing for “rereference” and “baseline correction” and “filtered”). The suffix is not necessary for the purposes of the EP Toolkit and are included only for your convenience.



Edit

It is now time to enter the newly processed average file into the working set of data. Click on Main to go back to the Main Menu and then Read. Read in the file as described earlier. Click Done and then click on the Edit button. This will bring up the Edit Window, which allows for editing the data file. If there is only one data file in the working set then it will automatically open, otherwise it will be necessary to click on the name of the one that is to be edited. If you had previously clicked on it and it is still highlighted, it will be necessary (on the Mac) first to command-click it to deselect it so that you can then select it again.



The initial pane of the Edit Window provides the general information about the file. The Data Name is the label by which it is identified in the EP Toolkit. Each data file in the working set needs to have a unique Data Name. Change it to “tutorial”. The Experiment Name is the name of the overall experiment, rather than the name of the specific file. Take this opportunity to provide an Experiment Name by typing it into the appropriate field (“SLI” in this case).

If one clicks on the "channel coordinates" field, one will be given the opportunity to select a .ced channel coordinates file. If the data already had channel coordinates specified, then the EP Toolkit will provide the opportunity to remap the voltage data according to the new electrode coordinates using interpolation.

If you make a mistake, clicking on Undo will take back the last edit made. Clicking on Undo again will redo the edit. Clicking on Cancel will end the edit session without making any changes to the file. Clicking Done keeps the changes but only in the working copy. The file must still be saved to make them permanent.

Click on the Subjects button to bring up the subject information. You'll want to enter in the correct subject numbers (under “names”). The “subjID” column is just a spec from the file and has no special role in the EP Toolkit). NetStation tends to lose this information when it exports files into EGIS format. The final column in the Subjects pane (you'll need to scroll over) contains the original file names of each subject. If need be you can shrink the size of the columns so that the “names” field and the “fileName” field can be

seen in the window at the same time. You can also drag the "fileName" column so it is next to the "names" field. Doing so will not change the file itself and if you later return to this file the fields will be back in the original order. The subjects should be in the order in which they were selected when the averaging step was conducted. It would be simplest if the subjects are in order so you should reorder them if necessary. To do so, you can type in the new number in the "order" column and the subject will immediately be moved to just below that number (so typing in "1") will move it to be the second (modifying this to work in a more intuitive manner and to allow for sorting is on the to-do list). Even easier, you can just select Names from the Sort pop-up menu in the left-hand column of controls.

	order	select	weights	names	type	RunDateMo	Rx
1	1	<input type="checkbox"/>		0 sub001	Avg	7	25
2	2	<input type="checkbox"/>		0 sub002	Avg	8	3
3	3	<input type="checkbox"/>		0 sub003	Avg	8	8
4	4	<input type="checkbox"/>		0 sub005	Avg	7	28
5	5	<input type="checkbox"/>		0 sub008	Avg	7	26
6	6	<input type="checkbox"/>		0 sub009	Avg	7	27
7	7	<input type="checkbox"/>		0 sub010	Avg	6	22
8	8	<input type="checkbox"/>		0 sub011	Avg	8	4
9	9	<input type="checkbox"/>		0 sub012	Avg	7	26
10	10	<input type="checkbox"/>		0 sub013	Avg	8	3

Also enter in the sex information as follows:

r	RunTimeHr	RunTimeMin	RunTimeSec	SubjID	Handed	Sex
1	17	17	5	0	0	F
2	16	36	42	0	0	F
3	16	31	39	0	0	M
4	15	37	14	0	0	F
5	15	38	41	0	0	M
6	15	25	35	0	0	M
7	10	34	36	0	0	F
8	16	10	16	0	0	M
9	16	16	17	0	0	M
10	15	54	18	0	0	M

This pane can also be used to delete selected subjects, add a grand average, appending more subjects, exporting the data from this pane to a text file, or adding/deleting columns (specs). They can also be reordered by changing the numbers in the order column.

When deleting subjects first click the checkboxes in the select column and then click Delete. The weights are not needed.

To append more subjects, click on Append and then indicate which file is to be added to the present file. It will be assumed that appended file has the same format as the present file. An error message will be generated if the appended file differs too much from the present file.

To add a grand average of a subset of the subjects, indicate in the weights column how much to weigh each subject and then click Add. The checkboxes are irrelevant. When using the weights to generate combinations, a running total of the weights will be maintained on the left side of the pane. **Note that any weights input into the pane will not take effect until one has clicked elsewhere or pressed enter.** Keep an eye on the running total to verify that each weight value you enter has been recognized. If the weights sum to zero then they will be weighted exactly as entered (e.g., a -2 and a 1 and a 1 one would result in the first subject being doubled and then subtracted from the sum of the other two). If the weights do not sum to zero (e.g., a 1 and a 1 and a 1) then they will be divided by the total weights to provide a mean value (e.g., the total in this case would be $1+1+1=3$ and so the three subjects' data would be added together and then divided by 3). Let's wait on generating a grand average till we've verified that all the subjects are acceptable.

Instead, let's shift to the Cells Pane. The Cells Pane lists the cells in the data. One can delete, reorder, rename, add combined cells, append more cells, or export the information.

Generate a da7+-da9+ difference wave by entering a weight of 1 by the first and a weight of -1 to the second.

	order	select	weights	names	types
1	1	<input type="checkbox"/>		1 da7+	SGL
2	2	<input type="checkbox"/>		-1 da9+	SGL
3	3	<input type="checkbox"/>		0 ga11	SGL
4	4	<input type="checkbox"/>		0 ga13	SGL

Then click Add. Note that the new condition is marked as having the type CMB to denote that it is a combined cell and is therefore not to be treated as a separate cell in the succeeding analyses (it will be ignored when doing PCAs or windowing data for example).

	order	select	weights	names	types
1	1	<input type="checkbox"/>		0 da7+	SGL
2	2	<input type="checkbox"/>		0 da9+	SGL
3	3	<input type="checkbox"/>		0 ga11	SGL
4	4	<input type="checkbox"/>		0 ga13	SGL
5	5	<input type="checkbox"/>		0 +da7+-da9+	CMB

Finally, rename the resulting new condition if you wish. Note that conditions must have unique names. In a session file, renaming a cell to have the same name as another cell results in their being combined.

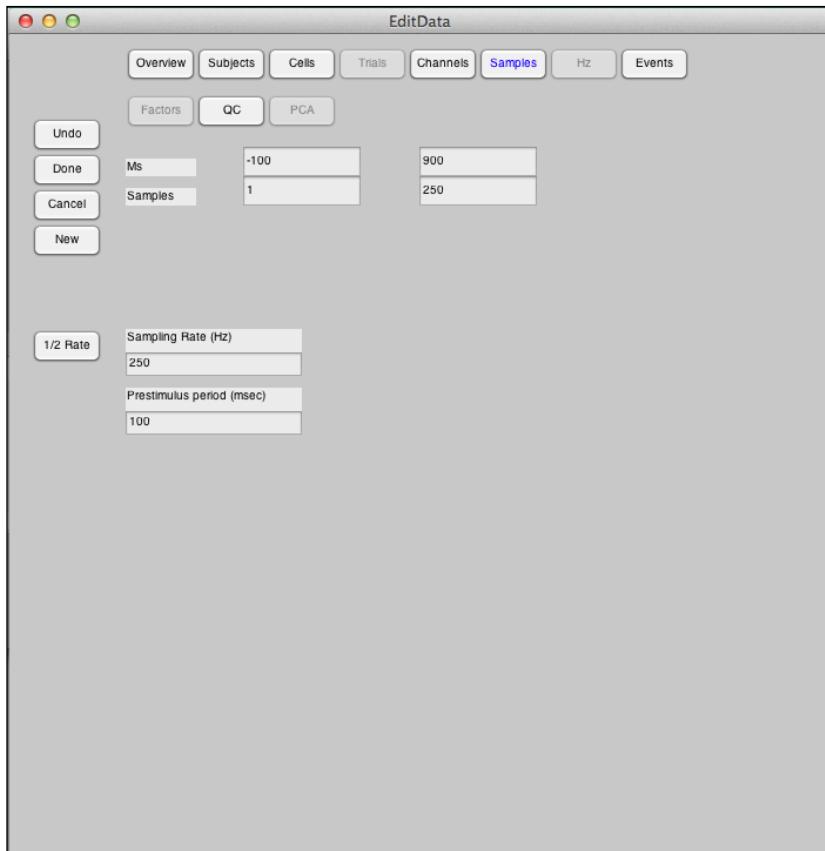
	order	select	weights	names	types
1	1	<input type="checkbox"/>		0 da7+	SGL
2	2	<input type="checkbox"/>		0 da9+	SGL
3	3	<input type="checkbox"/>		0 ga11	SGL
4	4	<input type="checkbox"/>		0 ga13	SGL
5	5	<input type="checkbox"/>		0 da7+-da9+	CMB

The Trials Pane is available only for session files and so its button is grayed out. Aside from listing all the trials and their trial specific data (like reaction time) if any, it provides an option to "Import" all the cell names from a text file, useful for epoch-marked Simple Binary files and a simple averaging function useful for taking a quick look at a session file's averaged waveforms.

The Channels Pane provides similar functionality for channels. One can, for example, generate regional channel averages (marked "REG") in the same manner. Sometimes there are also fiducial channels listed (marked "FID"). Fiducial channels are not data channels but rather standardized locations used for co-registration purposes. For BrainVision files, the impedance values will also be listed.

123	123	<input type="checkbox"/>	0 e123	EEG
124	124	<input type="checkbox"/>	0 e124	EEG
125	125	<input type="checkbox"/>	0 e125	EEG
126	126	<input type="checkbox"/>	0 e126	EEG
127	127	<input type="checkbox"/>	0 e127	EEG
128	128	<input type="checkbox"/>	0 e128	EEG
129	129	<input type="checkbox"/>	0 Cz	EEG
130	130	<input type="checkbox"/>	0 combined	REG
131	131	<input type="checkbox"/>	0 FidNz	FID
132	132	<input type="checkbox"/>	0 FidT9	FID
133	133	<input type="checkbox"/>	0 FidT10	FID

The Samples Pane provides some control over the temporal aspects of the data, including a button (1/2 Rate) to halve the sampling rate. Doing so also reduces the data itself by averaging consecutive pairs of time samples (e.g., 1&2, 3&4, etc.). This option is useful when the data was sampled at a higher rate than is now needed and reducing the size of the data file would be useful.



The Hz Pane provides similar functionality for frequency domain data. In this case it is grayed out.

The Events Pane provides a listing of the events in the file. The EGIS file format (that was used prior to translating the data over into EP format) does not represent events and so nothing is listed except for the points at which the Preprocessing function concluded that there was a blink or a saccade (if those options were turned on) and even these will only be present if the Drop Events option of the Averaging function was unchecked. If events were listed, they would be seen to generally follow the FieldTrip convention in which a .type field provides a general level of information (such as whether the event represents a stimulus event or something else) and a .value field that provides more specific information such as which stimulus. In order to support the mff file format, keys fields may also be present. The keys field of an event may contain any number of subfields holding additional parameters and information.

The Factors and the PCA buttons are only for factor data and so are grayed out.

The QC Pane provides quality control information by which problematic data can be detected. This information is generally only available if the EP Toolkit was used for the averaging process and the EP file format was used to store the results.

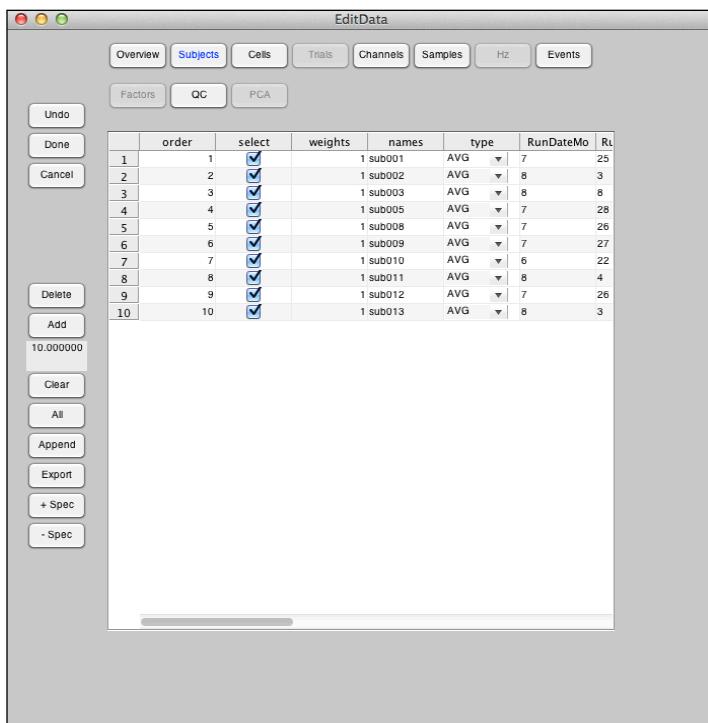
	names	type	da7+	da9+	ga11	ga13	+c
1	sub001	AVG	41.00	43.00	42.00	44.00	
2	sub002	AVG	28.00	24.00	23.00	18.00	
3	sub003	AVG	39.00	37.00	37.00	37.00	
4	sub005	AVG	40.00	39.00	40.00	40.00	
5	sub008	AVG	45.00	44.00	45.00	45.00	
6	sub009	AVG	45.00	46.00	45.00	46.00	
7	sub010	AVG	40.00	39.00	40.00	40.00	
8	sub011	AVG	37.00	40.00	39.00	39.00	
9	sub012	AVG	39.00	41.00	40.00	40.00	
10	sub013	AVG	39.00	38.00	39.00	40.00	
11	grand	GAV	393.00	391.00	390.00	389.00	

The first subpane (accessed by the buttons at the bottom of the pane) provides the number of trials going into each cell. The Subs Subpane provides the number of subjects going into each average. The Blinks Subpane indicates the proportion of good trials that contained blinks, according to the artifact correction step. The Saccades Subpane does the same for saccades. The Sacc Ms Subpane provides the estimate of the latency of the saccades.

The Move Subpane provides the proportion of good trials with movement artifacts. The BadTrials Subpane provides the proportion of bad trials in the cell. The BadChans Subpane provides the same information on bad channels (either the number that are bad if any are present, or the number that were bad and were dropped during the averaging

process, or otherwise the number that were replaced during the preprocessing. A label below the button will indicate which of the three is the case.). The Noise Subpane provides the magnitude of the noise in the cell, as estimated by the +/- reference (Schimmel, 1967) in which every other trial is inverted during averaging, resulting in an average in which the ERP has been cancelled out, leaving only noise. The numbers in the table are the root mean square (RMS) measures across all the channels and time points in those cells (meaning that the numbers were squared to eliminate negative signs, the mean was taken of the resulting squared numbers, and then the square root was taken of this final number in order to get back to the original metric, without any minus signs - basically just an elaborate way to get the average of the absolute values). Thus, larger numbers are higher levels of noise. This procedure is meaningless for frequency data. Outliers on this measure should be examined closely to determine if they are problematic. The numbers provided by these QC measures can allow for formal empirical criteria to be formulated and reported if it proves necessary to exclude bad subject data.

If the subjects prove to be acceptable, then a grand average can be generated. To do so, go to the Subjects Pane and click on All. This will give all the subjects a weight of one.



Then click on Add. The new entry is marked as a GAV type to keep it distinct from the subject averages which are AVG type. Rename it "grand"

The screenshot shows the 'EditData' window with the 'Subjects' tab selected. The main area displays a table with 11 rows, each representing a subject (sub001 to sub013) and a 'grand' row at the bottom. The columns are labeled: order, select, weights, names, type, RunDateMo, and Rr. The 'type' column contains 'AVG' for most subjects and 'GAV' for the 'grand' row. The 'RunDateMo' column shows dates ranging from 7 to 26. The 'weights' column contains checkboxes, all of which are checked for the first 10 subjects and unchecked for the 'grand' row.

	order	select	weights	names	type	RunDateMo	Rr
1	1	<input type="checkbox"/>		0 sub001	AVG	7	25
2	2	<input type="checkbox"/>		0 sub002	AVG	8	3
3	3	<input type="checkbox"/>		0 sub003	AVG	8	8
4	4	<input type="checkbox"/>		0 sub005	AVG	7	28
5	5	<input type="checkbox"/>		0 sub008	AVG	7	26
6	6	<input type="checkbox"/>		0 sub009	AVG	7	27
7	7	<input type="checkbox"/>		0 sub010	AVG	6	22
8	8	<input type="checkbox"/>		0 sub011	AVG	8	4
9	9	<input type="checkbox"/>		0 sub012	AVG	7	26
10	10	<input type="checkbox"/>		0 sub013	AVG	8	3
11	11	<input type="checkbox"/>		0 grand	GAV		

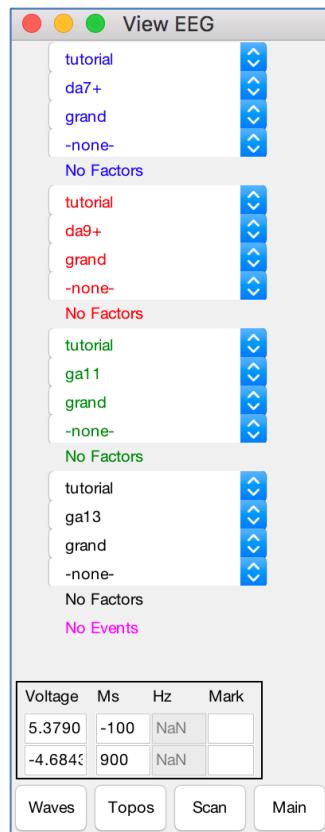
View Data

We can now proceed to view the data. Click on Done to return to the Read Pane of the Main Window (and to keep the changes you've made). If you changed the Data name, then it will ask you if you wish to make this be a new dataset in the working set or if you wish to rename and update the original dataset in the working set. Then click on Done to return to the Main Menu. Click on View to shift to the View EEG panel. This function allows one to view the waveforms directly. Four colors are available corresponding to four waves in the plots. For each color, there are controls indicating the data in the working set, the cell, the subject, the trial (or for averaged data various data range metrics), and the factor (where appropriate).

For datasets where there is event data like reaction time, one can also choose one or all of the event types to be marked on the figures using the magenta control. Choose one of the options in the magenta events popupmenu. Thick event bars will be added to the bottom of each waveform box, overlaying each other, color coded to correspond to the condition. If all events are chosen, they will not be distinguishable, so it is usually best to choose one of the event types (the Scan. At each sample where an event of that type occurs, the thick event bar will spike up. They are scaled so that the event with the greatest incidence will have a height equal to 25% of the waveform box (even if that event type was not chosen for display). For single-trial data, there will usually just be one of each event type at the most so all the event spikes will be of this height. For averaged data, all

the events from the contributing trials have been retained (if the EP Toolkit was used to conduct the averaging and the box was checked) so the event spikes will provide a histogram of the distribution of the events. Since the event used for epoching will usually be the event type with the greatest incidence (one per trial), it will be scaled to be 25% of the waveform box and the other events will be proportional to it. If there is an RT field in the trial specs, then this can also be chosen as an event marking.

In this case, set the controls to show the grand average for the four experimental cells by changing “sub001” to “grand” for all four of the colors.



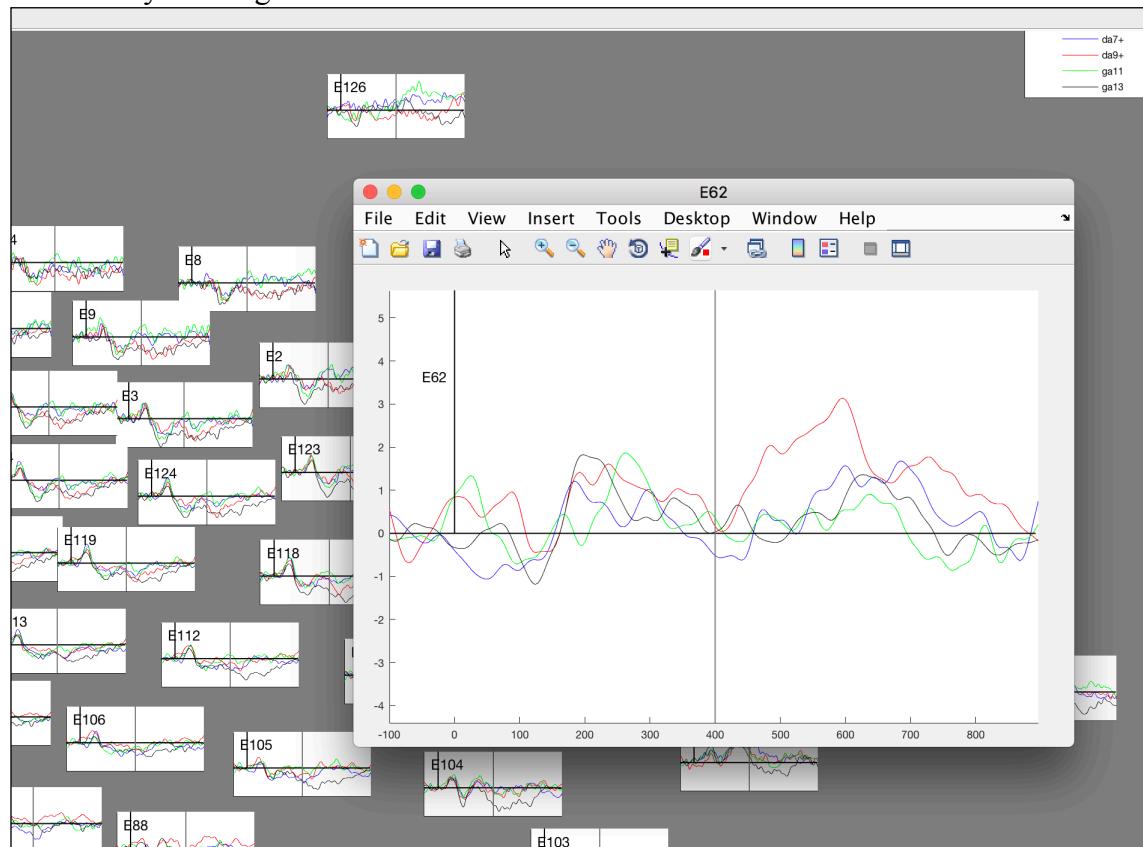
There are three options for viewing the data, Waves, Topos, and Scan. Note that the maximum and minimum voltages across all four colors is listed at the bottom under Voltages and these numbers are updated as the settings are changed. These numbers will be used to scale the data plots.

One can also change these settings manually if desired. The Epoch numbers show the ms to be displayed (dropping non-overlapping points if different datasets with different sized epochs are to be displayed together). If the Voltage, Mx, or Hz settings are manually set, their value will be pinned (and will change to blue) and will not change until a dataset is changed or the field is cleared, in which case they will revert to automatic values again.

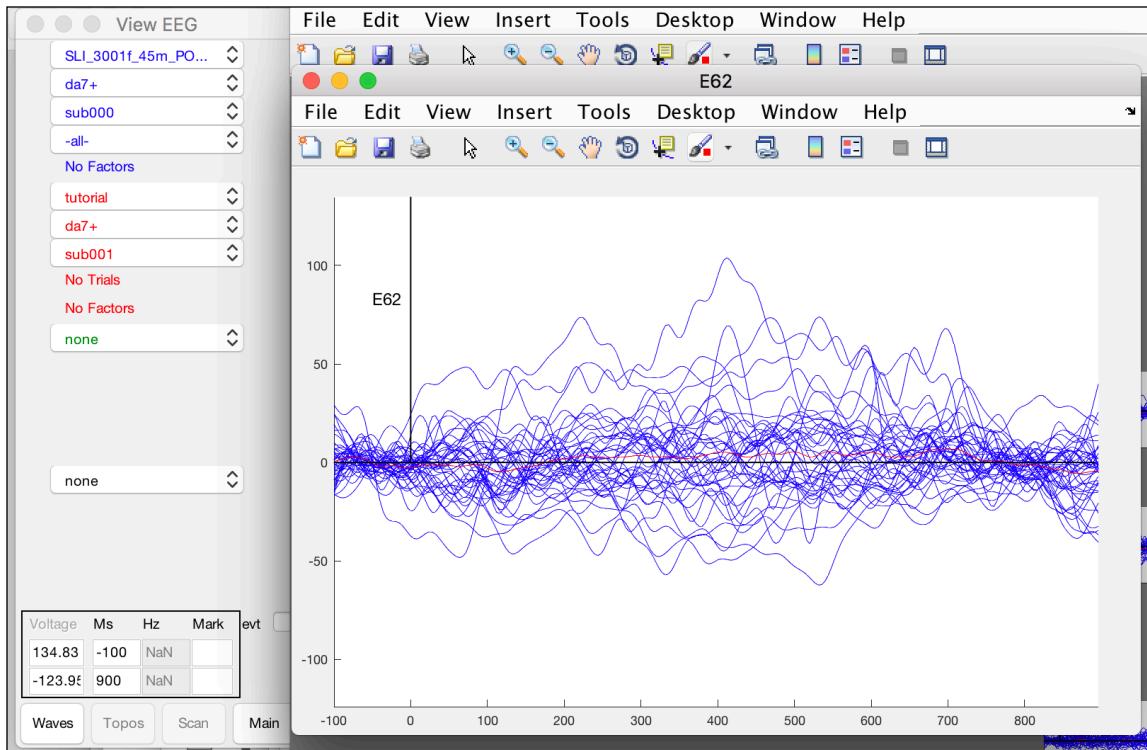
When one shifts to actually viewing the data by pressing the Waves or Topos buttons the

scaling will be updated to include the effect of the Ms and Hz controls to provide a better fit (this is especially important for spectral data as the range of values can be quite different between frequency bands). If the Voltage controls were manually set then the scaling will not be changed.

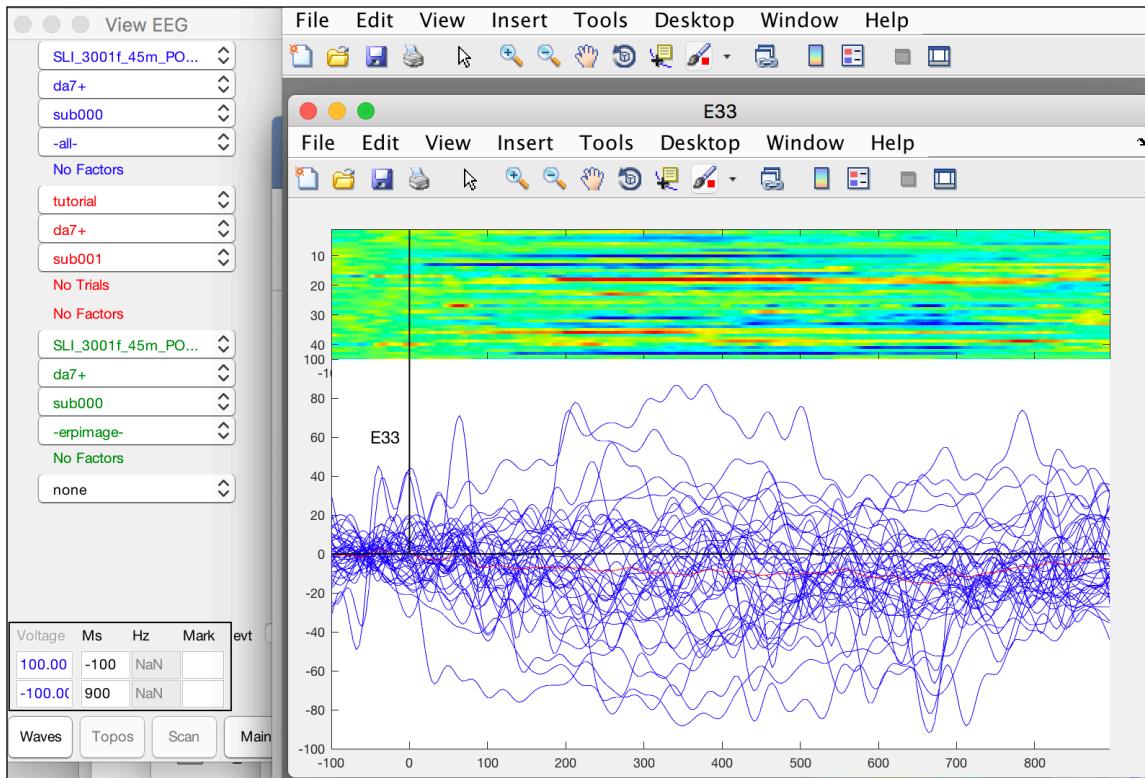
The marker fields allow for optional marker lines to be included on the waveforms. Enter 400 to indicate that one should be placed at 400 ms. Then click outside the box so that the number registers. Then click Waves. After a pause the waveforms should be displayed in a new window. A legend box will appear in the upper right corner and a scale will appear in the lower left corner. An expanded view of a waveform can be obtained by clicking on it.



One can also choose an “all” option in the Trials menu to overlay all the trials in a single-trial data file rather than just one. In the next figure this option has been used to plot all the trials (after first using Transform to baseline correct, rerefence, and low-pass filter the session file and then reading it into the working set) in blue and the resulting average waveform in red.



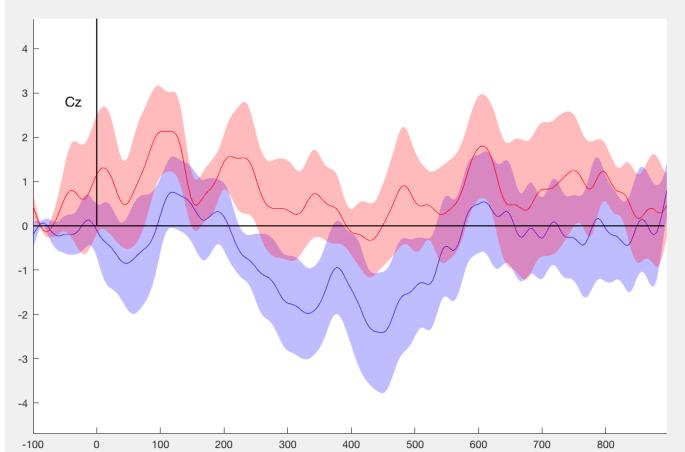
An erpimage (pioneered by Scott Makeig's group) option is also available. Every erpimage will be placed at the top of the channel window with any waveforms below them. Here is the same data with an erpimage added and with the scale pinned to -100 to +100 mv. In an erpimage, each pixel line is a different trial and the voltages are color coded. Thus, you can see the blue and red streaks corresponding to the trials that have sharp dips and peaks respectively. The -all- and -erpimage- options are also available for displaying cells, factors, and subjects. Event markings like reaction time can also be marked on these erpimages. If one has sorted the trials by reaction time using the Edit function, this can be quite informative.



For averaged voltage data, the trial menu instead provides several options for better understanding the variability of the data. -GFP- presents the global field power (Lehmann & Skrandies, 1984), basically the standard deviation of the voltage across all the channels at that time point, which provides a way of assessing the degree of ERP activity all over the head in a single waveform. This GFP waveform is present in every channel. I'm not a fan of the GFP because it encourages an overly serial view of ERPs but it can be helpful and is widely used.

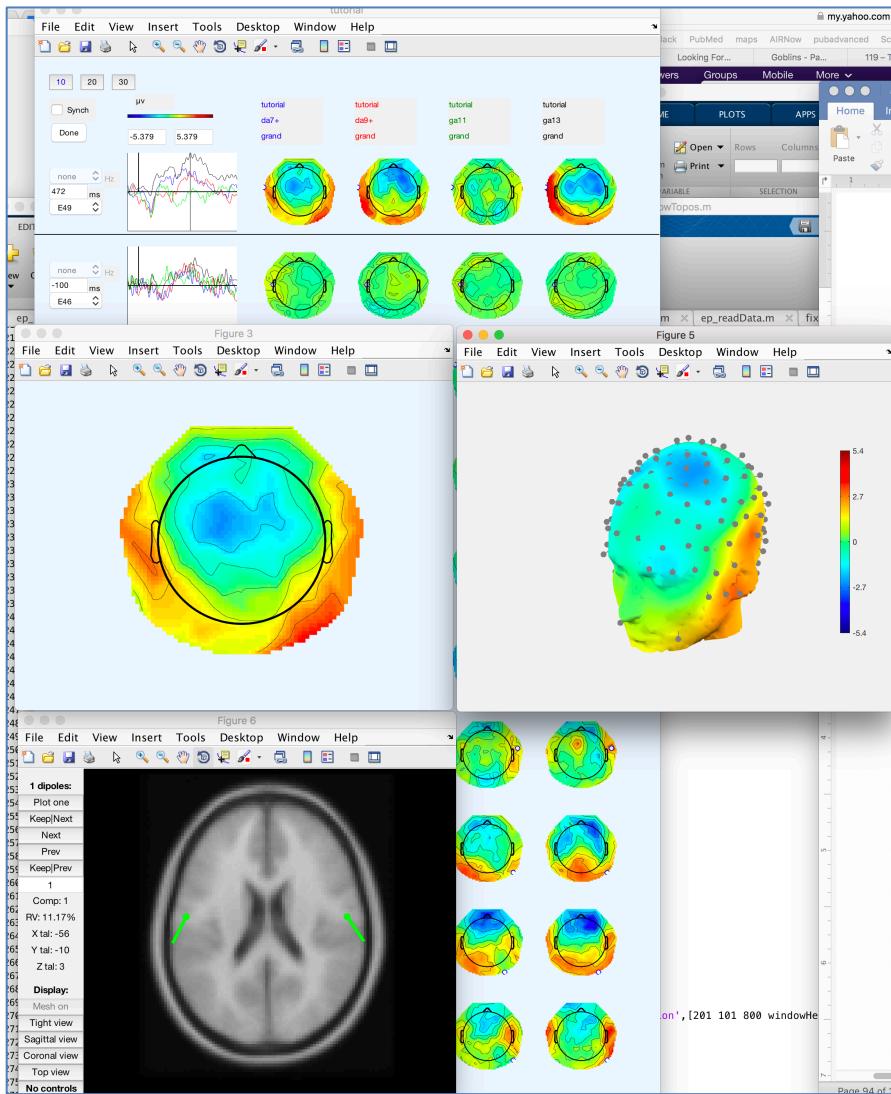
There are also three band options, each of which is presented as a band about the waveform. -noise- is generated using the +/- reference (Schimmel, 1967) and is computed by inverting every other trial, cancelling out the ERP components, and thus providing an estimate of the residual noise level. -StDev- does the same with the standard deviation. -CI- does the same with an 84% confidence interval. If 95% CI bands from two conditions do not overlap then that time point is statistically significant, ignoring the multiple comparison problem, but this approach is overly conservative (Schenker & Gentleman, 2001). To achieve a .05 alpha from this test, assuming equal standard errors, 84% CI is needed (Payton, Greenstone, & Schenker, 2003). If the Statistics toolbox is not installed, the EP Toolkit provides an estimate by using the coefficient of 1.44, which is appropriate for a sample size of n=30 when standard errors are equal. In order to deal with repeated measures for grand average data, the Cousineau-Morey correction (Baguley, 2012; Cousineau, 2005; Morey, 2008) is applied across the cells factor only, although it must be considered merely an estimate as it assumes circularity (Franz & Loftus, 2012). The important thing is to keep in mind that these

error bands merely provide a rough estimate and formal testing is required for conclusions. Also, these bands are also not computed using robust statistics as they have not yet been developed for this context. Also note that rereferencing eliminates the error band information so you need to rerefence prior to averaging if you wish to use this option. The bands for subject average data are based on the averaged trials. The bands for grand average data are based on the averaged subject averages.



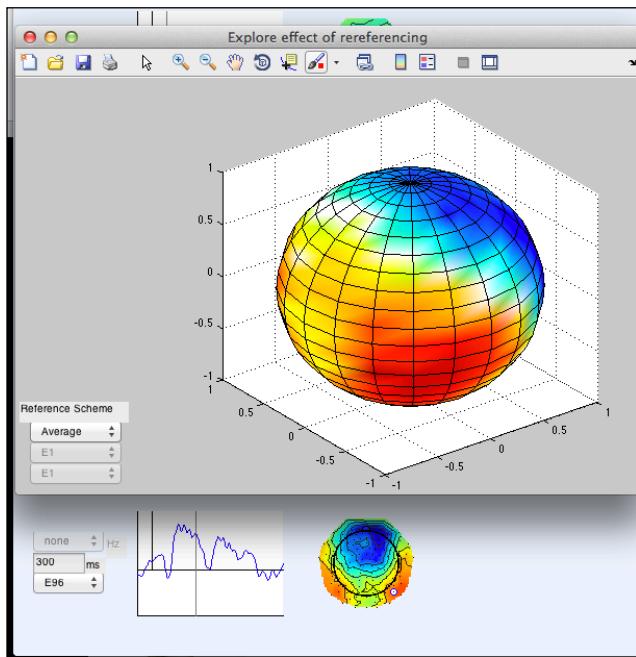
The Topos option provides an alternative viewing format in which the waveforms from one representative channel plus the scalp topography maps are provided (but the button will be grayed out if either the -all- or the -erpimage- options are chosen). Whatever dataset is listed first is used as the reference dataset. The waveforms for each line will be from the channel with the largest absolute voltages (in the reference dataset) and each topography plot will be from the time point with the largest absolute voltages (in the reference dataset). The gray line in the waveform figure indicates the time point corresponding to the topographical plots and the white dot in the topographical plots indicates the electrode corresponding to the waveform figure. You can change which channel and time point is being displayed using the controls on the left side. You may also change the channel by clicking directly on a scalp topography map. If you first click on the Synch checkbox then when you change the time or channel for one row, all of the rows will be changed to be the same. Black dots indicate the locations of the other channels but your click doesn't have to land precisely on the desired electrode location. You may change the voltage range of both the waveform figure and of the scalp topography maps by changing the numbers in the two boxes above the waveform figures. Note that you will need to change the number in a box, press enter or click outside the box, and then wait until the page is updated (you can use the Activity Monitor/Task Manager utility to see when it is done as well).

If you choose -all- in the View pane for any of the datasets, then whatever you chose (e.g., a factor) will be listed on each row. If you did not choose anything, then if the datasets are ERP or TFT data then each row will be time points spaced by 50 ms. If the reference dataset is FFT data then each row will be frequency bands spaced by 1 Hz. In these latter two cases, the first line will correspond to the peak latency/hz and will be set off with a gray line.



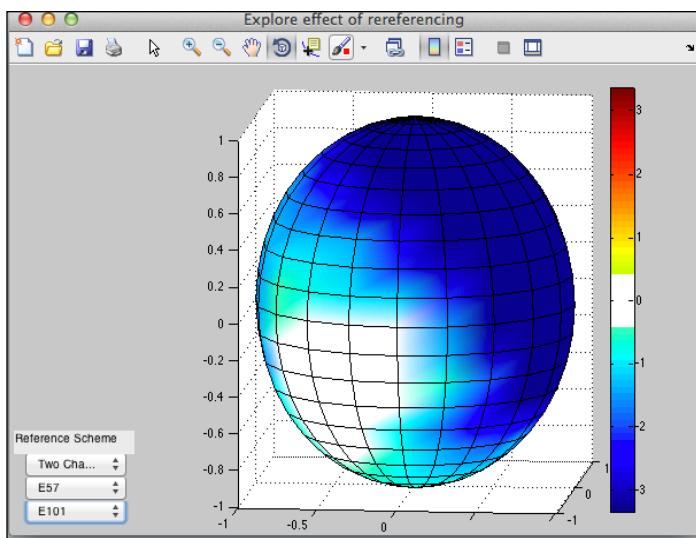
You may also right-click on the scalp topography plots to obtain: 1) an expanded 2D figure, 2) an expanded 3D head that may be rotated as needed, 3) rescaling of the topo plots based on the minimum and maximum of the clicked topo plot, 4) 2-Channels, which provides overplotting two channels from the 2D plot chosen and which can provide a sample-by-sample non-parametric t-test if the option box is checked (based on trials for single-trial data and on subjects for averaged data), 5) simple dipole analysis, 6) simple dipole analysis of jack-knife PCA results (for PCA results only). 7) illustration of effects of rereferencing. The former two are courtesy of EEGLab functions and the dipole analyses are courtesy of a FieldTrip function (using an EEGLab function to display the results).

Choosing the Rerefence option will not change the dataset but will help you evaluate the effects of different rerefencing schemes on the effects of interest. Here we can see the initial head topography (approximated as a sphere).



Clicking on the symbol adds the color scale (white marks the zero voltage region).

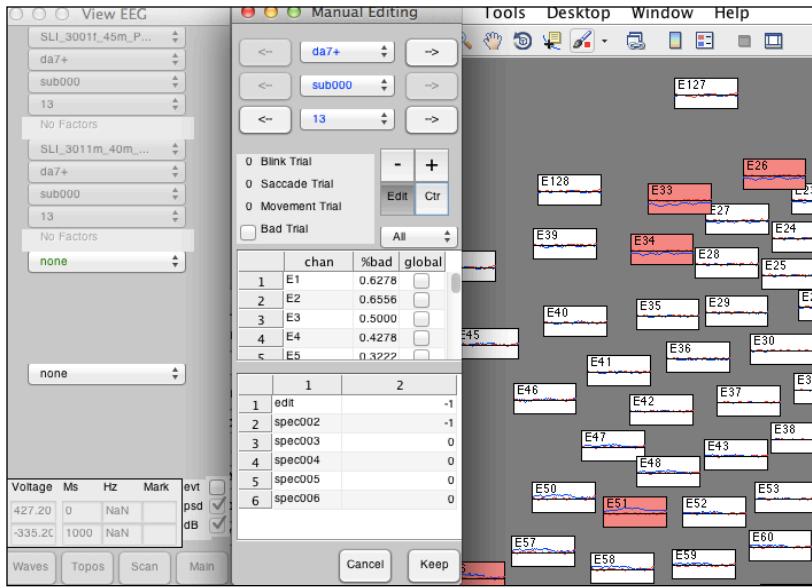
The symbol allows one to use the mouse to freely rotate the sphere. Since the data is average referenced, the reference menu starts with this option. Note how the sphere is roughly divided into half positive and half negative voltage regions, consistent with the biophysics of voltage fields in the head. In contrast, changing the settings to mean mastoids reference (channels 57 and 101 in the tutorial dataset) results in a very distorted voltage distribution. The difference between average reference with and without PARE correction is very subtle in this case.



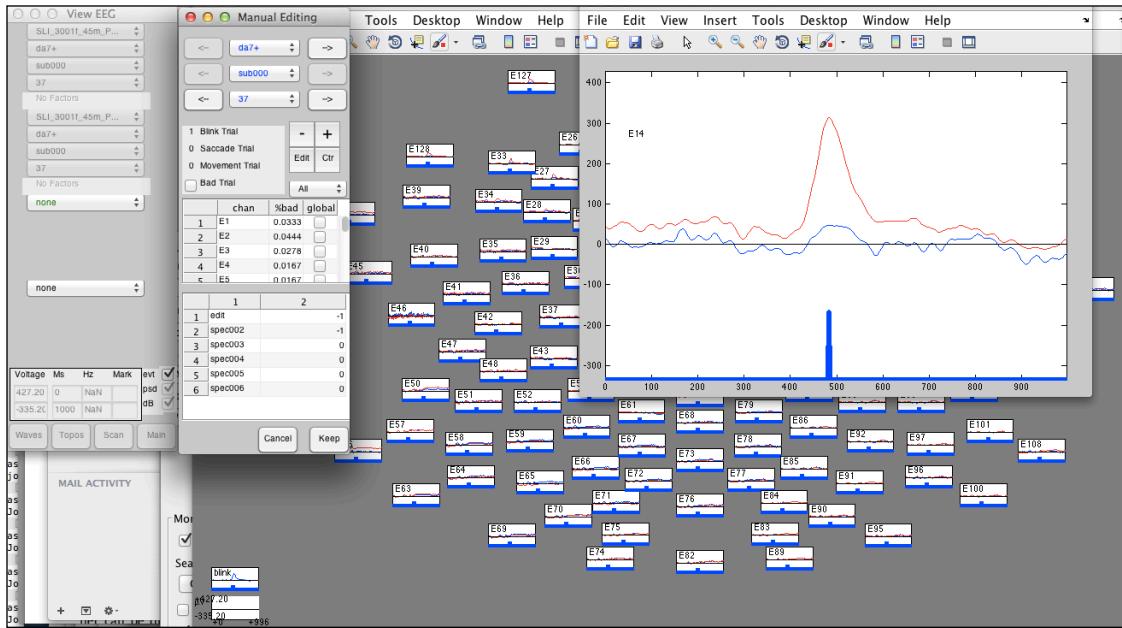
The first time you use the 3D head, EEGLab will need to generate a "spline file" which it will automatically place in the same location as the .ced file. You will need to wait while this is done. It only needs to be done once per .ced file that you are using. The dipole analysis is a bit trickier. In order to allow the function to work on multiple platforms, FieldTrip compiles a binary file on the fly. To do so, it needs a gcc compiler to be available (see installation instructions). If this was not done, then this function will not work. The dipole analysis program will attempt to fit two symmetric hemispheric dipoles. If they end up running into each other then it will try again with only one midline dipole. Note that this is a very simple implementation of dipole source analysis and does not seem to provide results as good as that provided by the more refined BESA program. In particular, it seems to have problems with the two hemispheric dipoles running into each other and then exploding into arbitrarily high amplitudes as they interact with each other. BESA provides parameters which help keep the dipoles from doing this. Nonetheless, this implementation of source analysis can be suggestive, especially when the dipoles have not collided. Press the Done button to return control to the View pane.

The Scan view allows one to scan through data to perform manual editing of bad channels and trials. The blue (first) dataset is the reference dataset that is being edited. If desired, other datasets can be selected. They will not be edited but can provide comparison waveforms. For example, in the following screenshot the blue dataset had undergone automatic bad channel/trial detection but no corrections were applied. The red dataset is the same data but after having undergone full automatic artifact correction (note, bad trials do not undergo channel replacement). Channels that were marked as being bad (but not replaced) are highlighted in red. One can turn this bad channel marking on and off by clicking on the channel if the Edit button is depressed, otherwise doing so will produce an expanded channel window. The Ctr button centers the display of each waveform on zero. The – and + buttons decrease and increase the scaling of the displayed waveforms by half. Bad Trials are indicated by a check mark in the Manual Editing window, and this too can be clicked on or off as desired. There is a table of all the channels that indicates the %age bad across all the good epochs for that subject and a checkbox that allows one to mark it as globally good or bad (will clear all bad channel markings if unchecked). Finally, there is a table that lists the trial specific information for this trial.

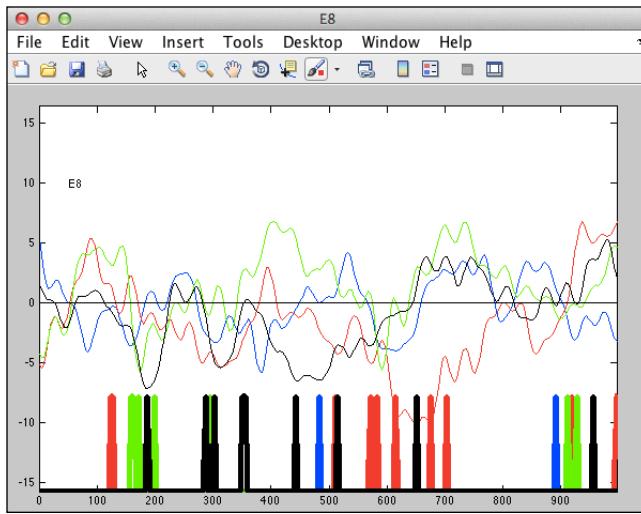
One can scan through the data by clicking on the appropriate arrows or choosing from the popup menu, for cell, subject, or trial. Once scanning is completed, one can either keep the manual edits by clicking on “keep” or discard them by clicking on “cancel”. Even if one keeps the manual edits, one will still need to Save the data to disk (see later section). These manual edits will then be corrected if one runs the file through the Preprocessing function with the editMode set to either Manual or Both.



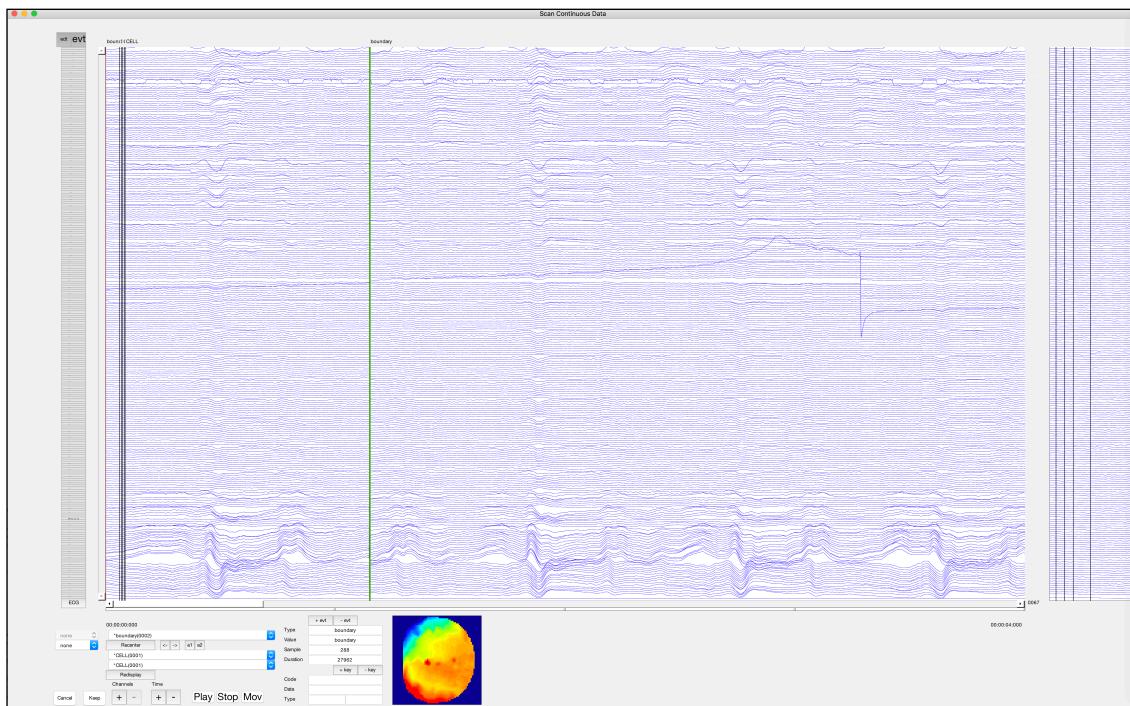
In the following screenshot of the fMRI-EEG dataset, it can be seen that the blink correction has left some residual artifact behind, so if there is a differential distribution of blinks between the conditions, it could result in an apparent experimental effect.



Once one averages the subject, one can then see the distribution of the blinks in the condition averages. In this particular case all the spikes are at the maximum height of 25% because the EGIS file format does not allow for event markers and so there is no event for the stimuli, which would normally be the most common event.



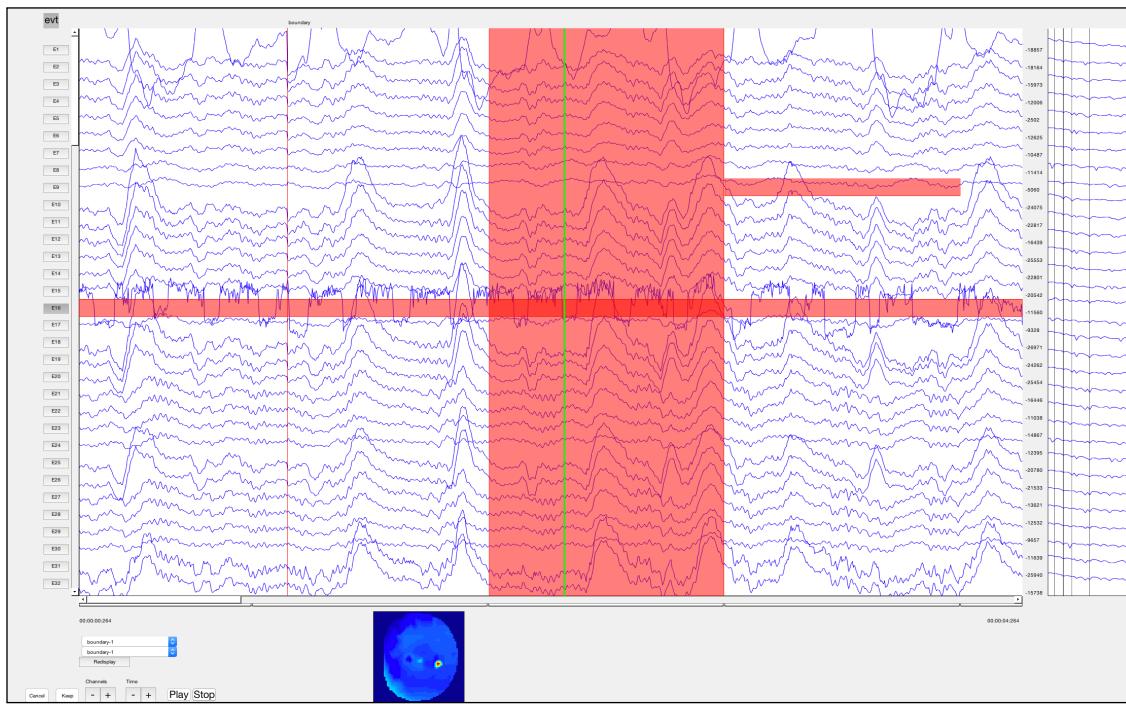
When the Scan function is utilized with a continuous dataset, such as the EEG-fMRI file, then it will present it in the form of a graph plot. Unfortunately this display can be quite sluggish as it is very data-intensive.



This graph plot has the following features. The channels are presented in a scrollable window. The channel names are placed along the left boundary. As before, multiple datasets can be overplotted. Event labels are located along the top boundary and black lines indicate their latency and will correspond to the blue (reference) dataset. The display of the events can be turned off by clicking on the "evt" toggle in the top left of the figure. Doing so can be helpful if there are so many events that they are bogging things.

down. Next to the "evt" toggle is a "edt" toggle that can turn off the red bad data markings that can otherwise obscure the data. Discontinuities in the recording are marked with a red line. A green line marks the time marker. The time marker can be moved by right-clicking anywhere in the graph plot. A 2D plot provides the scalp topography at the moment of the time marker (with additional 2D plots if multiple datasets are being overplotted). Clicking on a 2D plot generates a 3D figure of it. Along the right boundary the voltage value for each channel at the moment of the time marker is provided. Along the bottom boundary below the scroll bar, markings delineate one-second segments. Along the right side of the screen, a chart provides the spectral graph of the one-second segment currently occupied by the time marker. It has vertical lines at 4, 8, 12, and 20 Hz.

As before, the Cancel button returns one to the main pane without keeping any bad data edits while the Keep button retains bad data edits. The Channels - and + buttons zoom out and zoom in the number of channels while the Time - and + buttons do so for the time axis. The Play button causes the waveforms to start automatically scrolling, animating the 2D topo plot, while the Stop button stops this process. The Mov button also starts animating the display but will additionally save a movie file of the 2D plot(s) once finished.



Bad data are delineated by red shading (if the edt button is toggled on). To toggle global bad channel status, click on the channel name. To toggle bad channel in a single one-second segment, left-click on the channel row (in line with the channel name) within the one-second epoch delineated by the markings on the epoch bar below the horizontal scroll bar (for continuous data, the EP Toolkit divides it into one-second epochs for

purposes of editing and spectral analysis). To mark the entire one-second epoch bad, left-click on the epoch bar itself.

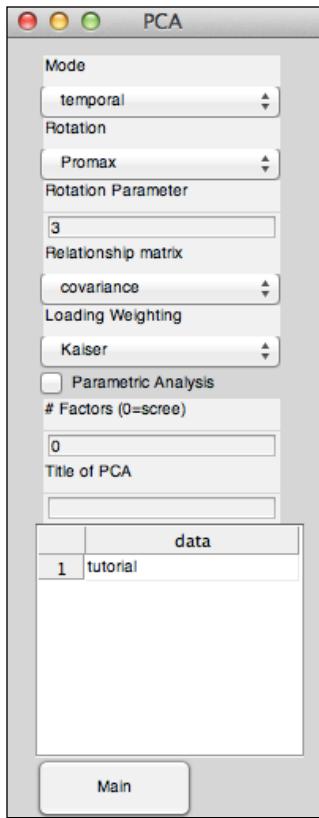
One can specify the display period in terms of two events by selecting them the two popup menus above the controls. The upper popup menu indicates the event marking the start of the display period and the lower popup menu indicates the event marking the end of the display period. Events that fall within the current display period are marked with an asterisk. Once the events have been selected, click on the Redisplay button below the two popup menus and the display will adjust accordingly. The events in the two popup menus are listed in alphabetical order. In case there are multiple instances of an event code, then the ordinal rank of the event will be listed in parentheses.

Alternatively, there is another popup menu above them that lists all the events in chronological order. One can select an event of interest and then recenter the display on it by pressing the Recenter button. The time marker will be placed at the sample of the selected event. The information fields associated with that event are listed to the right of these controls and can be edited. One can also shift the time marker to the prior or succeeding event by clicking on the <- and the -> buttons. One can also set the upper or the lower popupmenu to be the same as that of the top Recenter popupmenu by pressing the e1 and the e2 buttons respectively.

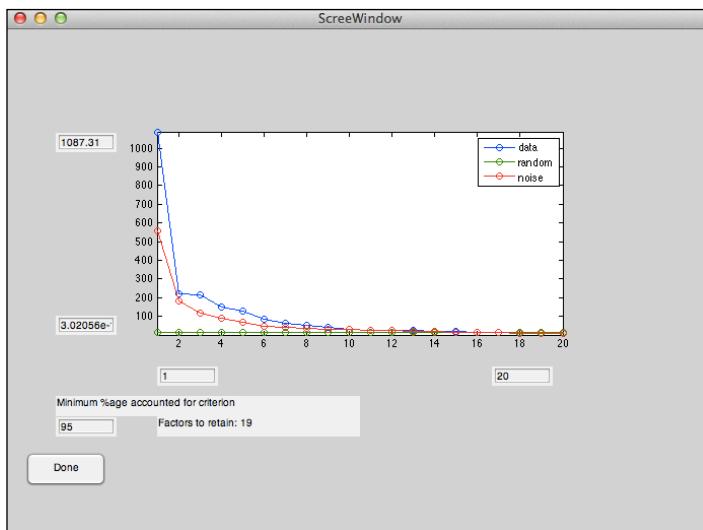
Principal Components Analysis (PCA)

The next step is to obtain a PCA of the data. I typically recommend using a two-step sequential PCA (Spencer, Dien, & Donchin, 1999; Spencer, Dien, & Donchin, 2001) in which the first step is a temporal Promax rotation and the second step is a spatial Infomax (ICA) rotation (Dien, 2010). Tutorials are available that discuss the principles of applying PCA to ERPs (Dien & Frishkoff, 2005) and the decisions that need to be made (Dien, 2012).

First click on Main to return to the Main Pane. Then click on PCA. I generally recommend using Promax with a covariance relationship matrix (Kayser & Tenke, 2003) and Kaiser weighting (Dien, Beal, & Berg, 2005) for this first step. The kappa for the Promax is generally set at 3 but does not make much difference (Dien, 2010). You will need to determine how many factors to retain for the initial step. Unfortunately, the question of how to best proceed remains unsettled at this point. Indeed, one recent paper concluded it is best to keep all the factors (Kayser & Tenke, 2003). At this point I find the data insufficient to convince me to change my analysis procedures, given the potential drawbacks of such an approach such as multiple comparison problems (Dien, 2006), but agree that it is a reasonable position and the data provided are intriguing. I therefore consider the question open and in need of further investigation. Leave the # Factors as zero to indicate that a Scree chart is needed. Click on the name of the dataset to begin.

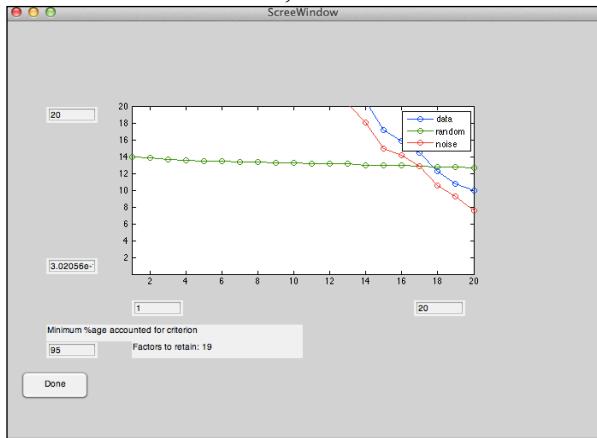


A Scree plot (Cattell, 1966; Cattell & Jaspers, 1967) is now displayed. The normal criterion is to choose the elbow but unfortunately, at least with ERP data, there are typically multiple elbows. The initial plot suggests 2 factors, for example, but if one expands the scaling then other elbows appear. Also whether one should choose the elbow or the point before it has been muddled.



Due to these ambiguities, I currently suggest the use of a parallel test (Horn, 1965), which compares the Scree of the dataset to that obtained from a fully random dataset. Adjust

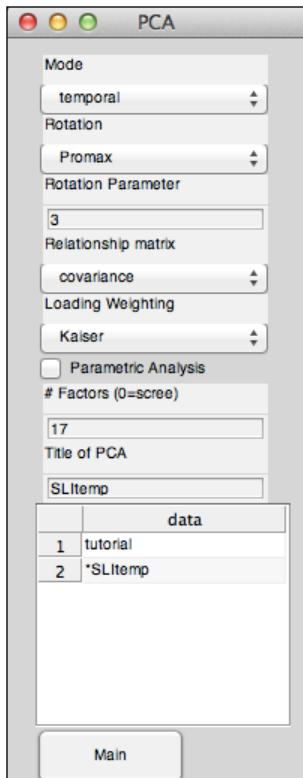
the scaling (on the left) to 20 to reveal the point at which the green line intersects with the blue line. In this case, 17 factors is the number indicated (the last point above the line).



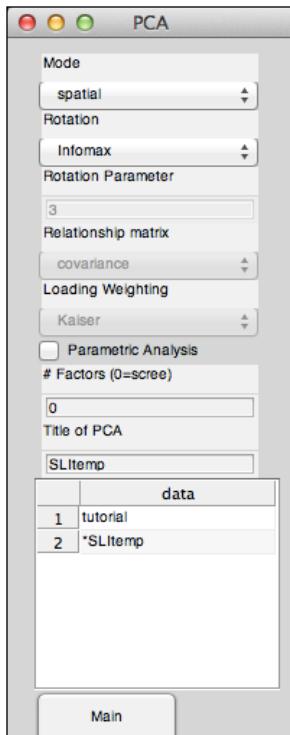
The red line represents the Scree plot of the noise data produced by the +/- reference (Schimmel, 1967). While I once recommended using it as the comparison Scree (Dien, 1998a), I no longer recommend its use as an effective PCA needs to represent coherent noise sources as well as the ERP components and so the random noise dataset is a more appropriate comparison. I am currently working on a more systematic treatment of these issues.

For completeness sake, the minimum %age accounted criterion is also available. Once finished, use the red close button in the upper left hand corner.

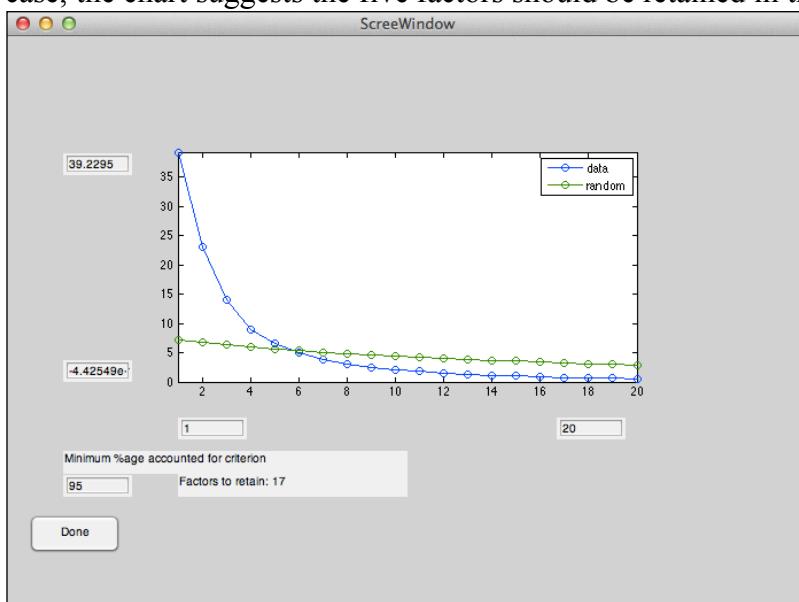
Set the # of factors to 17 and provide a title for the PCA, as in "SLItemp" and then click on the name of the dataset. It will first announce that it is computing jack-knife PCA Loadings. Basically, it is computing a set of PCAs in which each of the subjects in turn is let out of the sample, in order that one might later on determine how stable the PCA solution is to changes in the composition of the sample (see the Topos pane section of the tutorial for a further explanation). The PCA solution should be shortly added to the list of active datasets. It will have a star in front of the name to denote that it hasn't been saved yet.



Next, set it up for the second step by changing the settings to that of a spatial Infomax rotation. For Infomax, the rotation parameter, relationship matrix, and loading weighting does not apply. Make sure the number of factors is set at zero. Now click on the temporal PCA dataset.



The EP Toolkit generates a separate spatial PCA for each individual temporal factor, based on the argument that, for a given temporal factor, the other factors have nothing to contribute and can only distort the results (Dien, Spencer, & Donchin, 2003). This means that in the current example seventeen separate spatial PCAs are run. Currently, for simplicity's sake the EP Toolkit retains the same number of factors for each of the spatial PCAs. The scree chart is the average of all seventeen screes. This is obviously an oversimplification and the intention is to address this issue in a future update. In this case, the chart suggests the five factors should be retained in this second step.



Enter five for the # of factors and a title for this temporospatial PCA, such as SLIts and then click on the name of the temporal PCA.

At this point there was a memory fragmentation message:

??? Error using ==> zeros

Out of memory. Type HELP MEMORY for your options.

Error in ==> ep_PCAoutput at 434

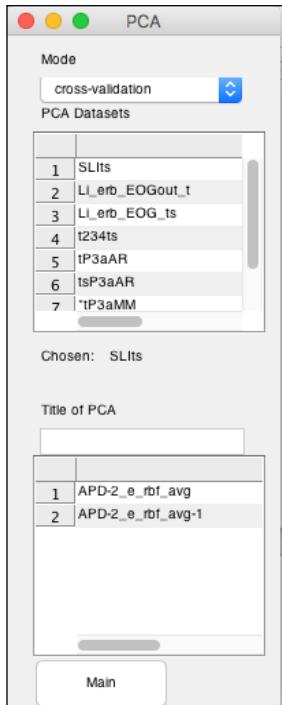
```
reconFacs = zeros(numChans, numPoints,numOutputCells,numSubs,NUM_FAC);
```

Error in ==> ep>pickPCAdata at 3715

```
[PCAoutput, peakLatency, peakSamp, peakChan] = ep_PCAoutput(FactorResults,  
cnames, cellcoll,  
exclChan, parametricData.data, parametricData.colheaders);
```

??? Error while evaluating uitable CellSelectionCallback

I therefore quit out of MATLAB without bothering to quit out of the EP Toolkit itself by going to MATLAB's File menu and choosing Quit. I then changed the current directory back to the one I had been using and typed ep at the command line. The EPwork directory retained the datasets that were being analyzed and so all that was needed was to go back to the PCA Pane and try the spatial step again as if nothing had happened. This time it worked fine. To purge a dataset from the working set, return to the Read Pane and click on the name of the dataset.

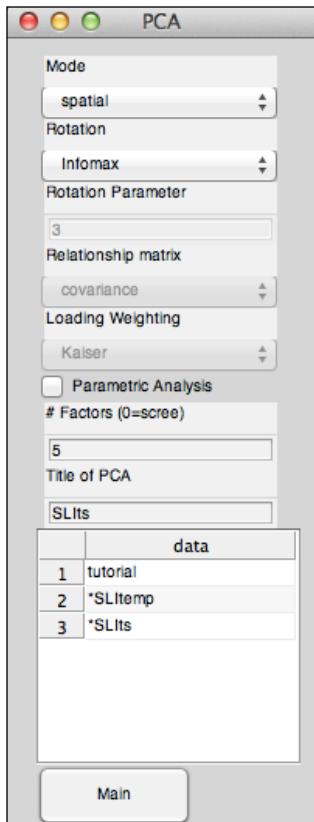


One can also cross-verify a PCA solution by applying the factor scoring coefficients directly to a different dataset, as long as it has the same number of relevant variables (timepoints for temporal, channels for spatial, bins for frequency). Cross-verification can be helpful if one wishes to rule out the possibility that differences in the factor structure of two separate PCAs were due to variations in the rotational process rather than differences in the latent structure of the datasets (e.g., Simons, Graham, Miles, & Chen, 2001).

It is important to understand that this procedure is not intended to allow one to apply a factor solution to entirely different datasets per se. A factor solution is specific to a dataset. For example, factor scoring coefficients reflect not just what is needed to measure a latent variable (e.g., ERP component) but also what is needed to disentangle it from other overlapping latent variables. So if both datasets had exactly the same P300 but only the first also had an N400, then applying the PCA results to the second dataset would be invalid. It would only be valid to apply the factor scoring coefficients from the PCA of one dataset to another dataset if the second dataset had exactly the same latent variables (e.g., same ERP components with exactly the same time course for a temporal PCA, differing only in amplitudes) and the same inter-factor correlations. This can rarely be said to be the case.

The sole intent is to allow one to compare two different factor solutions on the same dataset to quantitatively determine how similar they are (correlate the two sets of factor scores). I have chosen to call this procedure "cross-verification" to emphasize this point. To the extent that the latent structure of the second dataset varies from the first, you will also see the factor loading patterns (e.g., the waveforms in a temporal PCA) differ. Even if you apply it to the original data, you will see some minor differences due to rounding errors.

Select cross-verification from the Mode popupmenu. Then click on one of the PCA solutions in the upper table (so that its name is listed as being "chosen" underneath the table). Then click on a dataset in the lower table (only compatible datasets will be displayed there) and the same PCA solution will be applied to the new dataset. If the PCA was a two-step PCA then both steps will be applied to the new dataset.



If you click on Main and then use the Edit function to examine the temporo-spatial PCA data, you will find that the Factors and the PCA panes are now active. The PCA Pane for the temporo-spatial PCA shows the basic results for the PCA. The Summary subpane displays the basic parameters of the PCA. Note how the second step accounted for less total variance (69% vs. 93%) since additional noise variance was dropped from each of the spatial PCAs conducted on each of the temporal factors. The variance accounted for by each spatial PCA of each temporal PCA is provided in the table. Factor Variance is how much of the temporal factor was retained and Total Var is how much of the total original variance was retained by that second step.

The factor matrices are also available for inspection. For example, the FacPat Subpane displays the factor pattern matrix (one type of factor loading) from the initial temporal PCA step. The FacPatST displays it from the second spatial step. FacStr is the factor structure matrix, FacScr is the factor scores, FacCof is the factor scoring coefficients, and FacCor is the factor correlations. I don't have time to provide tutorials on factor analysis by e-mail but you're welcome to read my tutorial chapter (Dien & Frishkoff, 2005) or to consult books on factor analysis (Gorsuch, 1983; Tabachnick & Fidell, 1989). Note that there is normally no reason to export the factor scores. As I have argued elsewhere (Dien, 2012), it is much more useful to view the factors in the form of factor waveforms (the portion of the ERPs accounted for by each factor). These factors are in microvolt scaling and can therefore be directly compared to the original data. The PCA waveforms in the working set (in this case SLItemp and SLIts) have the full factor score information

so one can derive the necessary numbers to run ANOVAs from them (see the remainder of the tutorial).

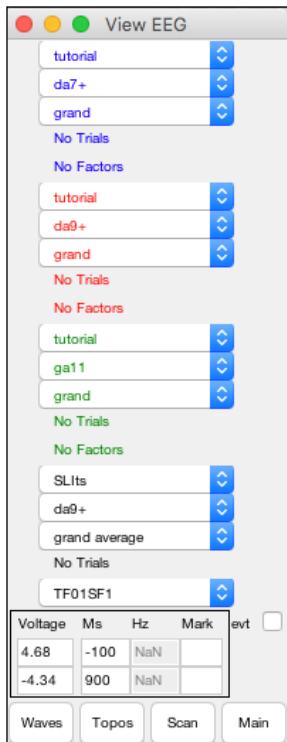


The Factors pane provides information on the individual factors. Peaklatency is the time point with the greatest absolute voltage (out of all the cells after computing the grand average). PeakNegChan is the channel with the most negative voltage (out of all the cells after computing the grand average) and PeakPosChan is the channel with the most positive voltage. PeakPolarity is whether the negative or the positive peak channel had the greater absolute voltage. Variance is the %age of the overall variance accounted for by the factor. Unique Variance is the %age variance that is uniquely accounted for by the factor (they are the same for orthogonal rotations where factors are not correlated). Notice that the factors from a two-step PCA are organized with the factors derived from the same first step factor clumped together (so the first five of the example are the five spatial factors derived from the first temporal factor).

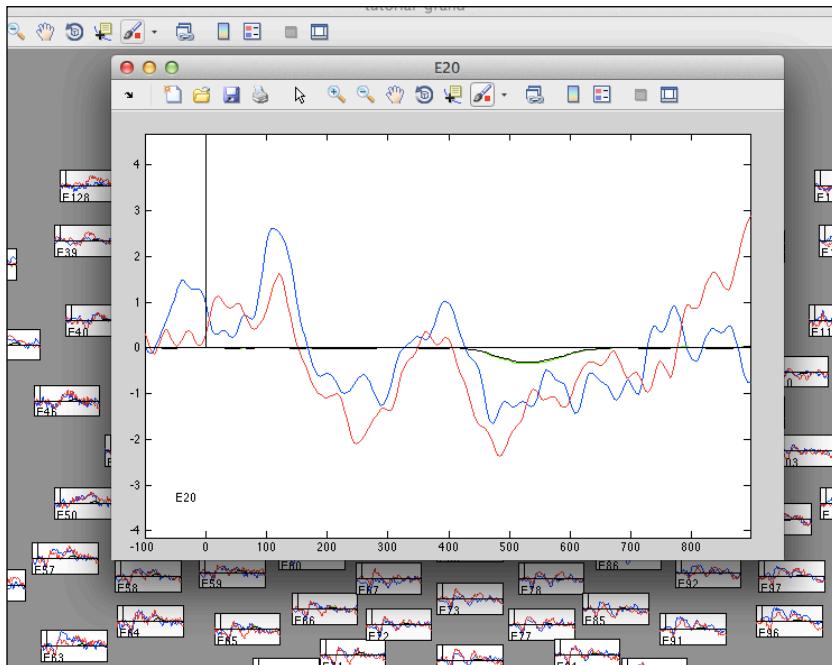
EditData

	order	select	weights	names	type	peakLatency
1	1	<input type="checkbox"/>	0	TF01SF1	SGL	300
2	2	<input type="checkbox"/>	0	TF01SF2	SGL	300
3	3	<input type="checkbox"/>	0	TF01SF3	SGL	300
4	4	<input type="checkbox"/>	0	TF01SF4	SGL	300
5	5	<input type="checkbox"/>	0	TF01SF5	SGL	300
6	6	<input type="checkbox"/>	0	TF02SF1	SGL	516
7	7	<input type="checkbox"/>	0	TF02SF2	SGL	516
8	8	<input type="checkbox"/>	0	TF02SF3	SGL	516
9	9	<input type="checkbox"/>	0	TF02SF4	SGL	516
10	10	<input type="checkbox"/>	0	TF02SF5	SGL	516
11	11	<input type="checkbox"/>	0	TF03SF1	SGL	388
12	12	<input type="checkbox"/>	0	TF03SF2	SGL	388
13	13	<input type="checkbox"/>	0	TF03SF3	SGL	388
14	14	<input type="checkbox"/>	0	TF03SF4	SGL	388
15	15	<input type="checkbox"/>	0	TF03SF5	SGL	388
16	16	<input type="checkbox"/>	0	TF04SF1	SGL	216
17	17	<input type="checkbox"/>	0	TF04SF2	SGL	216
18	18	<input type="checkbox"/>	0	TF04SF3	SGL	216
19	19	<input type="checkbox"/>	0	TF04SF4	SGL	216
20	20	<input type="checkbox"/>	0	TF04SF5	SGL	216
21	21	<input type="checkbox"/>	0	TF05SF1	SGL	740
22	22	<input type="checkbox"/>	0	TF05SF2	SGL	740
23	23	<input type="checkbox"/>	0	TF05SF3	SGL	740
24	24	<input type="checkbox"/>	0	TF05SF4	SGL	740
25	25	<input type="checkbox"/>	0	TF05SF5	SGL	740
26	26	<input type="checkbox"/>	0	TF06SF1	SGL	116
27	27	<input type="checkbox"/>	0	TF06SF2	SGL	116

One can also view the factors directly by going to the View Pane from the Main Pane of the Main Window. One could, for example, examine what portion of the grand average is accounted for by TFSF1 (the first spatial factor formed from the first temporal factor) by overlaying them using the Waves function.

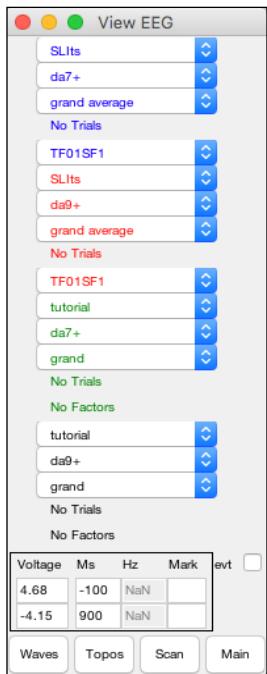


An expanded view of channel 20 (double click on it) reveals:

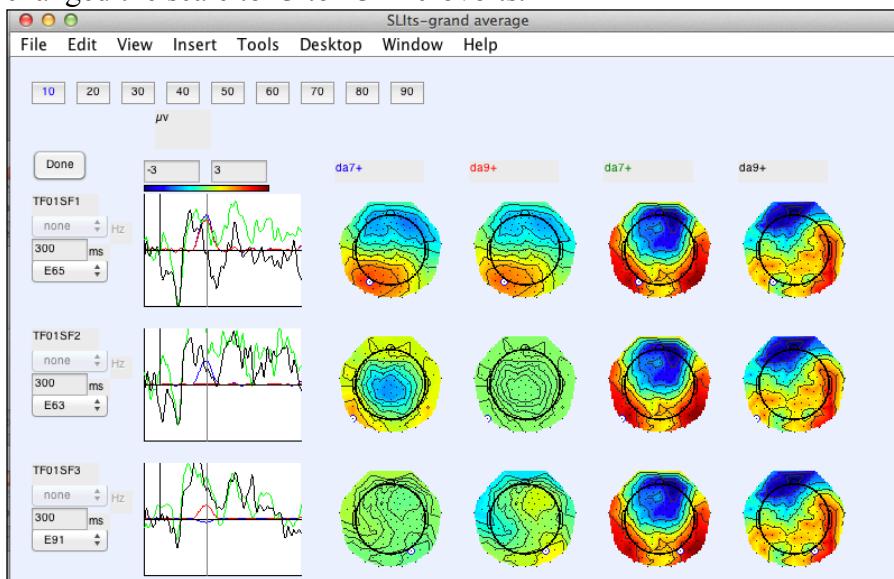


Alternatively, you can use the Topos function to examine the results. If a PCA dataset is examined, instead of only displaying the chosen factor, all of the factors will be displayed, each on a separate line. It is therefore an efficient method for screening for factors of interest. If the first (blue) dataset is the PCA dataset then it will serve as the

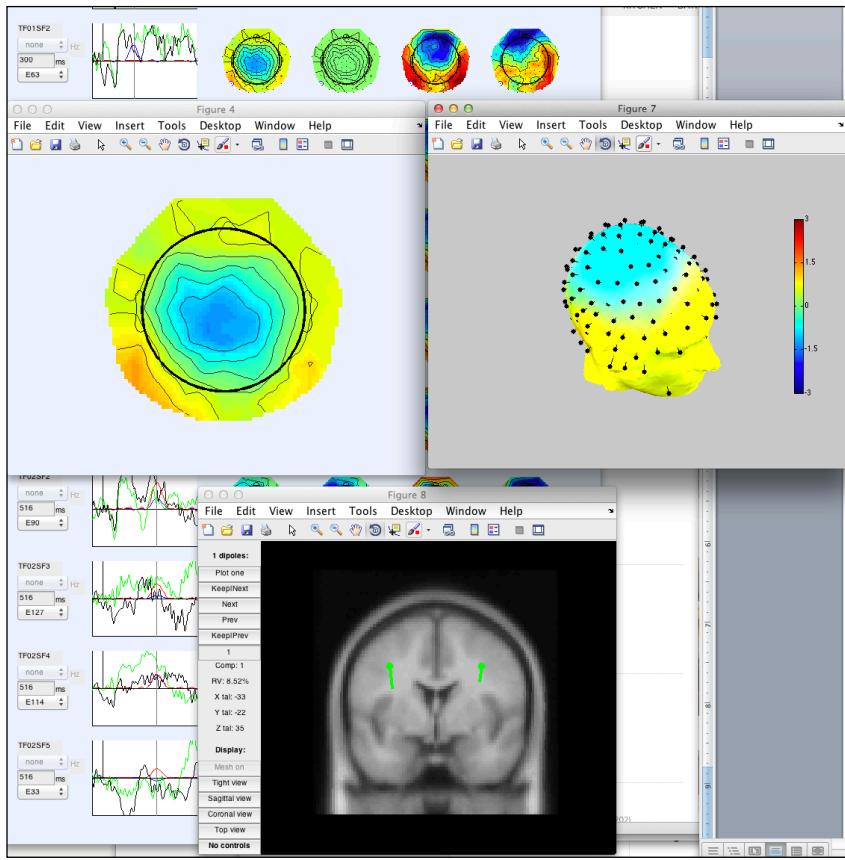
reference dataset and all the channels and time points will be the factor's most representative (largest amplitude) channel and timepoint.



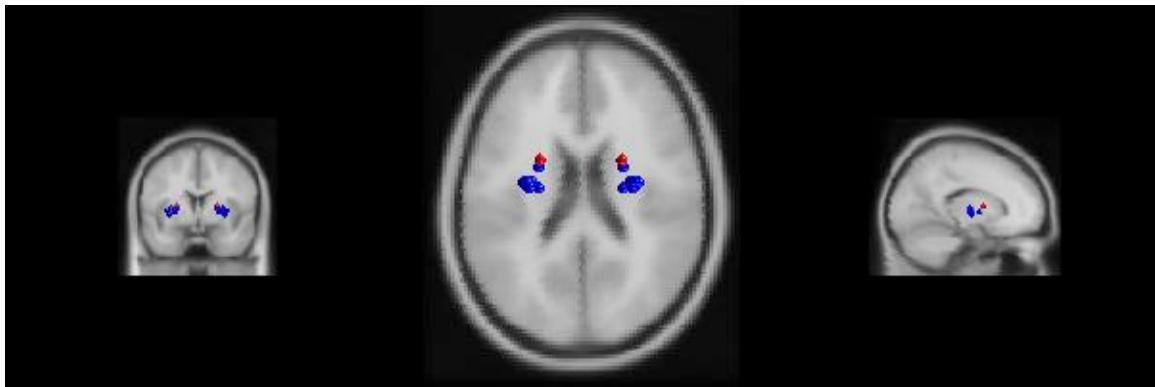
Press the Topos button. Plotting so much data will take some time so be patient. Only ten factors will be displayed on a page. The control at the top of the screen allows one to move between the pages of factors. In the following screenshot, TF01SF01 (the first spatial factor derived from the first temporal factor) had a peak latency of 524 ms and a peak channel at e112. The initial scaling left the color scheme too washed out so I changed the scale to -3 to +3 microvolts.



The figure below shows the results from TF01SF02, which appears at least to distinguish da7+ and da9+.



With the jack-knife option, what happens is that every time one does a PCA, a jack-knife analysis is automatically conducted in which a set of PCAs are computed in which one subject is left out (so twenty subjects results in twenty PCAs, each with nineteen of the subjects). For two-step PCAs, the jack-knife analysis is only conducted on the second step. The factor loadings from this are stored for later use. When the "jack-knife" option is chosen in the Topos function, a simple dipole analysis is conducted on each of the jack-knife solutions and the resulting cluster of solutions is generated, with the original location in red and the jack-knife solutions in blue. This provides a graphical representation of how stable the original solution was to individual subject variability (Foti, Weinberg, Dien, & Hajcak, 2011). Since this procedure is conducted on the factor loadings, it will only be done for a spatial PCA or for a temporo-spatial PCA. In addition, the jack-knife PCA procedure allows for a significance test to be conducted on the relative strength of the hemispheric dipole amplitudes, using a t-test that has been adapted for jack-knife analyses (Miller, Patterson, Ulrich, 1998), which is then printed out at the command line. Unfortunately, the corresponding test statistic is not yet available using robust statistics.



Sample Test

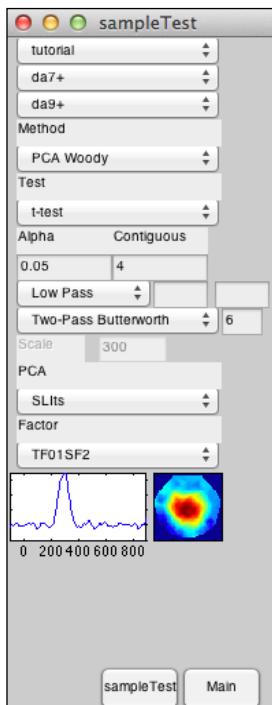
A next step can be to example sample-by-sample test statistics. A limitation of temporal PCA is that the factors are by definition a specific time course and so cannot be used to examine subtle latency shifts. Spatial PCA is capable of doing so but it tends to conflate multiple ERP factors, hence the need for the two-step PCA procedure. One way of proceeding is to use the PCA to identify ERP components of interest and then to use sample-by-sample tests to determine if there are any latency shifts. Sample-by-sample test statistics suffer from high multiple comparison rates so they need to either be highly constrained by a priori hypotheses or they need to be treated as highly exploratory. Go back to the Main Menu and click on SampleTest. This button will be grayed out if the Statistics Toolbox from Mathworks is not installed.

The first line is to indicate the dataset to be analyzed. It has to be part of the working set. It can be either single-trial or multi-subject averaged data. Choose the “tutorial” dataset. The next two lines are used to indicate which two cells are to be compared. At present only pairwise comparisons are available. If the dataset is frequency domain then the tests will be conducted across the frequency bins instead of time (bin-by-bin). If the dataset is time-frequency domain then the tests will be conducted across time (sample-by-sample) and this will be done individually for each frequency bin.

The Method menu allows one to choose one of three related methods:

- 1) Sample - is a sample-by-sample non-parametric in which each of the samples are individually tested. For single-trial data the Wilcoxon rank sum test is used and for averaged data the Wilcoxon signed rank test is used.
- 2) CWT - is a continuous wavelet transform analysis in which a Mexican Hat wavelet is generated and is slide across the epoch sample-by-sample. A cross-product fit statistic is generated at each sample and then tested. This is a simplified version of a published test procedure (Bostanov & Kotchoubey, 2006). The scale (or essentially the width) of the wavelet function can be specified in the Scale field and an image of the resulting wavelet is presented below.

3) PCA Woody - uses a PCA factor as a non-iterative Woody filter template (Woody, 1967) to slide across the epoch, generating a dot-product fit statistic (mean of the elementwise multiplication of the two matrices) at each lag and then tested. This PCA factor can be either a temporal PCA factor (temporal template only) or a temporospatial PCA factor (both temporal and spatial template). The PCA dataset (from the working set) and the template factor are specified below and the time course and the scalp topography (if temporospatial) is illustrated. If a spatial PCA is utilized on single-trial data, the latency and the amplitude of the maximum fit statistic will be saved in the trial specs. This latency information can then be used to with the latency-lock option of the Average function.



The test setting controls whether a sample-by-sample t-test is applied (either matched sample or two-sample depending on whether the data are multiple subject averages or single-trial data from a single subject) or a jack-knife test (Miller, Patterson, & Ulrich, 1998). The jack-knife test is applied to a single channel and will test whether there is a significant difference in when the waveform at that channel exceeds the threshold value (either above or below depending on whether the threshold value is positive or negative). The result of the test is output to the command window and is not saved with the dataset in any manner. This test seems to work quite well when the ERP is relatively robust, as in the lateralized readiness potential for which it was developed, but seems to me to be of less utility for other cases. If either of a subject's waveforms do not reach the threshold at all, the subject is counted as missing data and dropped from the test, as reflected in the smaller degrees of freedom.

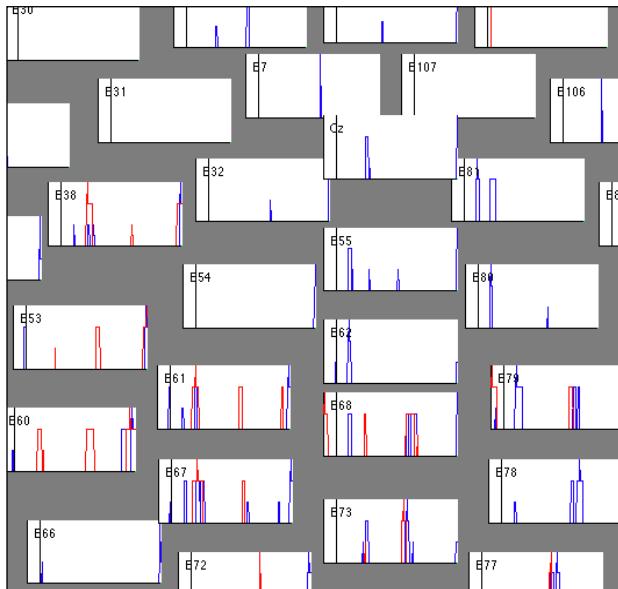
The Alpha field controls the alpha threshold used to determine whether a sample is to be considered statistically significant.

The Contiguous field controls a very crude multiple comparison control. If there is a series of contiguous samples at least as long as the value set in this field, then those samples will be highlighted when the results are viewed.

The next two lines are filtering controls that work as in the Transform function, except that they are only applied during the analysis and will not result in any lasting changes to the dataset itself.

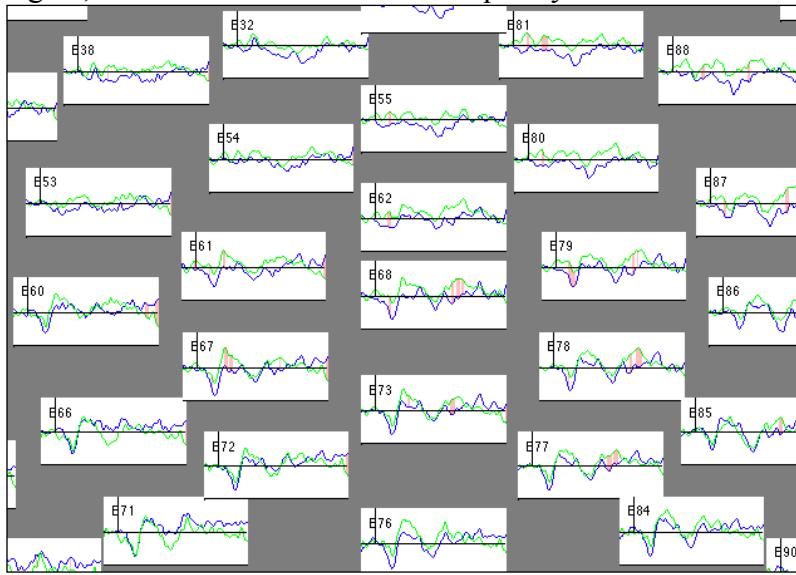
Try out all three methods on the da7+ and da9+ conditions in the tutorial dataset, using the t-test. The results will be saved to the tutorial dataset in a “subject” called “sampleTest” and cell names corresponding to the test and comparison made (e.g., CWT:da7+-da9+). If the same type of test and comparison is repeated, the results will overwrite the previous result. They can be viewed using the View function. The results take the form of waveforms where .25 marks a significant effect, .5 marks a significant effect which is part of a series of significant samples whose length exceeds the contiguity setting. A value of .75 marks the most significant sample.

In this case, the multiple comparison problem that is inherent in a sample-by-sample test makes it difficult to say for certain whether there is a substantive effect but sample test (in blue) looks suggestive at Cz, roughly the center of the TF1SF2 factor scalp topography. On the other hand, the CWT looks less promising and the PCA Woody did not generate any effects at all.



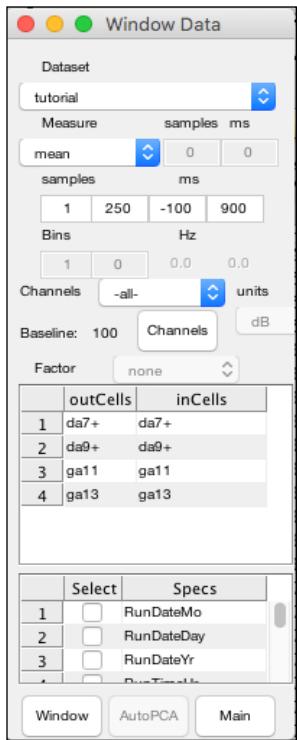
If one views the waveforms specifying one sample test waveform and two ERP waveforms and the fourth set at “none”, the sample test effects will be presented as a

filled in area between the two waveforms. Naturally this will only be meaningful if the two ERP waveforms represent the two conditions used to generate the sample test results. Again, this can also be done with frequency domain data.



Windowing

To test whether there are any statistically significant effects, go to the Window Pane of the Main Window. Let us first consider how subject averages would be analyzed and then address how to analyze PCA results.



Windowing Subject Average Data

First you need to indicate which of the datasets in the working set to analyze. Then which measure to use within the window. Min and max centroids (Dien, Spencer, & Donchin, 2004) are a way of measuring the latency of the overall area under the curve rather than just the peak, much as a mean measure does for amplitude. Use minimum centroid for negative components and maximum centroid for positive components. Mean is just the mean voltage in the window. While a methodology paper (Clayson, Baldwin, & Larson, 2013) reported that the centroid measure is "biased", the authors generously allowed me to examine the script that ran their simulation analyses and I found that contrary to their methods description they had not randomized the phase of the background sine waves (simulated noise), resulting in a confound. So in fact the "bias" results from the centroid measure was actually due to it being more sensitive to the presence of the confounded noise than the competing methods (which explains why this "bias" was stronger the larger the noise-to-signal ratio). The authors have issued an erratum to their paper.

Min and max peak are the minimum and maximum voltage values within the window. One can specify that some number of points surrounding the peak value are averaged together instead of measuring just the peak sample. Min and max latency are the latencies of the minimum and maximum voltage points within the window. Following (Luck, 2005), for the peak measures only a peak with smaller voltages on either side will

be counted as a peak. For peak amplitude measures only, there is also an option to have it average together the adjoining samples after locating the peak. This option is activated by first specifying a peak amplitude measure and then typing into the adjoining fields the number of neighboring samples to include (e.g., "1 sample" would indicate that a total of three samples would be averaged together, the peak and the samples on either side of it).

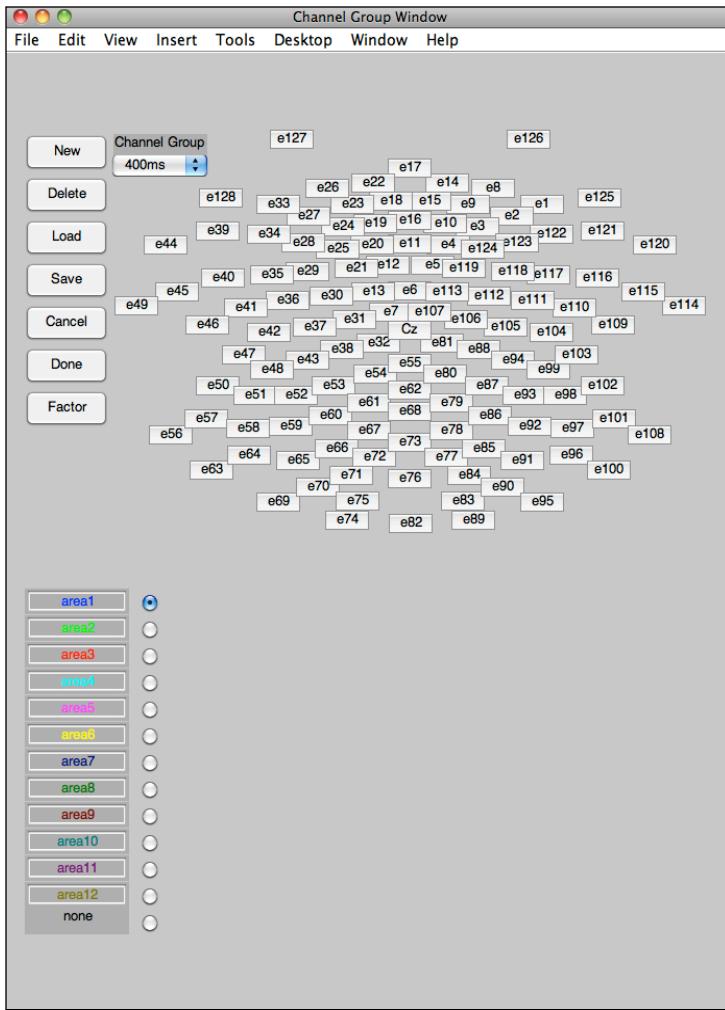
By default, the behavior is now to average together the channels in an Area and to measure the result, although there is an option under preferences to instead first measure each individual channel and then average together the resulting measures (the original behavior prior to EP Toolkit version 2.3).

Finally, if the trial specs include an RT field for reaction time and an ACC field for accuracy, one may choose "behavioral" to indicate that one wishes to generate text files suitable for ANOVAs for both the reaction time and the accuracy data (one for each).

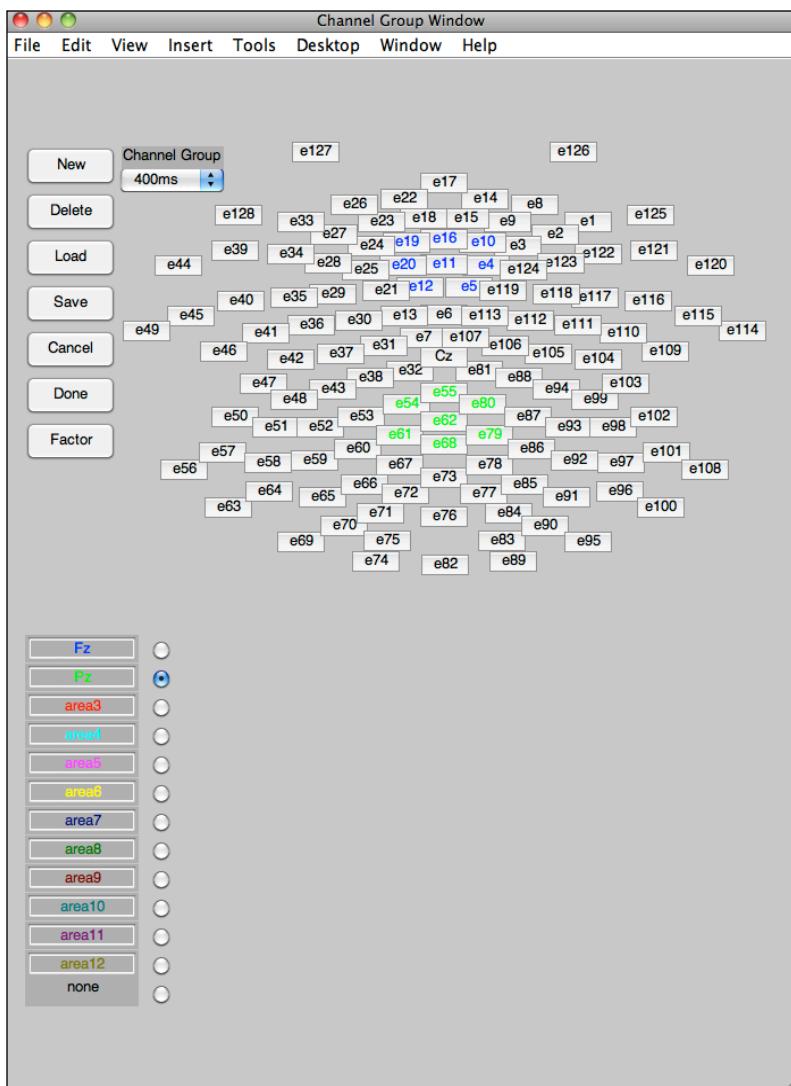
Let's choose the "Mean" option.

The time window also needs to be specified. Let's try a 300-500 ms window (although this tutorial dataset is too small to look for real effects) by entering in samples 100 to 150.

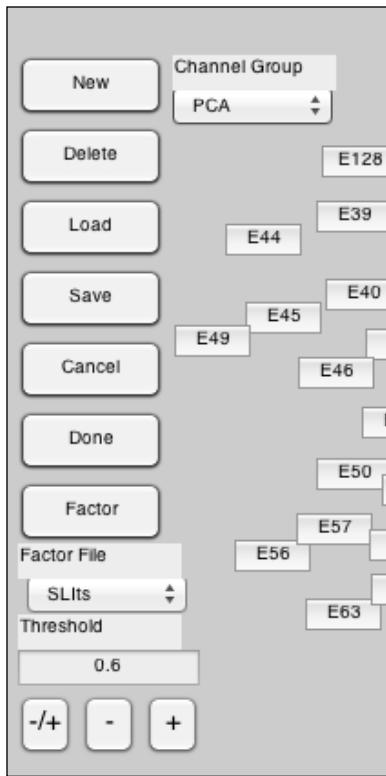
Next, the channels are specified by click on the Channels button. It will then bring up the electrode montage.



Click on the channels for the first electrode area. After the first channel is clicked, it will ask for a name for the new electrode grouping (the partition scheme for the electrodes, which in turn is divided into electrode areas that will be averaged together). Type in 400ms. You should also give the channel area a name by typing in the "area1" box, say Fz. Let's also add a posterior grouping around Pz by typing in Pz for area 2 and then clicking on the green box to activate the second area. Having clicked on the green box, any channels you click on will be added to the second area (and turned green) rather than the first box (and turned blue).

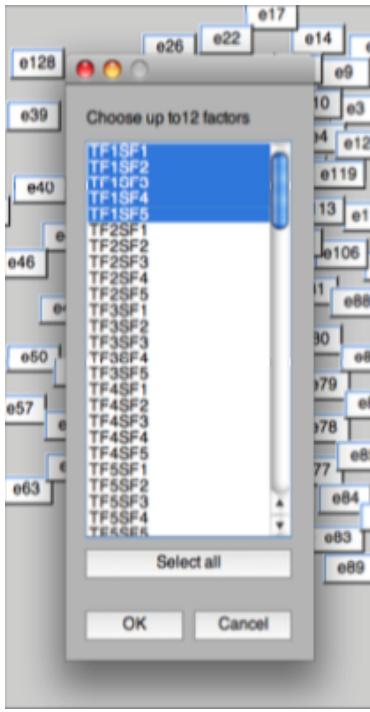


You could also define channel areas by using the results of a spatial PCA, if any are in the current working set. Click New to define a new channel grouping and give it the name PCA. Now click on the Factor button. It will give you a menu of the available spatial PCA solutions and the factor loading threshold to use (0.6 by default).

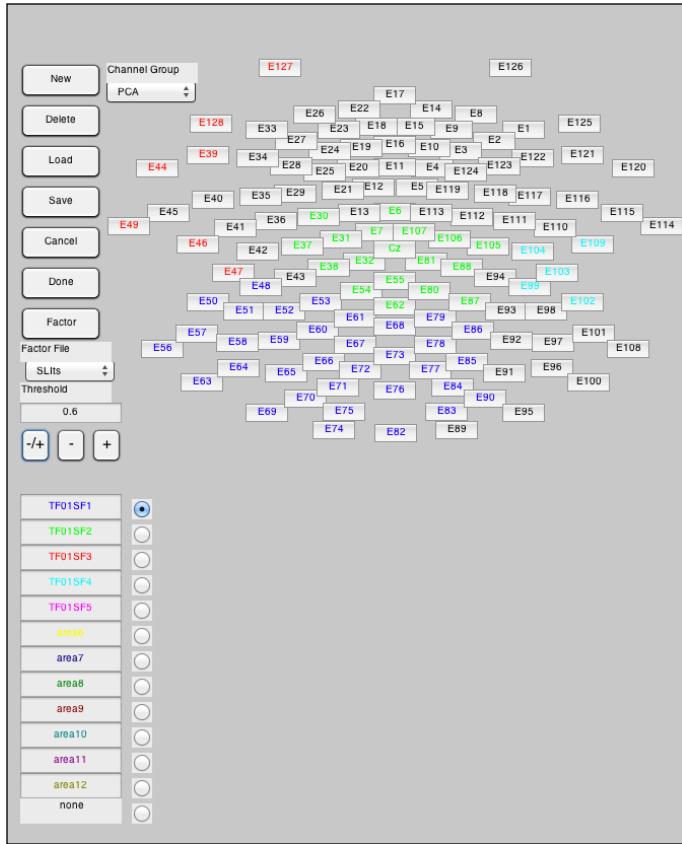


If you click on “-“ it will choose the factor loadings that are more negative than the threshold (e.g., -6). “+” will choose the factor loadings that are more positive than the threshold (e.g., +6). “+/-“ will choose the factor loadings whose absolute value is greater than the threshold. A negative threshold will be ignored and converted into a positive value. Note that the sign of the factor loading has no intrinsic meaning as it is essentially randomly determined. It is only the product of the factor loading and the factor score that has a direct relationship to the sign of the voltage data. Consider that for a spatial PCA, a channel with a negative loading can vary from having a positive to negative voltage reading over the course of the epoch. By itself, a negative loading only signifies that it correlates inversely with channels having a positive loading (and vice versa). The “-“ and “+” options are only provided so that a user can have more control over which set of channels are selected.

Click on +/--. It will then give you a listing of all the factors, of which you can choose 12. For this example, just choose the first five (on the Mac, hold down the command key or the shift key to choose more than one).



It will now choose label each channel according to which factor had the highest loading, as long as it passed the threshold that you specified (0.6 in this case). If a factor has both positive and negative loadings that pass the threshold and you pressed +/-, it will determine which polarity had the highest absolute amplitude and mark only loadings with that sign (otherwise you could end up with a windowed measure with both positive and negative voltages which would then cancel out when averaged together).

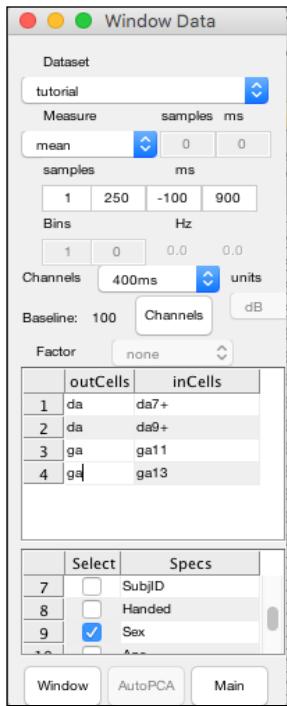


Once done, you can Save these channel groupings for later use and then press Done to go back to the Window Pane of the Main Window. For the tutorial, we'll just use the 400 ms channel grouping. As an alternative, the Channels pop-up menu also offers an “all” option which will simply window each and every EEG channel separately. This channel grouping cannot be edited.

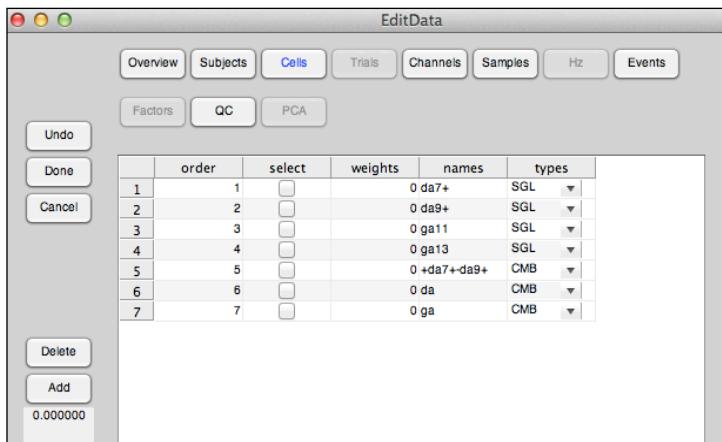
The Units setting is for frequency-domain data only and so will be grayed out at this point.

If you are windowing PCA data, then you will also need to specify the factor, otherwise it will be grayed out.

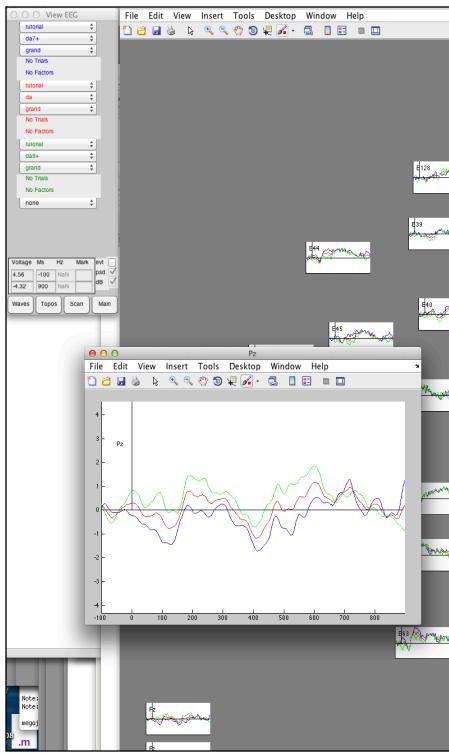
You will also need to specify the cells. It will list all the cells in the dataset (excluding any combined cells that you added). If you want any of them to be combined, rename the outcells accordingly. For this example, let's combine together the two ga cells and the two da cells. If you want to drop a cell, just delete the corresponding name in the outCells column (leaving it blank) and that cell will be left out. You can also freely change the order of the cells by retyping them. If you misname a cell, the function will let you know during the windowing process. Finally, you can specify if you want any of the subject specs (specifications) to be included in the output file. Let's click on Sex.



Once ready, click on the Window button. The windowing routine will check to see if the names of the output cells are different from those already in the dataset. If so, then it will add combined cells with those names to the dataset so that you can examine what the waveforms corresponding to the windowed measures looks like. Likewise, if the channel area names are different, then it will add new regional channels to the dataset so that you can again examine them.



If one goes back to the View Pane, the new regional channels show up in the lower left corner, right above the scale figure.

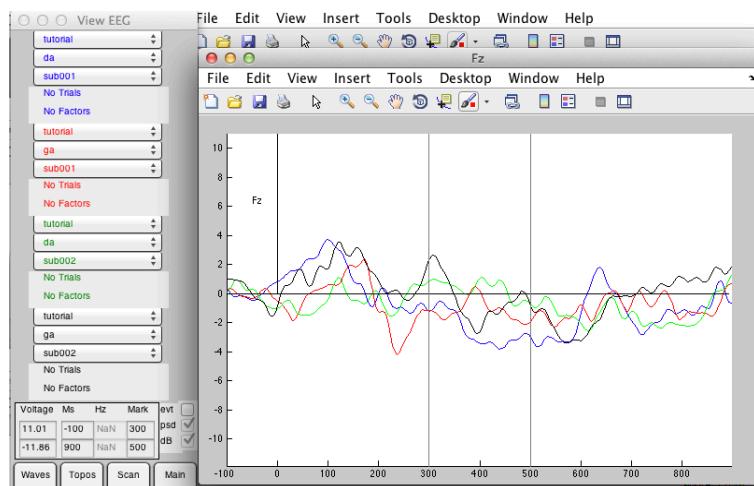


In this example, it can be seen how the red waveform (da) is the average of the blue (da7+) and green (da9+) waveforms.

Turning to the output of the windowing procedure, it generates a tab-delimited text file that can be examined in Excel or similar programs. After some header information it provides the windowed measures in a form suitable for direct use in a statistics program, along with the subjects specs requested (Sex) and the subject names. Note that “adds” (added summary data like grand averages and regional channels and combined cells) are excluded from windowing (and all other analyses like PCA and sample test) so they can be added to a dataset for inspection without concern that they might mess up the analyses.

	1	2	3	4	5	6
1	tutorial					
2	296-500 ms					
3	mean of voltage. Channels were collapsed together prior to taking the measure.					
4	400ms					
5						
6	da	da	ga	ga	Sex	
7	Fz	Pz	Fz	Pz	spec	
8	-2.475873	0.905479	-1.134573	1.713418	F	sub001
9	0.36906	-0.656594	-0.390182	0.563787	F	sub002
10	0.181165	-0.726983	0.211252	-0.198881	M	sub003
11	0.441973	0.557243	0.135876	-1.406489	F	sub005
12	-1.1636	-3.168842	-0.302876	1.122859	M	sub008
13	-0.532941	-0.960779	-2.631999	-2.704229	M	sub009
14	-1.853419	1.286228	-0.590128	0.338588	F	sub010
15	-0.108058	-0.517972	-0.389516	0.016304	M	sub011
16	-0.481424	-0.501067	2.0771	-0.746046	M	sub012
17	-3.956244	0.841574	-2.42548	0.778713	M	sub013
18						
19						
20						
21						
22						

As verification of the numbers, one can directly compare them with the waveforms. Set markers at 300 ms and 500 ms. See how the waveforms for subjects 1 and 2 correspond to the measures for da and ga in the Fz regional channel average. Note that there is a MATLAB bug that can prevent the baseline, onset, and marker lines from appearing if one clicks directly on the waveform lines. If this happens, just try again but clicking on the white background of the waveform box.



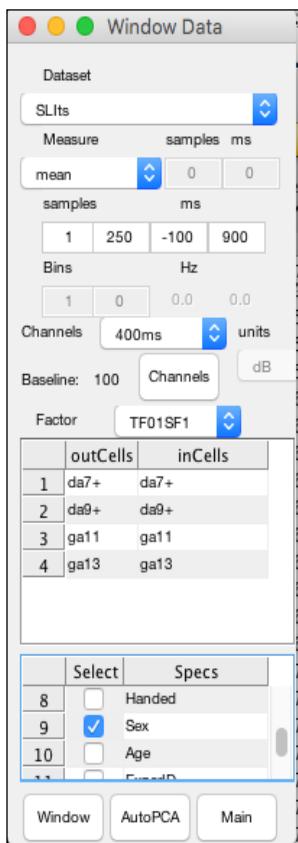
Windowing PCA Data

Analysis of PCA data is conducted in much the same way. The only difference is that one needs to specify the Factor in addition to everything else. Alternatively, if one is analyzing PCA data, one can click on the AutoPCA button and the Toolkit will run

through all the factors, choosing the peak channel and the peak time point for each factor. When using this option, the pane's settings for channel and for window will be ignored. It will only generate a windowed file for each factor whose size (variance accounted for) meets a minimum threshold (set in Preferences, .5% by default) to screen out factors that account for only small clumps of noise. This kind of selectivity is, in turn, helpful when controlling for multiple comparisons as one will not have to be as stringent as if one had included the noise factors. The command line will announce the number of factors that met the criterion.

The output of a PCA is expressed in voltages, corresponding to the voltage accounted for at the chosen time points and channels (the peak time point and channel if the AutoPCA option was chosen). The Toolkit has automatically converted the factor scores into microvolt scaling. One can use the View option to examine the actual factor waveforms, if desired, to see how they correspond.

In order to prepare for the next section, let's redo the cells so that we are not collapsing the ga and da cells together. For AutoPCA, the sample and the channel settings will be ignored so they do not need to be set. AutoPCA will generate one file per factor. You'll be asked to provide a root name for these files.



Now run the AutoPCA option. As can be seen in the resulting file for TF1SF2 (temporal factor 1/spatial factor 2), the peak channel is named as being electrode 32 and the peak

time point was at 300-304 ms (left to right side of the 4 ms long sample). The gender is also included as you had clicked on its checkbox.

	1	2	3	4	5	6	7
1	SLits						
2	300-304 ms						
3	One sample of voltage.						
4	autoPCA						
5	Factor: 2						
6	da7+	da9+	ga11	ga13	Sex		
7	E32	E32	E32	E32	spec		
8	-1.951025	-2.614924	-0.554821	1.586511	F	sub001	
9	-2.519095	-0.318395	-5.92596	0.97509	F	sub002	
10	-0.682695	0.099129	3.037135	3.731717	M	sub003	
11	-0.805911	3.937972	0.540423	-1.890388	F	sub005	
12	-1.574793	-3.132472	3.655785	0.146176	M	sub008	
13	-2.325759	2.402025	-3.072114	-3.156475	M	sub009	
14	-0.424296	-0.089724	0.091937	-2.015791	F	sub010	
15	-2.147196	2.046516	-0.760863	-3.989272	M	sub011	
16	2.861343	-3.314528	-1.658959	-3.068258	M	sub012	
17	-4.615623	0.740457	0.370576	-0.376168	M	sub013	
18							
19							

Robust ANOVA

About Robust Statistics

The robust statistics function generates inferential statistical tests comparable to ANOVAs that are designed to be more robust against violations of statistical assumptions. The statistical routines were translated from the SAS/IML routines posted by Lisa Lix (<http://www.usaskhealthdatalab.ca/sas-programs/>). The routines were fully described in the following publications (Keselman, Wilcox, & Lix, 2003; Keselman, Algina, Lix, Wilcox, & Deering, 2008). Also, the accompanying file "robust.pdf" is also included. A front-end has been added that automatically generates the necessary contrast matrices for omnibus ANOVAs and that organizes the results in an easy to read manner. Note that the routines take some time to run.

The effect size literature is rather confused at present (Lakens, 2013). The present code provides a Cohen's d type effect size wherein the effect size is presented as a proportion of the error standard deviation. With this type of statistic, the suggestion is that .2 is a small effect, .5 is a medium effect, and .8 is a large effect (Cohen, 1988). Of the many approaches for calculating the error standard deviation or standardizer (Keselman et al., 2008), the EP Toolkit utilizes the d* option (Equation 16). It also provides the 95% confidence interval for each effect.

The random aspect of bootstrapping results in some variability of the p-values. Based on some systematic testing (Dien, 2017), I'm recommending using 4999 simulation runs. The EP Toolkit runs this set of simulations eleven times to compute the standard deviation of the resulting p-values and reports the median one. If twice the standard

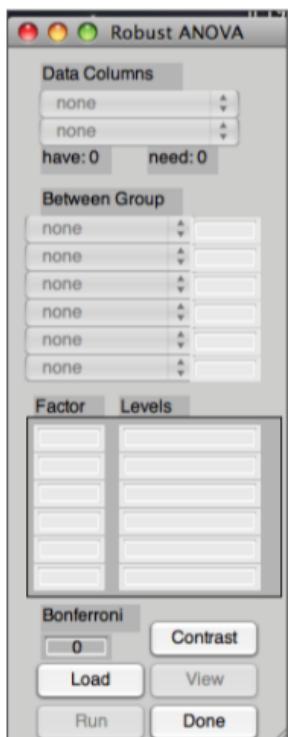
deviation of the p-values plus the median p-value exceeds the alpha threshold then a notation is given after the p-value that it was “(not confirmed)” and it should be treated as a borderline significant result. With smaller sample sizes some or all of the bootstrap runs may suffer from near-singularity, in which case they are dropped from the bootstrap computation. The EP Toolkit will report the %age of such runs on the next line, if they occur; if there is a sizable %age, then the results may be inaccurate.

Effect sizes and confidence intervals are also provided. Based on my exchanges with Lisa Lix (personal communication, Dec 2015), the contrast weights for the effect size calculations are normalized (i.e., the positive weights sum to 1 and the negative weights sum to -1). Also per her communications, effect sizes and confidence intervals are only available for between-group contrasts with one degree of freedom, pending further research. By convention, the effect sizes are always presented as an absolute value.

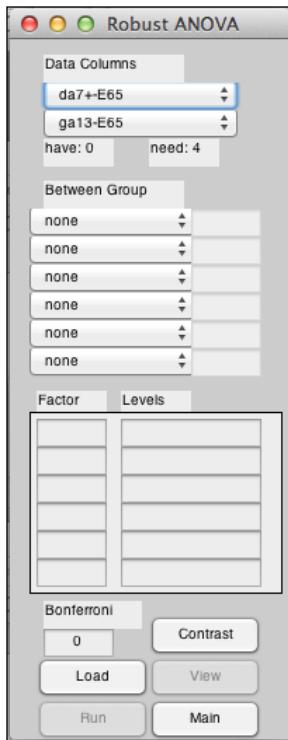
Psychophysiology has recommended the use of these robust statistics (specifically, statistical tests using non-pooled error terms) in its Guidelines to Authors. In brief, this robust statistic has the following three features: 1) trimmed means and winsorized variances/covariances to minimize effects of outliers; 2) bootstrapping routine to estimate the sample mean distribution rather than making the assumption that the data is normally distributed; 3) Welch-James approximate degrees of freedom statistic (resulting sometimes in decimal degrees of freedom) that avoids the assumption of homogeneous error variances/covariances. The latter also makes it unnecessary to use epsilon correction like G-G or H-F since sphericity is not assumed. In practice, it seems to generate results that are largely comparable to normal ANOVAs but that are more robust against violations of assumptions. For a direct comparison of ERP results against univariate and multivariate ANOVAs, see (Dien, Franklin, & May, 2006). A very approachable treatment of this robust statistic is available (Wilcox, 2001). A description of the issues involved in using conventional ANOVAs with ERP data is also available (Dien & Santuzzi, 2005). Further discussion of the issues in applying robust statistics to ERP data is also available (Dien, 2017).

General Procedures

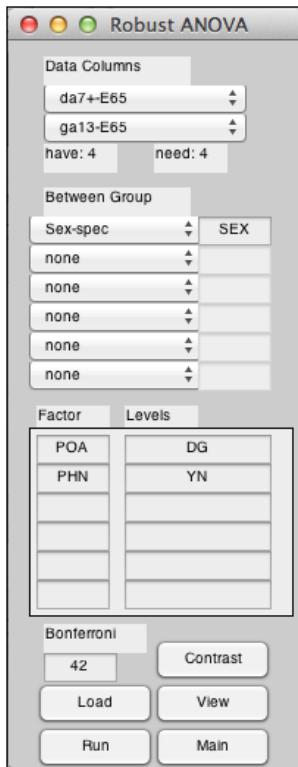
To use the robust statistics, first go back to the Main Pane of the Main Window and then click on the ANOVA button.



The ANOVA function is set up to assume that there will be a series of windowed files that have a similar structure (in terms of the cells). The first step is therefore to choose one of these files to serve as the template. Click on the Load button and then select one of the windowed factor files that you just generated with the AutoPCA option.



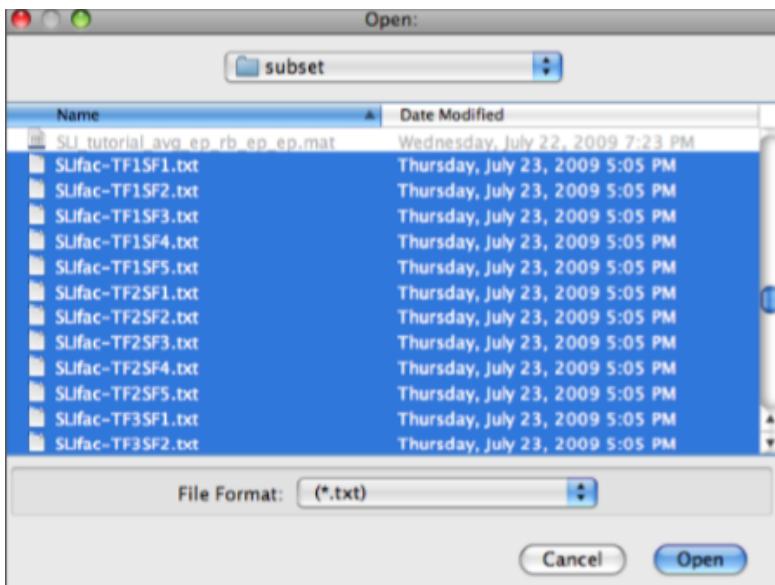
In this file, as you saw earlier, there were four data columns plus the Sex column. The first two menus are the leftmost and rightmost data columns to be analyzed. By default the Toolkit assumes that you will be analyzing all of the data columns but you can adjust the settings if you wish. Note that it indicates that 4 are needed. It means that the factor structure needs to accommodate four total within group cells. Enter in a POA (place of articulation) factor with a D and a G level and a PHN (phoneme) factor with a Y and an N level (yes a phoneme vs. no, not a phoneme). The lowest factor varies fastest as one goes across the columns. Note that the ANOVA factor name needs to have three letters and the ANOVA factor level names need to be one letter each. Also select Sex as a between group factor by selecting it and provide it with a three letter name, in this case "sex". Between group levels also need to be a single letter. If longer labels are provided, only the first letter will be used. It is therefore important that such labels start with different characters. Finally, enter the number of factors that met the variance criterion, 42, into the Bonferroni field (no need to use the Bonferroni if you are using a priori criteria to choose factors, such as their having the latency of prior interest). The pane should end up looking like the following figure:



You can verify that your factor structure mapped correctly onto the data by clicking on the View button.

	D Y da7+-E65	D N da9+-E65	G Y gall-E65	G N ga13-E65	Sex-spec
1	1.5127	4.1380	-2.0160	1.2298 F	
2	0.8658	-0.6245	3.1318	-5.0462 F	
3	0.4473	-0.1737	-0.1331	-0.7068 M	
4	2.2841	3.4818	2.4797	0.7257 F	
5	-3.6095	0.7649	0.1574	-0.4059 M	
6	2.5910	-1.0001	1.4467	3.3950 M	
7	2.8552	4.5168	8.5000	3.0694 F	
8	-2.7366	-2.4694	-3.1618	2.3809 M	
9	4.1334	-4.1966	-4.0864	-4.5724 M	
10	10.6428	12.0165	7.8742	8.6898 M	

Finally, click on the Run button. Enter in "SLIfacResults" as the ANOVA output name. Then click on the set of windowed files that you wish to run. In this case, we'll run all of them.



The Toolkit will start running a full ANOVA on the data (note, advanced options like ANCOVA and nested designs are not currently available). The output goes into an .html file with the name that you specified. The analysis will take some time, even on a fast computer. You can check on its progress by double-clicking on the html file. It should come up in a browser window that will show its current state. Click on the browser's refresh button periodically to follow its progress, if desired.

Some typical output follows. First it provides the basic parameters. Then each combination of between factor effects is presented. For each between factor effect combination, the within factor effects are provided. The section titled "NO BETWEEN EFFECTS" are the effects without interactions with the between group factors. The effect labeled " NO WITHIN EFFECTS" in the "sex MAIN EFFECT" is, conversely, the main effect of the between group effect of sex (thus having no interaction with the within group factors) and the "POA MAIN EFFECT" that follows it is the interaction with the sex main effect . Each effect lists the statistical test numbers (appropriate for directly copying into a manuscript). If the test reaches one-tailed significance (normally .10) then it is listed in green. If it reaches two-tailed significance but not Bonferroni corrected significance then it is listed in orange. If it reaches two-tailed significance even with the Bonferroni correction then it is listed in red. Finally, it lists the trimmed cell means underlying each of these tests.

```
#####
SLIfac-TF01SF2
WELCH-JAMES APPROXIMATE DF SOLUTION
TRIMMED MEANS & WINSORIZED VARIANCES
PERCENTAGE OF TRIMMING: 0.05
```

BOOTSTRAP CRITICAL VALUE FOR SINGLE TEST STATISTIC

NUMBER OF BOOTSTRAP SAMPLES: 4999

MEDIAN OF BOOTSTRAP RUNS: 11

STARTING SEED (multiplied by the run number): 1000

Number of subjects in each group: 4 6

Number trimmed from each end of the groups: 0 0

Uncorrected alpha criteria: 0.05

Corrected alpha criteria: 0.0011905

#####

NO BETWEEN EFFECTS

POA MAIN EFFECT

TWJt/c(1.0,7.9)=0.06, p=0.82, effect sizes only for between-group one degree of freedom contrasts.

Averaged Trimmed Cell Means:

D	G
+0.79	+0.60

PHN MAIN EFFECT

TWJt/c(1.0,5.7)=1.24, p=0.29, effect sizes only for between-group one degree of freedom contrasts.

Averaged Trimmed Cell Means:

Y	N
+0.50	+0.89

POA * PHN INTERACTION EFFECT

TWJt/c(1.0,7.2)=0.02, p=0.90, effect sizes only for between-group one degree of freedom contrasts.

Averaged Trimmed Cell Means:

DY	DN	GY	GN
+0.55	+1.02	+0.44	+0.77

#####

SEX MAIN EFFECT

NO WITHIN EFFECTS

TWJt/c(1.0,3.6)=2.47, p=0.20, d*=0.8, CI95=-0.04 to 2.55.

Averaged Trimmed Cell Means:

F +1.68

M -0.29

POA MAIN EFFECT

TWJt/c(1.0,7.9)=0.17, p=0.69, effect sizes only for between-group one degree of freedom contrasts.

Averaged Trimmed Cell Means:

D	G
F	+1.93+1.44
M	-0.36-0.23

PHN MAIN EFFECT

TWJt/c(1.0,5.7)=3.17, p=0.13, effect sizes only for between-group one degree of freedom contrasts.

Averaged Trimmed Cell Means:

Y	N
F	+1.17+2.20
M	-0.17-0.41

POA * PHN INTERACTION EFFECT

TWJt/c(1.0,7.2)=0.11, p=0.75, effect sizes only for between-group one degree of freedom contrasts.

Averaged Trimmed Cell Means:

DY	DN	GY	GN
F	+1.29+2.58+1.05+1.82		
M	-0.18-0.54-0.17-0.29		

A further feature of the Toolkit's output is that when an interaction is significant (uncorrected), the Toolkit will provide all the possible follow-up tests (i.e., for a three-way interaction, it will provide all the possible two-way interactions, where one level is held constant). If any of those are significant then the follow-up tests for that test are provided as well. In the following case, a sex by POA by PHN interaction is significant (uncorrected). It is known that this is an interaction with sex since it appears in the sex main effects section. It then follows up with all the possible two-way ANOVAs. It reports that the POA by PHN interaction is significant (uncorrected) for boys (level M of the sex factor). It then follows that up with the tests of the one-way ANOVAs for that interaction, the first of which is included below. Note that follow-up tests are in a smaller font to help set them off from the main tests. Also, follow-ups are indented deeper than the preceding level of results. Once the follow-ups to a test are completed then the results proceed to the next test. Devising a clearer format for these results tables is planned for a future release but it should suffice for now.

POA MAIN EFFECT

$T_{WJ}/c(1.0,7.9)=7.34$, $p=0.035$, effect sizes only for between-group one degree of freedom contrasts.

Averaged Trimmed Cell Means:

D	G
F	-0.07+0.05
M	+0.33-0.64

Holding level F of factor SEX constant.

#####
NO BETWEEN EFFECTS

POA MAIN EFFECT

$T_{WJ}/c(1.0,3.0)=0.21$, $p=0.62$, effect sizes only for between-group one degree of freedom contrasts.

Averaged Trimmed Cell Means:

D	G
-0.07+0.05	

#####
Holding level M of factor SEX constant.

#####
NO BETWEEN EFFECTS

POA MAIN EFFECT

$T_{WJ}/c(1.0,5.0)=10.09$, $p=0.078$, effect sizes only for between-group one degree of freedom contrasts.

Averaged Trimmed Cell Means:

D	G
+0.33-0.64	

#####
Holding level D of factor POA constant.

#####
SEX MAIN EFFECT

NO WITHIN EFFECTS

$T_{WJ}/c(1.0,7.4)=0.27$, $p=0.63$, $d^*=0.2$, $CI_{95}=-0.97$ to 0.68 .

Averaged Trimmed Cell Means:

F	-0.07
M	+0.33

#####
Holding level G of factor POA constant.

#####
SEX MAIN EFFECT

NO WITHIN EFFECTS

$T_{WJ}/c(1.0,7.4)=1.93$, $p=0.20$, $d^*=0.3$, $CI_{95}=-0.08$ to 1.21 .

Averaged Trimmed Cell Means:

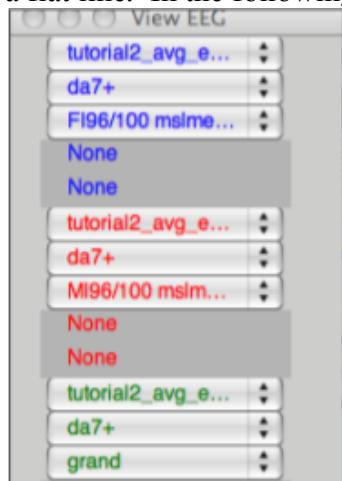
```
F +0.05  
M -0.64
```

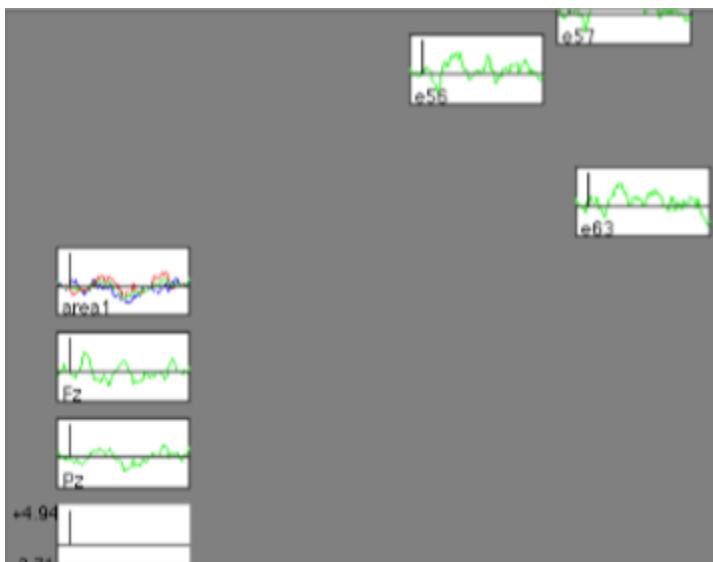
```
#####
```

Another feature of the Toolkit is that when an effect involves an electrode factor, it will provide the McCarthy and Wood (1985) vector test to determine if it does indeed indicate a change in the scalp topography rather than being artifact of the ANOVA model. For an explanation of this issue, see (Dien & Santuzzi, 2005). Such vector tests are set off from the rest of the results tables with italics.

Vector Scaling Test (is the scalp topography effect genuine?):
 $T_{WJr}/c(1.0,7.8)=295.24, p=0.00012$

The Toolkit will also examine whether the dataset name listed in the ANOVA text file is the same as any of the files in the current working set. If so, new combined subject conditions are added to the dataset with the waveforms (with the name of the corresponding between group cell) of each trimmed average of each cell in the ANOVA. They will only be added if the original dataset already has the corresponding cells and channels. Thus, it will now be possible to compare the ANOVA results to the exact waveforms that correspond to them. Bear in mind that this will only be done for channels (or regional channel averages) in the actual ANOVA so the other channels will be left as a flat line. In the following example, only area1 was in the ANOVA.





If needed, one can also perform follow-up contrasts. To do so, click on the Contrast button. From there one can specify up to five contrasts to be done. The numbers in the contrast should add up to zero. If no factors are desired of a certain type (no within or no between) then either put in all ones (the one exception to the add to zero rule) or leave them as zeroes and the Toolkit will change them to all ones.

	Cells	POA	PHN	Con1	Con2	Con3	Con4	Con5
1	da7-e7	D	Y	1	0	0	0	0
2	da9-e7	G	Y	-1	0	0	0	0
3	ga11-e7	D	N	0	0	0	0	0
4	ga13-e7	G	N	0	0	0	0	0

	sex	Con1	Con2	Con3	Con4	Con5
1	F	0	0	0	0	0
2	M	0	0	0	0	0

One then clicks on Run. As with the regular ANOVA, one is asked where to output the results and what ANOVA file to use. The results are rather barebones but functional:

SLIfac-TF1SF2
Contrast: 1
Within: 1 -1 0 0
Between: 1 1
 $T_{WJt}/c(1.0,5.3)=2.17, p=0.34$

Once finished with contrasts, click on Done to return to the Main Window.

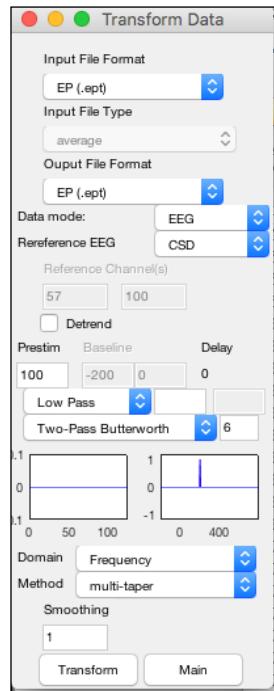
Behavioral Data

To use the ANOVA pane to analyze non-ERP data, use a spreadsheet program like Excel to have the following format:

- 1) The first line should contain the keyword "behavioral" without the quotation marks.
- 2) There should be four more lines whose contents will be ignored.
- 3) The next line is the column header line and should contain the names of the columns, separated by tabs. The Toolkit will ignore any additional columns that have no column name.
- 4) The next line will be ignored. Normally it would contain the channel region labels.
- 5) The remainder of the file should have the data with the values separated by tabs.

Spectral Analyses

The EP Toolkit can also be utilized to conduct spectral analyses. Since this is a new direction for the Toolkit, implementation is somewhat rudimentary. To do so requires a different stream of analysis. One can run the two streams of time-domain (ERP) and frequency-domain (FFT) analyses in parallel to obtain a more complete understanding of the data.



First set the appropriate Domain in the Transform function. “Frequency” means using Fourier analysis (with a Hanning filter) to measure oscillatory activity, such as alpha waves, using a function from FieldTrip. This option converts the data to frequency measures (complex amplitude), collapsing over the timepoints. One can also choose

whether the method used is multi-taper or the more traditional Hanning method to restrict the FFT to discrete one-second epochs. The FieldTrip team recommends the Hanning method when measuring frequencies below 30 Hz.

For continuous data, the data is divided into one-second epochs and each one serves as a separate “trial” that can be separately artifact-rejected or averaged together. The conventional Welch approach does so with each one second epoch overlapping half of the adjoining one second epochs so that the edges of the epochs are fully represented (the Hanning and multi-taper filters reduce the sensitivity of the FFT measures to zero towards the edges of the epoch to avoid edge artifacts and so the overlap approach allows those parts of the EEG recording to be fully utilized). However, taking this approach complicates artifact rejection so the EP Toolkit uses fully non-overlapping epochs. Whether this approach is optimal or not in this context will require further evaluation.

The Smoothing field is used to indicate the degree of smoothing in the spectral domain, with greater smoothing causing frequency peaks to become broader and more spread out.

The “Time-Frequency” option converts the data to time-frequency measures any of four different methods: Hanning, multi-taper, wavelet multiplication, and wavelet convolution. A half second window is used to generate the spectral measures and it is slide in 50 ms increments to produce a time course. The latency of each measure is attributed to the midpoint of the time window.

For the tutorial, choose the preprocessed session files (not the average file) and generate both “frequency” and “time-frequency” versions and using the CSD reference. This procedure will generate frequency versions of each session file (“_cs” for CSD frequency and “_cw” for CSD time-frequency). For each set, then run the average function to generate an average file for analysis. Note that the data in the tutorial files have already been low-pass filtered at 30Hz. Normally one would not do so for data intended for frequency analyses if one wished to inspect spectral analyses higher than or even in the vicinity of the 30Hz threshold.

As with the ERP data, read in the resulting averages and add a grand average using the Edit function. One can then view the results using the View function. One can view the data using four different common scaling: complex (cm), absolute amplitude (am), power (pw), and dB. Spectral results start in complex form with the real and imaginary parts coding for the cosine and sine components. Absolute amplitude converts these two parts into a single amplitude value. Power is the square of the amplitude.

Spectral measures follow a 1/f distribution, such that low frequencies have a high amplitude and higher frequencies have a much lower amplitude, which makes it harder to examine and gives the lower frequencies a disproportionate weight when averaging together frequency bands. The dB option helps address this problem by making the output log10-transformed (e.g., a value of 100 is 10^2 and the log10 of that is the exponent “2”, and then multiplied by a factor of 10 is “20”), evening out the frequency distribution.

By the original definition of dB, if the log transform is applied to the power values. The dB option will result in negative numbers for values less than one (e.g., the log10 of .1 is “-1” and the dB is “-10”).

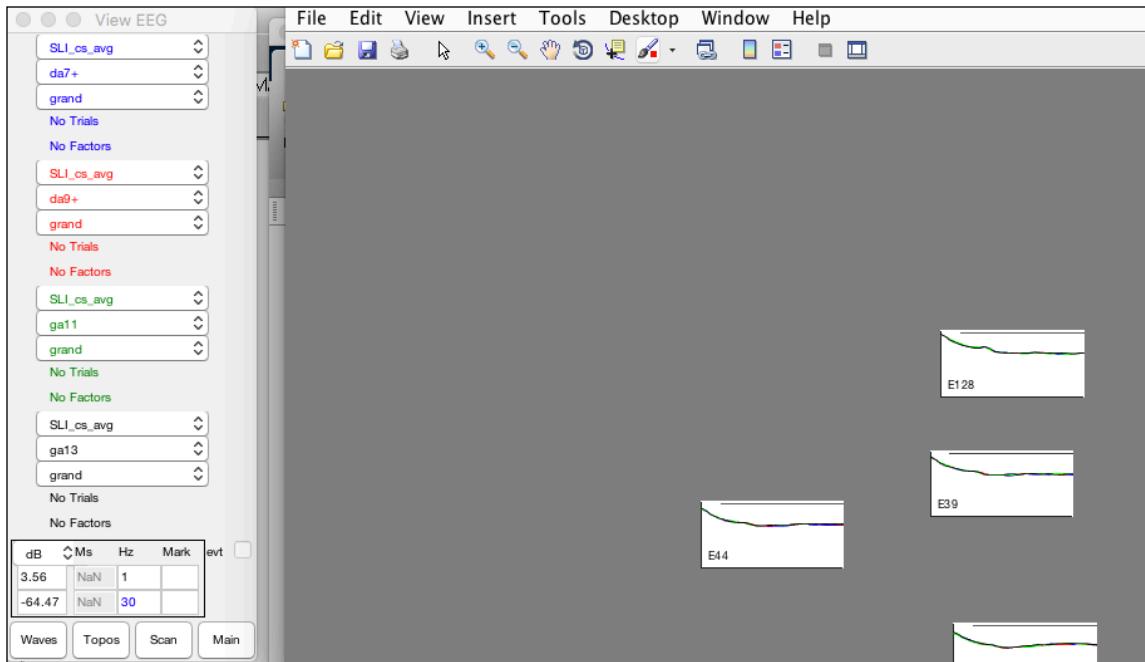
Internally, the EP Toolkit will represent the data in complex form to preserve the full information and will convert to the desired scaling upon output (whether as figures or for statistical analysis). Thus all the internal calculations are performed in complex scaling. There are two exceptions to this.

The first is that when data are added together (as in averaging or using the flexible segmenting or edit functions) there is a problem in that opposite signs can cancel out. While meaningful with voltages, when in complex scaling the signs just indicate phase differences. Thus two subjects might have equally large alpha waves but be 180 degrees out of synch. For most analyses this phase difference is irrelevant so when you add the data together you don't want them to cancel out. The EP Toolkit will therefore convert to absolute amplitude in such cases, although at the cost of losing the phase information. The exception to this is when adding channels together from the same segment. In this case the phase differences are meaningful as they reflect the bipolarity of the oscillating voltage fields (the two ends of the dipole will be 180 degrees out of phase) and preserving the sign information allows one to rereference the data. Thus, in this case the EP Toolkit will not convert the data to amplitude form.

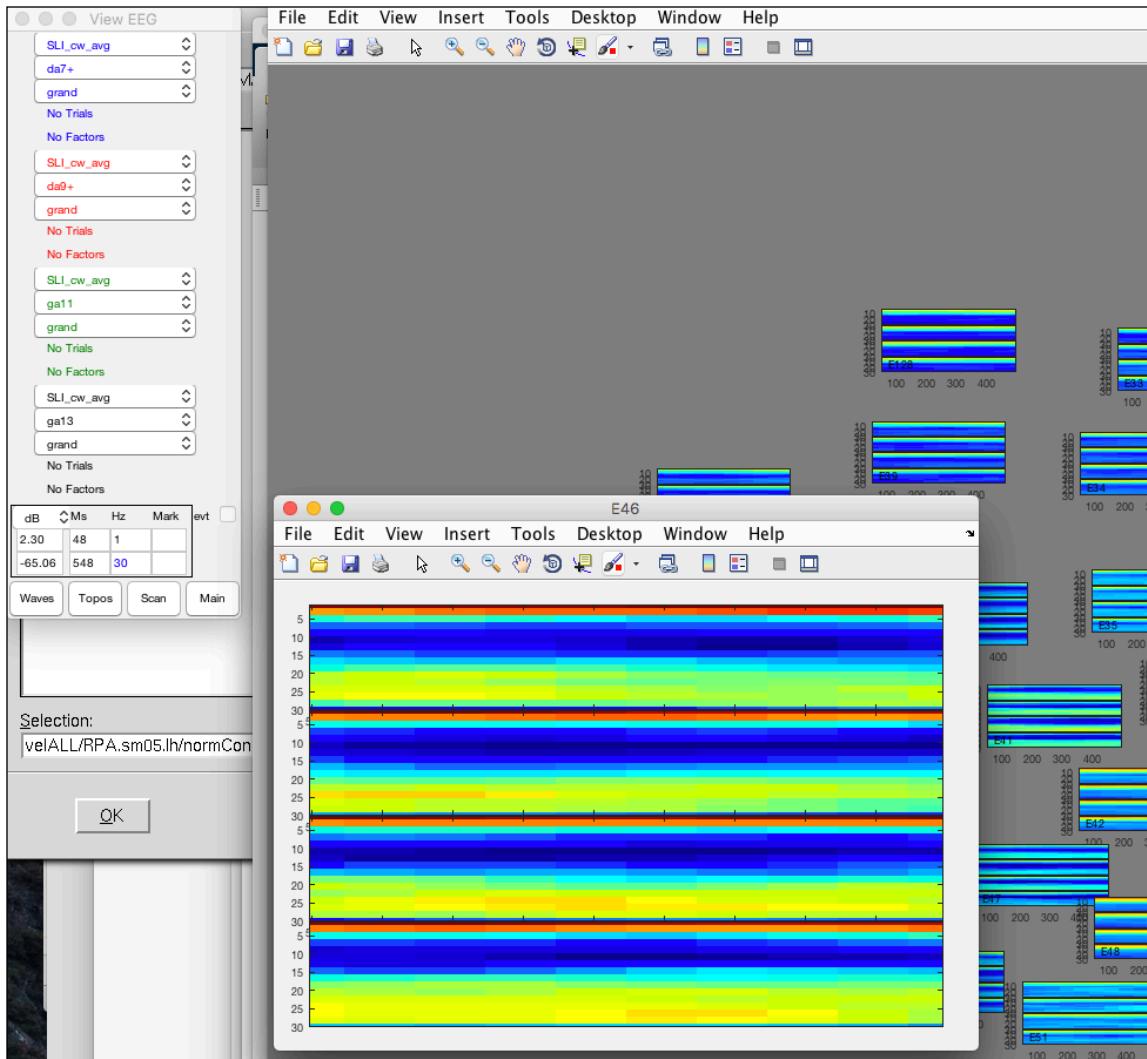
The second exception is that when windowing data preparatory to running ANOVAs, the scaling is applied to the individual numbers (cells and subjects) that are output to the text file. Thus, if one chose dB scaling, each number will be in dB and when the ANOVA is calculated, it will be performing these calculations on numbers that are already in dB form. The EP Toolkit does it this way to respect standard practice in the field.

Regardless of which of the four options is chosen, the EP Toolkit will always apply a spectral density correction to the output. The spectral density measure is intended to correct for a distortion produced by digitized as opposed to continuous data. This is computed by dividing by the size of the spectral bins, which in turn is determined by 1 over the epoch length in seconds (e.g., 1 Hz for 1 second epochs). By convention this is done in terms of power so amplitude measures are divided by the square root of the spectral bin size.

One can then view the results using the View function. For Frequency domain data, the results look much the same except that the lines represent the distribution across frequencies rather than across time. Since there will not be any frequencies above 30 Hz (due to the low-pass filtering), the frequency window should be set to 1-30 Hz.



For the Time-Frequency data, the display takes the form of color-coded charts in which the y-axis is the frequencies and the x-axis is the time. Each box is divided into the four different conditions, with Blue on top and Black on the bottom. If one sets the Hz control to only one frequency then the View function will present that one frequency bin as a line in the same manner as for time domain data. If one sets the time control to only one sample then the View function will present that one time point in the same manner as for frequency domain data. If you do both, the View function will not be able to present the data.

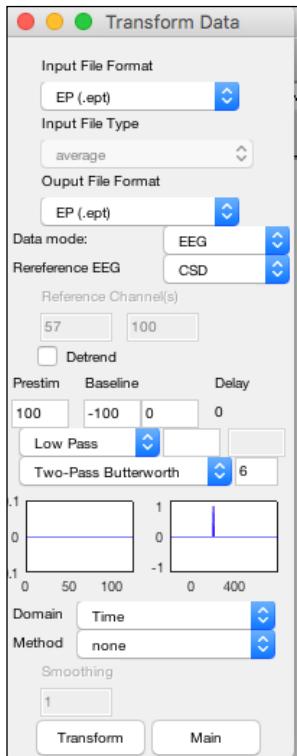


From here on out, the frequency data can be analyzed in a manner analogous to the voltage data.

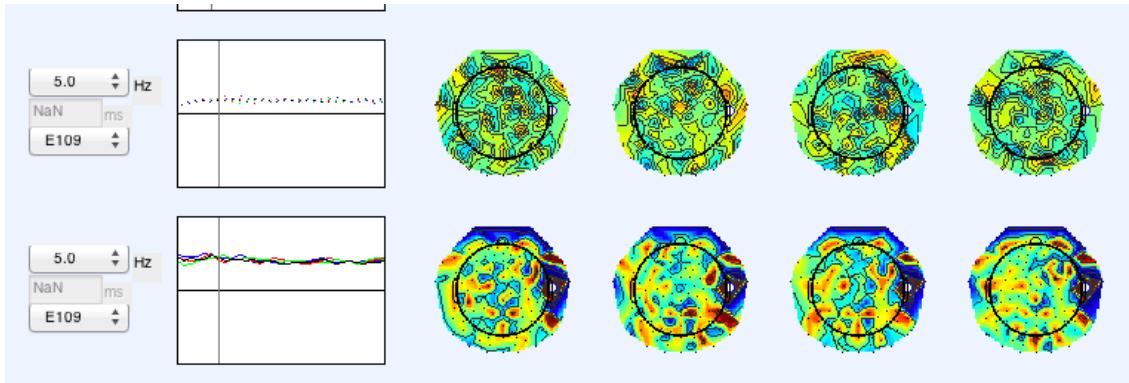
Finally, inter-channel spectral coherence may be calculated. In this procedure, what is essentially a correlation is computed between channels in each frequency band, producing a number between -1 (inversely synchronized) and 1 (synchronized). Since it needs to be computed across trials and results in a summary measure, the EP Toolkit treats it as a type of averaging. To invoke it, use the Average Data panel with the Procedure set on Frequency-Coherence. As with the spectral transforms, one can choose either the Hanning or the multi-taper options. The measure indicates the degree of synchrony between channels in a given spectral band, although it cannot distinguish between degree of synchrony and amplitude (vis a vis the background activity).

Before the inter-channel relationships are computed, a decision needs to be made about the reference scheme. Unlike with voltage data, the data can't be rereferenced after the averaging procedure. A recent paper (Thatcher, 2012) recommended against average

reference or CSD, although I didn't find its arguments to be especially persuasive; in fact, the review cited my own paper (Dien, 1998b) in a manner that did not reflect what it actually reported. However, this otherwise very informative review (Thatcher, 2012) also made a very well-taken caution that just like with ERPs, oscillating fields also have both positive and negative poles, so if two distant electrodes have high negative coherence or high phase-lock value, it may just reflect the measurement of two sides of the same field. I'll therefore use the CSD transform for this part of the tutorial as well as it helps avoid the opposite pole problem (in that it filters out activity distant from the electrode so it is likely to attenuate or eliminate the more distant pole). First run Transform on the _e session files, with rerefence set on CSD and the Domain set on Time (so no spectral transform yet) and a 100 ms baseline.



In the next figure, we can see the grand average of the coherence patterns. The dB and psd settings are irrelevant for coherence measures and so they were grayed out. Coherence measures yield both real and imaginary numbers and so two rows are needed to present the results. The real number row (with the solid waveform lines) shows that the channel with the overall highest real coherence numbers (mean of absolute coherence values with all other channels) in the 7 Hz theta band was E109. The pattern of coherences of this channel with all other channels is mapped by these topo maps. It shows what appears to be a cluster over the right temporal region.



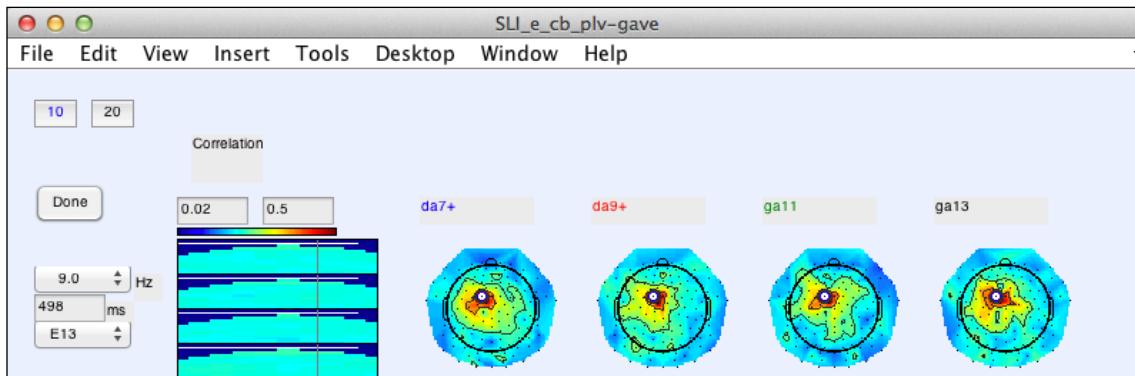
The imaginary row (with the dotted waveform lines) shows no clear pattern. While the imaginary component of coherence is often ignored, it is of interest because by definition it represents activity that is coherent with the index channel but at a fixed lag and hence is not due to the opposite side of the dipole (Nolte et al., 2004). The index channel itself will always have an imaginary value of zero, by definition.

When windowing coherence data, if there is one channel in an area then the correlations with all other channels will be used. The absolute value will be taken since otherwise they would tend to sum to zero (at least if average referenced). If a single common reference is used, it will be excluded since coherence with a flat channel produces a not-a-number result. If there is more than one channel in an area, then only the correlations between the channels in that area will be used. The absolute value will not be taken since the sign is meaningful and will not necessarily sum to zero. Separate files will be generated for the real and imaginary values.

Alternatively, one can use the coherence equivalent to the time-frequency transform, generating a time course of coherence changes. In this case the phase-lock statistic (Lachaux, Rodriguez, Martinerie, & Varela, 1999) is used as, unlike the coherence measure, it can help separate between amplitude and synchronization effects. As in the original report, the wavelet approach is used, although the Hilbert transform is often used, the results are the same if equivalent parameters are chosen (Bruns, 2004). The phase-lock statistic ranges from zero (no relation) to one (perfect phase synchrony). Also, unlike the coherence measure, phase-lock does not necessarily mean degree of synchrony but rather degree of stable phase-relationship. Thus, a phase-lock value would be a perfect one regardless of whether the oscillations at two electrodes are exactly in synchrony or exactly opposite to each other (180 degrees out of phase) as long as the phase relationship remains stable.

In the following figure, an area of phase-locked electrodes can be seen in the alpha band. The time-course clearly reveals the effects of approaching the edges of the epoch in blue, with the effects greater on low frequencies since they have a longer period. Otherwise the time-course does not clearly reflect the activity, perhaps because the EP Toolkit takes the mean across all the channel relationships with the index channel, thus watering it down. It may be that a better approach to presenting the activity needs to be

implemented. I will revisit this as I continue to work on this aspect of the EP Toolkit. Suggestions and requests are welcome.



References

- Blinn, K. A. (1955). Focal anterior temporal spikes from external rectus muscle. *Electroencephalogr Clin Neurophysiol*, 7(2), 299-302.

Some Publications Using The EP Toolkit

- Clementz, B. A., Brahmbhatt, S. B., McDowell, J. E., Brown, R., & Sweeney, J. A. (2007). When does the brain inform the eyes whether and where to move? An EEG study in humans. *Cereb Cortex, 17*(11), 2634-2643.
- Curran, T., & Dien, J. (2003). Differentiating amodal familiarity from modality-specific memory processes: An ERP study. *Psychophysiology, 40*, 979-988.
- Curran, T., DeBuse, C., Woroch, B., & Hirshman, E. (2006). Combined pharmacological and electrophysiological dissociation of familiarity and recollection. *J Neurosci, 26*(7), 1979-1985.
- Curran, T., & Friedman, W. J. (2004). ERP old/new effects at different retention intervals in recency discrimination tasks. *Brain Res Cogn Brain Res, 18*(2), 107-120.
- Dien, J. (1999). Differential lateralization of trait anxiety and trait fearfulness: evoked potential correlates. *Personality and Individual Differences, 26*(1), 333-356.
- Dien, J., Brian, E. S., Molfese, D. L., & Gold, B. T. (2013). Combined ERP/fMRI evidence for early word recognition effects in the posterior inferior temporal gyrus. *Cortex, 49*(9), 2307-2321.
- Dien, J., Franklin, M., & May, C. (2006). Is "blank" a suitable neutral prime for event-related potential experiments? *Brain and Language, 97*, 91-101.
- Dien, J., Frishkoff, G. A., Cerbone, A., & Tucker, D. M. (2003). Parametric analysis of event-related potentials in semantic comprehension: Evidence for parallel brain mechanisms. *Cognitive Brain Research, 15*, 137-153.
- Dien, J., Spencer, K. M., & Donchin, E. (2003). Localization of the event-related potential novelty response as defined by principal components analysis. *Cognitive Brain Research, 17*, 637-650.
- Dien, J., Spencer, K. M., & Donchin, E. (2004). Parsing the "Late Positive Complex": Mental chronometry and the ERP components that inhabit the neighborhood of the P300. *Psychophysiology, 41*(5), 665-678.
- Dien, J., Tucker, D. M., Potts, G., & Harry, A. (1997). Localization of auditory evoked potentials related to selective intermodal attention. *Journal of Cognitive Neuroscience, 9*(6), 799-823.
- Dien, J., Michelson, C. A., & Franklin, M. S. (2010). Separating the visual sentence N400

- effect from the P400 sequential expectancy effect: Cognitive and neuroanatomical implications. *Brain Res*, 1355, 126-140.
- Foti, D., & Hajcak, G. (2009). Depression and reduced sensitivity to non-rewards versus rewards: Evidence from event-related potentials. *Biological Psychology*, 81(1), 1-8.
- Foti, D., Hajcak, G., & Dien, J. (2009). Differentiating Neural Responses to Emotional Pictures: Evidence from Temporal-spatial PCA. *Psychophysiology*, 46(3), 521-530.
- Franklin, M. S., Dien, J., Neely, J. H., Waterson, L. D., & Huber, L. (2007). Semantic Priming Modulates the N400, N300, and N400RP. *Clinical Neurophysiology*, 118(5), 1053-1068.
- Frishkoff, G. A., Perfetti, C. A., & Westbury, C. (2009). ERP measures of partial semantic knowledge: left temporal indices of skill differences and lexical quality. *Biol Psychol*, 80(1), 130-147.
- Frishkoff, G. A., Perfetti, C. A., & Collins-Thompson, K. (in press). Lexical Quality in the Brain: ERP evidence for robust word learning from context. *Developmental Neuropsychology*.
- Hestvik, A., Maxfield, N., Schwartz, R. G., & Shafer, V. (2007). Brain responses to filled gaps. *Brain Lang*, 100(3), 301-316.
- Holroyd, C. B., Pakzad-Vaezi, K. L., & Krigolson, O. E. (2008). The feedback correct-related positivity: sensitivity of the event-related brain potential to unexpected positive feedback. *Psychophysiology*, 45(5), 688-697.
- Krigolson, O. E., & Holroyd, C. B. (2006). Evidence for hierarchical error processing in the human brain. *Neuroscience*, 137(1), 13-17.
- Krigolson, O. E., & Holroyd, C. B. (2007). Hierarchical error processing: different errors, different systems. *Brain Res*, 1155, 70-80.
- Krigolson, O. E., Holroyd, C. B., Van Gyn, G., & Heath, M. (2008). Electroencephalographic correlates of target and outcome errors. *Exp Brain Res*, 190(4), 401-411.
- Lister, J. J., Maxfield, N. D., & Pitt, G. J. (2007). Cortical evoked response to gaps in noise: within-channel and across-channel conditions. *Ear Hear*, 28(6), 862-878.
- Luu, P., Tucker, D. M., & Stripling, R. (2007). Neural mechanisms for learning actions in context. *Brain Res*, 1179, 89-105.
- Macnamara, A., Foti, D., & Hajcak, G. (2009). Tell me about it: neural activity elicited by emotional pictures and preceding descriptions. *Emotion*, 9(4), 531-543.

- Matsuda, I., Nittono, H., Hirota, A., Ogawa, T., & Takasawa, N. (2009). Event-related brain potentials during the standard autonomic-based concealed information test. *Int J Psychophysiol*, 74(1), 58-68.
- McDonald, C. G., Gabbay, F. H., Rietschel, J. C., & Duncan, C. C. (in press). Evidence for a new late positive ERP component in an attended novelty oddball task. *Psychophysiology*.
- Maxfield, N. D., Lyon, J. M., & Silliman, E. R. (2009). Disfluencies along the garden path: brain electrophysiological evidence of disrupted sentence processing. *Brain Lang*, 111(2), 86-100.
- O'Hare, A. J., & Dien, J. (2008). The Fear Survey Schedule as a measure of anxious arousal: Evidence from ERPs. *Neurosci Lett*, 441(3), 243-247.
- Fishman, I., Goldman, M. S., & Donchin, E. (2008). The P300 as an electrophysiological probe of alcohol expectancy. *Exp Clin Psychopharmacol*, 16(4), 341-356.
- Yang, C. L., Perfetti, C. A., & Schmalhofer, F. (2005). Less skilled comprehenders' ERPs show sluggish word-to-text integration processes. *Written Language & Literacy*, 8(2), 157-181.
- Yang, C. L., & Perfetti, C. A. (2006). Contextual constraints on the comprehension of relative clause sentences in Chinese: ERPs evidence. *Language and Linguistics*, 7(3), 697-730.
- Yang, C. L., Perfetti, C. A., & Schmalhofer, F. (2007). Event-related potential indicators of text integration across sentence boundaries. *J Exp Psychol Learn Mem Cogn*, 33(1), 55-89.

Bibliography

- Baguley, T. (2012). Calculating and graphing within-subject confidence intervals for ANOVA. *Behav Res Methods*, 44(1), 158-175.
- Blinn, K. A. (1955). Focal anterior temporal spikes from external rectus muscle. *Electroencephalogr Clin Neurophysiol*, 7(2), 299-302.
- Bostanov, V., & Kotchoubey, B. (2006). The t-CWT: a new ERP detection and quantification method based on the continuous wavelet transform and Student's t-statistics. *Clin Neurophysiol*, 117(12), 2627-2644.
- Bruns, A. (2004). Fourier-, Hilbert- and wavelet-based signal analysis: are they really different approaches? *J Neurosci Methods*, 137(2), 321-332.

- Cattell, R. B. (1966). The scree test for the number of factors. *Multivariate Behavioral Research*, 1, 245-276.
- Cattell, R. B., & Jaspers, J. (1967). A general plasmode (No. 3010-5-2) for factor analytic exercises and research. *Multivariate Behavioral Research Monographs*, 67-3, 1-212.
- Cohen, J. (1988). *Statistical power analysis for the behavioral sciences* (2nd ed.). New Jersey: Lawrence Erlbaum.
- Cousineau, D. (2005). Confidence intervals in within-subject designs: A simpler solution to Loftus and Masson's method. *Tutorials in quantitative methods for psychology*, 1, 42-45.
- De Vos, M., Vos, D. M., Riès, S., Vanderperren, K., Vanrumste, B., Alario, F. X., Van Huffel, S., Huffel, V. S., & Burle, B. (2010). Removal of muscle artifacts from EEG recordings of spoken language production. *Neuroinformatics*, 8(2), 135-150.
- Dien, J. (2006). Progressing towards a consensus on PCA of ERPs. *Clin Neurophysiol*, 117(3), 699-702; author reply 703.
- Dien, J. (2010). Evaluating Two-Step PCA Of ERP Data With Geomin, Infomax, Oblimin, Promax, And Varimax Rotations. *Psychophysiology*, 47(1), 170-183.
- Dien, J. (2012). Applying Principal Components Analysis to Event Related Potentials: A Tutorial. *Developmental Neuropsychology*, 37(6), 497-517.
- Dien, J. (2017). Best practices for repeated measures ANOVAs of ERP data: Reference, regional channels, and robust ANOVAs. *Int J Psychophysiol*, 111(1), 42-56.
- Dien, J. (1998a). Addressing misallocation of variance in principal components analysis of event-related potentials. *Brain Topography*, 11(1), 43-55.
- Dien, J. (1998b). Issues in the application of the average reference: Review, critiques, and recommendations. *Behavior Research Methods, Instruments, and Computers*, 30(1), 34-43.
- Dien, J., Beal, D. J., & Berg, P. (2005). Optimizing principal components analysis of event-related potential analysis: Matrix type, factor loading weighting, extraction, and rotations. *Clinical Neurophysiology*, 116(8), 1808-1825.
- Dien, J., Franklin, M., & May, C. (2006). Is “blank” a suitable neutral prime for event-related potential experiments? *Brain and Language*, 97, 91-101.
- Dien, J., & Frishkoff, G. A. (2005). Principal components analysis of event-related potential datasets. In T. Handy (Ed.), *Event-Related Potentials: A Methods Handbook* (pp. 189-208). Cambridge, Mass: MIT Press.

- Dien, J., & Santuzzi, A. M. (2005). Application of repeated measures ANOVA to high-density ERP datasets: A review and tutorial. In T. Handy (Ed.), *Event-Related Potentials: A Methods Handbook* (pp. 57-82). Cambridge, Mass: MIT Press.
- Dien, J., Spencer, K. M., & Donchin, E. (2003). Localization of the event-related potential novelty response as defined by principal components analysis. *Cognitive Brain Research*, 17, 637-650.
- Dien, J., Spencer, K. M., & Donchin, E. (2004). Parsing the “Late Positive Complex”: Mental chronometry and the ERP components that inhabit the neighborhood of the P300. *Psychophysiology*, 41(5), 665-678.
- Foti, D., Weinberg, A., Dien, J., & Hajcak, G. (2011). Event-related potential activity in the basal ganglia differentiates rewards from nonrewards: temporospatial principal components analysis and source localization of the feedback negativity. *Hum Brain Mapp*, 32(12), 2207-2216.
- Franz, V. H., & Loftus, G. R. (2012). Standard errors and confidence intervals in within-subjects designs: generalizing Loftus and Masson (1994) and avoiding the biases of alternative accounts. *Psychon Bull Rev*, 19(3), 395-404.
- Gorsuch, R. L. (1983). *Factor analysis* (2nd ed.). Hillsdale, NJ: Lawrence Erlbaum Associates.
- Horn, J. L. (1965). A rationale and test for the number of factors in factor analysis. *Psychometrika*, 30, 179-185.
- Junghöfer, M., Elbert, T., Tucker, D. M., & Braun, C. (1999). The polar average reference effect: A bias in estimating the head surface integral in EEG recording. *Clinical Neurophysiology*, 110(6), 1149-1155.
- Kayser, J., & Tenke, C. E. (2003). Optimizing PCA methodology for ERP component identification and measurement: Theoretical rationale and empirical evaluation. *Clinical Neurophysiology*, 114(12), 2307-2325.
- Keselman, H. J., Wilcox, R. R., & Lix, L. M. (2003). A generally robust approach to hypothesis testing in independent and correlated groups designs. *Psychophysiology*, 40, 586-596.
- Keselman, H. J., Algina, J., Lix, L. M., Wilcox, R. R., & Deering, K. N. (2008). A generally robust approach for testing hypotheses and setting confidence intervals for effect sizes. *Psychological Methods*, 13(2), 110.
- Lachaux, J. P., Rodriguez, E., Martinerie, J., & Varela, F. J. (1999). Measuring phase synchrony in brain signals. *Hum Brain Mapp*, 8(4), 194-208.

- Lakens, D. (2013). Calculating and reporting effect sizes to facilitate cumulative science: a practical primer for t-tests and ANOVAs. *Front Psychol*, 4, 863.
- Lehmann, D., & Skrandies, W. (1984). Spatial analysis of evoked potentials in man - a review. *Progress in Neurobiology*, 23, 227-250.
- Leonowicz, Z., Karvanen, J., & Shishkin, S. L. (2005). Trimmed estimators for robust averaging of event-related potentials. *J Neurosci Methods*, 142(1), 17-26.
- Lins, O. G., Picton, T. W., Berg, P., & Scherg, M. (1993). Ocular artifacts in EEG and event-related potentials. I: Scalp topography. *Brain Topogr*, 6(1), 51-63.
- Liu, Z., de Zwart, J. A., van Gelderen, P., Kuo, L. W., & Duyn, J. H. (2012). Statistical feature extraction for artifact removal from concurrent fMRI-EEG recordings. *Neuroimage*, 59(3), 2073-2087.
- Luck, S. J. (2005). *An Introduction to the Event-Related Potential Technique*. Cambridge, Mass: MIT Press.
- Luck, S. J. (2014). *An introduction to the event-related potential technique* (2nd ed.). MIT press.
- Miller, J., Patterson, T., & Ulrich, R. (1998). Jackknife-based method for measuring LRP onset latency differences. *Psychophysiology*, 35(1), 99-115.
- Morey, R. D. (2008). Confidence intervals from normalized data: A correction to Cousineau (2005). *reason*, 4(2), 61-64.
- Niazy, R. K., Beckmann, C. F., Iannetti, G. D., Brady, J. M., & Smith, S. M. (2005). Removal of FMRI environment artifacts from EEG data using optimal basis sets. *Neuroimage*, 28(3), 720-737.
- Nolte, G., Bai, O., Wheaton, L., Mari, Z., Vorbach, S., & Hallett, M. (2004). Identifying true brain interaction from EEG data using the imaginary part of coherency. *Clin Neurophysiol*, 115(10), 2292-2307.
- Payton, M. E., Greenstone, M. H., & Schenker, N. (2003). Overlapping confidence intervals or standard error intervals: what do they mean in terms of statistical significance. *Journal of Insect Science*, 3(1), 34.
- Perrin, F., Pernier, J., Bertrand, D., & Echallier, J. F. (1989). Spherical splines for scalp potential and current density mapping. *Electroencephalography and Clinical Neurophysiology*, 72, 184-0187.
- Schenker, N., & Gentleman, J. F. (2001). On judging the significance of differences by examining the overlap between confidence intervals. *The American Statistician*, 55(3), 182-186.

- Schimmel, H. (1967). The (+/-) reference: Accuracy of estimated mean components in average response studies. *Science*, 157, 92-94.
- Simons, R. F., Graham, F. K., Miles, M. A., & Chen, X. (2001). On the relationship of P3a and the Novelty-P3. *Biological Psychology*, 56, 207-218.
- Spencer, K. M., Dien, J., & Donchin, E. (1999). A componential analysis of the ERP elicited by novel events using a dense electrode array. *Psychophysiology*, 36, 409-414.
- Spencer, K. M., Dien, J., & Donchin, E. (2001). Spatiotemporal Analysis of the Late ERP Responses to Deviant Stimuli. *Psychophysiology*, 38(2), 343-358.
- Tabachnick, B. G., & Fidell, L. S. (1989). *Using multivariate statistics*. New York: Harper & Row, Publishers.
- Thatcher, R. W. (2012). Coherence, phase differences, phase shift, and phase lock in EEG/ERP analyses. *Dev Neuropsychol*, 37(6), 476-496.
- Wilcox, R. R. (2001). *Fundamentals of modern statistical methods: Substantially improving power and accuracy*. New York: Springer-Verlag.
- Woody, C. D. (1967). Characterization of an adaptive filter for the analysis of variable latency neuroelectric signals. *Medical and Biological Engineering*, 5, 539-553.
- Yuval-Greenberg, S., Tomer, O., Keren, A. S., Nelken, I., & Deouell, L. Y. (2008). Transient induced gamma-band response in EEG as a manifestation of miniature saccades. *Neuron*, 58(3), 429-441.