

Package ‘GCalcium’

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Type Package

Title A Data Manipulation and Analysis Package for Calcium Indicator Data

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Description Provides shortcuts in extracting useful data points and summarizing waveform data. It is optimized for speed to work efficiently with large data sets so you can get to the analysis phase more quickly. It also utilizes a user-friendly format for use by both beginners and seasoned R users.

Depends R (>= 2.10)

Imports stats, graphics, caTools, dplyr

License GPL-3

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VignetteBuilder knitr

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averaged_trials	<i>Averages signals across trials</i>
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Description

‘averaged_trials’ averages values over each time point, across the specified trials

Usage

```
averaged_trials(Dataframe, Trials)
```

Arguments

Dataframe	a GCalcium-format data frame or matrix
Trials	numbers of trials to be averaged across

Value

a data frame with observation times and averaged values

Examples

```
### Format data frame
df.new <- format_data(GCaMP)

### Plot the average fluorescence signal across trials 1-5
df.1thru5 <- averaged_trials(df.new, 1:5)

plot(x = df.1thru5$Time, df.1thru5$Values)
```

avg_curve_slope	<i>Get average curve slopes</i>
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Description

'avg_curve_slope' finds the average curve slopes for a trial using `inflect_points_df` and `lm`

Usage

```
avg_curve_slope(Dataframe, Trial)
```

Arguments

Dataframe	a GCalcium-format data frame or matrix
Trial	a single trial number

Value

vector of average rate of change for each curve

Note

curves of a single value will result in the average slope being labeled as NA

Examples

```
df.new <- format_data(data = GCaMP)
avg_curve_slope(Dataframe = df.new, Trial = 1)
```

between_trial_change	<i>Compare mean activity between trials</i>
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Description

'between_trial_change' finds the difference in means during same time range between sets of trials.

Usage

```
between_trial_change(Dataframe, TrialRange1, TrialRange2,
  Time.period = c(min(Dataframe[1]), max(Dataframe[1])))
```

Arguments

Dataframe	a GCaMP-format data frame or matrix
TrialRange1	range of trial numbers to be compared to second set of trials
TrialRange2	range of trial numbers to be compared to first set of trials
Time.period	range of time to be compared between sets of trials

Value

Number representing mean difference of trial set 2 and trial set 1

Examples

```
# How much did the mean value change 2s after epoch between trials 1-5 and trials 6-10?
df.new <- format_data(data = GCaMP)
between_trial_change(Dataframe = df.new, TrialRange1 = c(1, 5),
  TrialRange2 = c(6, 10), Time.period = c(0, 2))
```

centered_AUC

Compute centered area under curve

Description

‘centered_AUC’ computes the area under the curve (AUC) after centering values using a specified function, such as mean or min. Computed using trapezoidal integration.

Usage

```
centered_AUC(Dataframe, Trial, FUN = mean)
```

Arguments

Dataframe	a GCalcium-format data frame or matrix
Trial	a single trial number
FUN	a function to apply to each window

Value

Data frame of AUCs and curve number for each curve

Examples

```
# Get AUCs for trial 2, centered at the mean
df.new <- format_data(data = GCaMP)
centered_AUC(Dataframe = df.new, Trial = 2, FUN = mean)
```

`consecutive_trial_change`*Compare mean activity in consecutive trials*

Description

'consecutive_trial_change' finds the change in means between consecutive trials.

Usage

```
consecutive_trial_change(Dataframe, Trials, Time.period)
```

Arguments

Dataframe	a GCaMP-format data frame or matrix
Trials	range of trial numbers to be compared
Time.period	range of time to be compared

Value

Data frame with the "Mean.Change" column representing differences in means between trial n and trial n + 1 for the user-inputted range of trials.

Examples

```
### How much did the mean value change after epoc between consecutive trials in trials 1-10?  
df.new <- format_data(data = GCaMP)  
consecutive_trial_change(Dataframe = df.new, Trials = c(1, 10), Time.period = c(0, 4))
```

`find_peaks`*Get peaks/valleys in waveform data*

Description

'find_peaks' finds peaks or valleys in waveform by using inflection points, with filter of 'n' increasing/decreasing points on both sides of each inflection point.

Usage

```
find_peaks(x, n.points = 3)
```

Arguments

x	vector of numbers
n.points	the number of decreasing (peaks) or increasing (valleys) data points on left and right of inflection point required to be considered a "peak". A positive number as an input finds peaks, and a negative number finds valleys.

Value

a numeric vector of indices

Examples

```
### Format data frame
df.new <- format_data(GCaMP)

### How many peaks are there in trial 1 with 10 decreasing data points on each side?
peak.indices <- find_peaks(df.new$Trial1, n.points = 10)

### When do they occur?
data.frame(times = df.new$Time[peak.indices], vals = df.new$Trial1[peak.indices])
```

format_data	<i>Reformat and label data into GCalcium format</i>
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Description

‘format_data’ changes the format of data from wide time series to long format with labeled columns. If data is already in long format, the function simply re-labels the columns

Usage

```
format_data(data)
```

Arguments

data	A data set with observation times in the first row or column, and observed values from trials in each following row or column.
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Value

Data frame with labeled time and trial columns

Examples

```
df.new <- format_data(GCaMP)
```

GCaMP	<i>Pre-filtered GCaMP calcium activity waveforms</i>
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Description

A dataset containing calcium activity and observed times during a behavioral paradigm pilot study; organized into 10 individual trials

Usage

```
data(GCaMP)
```

Format

A data frame with 11 rows and 814 columns

Time observed times of Trial.n values, in seconds

Trial.n values of calcium activity signals for trial n ...

Source

Dr. David Root, Maier-Watkins laboratory

inflect_points	<i>Find inflection points</i>
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Description

'inflect_points' finds inflection points of waveform data

Usage

```
inflect_points(x)
```

Arguments

x A vector of numbers

Value

Inflection points of the input vector

Examples

```
df.new <- format_data(GCaMP)
inflect_points(df.new$Trial1)
```

inflect_points_df *Find inflection points and curve numbers*

Description

'inflect_points_df' finds inflection points of activity waves, returning a summarized data frame

Usage

```
inflect_points_df(Dataframe, Trial)
```

Arguments

Dataframe a GCalcium-format data frame or matrix
Trial a single trial number

Value

data frame with variables indicating the time, raw values, curve numbers, and inflection points corresponding to each data point of the input

Examples

```
df.new <- format_data(GCaMP)  
inflect_points_df(Dataframe = df.new, Trial = 1)
```

moving_window *Summarize data within windows of time*

Description

'moving_window' summarizes data within windows of a certain length.

Usage

```
moving_window(Dataframe, Trial, Window.length, FUN = mean)
```

Arguments

Dataframe a GCalcium-format data frame or matrix
Trial a single trial number
Window.length length of time each window encompasses
FUN a function to apply to each window

Value

a data frame with start and stop times of each window, the chronological number of each window, and summarized values

Examples

```
### Format data frame
df.new <- format_data(GCaMP)

### In trial 5, how does the average fluorescence change in 1 second time frames?
moving_window(Dataframe = df.new, Trial = 5, Window.length = 1, FUN = mean)
```

perc_baseline	<i>Find the percent change from baseline</i>
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Description

'perc_baseline' calculates the percent change from a user-specified baseline period

Usage

```
perc_baseline(Dataframe, Baseline.times, Baseline.frame = FALSE)
```

Arguments

Dataframe a GCalcium-format data frame or matrix
 Baseline.times range of time from Baseline.frame to compute the baseline value from
 Baseline.frame a GCalcium-format data frame or matrix containing the baseline period. If frame
 is not specified, Dataframe is automatically used

Value

a GCalcium-format data frame with values transformed to percent baseline

Examples

```
### Format data frame
df.new <- format_data(GCaMP)

### Transform into percent baseline: relative to -3s to -1s before epoc
perc_baseline(Dataframe = df.new, Baseline.times = c(-3, -1))
```

plot_trials	<i>Plot specified trials</i>
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Description

'plot_trials' plots the user-inputted trials. This function automatically adjusts the x- and y- axis limits to fit all data

Usage

```
plot_trials(Dataframe, Trials, ...)
```

Arguments

Dataframe	a GCalcium-format data frame or matrix
Trials	set of trials to be plotted
...	extra commands to be called to the blank base plot

Value

a single plot of user-specified trials

Examples

```
### Format data frame
df.new <- format_data(GCaMP)

### Specify and plot trials
my.trials <- c(1, 2, 7, 8)
plot_trials(Dataframe = df.new, Trials = my.trials)
```

within_trial_change	<i>Get mean activity change within a trial</i>
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Description

'within_trial_change' finds the change in mean values between beginning and end of entered time range.

Usage

```
within_trial_change(Dataframe, Trial, Beg.period = FALSE,
  End.period = FALSE)
```

Arguments

Dataframe	a GCalcium-format data frame or matrix
Trial	a single trial number
Beg.period	time frame of period 1 to be compared to period 2
End.period	time frame of period 2 to be compared to period 1

Value

vector with AUC for each curve in a trial

Examples

```
# In trial 1, how much did the mean value change between -2s and 0s, and 0 and 2s?
df.new <- format_data(data = GCaMP)
within_trial_change(Dataframe = df.new, Trial = 1, Beg.period = c(-2, 0), End.period = c(0, 2))
```

z_score	<i>Transform values into z scores</i>
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Description

'z_score' transforms input values to z scores. Allows user input of mu and sigma values for comparing distributions.

Usage

```
z_score(xvals, mu = FALSE, sigma = FALSE)
```

Arguments

xvals	vector of numbers
mu	the population mean
sigma	the population standard deviation

Value

a numeric vector of z scores

Examples

```
# Format data
df.new <- format_data(GCaMP)

# Split data
basevals <- df.new$Trial1[df.new$Time <= 0]
eventvals <- df.new$Trial1[df.new$Time > 0]

# Find baseline (pre-epoc) values
base.mu <- mean(basevals)
base.sigma <- sd(basevals)

# Compute values
z_score(x = eventvals, mu = base.mu, sigma = base.sigma)
```

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