

# Package ‘PupillometryR’

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**Type** Package

**Title** A Unified Pipeline for Pupillometry Data

**Version** 0.0.7

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

**BugReports** <https://github.com/samhforbes/PupillometryR/issues>

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

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

**Imports** fda, mgcv, signal, stats, stringr, tidyverse, utils, zoo

**RoxygenNote** 7.3.3

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Index****25****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

## 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)
```

---

### 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

```
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

```
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)
```

---

**calculate\_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**

```
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**

```
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 removes trials and participants who exceed specified thresholds for missing data. There are two main parameters for cleaning: one to remove trials with excessive missing data, and another to remove participants who drop more than a specified proportion of trials. An optional parameter allows you to specify the total number of trials expected for each participant, which is used to calculate the proportion of missing trials.

**Usage**

```
clean_missing_data(
  data,
  pupil,
  trial_threshold = 1,
  subject_trial_threshold = 1,
  total_trials_expected = NULL
)
```

**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 is considered lost.  
**subject\_trial\_threshold** A proportion of missing trials over which a participant is considered lost.  
**total\_trials\_expected** (Optional) The total number of trials expected for each participant. If specified, it will be used to calculate the proportion of missing trials. If not specified, the proportion is calculated based on the total number of trials in the data.

**Value**

A cleaned PupillometryR dataframe with trials and participants exceeding the thresholds removed.

**Examples**

```
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 PupillometryR 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)

**Value**

A Pupil\_difference\_data dataframe fitted with b-splines.

**See Also**

fda package

**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, basis = 10, order = 4)
```

create\_time\_windows    *Make PupillometryR 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 PupillometryR 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

**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))
```

**create\_window\_data** *Make PupillometryR 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)
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

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

### Arguments

data	dataset of class PupilometryR
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 data frame with blinks removed including forward and back, and data in blink column.

### Examples

```
## Not run:
Sdata <- make_pupilometryr_data(data = pupil_data,
  subject = 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)

## End(Not run)
```

---

**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

```
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

```
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**

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

**Arguments**

data	dataset of class PupilometryR
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 obervations to remove behind blink

**Value**

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

**Examples**

```
Sdata <- make_pupilometryr_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

```
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

```
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	<i>Run a filter on the data to smooth it out.</i>
-------------	---

---

## 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

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

## Arguments

data	a PupillometryR data frame
pupil	column name for pupil data
filter	option for filtering the data
degree	filter degree

## Value

filtered pupil 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)
```

---

GeomFlatViolin	<i>geom_flat_violin_HELPER2</i>
----------------	---------------------------------

---

## Description

Borrowed from [Ben Marwick](#). Original author David Robinson.

---

geom_flat_violin	<i>ggplot Flat Violin</i>
------------------	---------------------------

---

## 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
...	A value

## Details

Copy-pasted from <https://gist.github.com/benmarwick/2a1bb0133ff568cbe28d/raw/fb53bd97121f7f9ce947837ef1a> somewhat hackish solution to: <https://twitter.com/EamonCaddigan/status/646759751242620928> based mostly on copy/pasting from ggplot2 geom\_violin source: <https://github.com/hadley/ggplot2/blob/master/R/geom-violin.r> The original seems to be: sourced from: <https://gist.github.com/dgrtwo/eb7750e74997891d7c20>, Author is David Robinson. A key internal function for the raincloud plots used as a plotting option in this package. For information on raincloud plots see: Allen, M., Poggiali, D., Whitaker, K., Marshall, T. R., & Kievit, R. A. (2019). Raincloud plots: a multi-platform tool for robust data visualization. *Wellcome open research*, 4, 63. doi:10.12688/wellcomeopenres.15191.1

## Examples

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

---

gfv_helper1	<i>geom_flat_violin_HELPER1</i>
-------------	---------------------------------

---

## Description

Borrowed from <https://gist.github.com/benmarwick/2a1bb0133ff568cbe28d/raw/fb53bd97121f7f9ce947837ef1a>  
Original author David Robinson, from <https://gist.github.com/dgrtwo/eb7750e74997891d7c20>

---

interpolate_data	<i>Interpolate across the gaps in data</i>
------------------	--

---

## 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

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

## Arguments

data	a PupilometryR dataframe
pupil	Column name for pupil data to be interpolated
type	string indicating linear or cubic interpolation to be performed.
maxgap	numeric value specifying the maximum gap size (number of consecutive NAs) to interpolate. Default is Inf (interpolates gaps of any length).

**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')
```

**make\_pupillometryr\_data**

*Prepare data for pre-processing in PupillometryR*

**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 as 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 tidy 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,
  ...
)
```

**Arguments**

x	A PupillometryR dataframe
pupil	Column name of pupil data to be plotted
group	What to group the data by (none, condition, or subject)
geom	Geom to pass to ggplot. Either point, line, or pointrange.
model	Optional argument to plot against a fitted model
...	Ignored

**Value**

A ggplot object

**Examples**

```
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\_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**

```
## 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

**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)
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**

```
## 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, basis = 10, order = 4)
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

**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)
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.quebec.ca/pls/public/gscw031?owa\\_no\\_site=314&owa\\_no\\_fiche=3&owa\\_bottin=](https://oraprdnt.uqtr.quebec.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.quebec.ca/pls/public/gscw031?owa\\_no\\_site=314&owa\\_no\\_fiche=3&owa\\_bottin=](https://oraprdnt.uqtr.quebec.ca/pls/public/gscw031?owa_no_site=314&owa_no_fiche=3&owa_bottin=))

---

**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)
```

---

**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.

**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

## 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, basis = 10, order = 4)
ft_data <- run_functional_t_test(data = spline_data, pupil = mean_pupil, alpha = 0.05)
```

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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