Package: PhysioEDA (via r-universe)

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Title Electrodermal Activity Analysis for PhysioExperiment Objects

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Description Provides electrodermal activity (EDA / skin conductance) analysis functions for PhysioExperiment objects. Includes preprocessing (filtering, downsampling), artifact detection and correction, tonic/phasic decomposition (highpass, median, CDA, cvxEDA), SCR peak detection, feature extraction, data transformations, signal quality assessment, visualization, and event-related SCR analysis.

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`edaArtifact` *Detect and Correct EDA Artifacts*

Description

Identifies artifacts in electrodermal activity (EDA) signals using one or more detection methods (threshold, gradient, flatline) and optionally corrects them via interpolation or NA replacement.

Usage

```
edaArtifact(
  x,
  methods = c("threshold", "gradient", "flatline"),
  threshold_range = c(0.001, 60),
  gradient_max = NULL,
  flatline_sec = 5,
  correct = "interpolate",
  assay_name = NULL,
  output_assay = "cleaned"
)
```

Arguments

`x`	A PhysioExperiment object containing EDA data.
`methods`	Character vector of detection methods to apply. Any combination of `"threshold"`, `"gradient"`, and `"flatline"`. Default is all three.

`threshold_range`	Numeric vector of length 2 giving the acceptable range of EDA values in microsiemens (default: `c(0.001, 60)`). Values outside this range are flagged as artifacts.
`gradient_max`	Maximum allowable absolute gradient in microsiemens per sample. If NULL (default), computed as `10 / samplingRate(x)` (equivalent to 10 uS/sec).
`flatline_sec`	Minimum duration in seconds of a constant-value segment to be flagged as a flatline artifact (default: 5).
`correct`	Correction strategy: `"interpolate"` (linear interpolation across artifact regions), `"na"` (replace with NA), or `"none"` (detection only, no correction). Default is `"interpolate"`.
`assay_name`	Name of the input assay. If NULL, uses `defaultAssay(x)`.
`output_assay`	Name for the corrected output assay (default: `"cleaned"`). Only used when `correct != "none"`.

Value

A modified `PhysioExperiment` with artifact information stored in `metadata(x)$eda_artifacts`, a list containing:

mask Logical matrix (time x channels) where `TRUE` indicates an artifact sample.

summary A `data.frame` with columns `channel`, `method`, `n_artifacts`, and `pct` giving artifact counts per channel per detection method.

If `correct != "none"`, the corrected signal is stored in the `output_assay`.

References

Kleckner, I.R., et al. (2018). "Simple, transparent, and flexible automated quality assessment procedures for ambulatory electrodermal activity data." *IEEE Transactions on Biomedical Engineering*, 65(7), 1460-1467. doi:10.1109/TBME.2017.2758643

Boucsein, W. (2012). *Electrodermal Activity*. 2nd ed. Springer. doi:10.1007/9781461411260

See Also

`edaQuality` for signal quality assessment, `edaFilter` for frequency-domain filtering, `edaDecompose` for tonic/phasic decomposition

---

`edaDecompose` *Decompose EDA into Tonic and Phasic Components*

Description

Separates an electrodermal activity (EDA) signal into its slow-varying tonic component (skin conductance level, SCL) and fast-varying phasic component (skin conductance responses, SCR).

Usage

```
edaDecompose(
  x,
  method = c("highpass", "median", "cda", "cvxeda"),
  cutoff = 0.05,
  window_sec = 4,
  tau1 = 0.75,
  tau2 = 2,
  alpha = 0.01,
  gamma = 0.1,
  assay_name = NULL,
  output_tonic = "tonic",
  output_phasic = "phasic"
)
```

Arguments

`x`	A PhysioExperiment object containing EDA data.
`method`	Decomposition method: `"highpass"`, `"median"`, `"cda"`, or `"cvxeda"`. Default is `"highpass"`.
`cutoff`	Cutoff frequency in Hz for the highpass method (default: 0.05).
`window_sec`	Window length in seconds for the median method (default: 4).
`tau1`	SCR rise time constant in seconds for CDA/cvxEDA (default: 0.75).
`tau2`	SCR decay time constant in seconds for CDA/cvxEDA (default: 2.0).
`alpha`	L1 sparsity penalty for cvxEDA (default: 0.01). Ignored by other methods.
`gamma`	Smoothness weight for cvxEDA tonic component (default: 0.1). Ignored by other methods.
`assay_name`	Name of the input assay. If NULL, uses `defaultAssay(x)`.
`output_tonic`	Name for the tonic output assay (default: "tonic").
`output_phasic`	Name for the phasic output assay (default: "phasic").

Details

Four methods are available:

highpass FFT-based highpass/lowpass separation at a cutoff frequency.

median Sliding median filter for tonic extraction.

cda Continuous Decomposition Analysis (Benedek & Kaernbach, 2010). Deconvolution with a Bateman impulse response, Gaussian smoothing, and non-negativity constraint on the driver signal.

cvxeda Convex optimization-based decomposition (Greco et al., 2016). Iterative ADMM approach with Wiener deconvolution and L1 sparsity on the driver signal.

Value

A modified `PhysioExperiment` with new assays:

tonic The slow-varying skin conductance level (SCL) component.

phasic The fast-varying skin conductance response (SCR) component.

driver (CDA and cvxEDA only) The sudomotor nerve activity driver signal.

Decomposition parameters are stored in `metadata(x)$eda_decompose`.

References

Benedek, M., & Kaernbach, C. (2010). "A continuous measure of phasic electrodermal activity." *Journal of Neuroscience Methods*, 190(1), 80-91. doi:10.1016/j.jneumeth.2010.04.028

Greco, A., et al. (2016). "cvxEDA: A convex optimization approach to electrodermal activity processing." *IEEE Transactions on Biomedical Engineering*, 63(4), 797-804. doi:10.1109/TBME.2015.2474131

See Also

`edaPeaks` for SCR peak detection on the phasic signal, `edaFeatures` for feature extraction, `plotDecompose` for visualizing decomposition results

---

`edaDownsample` *Downsample EDA Signal*

Description

Reduces the sampling rate of an EDA signal by first applying an anti-aliasing lowpass filter at half the target sampling rate, then decimating the signal.

Usage

```
edaDownsample(x, target_sr, assay_name = NULL)
```

Arguments

`x`	A PhysioExperiment object containing EDA data.
`target_sr`	Target sampling rate in Hz. Must be lower than the current sampling rate.
`assay_name`	Name of the input assay. If NULL, uses `defaultAssay(x)`.

Value

A new `PhysioExperiment` with the downsampled signal in the `"raw"` assay and the sampling rate set to the actual achieved rate. Events are preserved. Downsampling parameters are stored in `metadata(x)$eda_downsample` (a list with `original_sr`, `target_sr`, `factor`, `original_n_time`, and `new_n_time`).

References

Boucsein, W. (2012). *Electrodermal Activity*. 2nd ed. Springer. doi:10.1007/9781461411260

See Also

`edaFilter` for frequency-domain filtering, `edaArtifact` for artifact detection and correction

---

`edaErscr` *Event-Related SCR Analysis*

Description

Performs event-related skin conductance response (ER-SCR) analysis by extracting SCR features time-locked to experimental events. For each event, the function searches for an SCR onset within a specified window and, if found, computes amplitude, latency, rise time, and 50 percent recovery time.

Usage

```
edaErscr(
  x,
  event_type = NULL,
  onset_window = c(1, 4),
  peak_window = c(0.5, 5),
  amplitude_min = 0.01,
  assay_name = NULL
)
```

Arguments

`x`	A PhysioExperiment object containing EDA data and events.
`event_type`	Character string specifying the event type to analyze. If NULL (default), all events are used.
`onset_window`	Numeric vector of length 2 giving the valid SCR onset latency window in seconds relative to event onset (default: c(1, 4)).
`peak_window`	Numeric vector of length 2 giving the minimum and maximum time from SCR onset to peak in seconds (default: c(0.5, 5)).
`amplitude_min`	Minimum SCR amplitude in microsiemens to be considered a valid response (default: 0.01).
`assay_name`	Name of the assay to use. If NULL, uses "phasic" if available, otherwise the default assay.

Value

A data.frame with one row per event per channel containing columns:

event_index	Integer index of the event.
event_onset	Numeric onset time of the event in seconds.
channel	Character name of the channel.
scr_present	Logical indicating whether a valid SCR was detected.
scr_amplitude	Numeric SCR amplitude (peak minus onset), or NA.
scr_latency	Numeric latency from event to SCR onset in seconds, or NA.
scr_rise_time	Numeric time from SCR onset to peak in seconds, or NA.
scr_recovery_time	Numeric time for 50 percent recovery from peak, or NA.

References

Bach, D.R., et al. (2010). "Modelling event-related skin conductance responses." *International Journal of Psychophysiology*, 75(3), 349-356. doi:10.1016/j.ijpsycho.2010.01.005

See Also

`edaPeaks` for general SCR peak detection, `edaDecompose` for tonic/phasic decomposition (run first), `edaFeatures` for summary feature extraction, `plotPeaks` for visualizing SCR peaks

---

`edaFeatures` *Extract EDA Features per Channel*

Description

Computes summary features from electrodermal activity data, including skin conductance response (SCR) statistics and skin conductance level (SCL) measures. Requires tonic/phasic decomposition to have been performed (via `edaDecompose`).

Usage

```
edaFeatures(x, peaks = NULL, window = NULL, assay_name = NULL)
```

Arguments

`x`	A PhysioExperiment object containing EDA data.
`peaks`	Optional pre-computed peaks data.frame from `edaPeaks`. If NULL, peaks are computed automatically using the gradient method.
`window`	Optional numeric vector of length 2 giving the time window in seconds as `c(start_sec, end_sec)` to restrict analysis.
`assay_name`	Name of the input assay for peak detection. If NULL, uses `defaultAssay(x)`.

Value

A `data.frame` with one row per channel and the following columns:

channel Character channel label.

scr_count Integer number of detected SCR peaks.

scr_rate_per_min Numeric SCR count per minute.

mean_amplitude Numeric mean SCR peak amplitude in microsiemens (0 if no peaks detected).

mean_scl Numeric mean tonic skin conductance level.

scl_sd Numeric standard deviation of the tonic signal.

auc_phasic Numeric area under the phasic curve (positive values only, in uS*s), or `NA` if no phasic assay exists.

ns_scr_freq Numeric non-specific SCR frequency (per minute).

References

Boucsein, W. (2012). *Electrodermal Activity*. 2nd ed. Springer. doi:10.1007/9781461411260

Benedek, M., & Kaernbach, C. (2010). "A continuous measure of phasic electrodermal activity." *Journal of Neuroscience Methods*, 190(1), 80-91. doi:10.1016/j.jneumeth.2010.04.028

See Also

`edaDecompose` for tonic/phasic decomposition (run first), `edaPeaks` for SCR peak detection, `edaErscr` for event-related SCR analysis

---

`edaFilter` *Filter EDA Signal*

Description

Applies a frequency-domain (FFT-based) filter to an EDA signal. Supports lowpass, highpass, and bandpass filter types using a smooth quadratic transition in the frequency domain.

Usage

```
edaFilter(
  x,
  type = c("lowpass", "highpass", "bandpass"),
  cutoff,
  order = 2,
  assay_name = NULL,
  output_assay = "filtered"
)
```

Arguments

`x`	A PhysioExperiment object containing EDA data.
`type`	Filter type: `"lowpass"`, `"highpass"`, or `"bandpass"`.
`cutoff`	Cutoff frequency in Hz. A single numeric value for lowpass or highpass, or a numeric vector of length 2 (`c(low, high)`) for bandpass.
`order`	Filter steepness parameter controlling the smoothness of the frequency transition (default: 2). Higher values produce sharper rolloff.
`assay_name`	Name of the input assay. If NULL, uses `defaultAssay(x)`.
`output_assay`	Name for the output assay (default: "filtered").

Value

A modified `PhysioExperiment` with filtered data stored in the `output_assay` and filter parameters recorded in `metadata(x)$eda_filter` (a list with `type`, `cutoff`, `order`, `assay_name`, and `output_assay`).

References

Boucsein, W. (2012). *Electrodermal Activity*. 2nd ed. Springer. doi:10.1007/9781461411260

See Also

`edaDownsample` for decimation with anti-aliasing, `edaArtifact` for artifact detection and correction, `edaDecompose` for tonic/phasic decomposition

---

`edaPeaks` *Detect Skin Conductance Response (SCR) Peaks*

Usage

```
edaPeaks(
  x,
  method = c("gradient", "threshold"),
  amplitude_min = 0.01,
  rise_time_min = 0.1,
  rise_time_max = 5,
  assay_name = NULL
)
```

Arguments

`x`	A PhysioExperiment object containing EDA data.
`method`	Detection method: `"gradient"` (first-derivative zero-crossing) or `"threshold"` (amplitude threshold). Default is `"gradient"`.
`amplitude_min`	Minimum SCR amplitude in microsiemens (default: 0.01).

`rise_time_min`	Minimum rise time in seconds (default: 0.1).
`rise_time_max`	Maximum rise time in seconds (default: 5.0).
`assay_name`	Name of the input assay. If NULL, uses `"phasic"` if available, otherwise `defaultAssay(x)`.

Value

A `data.frame` with one row per detected SCR and the following columns:

channel Character channel label.

onset_sample Integer sample index of SCR onset.

onset_sec Numeric onset time in seconds.

peak_sample Integer sample index of SCR peak.

peak_sec Numeric peak time in seconds.

amplitude Numeric SCR amplitude in microsiemens (peak minus onset).

rise_time Numeric rise time from onset to peak in seconds.

recovery_time Numeric 50\

Returns an empty `data.frame` with the same columns if no peaks are found.

Identifies SCR peaks in an EDA signal using either a gradient-based zero-crossing method or an amplitude threshold method. Returns onset, peak, amplitude, rise time, and recovery time for each detected SCR.

Bach, D.R., et al. (2010). "Modelling event-related skin conductance responses." *International Journal of Psychophysiology*, 75(3), 349-356. doi:10.1016/j.ijpsycho.2010.01.005

Benedek, M., & Kaernbach, C. (2010). "A continuous measure of phasic electrodermal activity." *Journal of Neuroscience Methods*, 190(1), 80-91. doi:10.1016/j.jneumeth.2010.04.028

`edaDecompose` for tonic/phasic decomposition (run first), `edaFeatures` for summary feature extraction, `plotPeaks` for peak visualization, `edaErscr` for event-related SCR analysis

---

`edaQuality` *Assess EDA Signal Quality*

Description

Computes per-channel signal quality metrics for electrodermal activity data, including basic statistics, flatline detection, artifact estimation, and an overall quality score.

Usage

```
edaQuality(x, assay_name = NULL)
```

Arguments

`x`	A PhysioExperiment object containing EDA data.
`assay_name`	Name of the input assay. If NULL, uses `defaultAssay(x)`.

Value

A data.frame with one row per channel and the following columns:

channel Channel label

mean_sc Mean skin conductance

sd_sc Standard deviation of skin conductance

min_sc Minimum skin conductance

max_sc Maximum skin conductance

pct_negative Percentage of samples <= 0

pct_flatline Percentage of signal in flatline segments (runs of consecutive near-zero differences longer than 1 second)

pct_artifact Percentage of gradient-based artifact samples

snr_db Estimated signal-to-noise ratio in dB (capped at 60)

quality_score Overall quality score from 0 to 100

quality_label "good" (>= 70), "acceptable" (>= 40), or "poor"

References

Kleckner, I.R., et al. (2018). "Simple, transparent, and flexible automated quality assessment procedures for ambulatory electrodermal activity data." *IEEE Transactions on Biomedical Engineering*, 65(7), 1460-1467. doi:10.1109/TBME.2017.2758643

See Also

`edaArtifact` for artifact detection and correction, `edaFilter` for frequency-domain filtering, `edaDecompose` for tonic/phasic decomposition

---

edaSimulate *Simulate Synthetic EDA Signals*

Description

Generates synthetic electrodermal activity (EDA) signals with known tonic (SCL) and phasic (SCR) components for testing and demonstration. SCRs are modeled as biexponential impulse responses (Bateman function).

Usage

```
edaSimulate(
  n_time = 6000,
  n_channels = 1,
  sr = 10,
  scr_count = 5,
  scl_level = 5,
```

```
  scr_amplitude = 0.5,
  noise_sd = 0.01,
  seed = NULL
)
```

Arguments

`n_time`	Number of time points (default: 6000).
`n_channels`	Number of EDA channels (default: 1).
`sr`	Sampling rate in Hz (default: 10).
`scr_count`	Number of SCRs to embed (default: 5).
`scl_level`	Baseline skin conductance level in microsiemens (default: 5.0).
`scr_amplitude`	Mean SCR amplitude in microsiemens (default: 0.5).
`noise_sd`	Standard deviation of Gaussian noise (default: 0.01).
`seed`	Random seed for reproducibility (default: NULL).

Value

A `PhysioExperiment` object with a single `"raw"` assay containing the simulated EDA signal (time x channels matrix). Channel metadata has `type` = `"EDA"` and `unit` = `"uS"`. The sampling rate is set to `sr`.

References

Boucsein, W. (2012). *Electrodermal Activity*. 2nd ed. Springer. doi:10.1007/9781461411260

Benedek, M., & Kaernbach, C. (2010). "A continuous measure of phasic electrodermal activity." *Journal of Neuroscience Methods*, 190(1), 80-91. doi:10.1016/j.jneumeth.2010.04.028

See Also

`edaDecompose` for tonic/phasic decomposition, `edaPeaks` for SCR detection, `edaFilter` for signal filtering

---

`edaTransform` *Transform EDA Data*

Description

Applies a mathematical transformation to EDA signal data. Common transformations include log and square root (to reduce skewness of SCR amplitudes), z-score standardization, and range normalization. Transformation parameters are stored in metadata so that `edaUntransform` can reverse the operation.

Usage

```
edaTransform(
  x,
  method = c("log", "sqrt", "zscore", "range"),
  assay_name = NULL,
  output_assay = NULL
)
```

Arguments

`x`	A PhysioExperiment object containing EDA data.
`method`	Transformation method: `"log"`, `"sqrt"`, `"zscore"`, or `"range"`.
`assay_name`	Name of the input assay. If NULL, uses `defaultAssay(x)`.
`output_assay`	Name for the output assay. If NULL, defaults to `"{method}_transformed"`.

Value

A modified PhysioExperiment with the transformed assay added and transformation parameters stored in `metadata(x)$eda_transform`.

References

Boucsein, W. (2012). *Electrodermal Activity*. 2nd ed. Springer. doi:10.1007/9781461411260

See Also

`edaUntransform` for reversing the transformation, `edaFeatures` for feature extraction, `edaDecompose` for tonic/phasic decomposition

---

`edaUntransform` *Reverse EDA Transformation*

Description

Reverses a transformation previously applied by `edaTransform`, using parameters stored in `metadata(x)$eda_transform`.

Usage

```
edaUntransform(x, assay_name = NULL, output_assay = NULL)
```

Arguments

`x`	A PhysioExperiment object that has been transformed via `edaTransform`.
`assay_name`	Name of the transformed assay to reverse. If NULL, uses the output_assay recorded in the transform metadata.
`output_assay`	Name for the untransformed output assay. If NULL, defaults to `"untransformed"`.

Value

A modified PhysioExperiment with the untransformed assay added.

References

Boucsein, W. (2012). *Electrodermal Activity*. 2nd ed. Springer. doi:10.1007/9781461411260

See Also

`edaTransform` for applying the initial transformation, `edaDecompose` for tonic/phasic decomposition

---

`make_eda` *Create a Simulated EDA PhysioExperiment*

Description

Generates a synthetic electrodermal activity (EDA) PhysioExperiment object with known tonic (SCL) and phasic (SCR) components. Useful for testing, demonstrations, and vignettes.

Usage

```
make_eda(n_time = 6000, n_channels = 1, sr = 10)
```

Arguments

`n_time`	Number of time points (default: 6000).
`n_channels`	Number of EDA channels (default: 1).
`sr`	Sampling rate in Hz (default: 10).

Value

A `PhysioExperiment` object with a single `"raw"` assay containing simulated EDA data. Channel metadata has `type = "EDA"` and `unit = "uS"`.

References

Boucsein, W. (2012). *Electrodermal Activity*. 2nd ed. Springer. doi:10.1007/9781461411260

See Also

`make_eda_with_scr` for EDA with stimulus events, `edaSimulate` for the underlying simulation function, `edaDecompose` for tonic/phasic decomposition

Examples

```
x <- make_eda()
x
```

`make_eda_with_scr` *Create a Simulated EDA PhysioExperiment with SCR Events*

Description

Generates a synthetic electrodermal activity (EDA) PhysioExperiment object with known SCR events time-locked to stimulus markers. The object includes regularly spaced stimulus events stored via `PhysioEvents`, making it suitable for testing event-related SCR analysis workflows.

Usage

```
make_eda_with_scr(
  n_time = 6000,
  n_channels = 1,
  sr = 10,
  n_events = 4,
  event_interval = 10
)
```

Arguments

`n_time`	Number of time points (default: 6000).
`n_channels`	Number of EDA channels (default: 1).
`sr`	Sampling rate in Hz (default: 10).
`n_events`	Number of stimulus events to embed (default: 4).
`event_interval`	Interval between events in seconds (default: 10). Note: events are spaced evenly within the usable signal duration rather than at exact fixed intervals.

Value

A `PhysioExperiment` object with a single `"raw"` assay containing simulated EDA data and stimulus events accessible via `getEvents`. Each event has `type = "stimulus"` and `duration = 0.5` seconds.

References

Bach, D.R., et al. (2010). "Modelling event-related skin conductance responses." *International Journal of Psychophysiology*, 75(3), 349-356. doi:10.1016/j.ijpsycho.2010.01.005

See Also

`make_eda` for basic EDA without events, `edaErscr` for event-related SCR analysis, `edaSimulate` for the underlying simulation function

Examples

```
x <- make_eda_with_scr()
x
```

`plotDecompose` *Plot EDA Decomposition*

Description

Displays the tonic/phasic decomposition of an EDA signal in a multi-panel layout. Requires that `edaDecompose()` has been run first so that "tonic" and "phasic" assays exist.

Usage

```
plotDecompose(
  x,
  channel = 1,
  time_range = NULL,
  main = "EDA Decomposition",
  ...
)
```

Arguments

`x`	A PhysioExperiment object with tonic and phasic assays.
`channel`	Integer or character specifying which channel to plot (default: 1).
`time_range`	Numeric vector of length 2 giving start and end times in seconds. If NULL, the full signal is plotted.
`main`	Character string for the overall plot title (default: "EDA Decomposition").
`...`	Additional arguments passed to `plot()`.

Value

Invisible NULL. Called for its side effect of producing a plot.

References

Boucsein, W. (2012). *Electrodermal Activity*. 2nd ed. Springer. doi:10.1007/9781461411260

See Also

`plotEda` for basic EDA time series plotting, `edaDecompose` for performing the decomposition, `plotPeaks` for SCR peak visualization

`plotEda` *Plot EDA Time Series*

Description

Plots electrodermal activity signals as time series using base R graphics. Multiple channels are displayed in stacked panels. Optionally overlays vertical event markers.

Usage

```
plotEda(
  x,
  channels = NULL,
  time_range = NULL,
  assay_name = NULL,
  show_events = TRUE,
  main = "EDA Signal",
  col = NULL,
  ...
)
```

Arguments

`x`	A PhysioExperiment object containing EDA data.
`channels`	Integer or character vector specifying which channels to plot. If NULL (default), all channels are plotted.
`time_range`	Numeric vector of length 2 giving start and end times in seconds for zooming (e.g., `c(10, 30)`). If NULL, the full signal is plotted.
`assay_name`	Name of the assay to plot. If NULL, uses `defaultAssay(x)`.
`show_events`	Logical; if TRUE (default) and events exist, draws vertical dashed lines at event onsets.
`main`	Character string for the plot title (default: "EDA Signal").
`col`	Vector of colors for the channels. If NULL, uses default palette.
`...`	Additional arguments passed to `plot()`.

Value

Invisible NULL. Called for its side effect of producing a plot.

References

Boucsein, W. (2012). *Electrodermal Activity*. 2nd ed. Springer. doi:10.1007/9781461411260

See Also

`plotDecompose` for decomposition visualization, `plotPeaks` for SCR peak visualization, `edaDecompose` for tonic/phasic decomposition

---

`plotPeaks` *Plot EDA Signal with SCR Peaks*

Description

Plots an EDA signal with detected SCR peaks, onsets, and amplitude lines annotated. If no peaks data.frame is supplied, peaks are computed automatically via `edaPeaks`.

Usage

```
plotPeaks(
  x,
  peaks = NULL,
  channel = 1,
  time_range = NULL,
  assay_name = NULL,
  main = "SCR Peaks",
  ...
)
```

Arguments

`x`	A PhysioExperiment object containing EDA data.
`peaks`	A data.frame as returned by `edaPeaks`, or NULL to compute peaks automatically.
`channel`	Integer or character specifying which channel to plot (default: 1).
`time_range`	Numeric vector of length 2 giving start and end times in seconds. If NULL, the full signal is plotted.
`assay_name`	Name of the assay to plot. If NULL, uses "phasic" if available, otherwise `defaultAssay(x)`.
`main`	Character string for the plot title (default: "SCR Peaks").
`...`	Additional arguments passed to `plot()`.

Value

Invisible NULL. Called for its side effect of producing a plot.

References

Boucsein, W. (2012). *Electrodermal Activity*. 2nd ed. Springer. doi:10.1007/9781461411260

See Also

`plotEda` for basic EDA time series plotting, `plotDecompose` for decomposition visualization, `edaPeaks` for SCR peak detection

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