Package ‘PupillometryR’

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Type Package

Title A Unified Pipeline for Pupillometry Data

Version 0.0.5

Description Provides a unified pipeline to clean, prepare, plot, and run basic analyses on pupillometry experiments.

BugReports https://github.com/samhforbes/PupillometryR/issues

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Encoding UTF-8

LazyData true

Depends R (>= 3.5.0), dplyr, ggplot2, rlang

Imports fda, itsadug, mgcv, signal, stats, stringr, tidyr, utils, zoo

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Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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baseline_data

Baseline pupil data to the average pupil size within a window

Description

This function is for use with the PupillometryR package to baseline each participant’s pupil size to the mean pupil size within a window. This may not be necessary if you are doing purely within-subject analyses, but it is convenient for comparison across subjects, and makes results more uniform.

Usage

baseline_data(data, pupil, start, stop)

Arguments

data a PupillometryR dataframe
pupil a column name denoting pupil data
start start time of baseline window
stop stop time of baseline window

Value

A PupillometryR dataframe, with baselined pupil
`calculate_mean_pupil_size`  

**Examples**

```r
data <- make_pupillometry_data(data = pupil_data,  
   subject = ID,  
   trial = Trial,  
   time = Time,  
   condition = Type)
regressed_data <- regress_data(data = Sdata, pupil1 = RPupil, pupil2 = LPupil)
mean_data <- calculate_mean_pupil_size(data = regressed_data, pupil1 = RPupil, pupil2 = LPupil)
base_data <- baseline_data(data = mean_data, pupil = mean_pupil, start = 0, stop = 100)
```

**calculate_mean_pupil_size**  

*Calculate a mean size across two pupils over time*

**Description**

This function is useful when you have left and right eye eyetracking data, and a mean of the two would be useful.

**Usage**

```r
calculate_mean_pupil_size(data, pupil1, pupil2)
```

**Arguments**

- `data`: a PupillometryR dataframe
- `pupil1`: column name indicating pupil size
- `pupil2`: column name indicating pupil size

**Value**

A PupillometryR dataframe with a mean pupil column

**Examples**

```r
data <- make_pupillometry_data(data = pupil_data,  
   subject = ID,  
   trial = Trial,  
   time = Time,  
   condition = Type)
regressed_data <- regress_data(data = Sdata, pupil1 = RPupil, pupil2 = LPupil)
mean_data <- calculate_mean_pupil_size(data = regressed_data, pupil1 = RPupil, pupil2 = LPupil)
```
**clean_missing_data**

*Calculate the missing data amount*

**Description**

This function can be used to assess the amount of samples that have problematic data from each trial, which helps assess cleaning parameters.

**Usage**

```r
calculate_missing_data(data, pupil)
```

**Arguments**

- `data` your data of class PupillometryR
- `pupil` a column name denoting pupil size

**Value**

A summary table with number of missing samples in each trial

**Examples**

```r
data(pupil_data)
Sdata <- make_pupillometryr_data(data = pupil_data,
subject = ID,
trial = Trial,
time = Time,
condition = Type)
new_data <- downsample_time_data(data = Sdata,
pupil = LPupil,
timebin_size = 50,
option = 'mean')
calculate_missing_data(data = new_data, pupil = LPupil)
```

---

**clean_missing_data**

*Clean missing data above an acceptable threshold*

**Description**

This function can be used to remove trials and participants who do not meet the threshold for a study. Note that there are two parameters for cleaning, one to remove trials above a threshold, the second to remove participants who drop more than a certain amount of trials.
create_difference_data

Usage

```r
clean_missing_data(
  data,
  pupil,
  trial_threshold = 1,
  subject_trial_threshold = 1
)
```

Arguments

- `data`: your data of class PupillometryR
- `pupil`: a column name denoting pupil size
- `trial_threshold`: a proportion of missing data over which a trial can be considered lost
- `subject_trial_threshold`: a proportion of missing trials over which a participant can be considered lost.

Value

A cleaned PupillometryR dataframe

Examples

```r
data(pupil_data)
Sdata <- make_pupillometryr_data(data = pupil_data,
subject = ID,
trial = Trial,
time = Time,
condition = Type)
new_data <- downsample_time_data(data = Sdata,
pupil = LPupil,
timebin_size = 50,
option = 'mean')
calculate_missing_data(data = new_data, pupil = LPupil)
```

create_difference_data

Create a difference data frame when dealing with a condition column with 2 levels

Description

The difference data frame is used when creating a dataframe to do the functional t-test analysis. This function would be the first step in that analysis, after doing the pre-processing. It creates a frame where it treats the condition data as level2 - level1. It will throw an error if there are more than two conditions.
Usage

create_difference_data(data, pupil)

Arguments

data a PupilometryR dataframe
pupil column name for pupil data

Value

A Pupil_difference_data data frame

Examples

Sdata <- make_pupillometryr_data(data = pupil_data,
subject = ID,
trial = Trial,
time = Time,
condition = Type)
mean_data <- calculate_mean_pupil_size(data = Sdata,
pupil1 = RPupil, pupil2 = LPupil)
base_data <- baseline_data(data = mean_data, pupil = mean_pupil, start = 0, stop = 100)
differences <- create_difference_data(data = base_data, pupil = mean_pupil)
plot(differences, pupil = mean_pupil, geom = 'line')

create_functional_data

Makes a functional data with splines from a Pupil_difference_data dataframe.

Description

This function turns difference data into fitted splines in order to carry out functional data analysis. Under the hood this passes basis and order to fda::Data2fd, and fda::create.bspline.basis, and is mandatory before running run_functional_t_test. It is recommended to read the documentation for package fda for further information.

Usage

create_functional_data(data, pupil, basis, order)

Arguments

data a Pupil_difference_data dataframe
pupil Column name indicating pupil data to fit
basis Integer specifying number of basis functions to create a b-spline basis
order Integer specifying order of b-splines (one higher than the degree)
create_time_windows

Value

A Pupil_difference_data dataframe fitted with b-splines.

See Also

tda package

Examples

Sdata <- make_pupillometryr_data(data = pupil_data,
                   subject = ID,
                   trial = Trial,
                   time = Time,
                   condition = Type
regressed_data <- regressed_data(data = Sdata, pupil1 = RPupil, pupil2 = LPupil)
mean_data <- calculate_mean_pupil_size(data = regressed_data, pupil1 = RPupil, pupil2 = LPupil)
base_data <- baseline_data(data = mean_data, pupil = mean_pupil, start = 0, stop = 100)
differences <- create_difference_data(data = base_data, pupil = mean_pupil)
spline_data <- create_functional_data(data = differences, pupil = mean_pupil, basis = 10, order = 4)

create_time_windows

Make PupilometryR dataframe into multiple time windows for easy analysis

Description

This function creates a single collapsed data frame for easy analysis with an anova or model, per condition. By comparison create_window_data allows collapsing all into a single time window.

Usage

create_time_windows(data, pupil, breaks)

Arguments

data a PupilometryR dataframe
pupil column name denoting pupil data to be used
breaks a vector or numbers indicating start times for each window

Value

a Pupil_window_data dataframe
create_window_data

Make PupilometryR dataframe into a single collapsed window for easy analysis

Description

This function creates a single collapsed data frame for easy analysis with a t-test or anova, per condition. By comparison create_time_windows allows dividing it into multiple windows per time.

Usage

create_window_data(data, pupil)

Arguments

data a PupillometryR dataframe
pupil column name denoting pupil data to be used

Value

a Pupil_window_data dataframe

Examples

Sdata <- make_pupillometryr_data(data = pupil_data,
    subject = ID,
    trial = Trial,
    time = Time,
    condition = Type)
regressed_data <- regress_data(data = Sdata, pupil1 = RPupil, pupil2 = LPupil)
mean_data <- calculate_mean_pupil_size(data = regressed_data,
pupil1 = RPupil, pupil2 = LPupil)
base_data <- baseline_data(data = mean_data, pupil = mean_pupil, start = 0, stop = 100)
time_window <- create_time_windows(data = base_data, pupil = mean_pupil,
    breaks = c(1000, 2000))

window <- create_window_data(data = base_data, pupil = mean_pupil)
p <- plot(window, pupil = mean_pupil, windows = FALSE, geom = 'boxplot')
p
**detect_blinks_by_column**

*detect blinks by a pre-existing labelled blink column that comes from the eyetracker*

**Description**

This allows the user to remove anything classed as a blink as a result of eyetracker output.

**Usage**

```r
detect_blinks_by_column(
  data,
  pupil,
  column,
  extend_forward = 0,
  extend_back = 0,
  .tag = 1
)
```

**Arguments**

- `data`: dataset of class PupillometryR
- `pupil`: column name for pupil data
- `column`: column that refers to blinks
- `extend_forward`: number of observations to remove forward of blink
- `extend_back`: number of observations to remove behind blink
- `.tag`: the variable in the blink column that represents a blink

**Value**

returns dataframe with blinks removed including forward and back, and data in blink column.

**Examples**

```r
## Not run:
Sdata <- make_pupillometryr_data(data = pupil_data, 
sample = ID, 
trial = Trial, 
time = Time, 
condition = Type)
Sdata2 <- detect_blinks_by_column(data = Sdata, 
pupil = LPupil, 
column = data_in_blink, 
extend_forward = 0, 
extend_back = 0)
```
**detect_blinks_by_size**  
*detect blinks by a change in pupil size*

**Description**
This allows the user to set a threshold for pupil size and remove anything classed as a blink as a result.

**Usage**
```r
detect_blinks_by_size(
    data,  
pupil, 
    threshold = 2.5,  
    extend_forward = 0,  
    extend_back = 0
)
```

**Arguments**
- `data` : dataset of class PupillometryR
- `pupil` : column name for pupil data
- `threshold` : velocity threshold for blink detection
- `extend_forward` : number of observations to remove forward of blink
- `extend_back` : number of observations to remove behind blink

**Value**
returns dataframe with blinks removed including forward and back, and data in blink column.

**Examples**
```r
Sdata <- make_pupillometryr_data(data = pupil_data,
                                 subject = ID,
                                 trial = Trial,
                                 time = Time,
                                 condition = Type)

Sdata2 <- detect_blinks_by_size(data = Sdata,
                                 pupil = LPupil,
                                 threshold = 2.5,
                                 extend_forward = 0,
                                 extend_back = 0)
```
detect_blinks_by_velocity

*detect blinks by a change in velocity*

**Description**

This allows the user to set a threshold for velocity and remove anything classed as a blink as a result.

**Usage**

```r
detect_blinks_by_velocity(
  data,
  pupil,
  threshold = 0.1,
  extend_forward = 0,
  extend_back = 0
)
```

**Arguments**

- `data`: dataset of class PupillometryR
- `pupil`: column name for pupil data
- `threshold`: velocity threshold for blink detection
- `extend_forward`: number of observations to remove forward of blink
- `extend_back`: number of observations to remove behind blink

**Value**

returns dataframe with blinks removed including forward and back, and data in blink column.

**Examples**

```r
Sdata <- make_pupillometryr_data(data = pupil_data,
                               subject = ID,
                               trial = Trial,
                               time = Time,
                               condition = Type)

Sdata2 <- detect_blinks_by_velocity(data = Sdata,
                                     pupil = LPupil,
                                     threshold = 0.1,
                                     extend_forward = 0,
                                     extend_back = 0)
```
downsample_time_data  

**Downsample frequency to reduce number of samples and data size**

Description

This function is useful if you were sampling at a very high frequency (eg 500Hz) causing the data size to be hard to manage, and high autocorrelation. Careful decisions should be made about the time bin size and appropriateness of this function, with respect to the data type.

Usage

```r
downsample_time_data(data, pupil, timebin_size, option = c("mean", "median"))
```

Arguments

- `data`: your data of class PupillometryR
- `pupil`: a column name denoting pupil size
- `timebin_size`: the size of the new timebin you wish to use
- `option`: what should be calculated in each timebin - mean or median. Defaults to mean.

Value

A downsampled dataframe of class PupillometryR

Examples

```r
data(pupil_data)
Sdata <- make_pupillometryr_data(data = pupil_data,
subject = ID,
trial = Trial,
time = Time,
condition = Type)
new_data <- downsample_time_data(data = Sdata,
pupil = LPupil,
timebin_size = 50,
option = 'mean')
```

filter_data  

**Run a filter on the data to smooth it out.**

Description

filter_data allows three different options for filtering, a butterworth lowpass filter, a hanning filter, or a median filter. You can also set the degree of this filter; we recommend a default of 11. This filters on one pupil, it can be re-run on a second pupil if needed. Lowpass makes use of the butterworth filter and filtfilt from package signal, median makes use of runmed.
Usage

```r
filter_data(
  data,
  pupil,
  filter = c("median", "hanning", "lowpass"),
  degree = 11
)
```

Arguments

- `data` a PupillometryR dataframe
- `pupil` column name for pupil data
- `filter` option for filtering the data
- `degree` filter degree

Value

filtered pupil data

Examples

```r
Sdata <- make_pupillometryr_data(data = pupil_data,
  subject = ID,
  trial = Trial,
  time = Time,
  condition = Type)
mean_data <- calculate_mean_pupil_size(data = Sdata,
  pupil1 = RPupil, pupil2 = LPupil)
filtered_data <- filter_data(data = mean_data,
  pupil = mean_pupil,
  filter = "hanning",
  degree = 11)
```

Description

Borrowed from Ben Marwick. Original author David Robinson.
Description

ggplot Flat Violin

Usage

geom_flat_violin(
  mapping = NULL,
  data = NULL,
  stat = "ydensity",
  position = "dodge",
  trim = TRUE,
  scale = "area",
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

Arguments

  mapping  A value
  data     A value
  stat     A value
  position A value
  trim     A value
  scale    A value
  show.legend A value
  inherit.aes A value
  ...

Details


Examples

```r
ggplot(diamonds, aes(cut, carat)) + geom_flat_violin() + coord_flip()
```

Description

Borrowed from https://gist.github.com/benmarwick/2a1bb0133ff568cbe28d/raw/fb53bd97121f7f9ce947837ef1a4c65a73bffb3f/geom_flat_violin.R.

Original author David Robinson, from https://gist.github.com/dgrtwo/eb7750e74997891d7c20

interpolate_data

Interpolate across the gaps in data

Description

Once data is smoothed, it is important to deal with missing observations, such as blinks. This allows simple interpolation over missing values, either linear, or cubic. Depending on the analysis planned, this may not be a necessary option, but it is strongly recommended for the functional analyses planned in this package.

Usage

```r
interpolate_data(data, pupil, type = c("linear", "cubic"))
```

Arguments

- `data` a PupilometryR dataframe
- `pupil` Column name for pupil data to be interpolated
- `type` string indicating linear or cubic interpolation to be performed.

Value

interpolated pupillometry data
Examples

Sdata <- make_pupillometryr_data(data = pupil_data,
   subject = ID,
   trial = Trial,
   time = Time,
   condition = Type)
mean_data <- calculate_mean_pupil_size(data = Sdata,
   pupil1 = RPupil, pupil2 = LPupil)
filtered_data <- filter_data(data = mean_data,
   pupil = mean_pupil,
   filter = 'hanning',
   degree = 11)
int_data <- interpolate_data(data = filtered_data,
   pupil = mean_pupil,
   type = 'linear')

Description

This should be the first function you run as part of using PupillometryR. This will make sure your data is in the right format for processing. This package is designed to deal with data at it comes out of the eyetracker in a long-form csv style format. Thus data input here would be a long dataframe, wherein each row is a single frame collected by the eyetracker.

Usage

make_pupillometryr_data(data, subject, trial, time, condition, other)

Arguments

data a raw, long form dataframe organised by subject, trial, and time. if your data is not long form, look at tidyr for examples of conversion.
subject column name indicating subject ID
trial column name indicating trial ID. This should be unique for participants
time column name indicating time column (should be numeric)
condition column name indicating experimental condition
other any other column you may wish to keep in the data frame for processing

Value

A dataframe ready to use in PupillometryR
Examples

Sdata <- make_pupillometryr_data(data = pupil_data,
subject = ID,
trial = Trial,
time = Time,
condition = Type)

mean2

Helper function mean2

Description

Somewhat useful function for ignoring NAs

Usage

mean2(x)

Arguments

x the object

plot.PupillometryR

Pre-prepared plots of PupillometryR data

Description

The plot functions are designed to run with just data and pupil selections, with some additional options for fun with plotting. This allows to see raw data as points, grouped by either subject or condition.

Usage

## S3 method for class 'PupillometryR'
plot(
  x,
pupil,
group = c("none", "condition", "subject"),
geom = c("point", "line", "pointrange"),
model = NULL,
...
)
plot.Pupil_difference_data

Pre-prepared plots of PupillometryR data

Description

The plot functions are designed to run with just data and pupil selections, with some additional options for fun with plotting. To see these plots, you must first use create_difference_data.

Usage

```r
## S3 method for class 'Pupil_difference_data'
plot(x, pupil, geom = c("point", "line"), colour = "black", ...)
```

Arguments

- `x`: A Pupil_difference_data dataframe
- `pupil`: Column name of pupil data to be plotted
- `geom`: String indicating whether made of connected points or a line
- `colour`: String indicating colour of geom, passed to ggplot2
- `...`: Ignored

Examples

```r
Sdata <- make_pupillometryr_data(data = pupil_data,
subject = ID,
trial = Trial,
time = Time,
condition = Type)
Sdata2 <- downsample_time_data(data = Sdata,
pupil = LPupil,
timebin_size = 100,
option = 'median')
p <- plot(Sdata2, pupil = LPupil, group = 'subject')
p
```
**plot.Pupil_test_data**

Value

A ggplot object

Examples

```r
Sdata <- make_pupillometryr_data(data = pupil_data,
subject = ID,
trial = Trial,
time = Time,
condition = Type)
regressed_data <- regress_data(data = Sdata, pupil1 = RPupil, pupil2 = LPupil)
mean_data <- calculate_mean_pupil_size(data = regressed_data,
pupil1 = RPupil, pupil2 = LPupil)
base_data <- baseline_data(data = mean_data, pupil = mean_pupil, start = 0, stop = 100)
differences <- create_difference_data(data = base_data,
pupil = mean_pupil)
p <- plot(differences, pupil = mean_pupil, geom = 'line')
p
```

---

**plot.Pupil_test_data Pre-prepared plots of PupillometryR data**

Description

The plot functions are designed to run with just data and pupil selections, with some additional options for fun with plotting. To see these plots, you must first use one of the run_functional tests.

Usage

```r
## S3 method for class 'Pupil_test_data'
plot(x, show_divergence = TRUE, colour = "black", fill = "grey", ...)
```

Arguments

- `x`: A Pupil_test_data dataframe
- `show_divergence`: logical indicating whether divergences are to be highlighted
- `colour`: string indicating colour of geom_line, passed to ggplot2
- `fill`: string indicating fill hue of divergence highlights, passed to ggplot2
- `...`: Ignored

Value

A ggplot object
Examples

Sdata <- make_pupillometryr_data(data = pupil_data,
subject = ID,
trial = Trial,
time = Time,
condition = Type)
regressed_data <- regress_data(data = Sdata, pupil1 = RPupil, pupil2 = LPupil)
mean_data <- calculate_mean_pupil_size(data = regressed_data,
pupil1 = RPupil, pupil2 = LPupil)
base_data <- baseline_data(data = mean_data, pupil = mean_pupil, start = 0, stop = 100)
differences <- create_difference_data(data = base_data,
pupil = mean_pupil)
spline_data <- create_functional_data(data = differences, pupil = mean_pupil)
ft_data <- run_functional_t_test(data = spline_data,
pupil = mean_pupil)
p <- plot(ft_data, show_divergence = TRUE, colour = 'red', fill = 'orange')
p

plot.Pupil_window_data

Pre-prepared plots of PupillometryR data

Description

The plot functions are designed to run with just data and pupil selections, with some additional options for fun with plotting. To see these plots, you must first use create_window_data.

Usage

## S3 method for class 'Pupil_window_data'
plot(
x,
pupil,
windows = c(FALSE, TRUE),
geom = c("raincloud", "violin", "boxplot"),
...
)

Arguments

x A Pupil_window_data dataframe
pupil Column name of pupil data to be plotted
windows Whether you want to include time windows in the plot - logical
geom violin plots or boxplots. The newest version adds raincloud plots using Ben Marwick’s flat violin plot.
... Ignored
**pupil_data**

**Value**

A ggplot object

**Examples**

```r
data <- make_pupillometryr_data(data = pupil_data,
  subject = ID,
  trial = Trial,
  time = Time,
  condition = Type)
regressed_data <- regress_data(data = Sdata, pupil1 = RPupil, pupil2 = LPupil)
mean_data <- calculate_mean_pupil_size(data = regressed_data,
  pupil1 = RPupil, pupil2 = LPupil)
base_data <- baseline_data(data = mean_data, pupil = mean_pupil, start = 0, stop = 100)
window <- create_window_data(data = base_data, pupil = mean_pupil)
p <- plot(window, pupil = mean_pupil, windows = FALSE, geom = 'boxplot')
p
```  

---

**pupil_data**  
Data collected in a pupillometry study by Sylvain Sirois

**Description**

Data from a simple study measuring pupil dilation as participants answer hard or easy maths problems. Original data sourced and reformatted from Sylvain Sirois’ Pupillometry tutorial available at https://oraprdnt.uqtr.uquebec.ca/pls/public/gscw031?owa_no_site=314&owa_no_fiche=3&owa_bottin=

**Usage**

pupil_data

**Format**

A data frame with 28800 rows and 7 variables:

- **ID** Unique participant ID
- **Trial** Unique trial code (also unique for each participant)
- **RPupil** Right pupil size
- **LPupil** Left Pupil Size
- **Timebin** Ordered timebin within each trial
- **Time** Elapsed time within trial
- **Type** Hard or easy trial?

**Source**

(https://oraprdnt.uqtr.uquebec.ca/pls/public/gscw031?owa_no_site=314&owa_no_fiche=3&owa_bottin=)
replace_missing_data

replace_missing_data replaces missing observations if you have some degree of incomplete observations

Description

This is a useful function if you have a dataset where certain timepoints have been removed for whatever reason, but you want continuous time data. This will make assumptions about trials being the same length though, so may not be appropriate for all data types. This should only be run after running make_pupillometry_data.

regress_data

Regress one pupil against another for extra smoothing

Description

regress_data runs a simple linear regression of pupil1 against pupil2 and the reverse. This can help to account for small amount of bumpiness in the data. The regression runs over each participant and each trial, per time.

Usage

regress_data(data, pupil1, pupil2)

Arguments

data a PupillometryR dataframe

pupil1 Column name for first pupil data

pupil2 Column name for second pupil data

Value

a PupillometryR dataframe with smoothed pupil values

Examples

Sdata <- make_pupillometryr_data(data = pupil_data,
subject = ID,
trial = Trial,
time = Time,
condition = Type)
regressed_data <- regress_data(data = Sdata,
pupil1 = RPupil,
pupil2 = LPupil)
mean_data <- calculate_mean_pupil_size(data = regressed_data,
pupil1 = RPupil, pupil2 = LPupil)
run_functional_t_test

Usage

replace_missing_data(data)

Arguments

data your data of class pupillometryR

Value

A time-stepped data frame

Examples

data(pupil_data)
Sdata <- make_pupillometryr_data(data = pupil_data,
subject = ID,
trial = Trial,
time = Time,
condition = Type)
new_data <- replace_missing_data(data = Sdata)

run_functional_t_test

Run a functional t-test on a dataframe previously fitted with b-splines.

Description

This allows running of a functional t-test for a given alpha on pupil data that has been fitted with b-splines. This is only appropriate for functional difference data, as it assumes we are dealing with condition A - condition B.

Usage

run_functional_t_test(data, pupil, alpha = 0.05)

Arguments

data a Pupil_difference_data fitted with b-splines
pupil column name indicating pupil data to test
alpha an alpha level to be set for the t-test

Value

A Pupil_test_data dataframe
subset_data

Subset data to provide start and finish time windows

Description

subset_data can be used on a PupillometryR dataframe to subset the time into relevant chunks. This, ideally should be one of the first functions run, before anything analytical. Use this to indicate a start and stop time to create a new resized dataframe.

Usage

subset_data(data, start = NULL, stop = NULL, rezero = T, remove = T)

Arguments

data a PupillometryR dataframe
start a single number indicating start time of new dataframe
stop a single number indicating end time of new dataframe
rezero logical, whether time should start from zero
remove logical, remove observations outside of start and stop

Value

a subsetted PupillometryR dataframe

Examples

Sdata <- make_pupillometryr_data(data = pupil_data,
  subject = ID,
  trial = Trial,
  time = Time,
  condition = Type)

subset_data(Sdata, start = 100, stop = 10000, rezero = TRUE, remove = TRUE)
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