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Breathe Easy EDA: a MATLAB toolbox for psychophysiology data management, cleaning, and analysis

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Breathe Easy EDA: a MATLAB toolbox

for psychophysiology data management, cleaning, and analysis

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Abstract

Electrodermal activity (EDA) recordings are widely used in experimental psychology to evaluate fluctuations in skin electrical conductance, a measure of sympathetic nervous system arousal. Respiration patterns influence EDA, such that irregular breathing can cause EDA fluctuations that are difficult to distinguish from genuine arousal-related sympathetic skin conductance responses. Thus, it is crucial to control for respiration-related EDA artifacts. Here we developed a novel MATLAB toolbox that facilitates identifying respiration-related artifacts in EDA recordings, called Breathe Easy EDA (BEEDA). The flexible toolbox enables users to eliminate EDA respiration artifacts and analyze EDA data and is distributed freely. The EDA analysis capabilities include tonic and phasic EDA measurements, following from standard methodological implementations. The toolbox is suitable for any experiment recording both EDA and respiration data, and flexibly adjusts to experiment-specific parameters (e.g., trial structure and analysis parameters).

Keywords: respiration artifact, electrodermal activity, skin conductance,

Introduction

Electrodermal activity (EDA) methods evaluate fluctuations in skin electrical conductance caused by changes in sweat gland production. As the sympathetic nervous system innervates sweat glands, corresponding changes in the skin's conductance are thought to measure sympathetic nervous system arousal (Bach, Friston, & Dolan, 2010). Importantly, EDA recordings have become a valuable and popular psychophysiological measurement in studies of affect and cognition (Boucsein et al., 2012).

It is well known that respiration and electrodermal activity (EDA) influence each other (Schneider, Schmidt, Binder, Schafer, & Walach, 2003). In laboratory settings, researchers often use this relationship to check the integrity of a psychophysiology set-up by asking participants to take a deep breath in order to observe concurrent deflections in both waveforms. EDA is typically recorded using electrodes places on the palmar or plantar surfaces where eccrine sweat glands—innervated by the sympathetic nervous system—are densely located. Respiration, typically recorded using a belt secured around the diaphragm, is an oscillatory event that approximates a sine wave with regular breathing. However, irregular respiration, or abnormalities in the respiration waveform (frequency or amplitude), are associated with non-specific changes in the EDA waveform. These physiological respiration-related artifacts can cause researchers to overestimate the presence or magnitude of skin conductance responses (SCRs) in experiments (Schneider et al., 2003).

While EDA and respiration influence each other, prior work has shown that EDA and respiratory signals are not *strictly* coupled (Rittweger, Lambertz, & Langhorst, 1996), which might be related to differences in their physiological origin. Physiologically, the emotion-reactive palmar and plantar eccrine sweat glands are maximally innervated by cholinergic (Sato & Sato, 1981) sudomotor fibers leaving the ventral root of the spinal cord (Boucsein, 2012, p. 20). While eccrine sweat glands are modulated by the sympathetic nervous system, the transmission related to EDA is mainly cholinergic, not noradrenalergic (Sato & Sato, 1981; Stern, Ray, & Quigley, 2001). However, deep breathing has been associated with sudden increases in free-circulating adrenaline, producing sweat responses (Boucsein, 2012, p. 32) which mimic SCRs on EDA recordings. As mentioned above, this relationship is useful for checking

psychophysiological signal integrity but can also bias the analysis of SCRs of interest. Identifying respiration artifacts might be particularly important over longer trial epochs (e.g., > 5 seconds)—such as viewing video clips or recalling autobiographical memories—when the standard stimulus-response latency window for identifying event-related SCRs (1-4s) may no longer be suitable.

While movement-induced EDA artifacts are fairly straightforward to identify (e.g., unusually steep rise in the waveform), physiologically derived artifacts appear similar to arousal-related waveforms (Boucsein, 2012). Developing methods for identifying respiration-related artifacts has been a challenge for the field of psychophysiological research due to high intersubject and intrasubject variability in respiration activity, yielding a wide range of waveform characteristics (Schneider et al., 2003). A lack of analytical solutions has motivated software development within this field since the early 1990's, with the goal of improving how researchers inspect and manipulate respiration data (Wilhelm & Roth, 1993).

Recently the Society for Psychophysiological Research, which oversees the journal *Psychophysiology*, recommended that all manuscript submissions that report EDA results should also outline artifact elimination procedures (Boucsein et al., 2012). It is common practice to employ time-consuming visual inspection of the respiration trace to remove artifact EDA responses, but visual inspection is not without bias or subjectivity and the criteria are not standard across laboratories. Prior work has offered artifact detection methods, but easy-to-use and freely available software that expedites EDA data cleaning is not yet available. For example, Schneider et al. (2003) provide a useful decision tree for discarding artifact EDA responses based on a set of criteria. An algorithmic approach has also been proposed recently, although this method still requires researchers to manually adjust parameters for each participant according to their own subjective criteria (Blain, Power, Sejdic, Mihailidis, & Chau, 2010). In both cases, the software necessary to implement the method was not developed. While purely computational or analytical methods for artifact identification are not presently available, new advances in modeling respiration physiology may one day provide these capabilities (Bach, Gerster, Tzovara, & Castegnetti, 2016).

Currently, there is a need for easy-to-use, flexible, and interoperable software that facilitates EDA artifact elimination via the widely employed method of visual inspection. We have developed a novel MATLAB toolbox for efficiently eliminating EDA respiration artifacts and analyzing EDA data, which we freely distribute as Breathe Easy EDA or 'BEEDA'. BEEDA's streamlined artifact removal interface allows users to quickly identify and clean EDA data, expediting EDA analysis without compromising analysis integrity. Additionally, BEEDA's integrated EDA analysis functionality allows users to seamlessly analyze cleaned EDA data within the toolbox.

The BEEDA toolbox is controllable through a graphical user interface (GUI), and requires no programming skill to operate. This toolbox may be used either for simple artifact detection, EDA analyses, or for both artifact elimination and subsequent EDA analyses—as illustrated in Figure 1. This flexibility allows users to take advantage of BEEDA's functionality without restricting the use of complementary software such as Mindware (MindWare Technologies Ltd., Gahanna, OH), Ledalab (Benedek & Kaernbach, 2010), ANSLAB (Wilhelm & Peyk, 2005), or AcqKnowledge (Braithwaite, Watson, Jones, & Rowe, 2013). For instance, one could use BEEDA only for marking artifacts in a dataset, and then use the artifact information file BEEDA produces with an alternative EDA analysis program. Furthermore, BEEDA is suitable for any experiment where both EDA and respiration data were collected, and parameters specific to individual experiments can easily be modified through the GUI (e.g., trial structure and analysis options). This permits a great deal of functional flexibility, without encumbering the toolbox's usability.

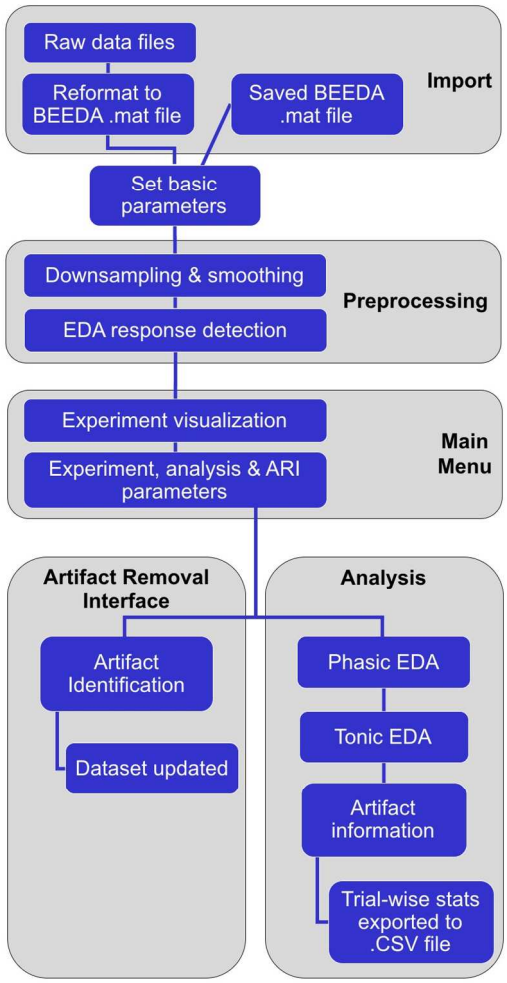

Figure 1. Illustration of the Breathe Easy EDA (BEEDA) processing workflow.

Toolbox design and workflow

A. Loading an experiment into BEEDA

Initializing the BEEDA toolbox (executing *BreatheEasyEDA.m*) immediately launches the data loading GUI. This interface allows users to either load data files for a new session, or load data from a previously saved session. If a new session is started, BEEDA copies and reformats raw data files into a MATLAB structure variable (*BEEDAdata*). The *BEEDAdata* variable is the toolbox's primary data structure; all user defined parameters (e.g. analysis settings) and analysis actions (e.g. artifact removal)

are written to this *BEEDAdata* structure. Resuming a previous session reads information from a saved *BEEDAdata* structure and launches into the main menu.

For new sessions, basic analysis parameters are also specified in the data loading GUI. These basic settings are: downsampling and Skin Conductance Response (SCR) parameters. Importantly, once downsampling and SCR options are chosen, these settings are permanently fixed for the current BEEDA session (even if the session is saved and resumed). If a downsampling factor is specified, both the EDA and respiration data are immediately downsampled within *BEEDAdata*. This downsampling functionality is provided because the sampling rate capabilities of modern EDA systems (e.g. > 1000 Hz) far exceed the resolution necessary for EDA analyses. Downsampling datasets to lower temporal resolutions can dramatically reduce a dataset's size, consequently improving BEEDA's memory and hard disk requirements, computation time, and GUI responsiveness.

B. Main menu

The main menu provides a visual summary of your experiment, trial information, analysis settings, and display settings (Figure 2A). The main menu also allows users to save the current BEEDA session, start the artifact removal interface, and export final analysis results.

Before displaying the experiment summary panel, the EDA data is first smoothed via convolution with a Gaussian kernel (as in Benedek and Kaernbach (2010)). Smoothing removes minor signal noise, which may originate from a variety of sources (e.g. recording equipment or downsampling). Next, valid SCRs are identified based on previously specified threshold and rejection-rate parameters. The experiment summary panel plots the entire experiment's EDA timecourse, marking onset times for trials, and valid SCRs (Figure 2). This window provides users with an overview of the experiment's EDA data, allowing users to easily confirm the indented dataset has loaded correctly.

All unique trial-types are displayed in the trial-type information window, and the current BEEDA session's settings are displayed in the setting information window (Figure 2). From the main menu, users can easily set a number of session settings: SCR latency tolerances, valid trials for analysis, and display settings (see GUI display options). SCR latency tolerances establish the stimulus time-locked window

when SCRs may be appropriately attributed to the preceding stimulus (see Main EDA analysis parameters), typically a 3-second window between 1-4 seconds post-stimulus onset (Boucsein, 2012), but shorter windows have been proposed (e.g., 2 seconds or less; Barry, 1990; Levinson & Edelberg, 1985). Additionally, if end-of-trial events were omitted during an experiment's data collection, specifying a maximum SCR latency parameter effectively creates these events. Specifying the valid trials for analysis determines which trial-types are available for artifact cleaning and EDA analysis. All unique events recorded during data collection may be declared as valid trial-types; this allows users to disregard inter-trial events, baseline events, or events not corresponding to trials of interest.

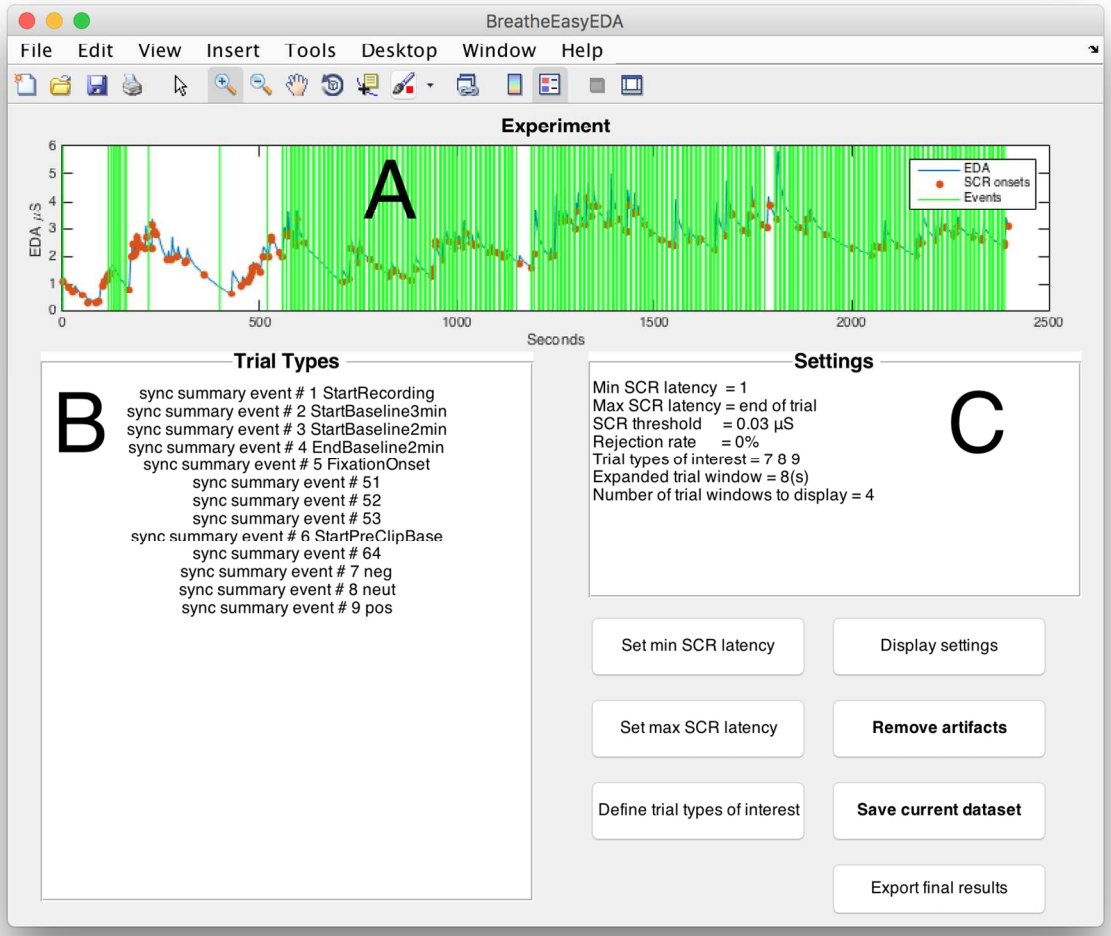

Figure 2. Main menu after data has been loaded into BEEDA. (A) Visual experiment summary; the EDA timecourse is plotted in blue, red points mark valid SCR onsets, and vertical green lines mark recording

events (e.g. trial onsets). (B) Trial-type window displays each type of recording event imported with the dataset. (C) Current settings.

C. Artifact removal interface

Selecting "Remove artifacts" from the main menu will launch the Artifact Removal Interface (ARI). The ARI allows users to efficiently clean EDA data via streamlined data presentation and easy to use controls. Users can easily scroll through 'pages' of trials, examining each trial for irregular respiration waves, as shown in Figure 3. If problematic respiration waves are identified, users can clean the data with either 'SCR delete mode' or 'drag delete mode'. Drag delete mode removes entire time segments of EDA data, whereas SCR delete mode only removes SCRs from analysis consideration. Therefore, drag delete mode is recommended for Skin Conductance Level (SCL) analyses and thorough artifact elimination, whereas SCR delete mode is only recommended for SCR analyses (see EDA analysis functionality).

In the ARI, user defined trials of interest are individually displayed by plotting SCR onset timepoints directly onto the trial's respiration data (Figure 3). This presentation simplifies the manual identification of problematic breathing (e.g. Figure 4), and the recommended procedures for EDA respiration artifact scrubbing can be found in Schneider et al. (2003). All user actions (e.g., data cleaning) are immediately applied to *BEEDAdata* and can be saved through the main menu.

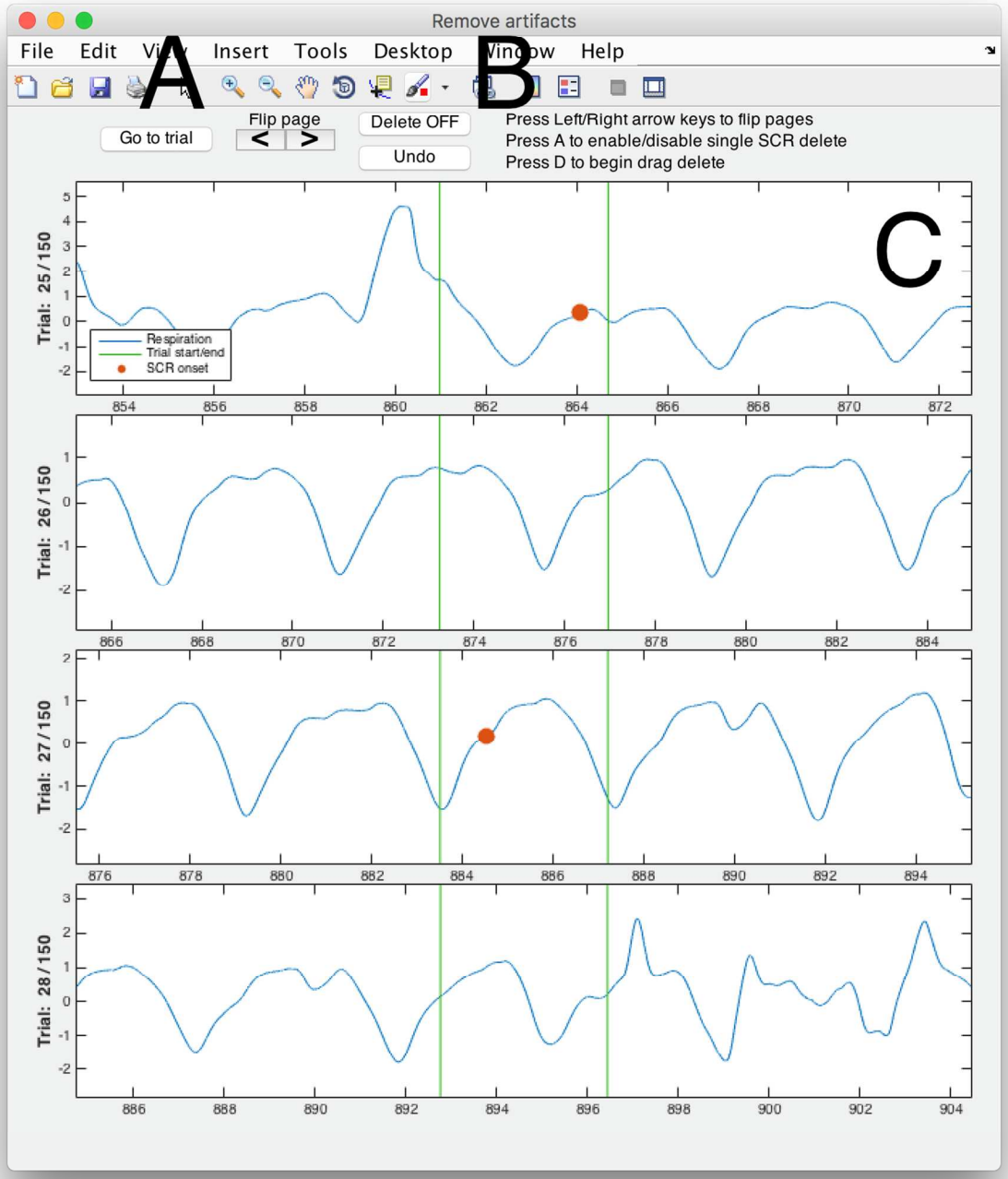

Figure 3. Artifact removal interface displays a page of four trials. (A) Event navigation controls. (B) Data manipulation controls and hotkey guide. (C) Respiration timecourse is plotted in blue, red points mark valid SCR onsets, and vertical green lines mark an event's start and end.

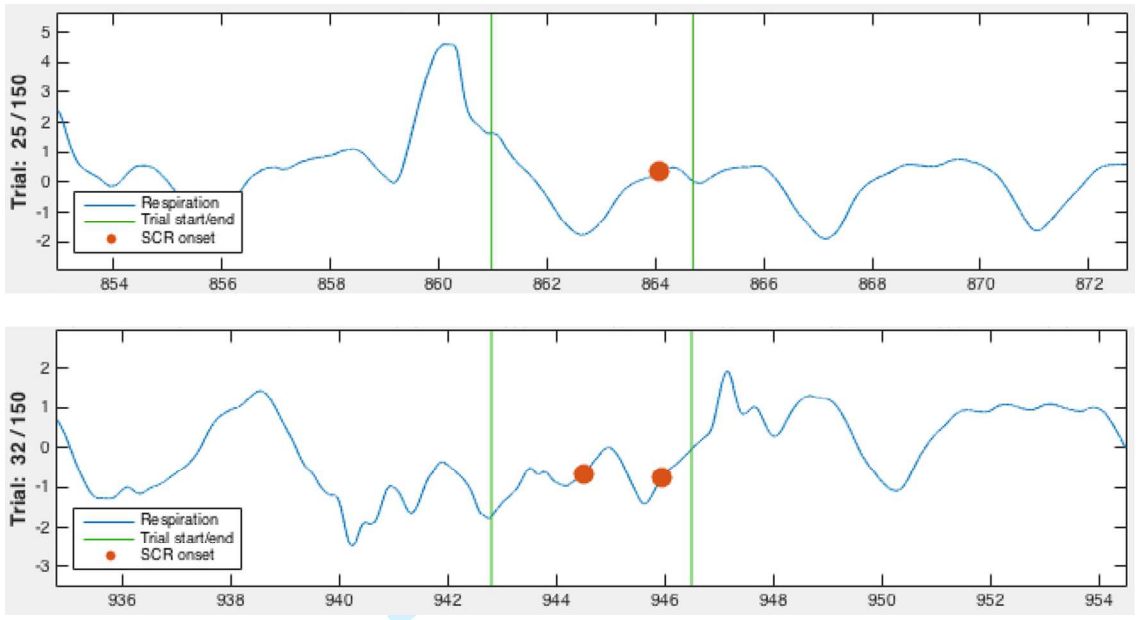

Figure 4. Two examples of artifact SCRs displayed in the artifact removal interface. The presentation simplifies inspecting data for a sudden deep breath (Panel A) or highly irregular breathing pattern (Panel B) preceding an SCR onset.

D. Exporting results and artifact information

Selecting "export final results" in the main menu will analyze the user-defined trials-of-interest and export the analysis results to a Microsoft Excel spreadsheet (.XLS file). 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. In this way, one may simply use BEEDA's GUI to mark artifacts within an EDA dataset, then use the artifact information output with another EDA analysis software. Similarly, the artifact information output allows experimenters to easily compare the interrater reliability of multiple artifact scorers within a dataset.

GUI display options

The *Display settings* main menu button allows users to customize the Artifact Removal Interface. The *Expanded trial window* parameter controls the additional timecourse data displayed before and after each trial in the artifact removal interface. For instance, setting expanded trial window to 5 (seconds) will

display the 5 seconds before every trial and the 5 seconds after every trial. This option may help users evaluate how respiration immediately preceding or following a trial relates to respiration during a trial. Additionally, users who wish to remove artefactual respiration may benefit from more contextual information about each trial within the experiment's timecourse.

The *Number of trial windows to display* parameter controls the number of trials simultaneously displayed in the artifact removal interface. This option may be particularly useful when running the BEEDA toolbox on computers with lower resolution computer monitors, as users can adjust the number of trials in each ARI page to best fit their display configuration.

EDA analysis functionality

The BEEDA toolbox features integrated EDA analysis functionality, which may be used with or without prior artifact removal. Selecting the *Export final results* main menu button will initialize EDA analyses and export the subsequent results as a spreadsheet. These analyses measure tonic and phasic EDA using standard methodology (Boucsein, 2012). Tonic EDA is defined as the slow change in SCLs over a timecourse of interest. BEEDA determines the mean and standard deviation of each trial's EDA levels, and these statistics are included in the results output. Data segments marked as artifacts using the *Drag delete mode* are not included in SCL analyses.

Phasic EDA measurements are determined via the trough-to-peak detection of SCRs (Boucsein, 2012). SCRs are quickly changing EDA levels that exceed an amplitude threshold and occur within a response window time-locked to a stimulus. The SCR amplitude is defined as the SCR's peak EDA level minus the SCR's initial trough EDA level. Users can explicitly specify an SCR amplitude threshold, and this practice is typical for trough-to-peak SCR detection. Alternately, the amplitude threshold can be flexible and data driven via setting an SCR rejection rate (Kim, Bang, & Kim, 2004). In BEEDA, specifying an explicit SCR threshold of 0μS and a rejection rate of 10% emulates the algorithmic SCR thresholding procedure described in Kim et al. (2004). While this thresholding procedure is not typically employed, BEEDA includes this functionality to mirror proprietary EDA analysis software packages which offer similar analysis options (Braithwaite et al., 2013).

For phasic EDA analyses, BEEDA detects valid SCRs and exports the following statistics for each trial: number of SCRs, average SCR magnitude, cumulative SCR magnitude, and maximum SCR magnitude. SCRs in data segments removed with *Drag delete mode,* in addition to SCRs marked as artifacts with *SCR delete mode*, are not included in SCR analyses.

EDA analysis statistics

- *Number of SCRs*: the number of valid 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 EDA signal within a trial
- *SCL(standard deviation)*: the standard deviation of a trial's EDA signal

Main EDA analysis parameters

- *SCR threshold*: Only EDA responses above this amplitude threshold are considered valid SCRs. Typically an amplitude threshold of .05μS is used, although some researchers advocate for thresholds as low as .01μS (Braithwaite et al., 2013). Schmidt and Walach (2000) recommend that sampling resolution should be taken into account when considering low thresholds, and thresholds lower than .01μS should not be used.
- *Rejection rate*: If a rejection rate greater than 0 is specified, within each trial, SCR amplitudes must also exceed this percentage of the trial's largest SCR amplitude. For example, if the rejection rate is 10% and a trial's largest SCR amplitude is 4μS, SCRs with amplitudes below .4 μS are rejected in that trial.
- *Min SCR latency*: The minimum time after a trial's start when EDA data can be considered for analyses (i.e. the stimulus response window). Valid SCRs onsets must begin after the specified minimum latency time, and EDA levels before minimum latency time will be excluded from SCL

analyses. Benedek and Kaernbach (2010) report that a minimum latency of 1 second post-stimulus is typical.

- *Max SCR latency*: The time after a trial's start when EDA data cannot be considered for analyses. Valid SCRs must begin before the specified maximum latency, and EDA signal after the maximum latency is excluded from SCL analyses. Benedek and Kaernbach (2010) report that a maximum latency of 3 or 5 seconds post-stimulus is typical.

Conclusion

Breathe Easy EDA is a novel MATLAB toolbox developed for analyzing EDA data. This software was specifically built to facilitate the methodical considerations of psychophysiology researchers through a simple, flexible, interoperable, and tolerant design. BEEDA's simplified data presentation allows efficient data inspection and cleaning, without sacrificing functionality in the GUI. In fact, the intuitive interface includes features that are absent from widely used contemporary EDA software, but still essential to researchers (e.g., the "undo" function). The toolbox's common output-file format and range of analysis capabilities also allows users to integrate BEEDA in their analysis pipelines without precluding alternate software packages. Furthermore, BEEDA was built to handle any experiment where both respiration and EDA data were collected, even in non-ideal, or creative, event recording circumstances. In these ways, this software provides researchers with optimized tools for psychophysiology analysis.

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