Package: eyetools (via r-universe)

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Type Package

Title Analyse Eye Data

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Description Enables the automation of actions across the pipeline, including initial steps of transforming binocular data and gap repair to event-based processing such as fixations, saccades, and entry/duration in Areas of Interest (AOIs). It also offers visualisation of eye movement and AOI entries. These tools take relatively raw (trial, time, x, and y form) data and can be used to return fixations, saccades, and AOI entries and time spent in AOIs. As the tools rely on this basic data format, the functions can work with data from any eye tracking device. Implements fixation and saccade detection using methods proposed by Salvucci and Goldberg (2000) <doi:10.1145/355017.355028>.

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`AOI_seq` *Sequence analysis of area of interest entries*

Description

Analyses the sequence of entries into defined AOI regions across trials. Can only be used with fixation data with a "fix_n" column denoting fixation events. Assumes that AOIs are non-overlapping and hasn't been tested with overlapping AOIs. Consecutive fixations within an AOI are grouped together as a single entry. Non-consecutive fixations in the same AOI (i.e., with an intervening fixation in no AOI) are treated as two separate entries.

Usage

```
AOI_seq(data, AOIs, progress = TRUE)
```

Arguments

data	A dataframe with fixation data (from fixation_dispersion). Either single or multi participant data
AOIs	A dataframe of areas of interest (AOIs), with one row per AOI (name, x, y, width_radius, height).
progress	Display a progress bar

Value

a dataframe containing the sequence of entries into AOIs on each trial, entry/exit/duration time into AOI

Examples

```
data <- combine_eyes(HCL)
fix_d <- fixation_dispersion(data)

AOI_seq(fix_d, AOIs = HCL_AOIs)
```

AOI_time *Analysis of time spent in areas of interest*

Description

Analyses total time on defined AOI regions across trials. Works with fixation and raw data as the input (must use one or the other, not both).

Usage

```
AOI_time(data, data_type = NULL, AOIs, as_prop = FALSE, trial_time = NULL)
```

Arguments

data	A dataframe of either fixation data (from fix_dispersion) or raw data
data_type	Whether data is a fixation ("fix") or raw data ("raw")
AOIs	A dataframe of areas of interest (AOIs), with one row per AOI (name, x, y, width_radius, height).
as_prop	whether to return time in AOI as a proportion of the total time of trial
trial_time	needed if as_prop is set to TRUE. a vector of the time taken in each trial. Equal to the length of x trials by y participants in the dataset

Details

Analyses data separately for each unique combination of values in `pID` and `trial`. Returned values can be absolute time or proportion of time over the period.

Value

a dataframe containing the time on the passed AOIs for each trial. One column for each AOI separated by trial.

Examples

```
data <- combine_eyes(HCL)
fix_d <- fixation_dispersion(data)

# fixation data
AOI_time(data = fix_d, data_type = "fix", AOIs = HCL_AOIs)

#raw data
AOI_time(data = data, data_type = "raw", AOIs = HCL_AOIs)

#as proportional data
AOI_time(data = fix_d, data_type = "fix", AOIs = HCL_AOIs,
         as_prop = TRUE, trial_time = HCL_behavioural$RT)
```

AOI_time_binned *Binned time analysis of area of interest entries*

Description

Analyses total time on defined AOI regions across trials separated into bins. Works with raw data as the input. Data can be separated into bins of a given length of time and the number of bins per trial is calculated automatically, keeping the bin length consistent across varying lengths of trial. Any data that cannot fill a bin (typically the last few milliseconds of the trial) are dropped to ensure that bins are of a consistent length

Usage

```
AOI_time_binned(
  data,
  AOIs,
  bin_length = NULL,
  max_time = NULL,
  as_prop = FALSE
)
```

Arguments

data	A dataframe of raw data
AOIs	A dataframe of areas of interest (AOIs), with one row per AOI (name, x, y, width_radius, height).
bin_length	the time duration to be used for each bin.
max_time	maximum length of time to use, default is total trial length
as_prop	whether to return time in AOI as a proportion of the total time of trial

Details

AOI_time_binned can take either single participant data or multiple participants, where participants are demarcated by values in the "pID" column.

Value

a dataframe containing the time on the passed AOIs for each trial. One column for each AOI separated by trial.

Examples

```
data <- combine_eyes(HCL)


#with bins of 100ms each and only for the first 2000ms
AOI_time_binned(data = data, AOIs = HCL_AOIs,
    bin_length = 100, max_time = 2000)
```

ASC_to_df *Read Eyelink ASC Sample Data*

Description

Reads gaze sample data from an EyeLink ASC file, parses binocular or monocular recordings, segments samples into trials based on gaps in the timestamp sequence, and returns a tidied data frame with time reset to zero at the start of each trial.

Usage

```
ASC_to_df(
  file,
  recording = c("binocular", "monocular"),
  pID = NA,
  frequency = NA
)
```

Arguments

file	Character string. Path to the EyeLink ASC (.asc) file to read.
recording	Character string. Type of recording to parse, either "binocular" or "monocular". Defaults to c("binocular", "monocular"), with "binocular" used if unspecified.
pID	Participant identifier to attach to every row of the output. Required; the function will error if left as NA.
frequency	Numeric. Sampling frequency in Hz of the recording (e.g. 500, 1000). Used to determine the inter-sample gap threshold for trial segmentation. The function will estimate the frequency as the median difference between samples if left as NA.

Details

Lines in the ASC file are treated as gaze samples if they begin with a digit. Columns are split on whitespace, EyeLink's missing-value marker (".") is converted to NA, and all columns are coerced to numeric. For binocular recordings the first 7 columns are expected (time, left x/y/pupil, right x/y/pupil); for monocular recordings the first 4 columns are expected (time, x, y, pupil).

Value

A data frame with one row per gaze sample, with columns:

pID Participant ID, as supplied.

trial Integer trial number, incremented whenever the gap between consecutive samples exceeds twice the expected sampling interval.

left_x, left_y, right_x, right_y Gaze coordinates for each eye (binocular recordings only).

x, y Gaze coordinates (monocular recordings only).

time Sample timestamp, reset to zero at the start of each trial.

Examples

```
## Not run:
samples <- read_eyelink_samples(
  file = "participant01.asc",
  recording = "binocular",
  pID = "P01",
  frequency = 1000
)

## End(Not run)
```

`combine_eyes` *Combine binocular data into single X/Y coordinate pairs*

Description

Combines the data from binocular samples into X/Y coordinate pairs. Two methods can be used: "average" or "best_eye". For "average", the result is based on the average of the two eyes for each sample, or for samples where there is data from only a single eye, that eye is used. For "best_eye", a summary of the proportion of missing samples is computed, and the eye with the fewest missing samples is used.

Usage

```
combine_eyes(data, method = "average", progress = TRUE)
```

Arguments

`data`	raw data with columns time, left_x, left_y, right_x, right_y, and trial
`method`	either "average" or "best_eye" - see description.
`progress`	whether to provide a progress bar or not.

Value

a dataframe of x-2 variables (with left_x and right_x condensed to x, and left_y and right_y condensed to y) and the same number of observations as the input data

Examples

```
combine_eyes(HCL, method = "average")
```

`compare_algorithms` *A battery of metrics and plots to compare the two algorithms (dispersion and VTI)*

Description

A tool for comparing the two different algorithms present in this package. This function is useful for assessing the data as well as exploring which algorithm is likely to fit data more appropriately. The raw data is run through both algorithms (using the same specified dispersion tolerances, etc.) before making comparisons of the underlying data. Can only be used for single participant data.

Usage

```
compare_algorithms(
  data,
  plot_fixations = TRUE,
  print_summary = TRUE,
  threshold = 100,
  min_dur = 150,
  min_dur_sac = 20,
  disp_tol = 100,
  NA_tol = 0.25,
  smooth = FALSE
)
```

Arguments

data	A dataframe with raw data (time, x, y, trial) for one participant
plot_fixations	Whether to plot the detected fixations. default as TRUE
print_summary	Whether to print the summary table. default as TRUE
threshold	velocity threshold (degrees of VA / sec) to be used for identifying saccades. Supplied to the VTI algorithm
min_dur	Minimum duration (in milliseconds) of period over which fixations are assessed. Supplied to both algorithms.
min_dur_sac	Minimum duration (in milliseconds) for saccades to be determined. Supplied to the VTI algorithm
disp_tol	Maximum tolerance (in pixels) for the dispersion of values allowed over fixation period. Supplied to both algorithms
NA_tol	the proportion of NAs tolerated within any window of samples that is evaluated as a fixation. Supplied to the dispersion algorithm
smooth	include a call to eyetools::smoother on each trial. Supplied to the VTI algorithm

Value

a list of the fixation data, correlation output, and data used for plotting

Examples

```
data <- combine_eyes(HCL)
data <- interpolate(data)
compare_algorithms(data[data$pID == 119,])
```

conditional_transform *conditional_transform*

Description

A function to perform conditional transformations of the x/y raw data. The function takes the dataframe and performs a single axis flip based on the values specified in the cond_column. The primary use of this function is to correct or normalise the data when counterbalancing stimulus placement within experiments (e.g., having a target stimulus appear on the left and right equally often) The screen width and height in pixels can be set using tracker_properties_set().

Usage

```
conditional_transform(
  data,
  flip = c("x", "y"),
  cond_column,
  cond_values,
  message = TRUE
)
```

Arguments

data	a dataframe that includes columns x and y and the column specified in cond_column. Can be raw, fixation, or saccade data.
flip	either "x", to flip across vertical midline, or "y" to flip across horizontal midline
cond_column	a column name, on which the flips are conditional
cond_values	a single value or vector stating which values in con_column result in a flip
message	whether to output messages during function. Useful to turn off when using in a vectorised fashion where it is running multiple times

Value

a dataframe of the equivalent format as the input data

Examples

```
data <- combine_eyes(HCL)
data <- merge(data, HCL_behavioural)
conditional_transform(data, flip = "x",
                      cond_column = "cue_order",
                      cond_values = 2)
```

create_AOI_df *Create a blank data frame for populating with AOIs*

Description

Used to define a set of AOIs for use across various functions within the eyetools package.

Usage

```
create_AOI_df(num_AOIs = 3, AOI_data = NULL, AOI_names = NULL)
```

Arguments

num_AOIs	number of AOIs, setting the number of rows
AOI_data	a list containing data for each AOI, ordered by x, y, width_radius, and height (NA if circular)
AOI_names	a vector of names for the AOIs specified in AOI_data

Value

an AOI dataframe in the format required for several AOI functions in eyetools

Examples

```
# create an empty data frame with 3 AOIs
create_AOI_df(3)

# create an AOI dataframe with data, the second of which is circular, with names
create_AOI_df(num_AOIs = 3,
              AOI_data = list(c(460,840,400,300), c(1460,840,400,NA), c(960,270,300,500)),
                AOI_names = c("AOI_1", "AOI_2", "AOI_3"))
```

dist_to_visual_angle *Compute visual angle from distance metrics*

Description

Takes a single value or vector of distances and returns the visual angle equivalent.

Usage

```
dist_to_visual_angle(vector, dist_type = "cm")
```

Arguments

vector	vector of distances (or single distance)
dist_type	default is "cm". Specify "pixel" for conversion from pixel values.

Value

an equivalent-sized object to the input

Examples

```
# calculate visual angle for stimulus of 5cm
dist_to_visual_angle(5)

# calculate visual angle of stimuli 2cm and 10cm width
dist_to_visual_angle(c(2,10))

# calculate visual angle of 150 pixel wide
dist_to_visual_angle(150, dist_type = "pixels")
```

---

fixation_dispersion *Fixation detection using a dispersion method*

Description

Detects fixations by assessing dispersion of the eye position, using a method that is similar to that proposed by Salvucci & Goldberg (2000). Evaluates the maximum dispersion (distance) between x/y coordinates across a window of data. Looks for sufficient periods in which this maximum dispersion is below the specified dispersion tolerance. NAs are considered breaks in the data and are not permitted within a valid fixation period.

Usage

```
fixation_dispersion(
  data,
  min_dur = 150,
  disp_tol = 100,
  NA_tol = 0.25,
  progress = TRUE
)
```

Arguments

data	A dataframe with raw data (pID, time, x, y, trial), the standardised raw data form for eyetools
min_dur	Minimum duration (in milliseconds) of period over which fixations are assessed
disp_tol	Maximum tolerance (in pixels) for the dispersion of values allowed over fixation period
NA_tol	the proportion of NAs tolerated within any window of samples that is evaluated as a fixation
progress	Display a progress bar

Details

It can take either single participant data or multiple participants, where participants are demarcated by values in the "pID" column.

Value

a dataframe containing each detected fixation by trial, with mean x/y position in pixel, start and end times, and duration.

References

Salvucci, D. D., & Goldberg, J. H. (2000). Identifying fixations and saccades in eye-tracking protocols. Proceedings of the Symposium on Eye Tracking Research & Applications - ETRA '00, 71–78.

Examples

```
data <- combine_eyes(HCL)
fixation_dispersion(data)
```

---

fixation_VTI *Fixation detection using a velocity threshold identification method*

Description

Determine fixations by assessing the velocity of eye-movements, using a method that is similar to that proposed by Salvucci & Goldberg (2000). Applies the algorithm used in VTI_saccade and removes the identified saccades before assessing whether separated fixations are outside of the dispersion tolerance. If they are outside of this tolerance, the fixation is treated as a new fixation regardless of the length of saccade separating them. Compared to fixation_dispersion(), fixation_VTI() is more conservative in determining a fixation as smaller saccades are discounted and the resulting data is treated as a continued fixation (assuming it is within the pixel tolerance set by disp_tol). Returns a summary of the fixations found per trial, including start and end coordinates, timing, duration, mean velocity, and peak velocity.

Usage

```
fixation_VTI(
  data,
  threshold = 100,
  min_dur = 150,
  min_dur_sac = 20,
  disp_tol = 100,
  smooth = FALSE,
  progress = TRUE
)
```

Arguments

data	A dataframe with raw data (pID, time, x, y, trial), the standardised raw data form for eyetools
threshold	velocity threshold (degrees of VA / sec) to be used for identifying saccades.
min_dur	Minimum duration (in milliseconds) of period over which fixations are assessed
min_dur_sac	Minimum duration (in milliseconds) for saccades to be determined
disp_tol	Maximum tolerance (in pixels) for the dispersion of values allowed over fixation period
smooth	include a call to eyetools::smoother on each trial
progress	Display a progress bar

Details

Analyses data separately for each unique combination of values in `pID` and `trial`.

Value

a dataframe containing each detected fixation by trial, with mean x/y position in pixel, start and end times, and duration.

References

Salvucci, D. D., & Goldberg, J. H. (2000). Identifying fixations and saccades in eye-tracking protocols. Proceedings of the Symposium on Eye Tracking Research & Applications - ETRA '00, 71–78.

Examples

```
data <- combine_eyes(HCL)
data <- interpolate(data)
fixation_VTI(data)
```

HCL

Example dataset from that contains binocular eye data from two participants from a simple contingency learning task (the data are from Beesley, Nguyen, Pearson, & Le Pelley, 2015). In this task there are two stimuli that appear simultaneously on each trial (to the left and right of the screen). Participants look at these cues and then make a decision by selecting an "outcome response" button. Data was recorded with a Tobii TX300 sampling at 300Hz. Participant sat approximately 60 cm from the screen. The screen resolution was 1920 x 1080.

Description

The dataset contains data from two participants and the first six trials of the study.

Usage

```
HCL
```

Format

A dataframe of 31,041 observations and seven variables

pID participant ID

time timestamp of the sample (milliseconds)

left_x x coordinate of the left eye

left_y y coordinate of the left eye

right_x x coordinate of the right eye

right_y y coordinate of the right eye

trial trial number ...

HCL_AOIs *Example AOIs for use with HCL*

Description

This dataframe contains three rectangular areas of interest (AOIs), set out for use with the HCL dataset. Values are in pixels. This is the standard AOI format required by many functions in the package. A template dataframe can be created using create_AOI_df()

Usage

```
HCL_AOIs
```

Format

A data frame with 3 rows and 5 variables:

name custom name for the AOI

x centred x coordinate of the AOI

y centred y coordinate of the AOI

width_radius either the width of the AOI, or the radius for circular AOIs

height the height of the AOI; should be NA for circular AOIs ...

HCL_behavioural *Example dataset of behavioural data to complement dataset HCL.*

Description

This contains information on stimuli (such as the side the predictive cue was presented on) as well as response data, including accuracy and response times

Usage

```
HCL_behavioural
```

Format

A dataframe of 12 observations and eight variables

pID participant ID

trial trial number

P_cue Are these necessary columns?

NP_cue Are these necessary columns?

cue_order whether the predictive cue os presented on the left (1) or the right (2)

correct_out NAre these necessary columns?

accuracy response accuracy

RT response time in milliseconds ...

hdf5_get_event *Get messages stored in TOBII-generated HDF5 files*

Description

A function to get the message event files from a TOBII-generated hdf5 file to dataframe. Used when a Psychopy experiment uses the io.sendMessageEvent() to record events

Usage

```
hdf5_get_event(filename)
```

Arguments

filename	the hdf5 file generated from TOBII

Value

A dataframe of message events as recorded by TOBII eye trackers

Examples

```
## Not run:
raw_data <- hdf5_get_event("example_TOBII.hdf5")

## End(Not run)
```

`hdf5_to_df` *Convert TOBII-generated HDF5 files to dataframe*

Description

A function to convert TOBII-generated hdf5 files to a dataframe

Usage

```
hdf5_to_df(filename)
```

Arguments

`filename`	the hdf5 file generated from TOBII

Value

A list of dataframes collected from the eyetracker content, if only one eyetracking event is present, return this as a single dataframe

Examples

```
## Not run:
raw_data <- hdf5_to_df("example_TOBII.hdf5")

## End(Not run)
```

`interpolate` *Interpolation of missing data (NAs)*

Description

Extends the zoo::na.approx and zoo::na.spline functions to include a report which provides the proportion of missing data before and after the interpolation process. This is handy for evaluating the effectiveness of the repair.

Usage

```
interpolate(
  data,
  vel_threshold = 35,
  maxgap = 150,
  method = "approx",
  report = FALSE,
  progress = TRUE
)
```

Arguments

data	A dataframe with raw data (pID, time, x, y, trial), the standardised raw data form for eyetools
vel_threshold	the maximum velocity that is tolerated between start and end points of periods of missing data
maxgap	maximum time gap of consecutive trackloss to fill (in ms). Any longer gaps will be left unchanged (see zoo package)
method	"approx" for linear interpolation or "spline" for cubic spline interpolation
report	default is FALSE. If TRUE, then the return value is a list containing the returned data frame and the report.
progress	Display a progress bar

Details

Analyses data separately for each unique combination of values in `pID` and `trial`.

Value

a dataframe of the same shape of the input data

Examples

```
data <- combine_eyes(HCL)
interpolate(data, maxgap = 150)
```

---

plot_AOI_growth *Plots absolute or proportional time spent in AOIs over time*

Description

A visualisation tool for plotting the changes in defined AOI regions across a single trial time.

Usage

```
plot_AOI_growth(
  data = NULL,
  pID_values = NULL,
  trial_values = NULL,
  AOIs = NULL,
  type = "abs",
  plot_time_not_in_AOI = FALSE
)
```

Arguments

data	raw data in standard raw data form (time, x, y, trial)
pID_values	specify particular values within 'pID' to plot data from certain participants
trial_values	can be used to select particular trials within the data
AOIs	A dataframe of areas of interest (AOIs), with one row per AOI (name, x, y, width_radius, height)
type	either "abs" (absolute) or "prop" (proportion)
plot_time_not_in_AOI	boolean as to whether to include proportion of time spent outside AOIs

Value

a plot of the raw data

Examples

```
data <- combine_eyes(HCL)
data <- interpolate(data)
# plot absolute and then proportional
plot_AOI_growth(data = data, AOIs = HCL_AOIs, type = "abs")
plot_AOI_growth(data = data, AOIs = HCL_AOIs, type = "prop")
```

---

plot_heatmap *Plot heatmap of raw data*

Description

Plots a heatmap of raw data.

Usage

```
plot_heatmap(
  data = NULL,
  pID_values = NULL,
  trial_values = NULL,
  bg_image = NULL,
  flip_y = FALSE,
  plot_type = "density",
  alpha_range = c(0.1, 0.8),
  plot_header = FALSE
)
```

Arguments

data	data in standard raw data form (time, x, y, trial)
pID_values	specify particular values within 'pID' to plot data from certain participants
trial_values	specify particular values within 'trial' to plot data from certain trials
bg_image	The filepath of a PNG image to be added to the plot, for example to show a screenshot of the task.
flip_y	reverse the y axis coordinates (useful if origin is top of the screen)
plot_type	Specify the nature of the data displayed. Either "density" (default) or "hex"
alpha_range	a pair of values between 0 and 1. The first is a cut off, whereby lower values are not displayed. The second value sets the transparancy of the visible poitns.
plot_header	display the header title text which explains graphical features of the plot.

Value

a plot of the raw data

Examples

```
data <- combine_eyes(HCL)
# plot all trials data
plot_heatmap(data, pID_values = 118, alpha_range = c(0.3,0.8))

#plot one trial
plot_heatmap(data, trial_values = 1)
```

plot_seq *Plot of raw data over time*

Description

A tool for visualising the timecourse of raw data over a single trial. Participant and trial values can be selected from the data. If values for these parameters are not provided then a single participant and a single trial will be sampled at random. Data can be split into bins by time or by the number of bins.

Usage

```
plot_seq(
  data = NULL,
  AOIs = NULL,
  trial_values = NULL,
  pID_values = NULL,
  bg_image = NULL,
  flip_y = FALSE,
  plot_header = FALSE,
  bin_time = NULL,
  bin_range = NULL
)
```

Arguments

data	A dataframe with raw data. If multiple trials are used, then one trial is sampled at random.
AOIs	A dataframe of areas of interest (AOIs), with one row per AOI (name, x, y, width_radius, height).
trial_values	specify particular values within 'trial' to plot data from certain trials
pID_values	specify particular values within 'pID' to plot data from certain participants
bg_image	The filepath of a PNG image to be added to the plot, for example to show a screenshot of the task.
flip_y	reverse the y axis coordinates (useful if origin is top of the screen)
plot_header	display the header title text which explains graphical features of the plot.
bin_time	if wanting to split data into bins, the time (in ms) for each bin of data to be displayed
bin_range	if wanting to split data into bins, the first and last bin to be display, e.g., c(1,5)

Value

a plot of the raw data representing changes over time

Examples

```
data <- combine_eyes(HCL)

# plot the raw data
plot_seq(data)

# with AOIs
plot_seq(data, AOIs = HCL_AOIs)

# plot raw data with bins
plot_seq(data, bin_time = 500)
```

`plot_spatial` *Plot raw data and fixations*

Description

A tool for visualising raw eye-data, processed fixations, and saccades. Can use all three data types together and independently. Fixations can be labeled in the order they were made. Can overlay areas of interest (AOIs) and customise the resolution.

Usage

```
plot_spatial(
  raw_data = NULL,
  fix_data = NULL,
  sac_data = NULL,
  AOIs = NULL,
  pID_values = NULL,
  trial_values = NULL,
  bg_image = NULL,
  flip_y = FALSE,
  show_fix_order = TRUE,
  plot_header = FALSE
)
```

Arguments

`raw_data`	data in standard raw data form (time, x, y, trial)
`fix_data`	data output from fixation function
`sac_data`	data output from saccade function
`AOIs`	A dataframe of areas of interest (AOIs), with one row per AOI (name, x, y, width_radius, height). If using circular AOIs, then the column width_radius is used for the radius and the height should be set to NA.
`pID_values`	specify particular values within 'pID' to plot data from certain participants

trial_values	specify particular values within 'trial' to plot data from certain trials
bg_image	The filepath of a PNG image to be added to the plot, for example to show a screenshot of the task.
flip_y	reverse the y axis coordinates (useful if origin is top of the screen)
show_fix_order	label the fixations in the order they were made
plot_header	display the header title text which explains graphical features of the plot.

Value

a plot of the raw data

Examples

```
data <- combine_eyes(HCL)
# plot the raw data
plot_spatial(raw_data = data, pID_values = 118)

# plot both raw and fixation data together
plot_spatial(raw_data = data, fix_data = fixation_dispersion(data), pID_values = 118)

#plot one trial
plot_spatial(raw_data = data, fix_data = fixation_dispersion(data), trial_values = 6)
```

---

saccade_VTI *Velocity threshold identification of saccades*

Description

Use the velocity threshold algorithm from Salvucci & Goldberg (2000) to determine saccadic eye movements. Returns a summary of the saccades found per trial, including start and end coordinates, timing, duration, mean velocity, and peak velocity.

Usage

```
saccade_VTI(data, threshold = 150, min_dur = 20)
```

Arguments

data	A dataframe with raw data (pID, time, x, y, trial), the standardised raw data form for eyetools
threshold	velocity threshold (degrees of VA / sec) to be used for identifying saccades
min_dur	minimum duration (ms) expected for saccades. This helps to avoid identification of very short saccades occurring at the boundary of velocity threshold

Details

Analyses data separately for each unique combination of values in `pID` and `trial`.

Value

a data frame giving the saccades found by trial

References

Salvucci, D. D., & Goldberg, J. H. (2000). Identifying fixations and saccades in eye-tracking protocols. Proceedings of the Symposium on Eye Tracking Research & Applications - ETRA '00, 71–78.

Examples

```
data <- combine_eyes(HCL)
saccade_VTI(data)
```

`smoother` *Smoothing of raw data*

Description

A wrapper for the stats::loess function, with default parameters suitable for smoothing raw eye data

Usage

```
smoother(data, span = 0.05, plot = FALSE)
```

Arguments

`data`	A dataframe with raw data (time, x, y, trial) for one participant
`span`	From stats::loess. The parameter alpha which controls the degree of smoothing.
`plot`	whether to plot the raw and smoothed plot for inspection

Details

Analyses data separately for each unique combination of values in `pID` and `trial`.

Value

a dataframe of the same shape as the input data

Examples

```
data <- combine_eyes(HCL)

smoother(data)

#with an inspection plot
smoother(data, span = .02, plot = TRUE)
```

`tracker_properties_get` *Get Current Eyetracker Properties*

Description

Returns a list containing the current global eyetracker settings.

Usage

```
tracker_properties_get()
```

Value

A named list of the current tracker parameters.

`tracker_properties_set` *Set the properties of the eye-tracker that was used in recording the data*

Description

This function is used to specify the properties of the eye-tracker used to record the data. Users can update one or more parameters. Unnamed parameters retain previous values. If these are not set by the user, then default parameters are set and a warning is issued in every call to relevant functions

Usage

```
tracker_properties_set(
  sample_frequency = NULL,
  viewing_distance_cm = NULL,
  screen_width_cm = NULL,
  screen_height_cm = NULL,
  screen_width_pixels = NULL,
  screen_height_pixels = NULL
)
```

Arguments

`sample_frequency`
: Numeric frequency.

`viewing_distance_cm`
: Distance in cm.

`screen_width_cm`
: Width in cm.

`screen_height_cm`
: Height in cm.

`screen_width_pixels`
: Width in pixels.

`screen_height_pixels`
: Height in pixels.

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