Breathe Easy EDA User Guide

1) Introduction

The BEEDA toolbox is designed for efficiently eliminating EDA respiration artifacts and analyzing EDA data. BEEDA's streamlined artifact removal interface allows users to quickly identify and clean EDA data, expediting EDA analysis without compromising analysis integrity. Aditionally, BEEDA's integrated EDA analysis functionality allows users to seamlessly analyze cleaned EDA data within the toolbox.

1a) System requirements

- Matlab 2014b or newer
- Matlab Siginal Processing Toolbox

1b) Installing BEEDA

step 1: Download and unzip the compressed BreatheEasyEDA.zip file.
step 2: Add the extracted BreatheEasyEDA folder to the Matlab Path. Adding subdirectories of the main folder is not necessary.

2) Data files

BEEDA requires two files from your EDA experiment, a data file and a corresponding event file. The experiment data file contains the raw data collected during your experiment, and the event file contains information about your experiment's trials and time-course. BEEDA accepts data in Biolab formatted .txt files, or data in generic .csv format. The following sections (2a) & (2b) describe how to obtain these files easily through Biolab, or alternately how to format them yourself in .csv.

2a) Raw data files

----How to obtain from Biolab

BioLab can export your experiment data into the properly formatted .txt file through the following steps:

Step 1:

Open BioLab, then use the BioLab dropdown file menu to open your experiment's .mw file.

Step 2:

In the channels tab menu, select GSC (EDA data) and Transducer (respiration data). Leave all other channels unselected.

Step 3:

Click the "View" button (large green button located at the bottom)

Step 4:

Click the "Save all text" button (powder blue button located at top left)

Step 5:

Save your raw data .txt file with the prompt

Raw data .txt files should take the format:

Sample Rate:	1000.000000		
Time (s)	GSC_Ch4	Transducer_Ch9	synch summary
0.000000	0.000001	0.000315	0.639954
0.001000	0.000005	0.001562	0.639954
0.002000	0.000013	0.004016	0.639954

Where the first column is sample time, the second column is EDA data, and the third column is respiration data. These three columns are the only necessary data columns for BEEDA, and must be in this order. In the example shown, the fourth column corresponds to your experiment event codes. BioLab will export your experiment event code data in the last column position by default, although this data will not be used by BEEDA (or interfere with BEEDA, so long as the event code data is not in columns 1 through 3). Additionally, BioLab will export sample time data in the first column by default.

----How to create your own .csv raw data file

Create your own .csv data file with three columns. The first column is sample time (starting at 0), the second column is EDA data, and the third column is respiration data. The .csv file does not contain header labels (column labels). If you want to use BEEDA without respiration data, simply populate the third column with zeros.

2b) Event files

----How to obtain from Biolab

A file containing your experiment's time-course information should be created as an "event.txt" file automatically after data collection. This file should take the format:

Event Type	Name	Date	Time
rising trigger	acquisition started	07/23/2015	09:05:48.453 AM
sync summary event # 1	StartRecording	07/23/2015	09:05:49.504 AM
sync summary event # 5	FixationOnset	07/23/2015	09:07:44.304 AM
sync summary event # 6	StartPreClipBase	07/23/2015	09:07:51.875 AM
sync summary event # 53		07/23/2015	09:07:56.936 AM
sync summary event # 5	FixationOnset	07/23/2015	09:08:00.730 AM
sync summary event # 6	StartPreClipBase	07/23/2015	09:08:06.282 AM
sync summary event # 51		07/23/2015	09:08:11.340 AM
sync summary event # 5	FixationOnset	07/23/2015	09:08:15.034 AM
sync summary event # 6	StartPreClipBase	07/23/2015	09:08:24.587 AM
sync summary event # 52		07/23/2015	09:08:29.651 AM
sync summary event # 2	StartBaseline3min	07/23/2015	09:09:26.655 AM
sync summary event # 3	StartBaseline2min	07/23/2015	09:12:27.409 AM
sync summary event # 4	EndBaseline2min	07/23/2015	09:14:27.894 AM
sync summary event # 64		07/23/2015	09:15:05.879 AM

BioLab generates this file in the correct formatting automatically. If necessary, BioLab may also be able to generate this file through the "synchronous events" tab. However, creating this file manually should not be necessary as BioLab automatically generates this file after your experiment's data collection finishes.

----How to create your own .csv event file

Create your own .csv data file with two columns. The first column is event name, the second column is event time. The .csv file does not contain header labels (column labels). The file should look like:

acquisition started	07/23/2015 12:05:48 AM
StartRecording	07/23/2015 12:05:49 AM
FixationOnset	07/23/2015 12:07:44 AM
StartPreClipBase	07/23/2015 12:07:52 AM

3) Loading an experiment into BEEDA

Opening BEEDA and loading your experiment are always the first two steps when running the toolbox. This process is explained in (3a) & (3b).

3a) Opening BEEDA

In your Matlab command window, type the following text and hit enter:

BreatheEasyEDA

This will launch the BEEDA toolbox and immediately prompt you to load your experiment's data (see 3b).

3b) Loading experiment data

Step 1:

When loading an experiment's data for the first time, select either "Load BioPac .txt files" or "Load generic .csv files" button.

Step2:

A prompt titled "Select .txt data file" or "Select .csv data file" will open, select your data file here.

Step3:

A second prompt titled "Select event .txt file" or "Select event .csv file" will open, select your event file here. After selecting this file, the "Load BioPac .txt files"/"Load generic .csv files" button will inactivate and display "Loading… Please wait". Loading the raw data files may take a few minutes on slower computers.

Step4:

A third prompt titled "Save BEEDA .mat file" will open, save your experiment as a BEEDA toolbox .mat file. From this point forward, you can save/load your experiment as a BEEDA toolbox .mat file.

After saving your BEEDA .mat file, you should see the following lines printed to your Matlab command window:
reading in data file
reading in event file
reformatting and saving EDA experiment data

4) Setting basic analysis parameters

After loading your experiment .txt files and saving the experiment's new .mat file, the next step is setting basic parameters for your analysis. Importantly, these basic parameters may not be changed at a later point in the same analysis! After setting these parameters, they are permanently fixed for this BEEDA analysis (even after saving and reloading the .mat file). In order to use new basic parameters for your experiment, you must re-load the experiment .txt files and start from scratch.

Note: Future versions of this toolbox may include greater flexibility with regard to changing basic parameters during an analysis.

4a) Downsampling

A downsampling prompt will open after (3b) is completed. This prompt will display your experiment's original sampling rate, and you may choose to down sample your data here. Downsampling will decrease your experiment file sizes and potentially improve performance on slower computers.

If you choose to downsample your data, enter your downsampling factor into the subsequent prompt. Your downsampling factor is:

[Original sampling rate(Hz)] / [downsampling factor] = [downsampled rate(Hz)]

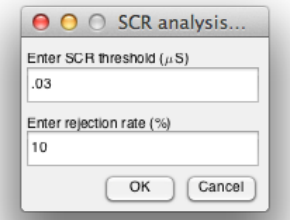
For instance, if your experiment was originally sampled at 1000Hz and you wish to downsample your data to 20Hz, your downsampling factor should be entered as 50.

[1000(Hz)] / [50] = [20Hz]

After entering your downsampling factor, your experiment's new sampling rate will print to the Matlab command window and briefly display in a pop-up window.

4b) SCR parameters

After choosing your downsampling parameters (4a), the next step is entering your SCR parameters. The SCR parameter prompt will appear as:

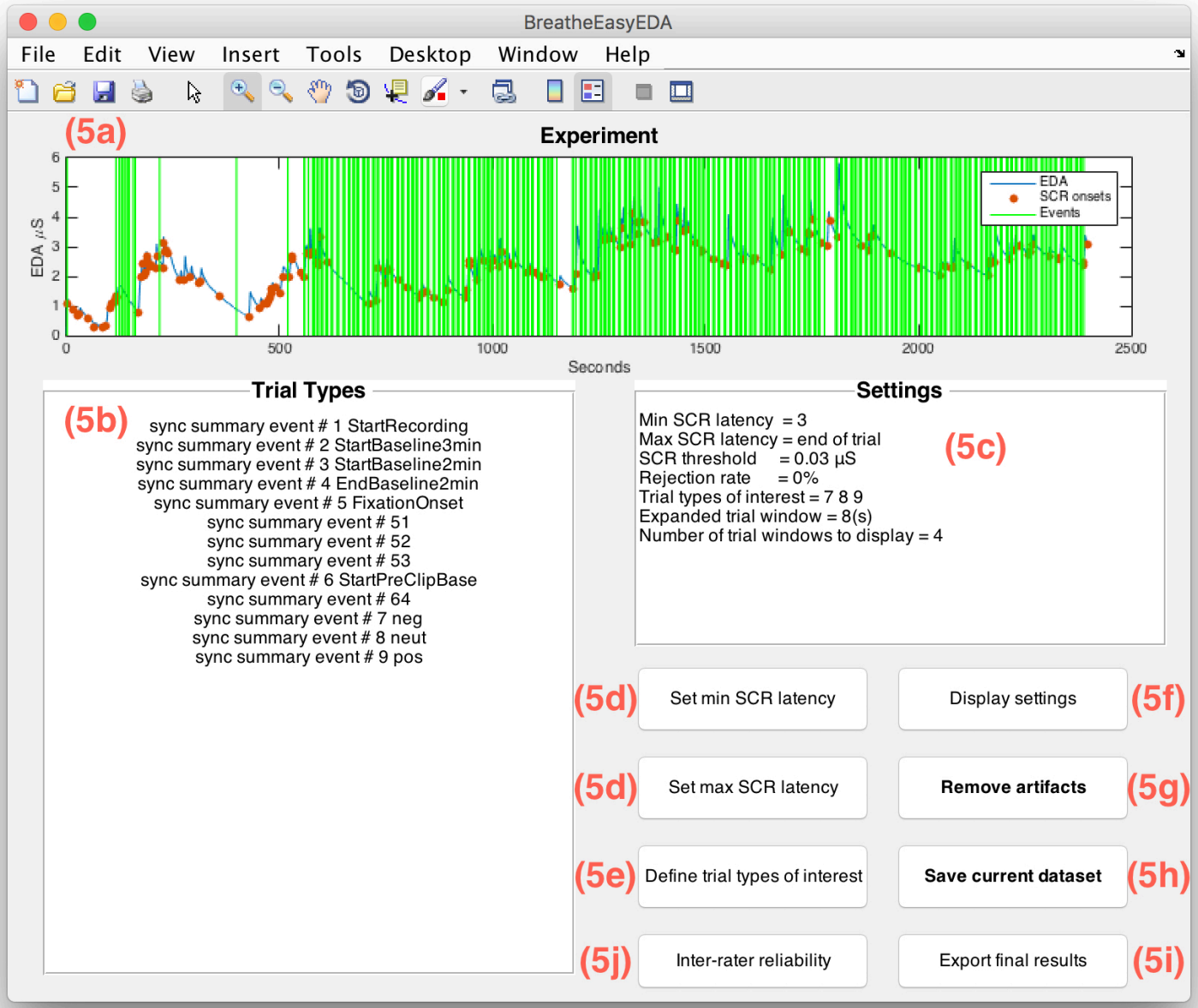


The top field specifies the SCR amplitude threshold, BEEDA will ignore EDA responses below this amplitude threshold. The default value is .03 microsiemens.

The bottom field specifies SCR rejection rate. If a rejection rate greater than 0 is entered, within each trial, SCRs with amplitudes below x% of the trial's largest amplitude are ignored. For example, if the rejection rate is set at 10% and a trial's largest SCR amplitude is 4μS, SCRs below .4 μS will be ignored in that trial. The default value is 10%, and entering 0% disables rejection rate exclusion.

5) Main Menu

The main menu will launch after an experiment's data is loaded and basic analysis parameters are set. This menu provides a basic visual summary of your experiment, trial information, analysis & display settings, in addition to the options for starting artifact removal, saving, and exporting final results.



5a) Experiment summary

A visual summary of your experiment is located at the top of the Main Menu. Here the X axis is time from the start of the experiment (in seconds), and the Y axis is EDA (in microsiemens). EDA data is shown as a blue line, and above-threshold SCR onsets (troughs) are shown as red dots. Vertical green lines mark the start of every event found in the experiment's event .txt file. This visual summary provides a sanity-check to ensure experiments were properly loaded.

5b) Trial type information

A list of all event types found in the experiment event .txt file is located on the main menu's left hand side. Each event listed will take the format:

sync summary event # 1 StartRecording

Where "sync summary event" is BioLab's label for an experiment event, "#1" indicates the event type number, and "StartRecording" is an event label previously defined by the experiment creator (not in BEEDA). You can determine the information relevant to your experimental trials of interest here.

5c) Settings

The settings display is located below the visual experiment summary on the right hand side of the main menu. This shows your toolbox display settings and analysis parameters. These settings will automatically start at BEEDA defaults when beginning a new analysis, except for "Trial types of interest" which does not have a default value.

Settings & parameter information:

Min SCR latency: Time after the start of a trial (in seconds) when SCRs will be considered. For instance, if Min SCR latency is set to 3, above-threshold SCRs with onsets starting sooner than 3 seconds after the start of a trial will be ignored (only onsets occurring after T+3(s) will be considered). Additionally, SCL during this time will be ignored during analysis. Default value is 3 seconds, this setting can be specified in the "Min SCR latency" main menu button.

Max SCR latency: Time after the start of a trial (in seconds) when SCRs will be ignored. For instance, if max SCR latency is set to 15, above-threshold SCRs with onsets starting later than 15 seconds after the start of a trial will be ignored (only onsets occurring before T+15(s) will be considered). Additionally, SCL during this time will be ignored during analysis. Default value is "end of trial", this setting can be specified in the "Max SCR latency" main menu button.

SCR threshold: Set during (4b), cannot be changed after an analysis has started. SCR amplitude threshold, BEEDA will ignore EDA responses below this amplitude threshold. The default value is .03 microsiemens.

Rejection rate: Set during (4b), cannot be changed after an analysis has started. When rejection rates greater than 0 are specified, within each trial, SCRs with amplitudes below x% of the trial's largest amplitude are ignored. For example, if the rejection rate is set at 10% and a trial's largest SCR amplitude is 4μS, SCRs below .4 μS will be ignored in that trial. The default value is 10%, and entering 0% disables rejection rate exclusion. NOTE: if you change the trial-types of interest during your analysis (i.e. switch the trials you're analyzing), the rejection rate threshold will change as well. This is because the threshold calculation only uses analysis-relevant data (i.e. from trials of interest). Redefining the analysis-relevant data will correspondingly change the rejection rate threshold.

Trial types of interest: The event type numbers for trials/events that will be processed in artifact removal and EDA analysis. Only trials specified here can be loaded in the artifact removal interface or analyzed.

This option can be specified in the “Define trial types of interest” main menu button. Trial types of interest should be entered as space-separated event type numbers, for instance:

7 8 9

Event type numbers for all trial types can be found in the Trial Types display (5b), and must be defined before artifact removal or analysis can begin. If this setting has not been specified before artifact removal or analysis is attempted, the following error will print to the command window:

ERROR: Trials of interest must be defined first

Defining trial types of interest and re-attempting artifact or analysis will solve this error.

While not strictly advised, you may respecify the trial-types of interest during your analysis. The toolbox will handle this gracefully, and any previous actions (artifact editing, etc) will be stored and can be recovered by resetting the trial-types of interest again. Please note, rejection-rate thresholds will also change if you respecify the trial-types of interest (see rejection rate section above).

Expanded trial window: The additional time displayed before and after a trial begins/ends in the artifact removal interface (in seconds). For instance, setting expanded trial window to 5(s) will display the 5(s) before every trial and the 5(s) after every trial. The default value is 3, this setting can be specified in the “Display settings” main menu button.

Number of trial windows to display: The number of trials simultaneously displayed in the artifact removal interface. Default value is 4, this setting can be specified in the “Display settings” main menu button.

5d) Set min/max SCR latency

This button allows you to specify the “Min SCR latency” and “Max SCR latency“ settings. See (5c) for more information about these settings.

5e) Define trial types of interest

This button allows you to specify the “Trial types of interest”. See (5c) for more information about this setting.

5f) Display settings

This button allows you to specify the “expanded trial window” and “number of trial windows to display “settings. See (5c) for more information about these settings.

5g) Remove artifacts

Start the artifact removal interface.

5h) Save current dataset

Save your current analysis session as a BEEDA toolbox .mat file.

5i) Export final results

Selecting this button will analyze the current experiment's EDA data and export EDA analysis statistics in addition to trial-wise artifact removal information. This analysis will not consider any EDA data removed through the artifact removal interface.

Exporting final results will also clear all data from the current BEEDA toolbox session after competition. After selecting this option, a prompt will always ask if you would like to continue exporting your results or return to the main menu (where you can save your current session). Select "No" to return to the main menu, "Yes" to continue exporting final results. Saving your current BEEDA session before exporting final results will prevent data loss, and is highly recommended. See (8) for more information on this function.

Common Errors (printed to command window):

1) ERROR: No trials of interest defined

This error occurs when attempting to export final results before defining trials of interest (see (5c)). Simply define your trials of interest and try exporting again.

2) WARNING: BEEDA artifact removal not used with this dataset

This message is not strictly an error message, as exporting will continue without issue even when this message is displayed. This warning message indicates that the BEEDA artifact removal interface was never initiated for the current experiment.

5j) Inter-rater reliability

Selecting this option will perform an inter-rater reliability (IRR) analysis on artifacts defined in BEEDA result files (see (5i) and (8)). This is useful for evaluating how consistently a dataset was cleaned by different users. The IRR analysis requires at least two BEEDA result files originating from the same dataset (i.e. two users cleaned the same dataset). Files from different datasets, or with different trial-type parameters (5b) will cause an error.

In addition to the BEEDA result files, an IRR information spreadsheet (.csv) must be made. This spreadsheet simply contains the BEEDA result filenames in column 1, and the corresponding users' names in column 2. An example of what this spreadsheet looks like:

Rater_1_results	Jack
Rater_2_results	Sally

Rater_3_results	Topher

In this example, Jack's result file is *Rater_1_results.csv*, Sally's file is *Rater_2_results.csv*, etc. This IRR information spreadsheet must be saved as a .csv (comma separated value) file. CRITICALLY, the BEEDA result files must be located in the same directory as the IRR information spreadsheet; BEEDA will look for result files in that directory. For instance, if the above IRR info spreadsheet is saved to Jack's desktop as *IRRinfo.csv* then all the results files must also be located on the desktop. The following file organization is needed:

/Users/ksander/Desktop/IRRinfo.csv
/Users/ksander/Desktop/Rater_1_results.csv
/Users/ksander/Desktop/Rater_2_results.csv
/Users/ksander/Desktop/Rater_3_results.csv

Once the information file has been created, selecting the IRR analysis button will show a prompt with two options: "Only trials with SCRs" and "All trials". This prompt specifies which trials will be considered in the IRR analysis. "Only trials with SCRs" will only perform the IRR analysis on trials containing an SCR, as defined by the SCR threshold parameters (4b). "All trials" will perform the analysis on all trials of interest (5e). Selecting the latter option would be more appropriate for SCL analyses (see the manuscript for a more detailed discussion).

After specifying the data to consider, a new file prompt will open. Select the IRR info spreadsheet in this prompt (e.g. *IRRinfo.csv*). The IRR calculation is very fast, and a new prompt will appear where you can save the IRR results. The results file will contain a matrix showing the pairwise Cohen's κ between all raters, labeled with the names provided in *IRRinfo.csv*.

Common Errors:

1) ERROR: the files do not exist, or are not located in the directory…

Result files specified in the IRR information spreadsheet could not be found. The most likely issue is those result files are not saved in the same directory as the IRR information spreadsheet. See above.

2) ERROR: raters have inconsistent trial numbers

Every result file does not have the same number of trials. This is most likely because they came from different datasets, or used different parameters that effect trial numbers (e.g. (5e)).

6) Artifact removal interface

After specifying all settings and parameters, selecting the main menu "remove artifacts" button (5g) will launch the artifact removal interface (ARI). ARI display options can be modified using the "Display settings" main menu button (5f).

6a) Trial window

Trial windows display respiration data, trial start/end markers*, and SCR onsets** (troughs) for user-specified trials of interest. The Y axis is transducer voltage (respiration measurement), and the X axis is time from the start of the experiment (in seconds). Respiration is shown as a blue trace, trial start/end markers are shown as green vertical lines, and SCR onsets are shown as red dots.

SCR onsets (red dots) are always marked on top of the blue respiration trace. In this way, the blue respiration trace must not be confused with an EDA data trace, *since the blue trace is always respiration data in a trial window*. EDA onsets are plotted on top of respiration data in order to simplify artifact removal. Since irregular breathing is thought to cause EDA artifacts, visualizing EDA traces is irrelevant to identifying and removing problematic data. Respiration traces are the signal of interest in identifying irregular breathing, and SCR onsets are shown overlaying respiration traces in order to better indicate onset times relative to corresponding respiration time-courses. Even though EDA signal traces are irrelevant to artifact removal (and may hinder/delay artifact removal, since users must consider more data traces simultaneously), SCR onsets are still displayed in the ARI in order to accommodate artifact removal focused solely on SCRs (see (7a) for more information on this).

*only if expanded trial window is set to greater than 0(s), otherwise the trial window boundaries themselves mark a trial's start/end.
**only SCRs eligible for analysis will be displayed (i.e. SCRs occurring after the Min SCR latency, above the rejection rate/threshold parameters, etc.)

6b) Trial number information

Trial numbers are listed vertically to the left of each trial window. These numbers correspond to the chronological order of trials in your experiment, and take the form:

Trial: 1/150
Trial: [trial number]/[total trials of interest]

User defined trial labels are intentionally omitted from the ARI in order to help reduce user-biased artifact removal.

6c) Flip page

The "Flip page" arrow buttons located at the top of the ARI will display the next/previous set of trial windows. Pressing the keyboard Left and Right arrow keys will also perform the same function as the "Flip page" buttons. The number of trial windows per set can be specified in the "Display settings" main menu button (5f).

6d) Go to trial

The “Go to trial” button located at the top of the ARI will navigate to a specific trial number. This can be useful when cycling through numerous sets of trials with the “flip page” button becomes tedious. Specific trial numbers correspond to the trial number labels detailed in (6b).

6e) Delete button

Clicking the delete button enables/disables the SCR delete mode. When enabled, the delete button will turn red and read “Delete ON”. When disabled, the Delete button will turn gray and read “Delete OFF”. Pressing the “a” key on the keyboard performs the same action as clicking on the delete button. The delete button cannot be toggled on/off when the drag delete mode is active (6f). For more information on SCR delete mode, see (7a)

6f) Drag delete key

Pressing the “d” key on the keyboard enables/disables drag delete mode. When enabled, the delete button (6e) will turn yellow and read “Drag Delete ON” *. When disabled, the Delete button will turn gray and read “Delete OFF”. Drag delete mode may not be toggled on/off when SCR delete mode (6e) is active. Drag delete mode may only be toggled through the “d” key, as there is no drag delete button. For more information on drag delete mode, see (7b).

*In many cases, the ARI window may not be wide enough to fully display the “Drag Delete ON” text. Instead, the button may read something like “Drag Delete …”, however the button will always turn yellow when drag delete mode is active.

6g) Undo

Clicking the undo button will restore the previously deleted SCR or data segment. This button may be clicked multiple times, and data will be restored in the order in which it was deleted. Deleted data will be re-added to the experiment, visible in the ARI, and eligible for later analysis (unless otherwise ineligible). Every time the undo button is clicked, a message will print to the Matlab command window indicating the action taken. For instance:

Undo: Data segment added back to trial #51/150

BEEDA’s undo function stores every instance of deleted data, so there is no limit on how many times the undo function may be called. Pressing the undo button repeatedly will eventually restore the experiment data to its original state. If this occurs, pressing the undo button will print this message to the Matlab command window:

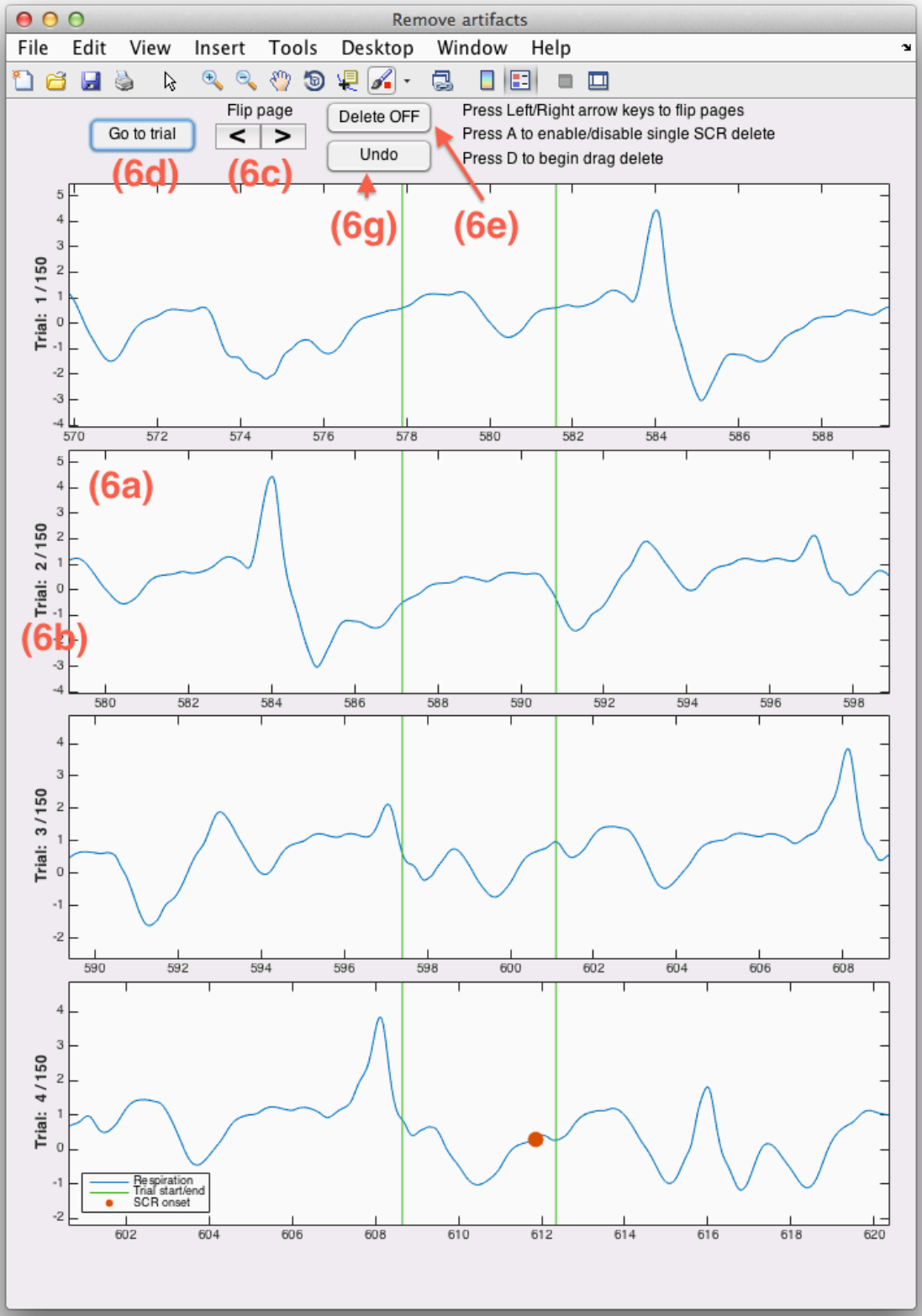
No previously deleted SCRs or data segments data found in memory

If both an SCR and a data segment were simultaneously deleted (i.e. drag delete was used to remove a segment with an SCR onset see (7b)), the undo button must be clicked twice to add both the SCR onset and the data segment back into the experiment. The undo button never reinstates deleted

SCRs and data segments simultaneously, even if they were deleted as such. You should see the corresponding messages printed to the Matlab command window, for instance:

Undo: Data segment added back to trial #50/150
Undo: SCR added back to trial #50/150

Additionally, deleted data is never cleared from the undo function memory, even after closing the ARI. The undo function memory will also be preserved in saved BEEDA toolbox .mat files (i.e. loading a saved BEEDA session will load the previous undo function memory).


Remove artifacts
File Edit View Insert Tools Desktop Window Help
Go to trial
Flip page
< >
Delete OFF
Undo
Press Left/Right arrow keys to flip pages
Press A to enable/disable single SCR delete
Press D to begin drag delete
(6a)
(6b)
(6c)
(6d)
(6e)
(6g)
Trial: 1 / 150
Trial: 2 / 150
Trial: 3 / 150
Trial: 4 / 150
Respiration
Trial start/end
SCR onset

7) Removing artifacts/using the ARI

The ARI (artifact removal interface) allows users to efficiently clean EDA data via streamlined data presentation and easy to use controls (for more detailed information, see section (6)). Users can scroll through "pages" of trials, examining each trial for problematic respiration waves. If problematic respiration waves are found, users can clean the data with SCR delete mode or drag delete mode. Drag delete mode is recommended for a more thorough data cleaning, while SCR delete mode is only recommended for SCR analyses (not SCL analyses). See (7a) and (7b) for more detailed information about these two delete modes.

7a) SCR delete mode

Activate SCR delete mode with the "a" key or the ARI delete button (see (6e) for more detail). Once activated, clicking on SCR onsets (red dots) will delete the SCRs and remove them from the experiment. Deleting an SCR will cause the trial window to briefly flash red and print a message to the Matlab command window such as:

Delete: SCR deleted from trial #25/150

SCRs deleted in this mode will not be visible in the ARI, and will not be considered for SCR analyses (average/cumulative/max SCR magnitude & number of SCRs statistics). However, deleting SCRs in SCR delete mode has no effect on skin conductance level (SCL) analyses. For example, a deleted SCR will not be considered for any SCR analyses, but SCL analyses will incorporate the deleted SCR's EDA levels when calculating SCL statistics (SD, average SCL). Consequently, SCR delete mode is not recommended for users planning to use SCL statistics (see (7b)). SCR delete mode will remain active until deactivated by the user.

Common errors:

1) Selecting a point before a trial starts or after a trial ends will cause this error message in the Matlab command window:

ERROR: only select points within trial range

To avoid this error when deleting SCRs, click directly on SCR onsets.

2) If clicking an SCR onset fails to delete the SCR or instead deletes an unintended SCR (e.g. from another trial), this is likely due to a graphics speed error (see (9-1)). Closing and reopening the ARI should resolve this, and avoiding rapid selections/clicking will help prevent this error from occurring again.

3) If activating/deactivating SCR delete mode fails, this is likely due to a graphics speed error (see (9-1)). Closing and reopening the ARI should resolve this, and avoiding rapid selections/clicking will help prevent this error from occurring again. Additionally, activating SCR delete mode or drag delete mode when the other is already active may increase the potential for such errors.

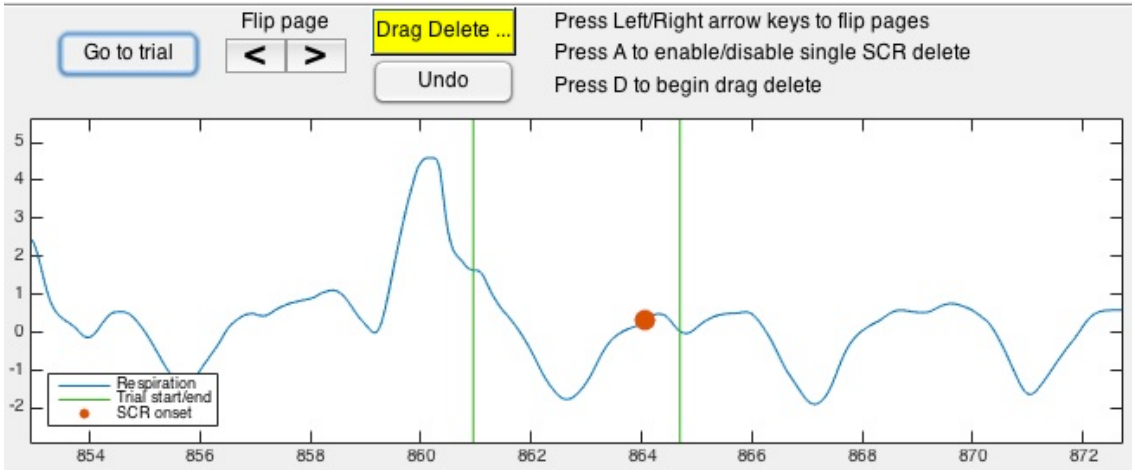
7b) Drag delete mode

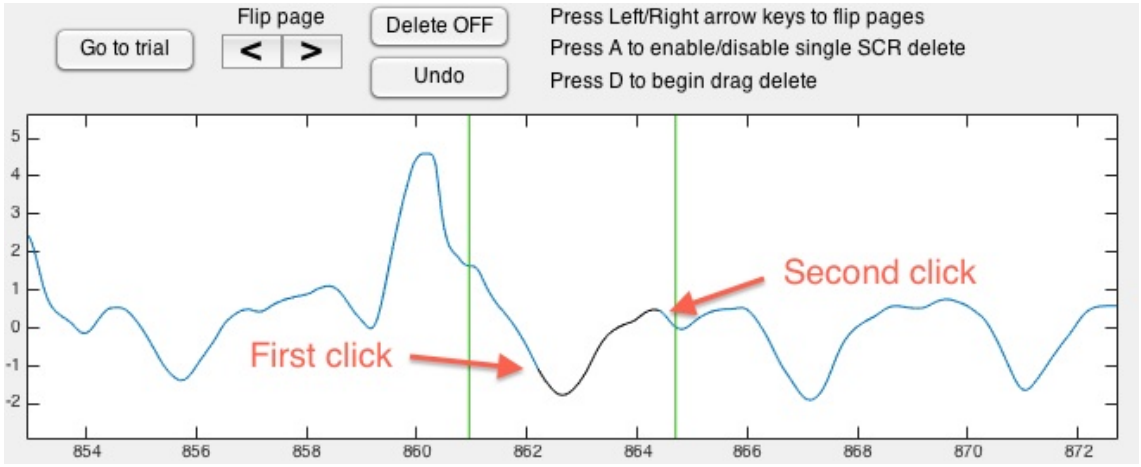
This mode allows users to delete continuous data segments from the experiment. Deleted data segments will be ignored in all SCL and SCR analyses. Activate drag delete mode with the "d" key (see (6f) for more detail). Once activated, click once at the beginning of a data segment and then a second time at the end of a data segment. This will delete all data between the first and second click, then deactivate drag delete mode. Unlike SCR delete mode, drag delete mode will not remain active after deleting data, and must be reactivated to delete additional segments. Deleting a data segment will cause the trial window to briefly flash red, turn the corresponding respiration trace black, and remove SCR onsets located within the segment. The following message will print to the Matlab command window:

Delete: data segment deleted from trial #25/150

If an SCR was included in the segment, an additional message will print regarding the SCR deletion.

Example drag delete:





Drag delete is recommended for users who plan to use SCL statistics, since the SCR delete mode has no effect on SCL analysis (see (7a)). Only drag delete mode cleans SCL data. Additionally, any trial can be flagged for artifacts using drag delete mode (see (8)), whereas SCR delete can only flag trials by removing SCR onsets (every trial may not have an SCR to remove). Overall, drag delete is recommended for more comprehensive EDA data cleaning.

Common Errors:

1) If activating/deactivating drag delete mode fails, this is likely due to a graphics speed error (see (9-1)). Closing and reopening the ARI should resolve this, and avoiding rapid selections/clicking will help prevent this error from occurring again. Additionally, activating SCR delete mode or drag delete mode when the other is already active may increase the potential for such errors.

2) ERROR: only select points within trial range

To avoid this message, do not select data segment points before a trail start or after a trial end.

3) If it appears the undo function has failed to restore a previous drag delete, see (6g) regarding simultaneously deleted SCRs and data segments. Undo restores drag deleted SCRs separately from data segments.

8) Exporting results and artifact information

After problematic data has been deleted, use the main menu "export final results" button to analyze your trials of interest (see (5i) for additional information). This will export EDA statistics and artifact removal information to an excel spreadsheet.

This spreadsheet will show trial-wise EDA statistics, in addition to whether or not the trial was flagged for artifacts. A trial will show "flagged for artifacts" if any SCR or data segment was deleted from the trial. Trials are listed in chronological order, with the first trial occurring earliest in the experiment. An artifact cleaning inter-rater reliability (IRR) analysis can be directly performed on these files, see (5j).

8a) EDA statistics

Number of SCRS: the number of SCRs in a trial

Average SCR magnitude: average trial SCR amplitude
Max SCR magnitude: the largest SCR amplitude within a trial
Cumulative SCR magnitude: the sum of all trial SCR amplitudes
SCL(average): mean trial EDA signal
SCL(standard deviation): trial EDA signal standard deviation
All units are in microsiemens, except number of SCRs.

9) Common general errors/issues

1) Graphics speed error: BEEDA's graphics are much slower than the actual toolbox processes, and sometimes this causes minor glitches and errors. In the current version, most BEEDA errors are caused by this graphics speed problem. These errors can manifest in different ways, although the solution is simply:

If the error occurs in the ARI, close & reopen the ARI.
If the error does not occur in the ARI, save the current session and reopen BEEDA.

Graphics speed errors can be easily avoided by refraining from rapid selections! Pressing buttons/clicking rapidly will cause graphics speed errors, working deliberately should rarely cause a problem.

2) Trial end markers: BEEDA defines an event's end as the start of the next event. (i.e. the end of event 1 is defined as the start of event 2). This can cause irregularities if an experiment's real trial time-course ends before the next event occurs. For instance, experiment A involves showing 20 second videos with 5-second breaks in between. However, experiment A only has event codes for each video's start time, with no events corresponding to the breaks. In this example, BEEDA will assume Experiment A's video trials are 25 seconds long. An easy workaround for this issue is simply setting the max SCR latency (see (5c) for more details), since no data will be analyzed after the max SCR latency parameter.

3) For errors related to specific functions (i.e. deleting an SCR in SCR delete mode, trial type definition errors), please check the function's specific section (e.g. (7a) for SCR delete mode issues, (5e) for trial type definition problems).