

# Package ‘gazepath’

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**Type** Package

**Title** Parse Eye-Tracking Data into Fixations

**Version** 1.4

**Date** 2026-05-28

**Description** Eye-tracking data must be transformed into fixations and saccades before it can be analyzed. This package provides a non-parametric speed-based approach to do this on a trial basis. The method is especially useful when there are large differences in data quality, as the thresholds are adjusted accordingly. The same pre-processing procedure can be applied to all participants, while accounting for individual differences in data quality. The method is described in van Renswoude et al. (2018) <[doi:10.3758/s13428-017-0909-3](https://doi.org/10.3758/s13428-017-0909-3)>.

**License** GPL-2

**Imports** sp, jpeg, zoo, scales, shiny

**NeedsCompilation** no

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gaze-path-package

*Parse Eye-Tracking Data into Fixations*

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### Description

Eye-tracking data must be transformed into fixations and saccades before it can be analyzed. This package provides a non-parametric speed-based approach to do this on a trial basis. The method is especially useful when there are large differences in data quality, as the thresholds are adjusted accordingly. The same pre-processing procedure can be applied to all participants, while accounting for individual differences in data quality.

### Details

Package: gaze-path  
Type: Package  
Version: 1.4  
Date: 2026-05-28  
License: GPL-2

### Author(s)

Ingmar Visser & Daan van Renswoude

Maintainer: Ingmar Visser <i.visser@uva.nl>

### References

van Renswoude, D. R., Raijmakers, M. E. J., Koornneef, A., Johnson, S. P., Hunnius, S. and Visser, I. (2018). Gaze-path: An eye-tracking analysis tool that accounts for individual differences and data quality. *Behavior Research Methods*, 50(2), 834-852. doi:10.3758/s1342801709093

Mould, M. S., Foster, D. H., Amano, K. and Oakley, J. P. (2012). A simple nonparametric method for classifying eye fixations. *Vision Research*, 57, 18-25.

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eye\_dat

*Eye\_Data*

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### Description

eye-tracking data of an 11-month-old infant watching 15 real-world scene stimuli

### Usage

data(eye\_dat)

**Format**

A dataframe with 4 variables (x- and y-coordinates of gaze position in pixels, stimuli name and distance to the screen in mm)

**Source**

S. P. Johnson

**References**

S. P. Johnson

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gazeopath

*Transform Raw Eye-Tracking Data into Fixations and Saccades*

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**Description**

This function transforms raw eye-tracking data into fixations and saccades using a non-parametric speed-based approach to do this on a trial basis. The method is especially useful when there are large differences in data quality between or within participants. Lower data quality results in more conservative thresholds, thereby controlling for noise levels.

**Usage**

```
gazeopath(data, x1, y1, x2 = NULL, y2 = NULL, d1, d2 = NULL, trial,
height_px, height_mm, width_px, width_mm, extra_var = NULL,
res_x = 1280, res_y = 1024, samplerate = 500,
method = "Mould", posthoc = FALSE, thres_vel = 35,
thres_dur = 100, min_dist = 250, in_thres = 150)
```

```
## S3 method for class 'gazeopath'
summary(object, ...,
complete_only = FALSE, fixations_only = FALSE)
## S3 method for class 'gazeopath'
plot(x, ..., trial_index = 1)
## S3 method for class 'gazeopath'
print(x, ...)
## S3 method for class 'gazeopath'
head(x, ...)
## S3 method for class 'gazeopath'
tail(x, ...)
```

**Arguments**

data	The dataframe with at least the raw x- and y-coordinates, the distance to the screen in mm and a trial index.
x1	The column name (between quotes, e.g. 'x1') or the number of the column in the dataframe containing the x-coordinates
y1	The column name (between quotes, e.g. 'y1') or the number of the column in the dataframe containing the y-coordinates
x2	When tracking was binocular, the column name (between quotes, e.g. 'x2') or number of the dataframe containing the x-coordinates of the second eye
y2	When tracking was binocular, the column name (between quotes, e.g. 'y2') or number of the dataframe containing the y-coordinates of the second eye
d1	The column name (between quotes, e.g. 'd1') or number of the dataframe containing the distance in mm
d2	When tracking was binocular, the column name (between quotes, e.g. 'd2') or number of the dataframe containing the distance in mm of the second eye
trial	The column name (between quotes, e.g. 'TRIAL_INDEX') or number of the dataframe containing the trial or stimuli index
height_px	The height of the stimuli in pixels, can be a single value or a vector of length number of trials when stimuli differ in size per trial
height_mm	The height of the stimuli in mm, can be a single value or a vector of length number of trials when stimuli differ in size per trial
width_px	The width of the stimuli in pixels, can be a single value or a vector of length number of trials when stimuli differ in size per trial
width_mm	The height of the stimuli in pixels, can be a single value or a vector of length number of trials when stimuli differ in size per trial trials
extra_var	A vector of names of the variables that must return in the output file, for example, condition, stimuli name, etc.
res_x	The horizontal resolution of the monitor in pixels
res_y	The vertical resolution of the monitor in pixels
samplerate	The samplerate, e.g., 60 for a 60 Hz scanner, 500 for a 500 Hz scanner
method	<p>Must be one of the following methods: Mould, MouldDur, Mould.all, Mould.allDur, gazePath, dispersion, velocity.</p> <p>Mould estimates velocity threshold per trial and duration thresholds per person (recommended for high, &gt; 250 Hz, samplerate and high quality data)</p> <p>MouldDur estimates velocity threshold per trial and uses the duration thresholds specified under 'thres_dur' (recommended for low, &lt; 250 Hz, samplerate data and data of low quality)</p> <p>Mould.all estimates velocity threshold and duration threshold for all trials (recommended for high, &gt; 250 Hz, samplerate data and data with short trial times, &lt; 2 seconds)</p> <p>Mould.allDur estimates one velocity threshold for all trials and uses the duration threshold specified under 'thres_dur' (recommended for high, &gt; 250 Hz, samplerate data and data with short trial times, &lt; 2 seconds and few trials)</p>

gazePath estimates velocity thresholds per person and uses the duration thresholds specified under 'thres\_dur'. Furthermore, extra preprocessing steps are performed, such as, last point interpolation of missing data sequences of length in\_thres and combining successive fixations that overlap in space.

dispersion derives fixations and saccades based on a dispersion threshold of .9 degrees of visual angle

velocity classifies saccades as sequences of samples (> 4ms) that have a velocity over 35 deg/s. Fixations are the sequences of samples that are not saccades and pass the duration threshold of 100 ms

posthoc	TRUE or FALSE (default). When TRUE successive fixations close in space are merged.
thres_vel	The desired velocity threshold, will only be used for method 'velocity'
thres_dur	The desired duration threshold, will be used for methods 'gazePath', 'velocity' and 'MouldDur'
min_dist	The minimal distance from the screen in mm, samples below this distance are considered unreliable and are omitted from further analysis.
in_thres	The durations threshold in msec used by the gazePath method to interpolate.
object	Object of class 'gazePath' can be used in the plot, summary and print function
x	Object of class 'gazePath' can be used in the plot, summary, head, tail and print function
trial_index	Argument of the plot function, referring to the trial to be plotted
complete_only	Argument (TRUE/FALSE) to indicate whether only fixations that have incoming out outgoing saccades and saccades that are between two fixations should be selected
fixations_only	Argument (TRUE/FALSE) to indicate whether only fixations should be returned by summary, instead of fixations and saccades
...	Not used currently

### Details

no details

### Value

gazePath returns a list of 16 items. names(list) and be used to extract useful information, the plot() and summary() functions can be used to verify the procedure and obtain the fixations.

#### 1. Classifications

List of length number of trials with a vector indicating whether a sample is classified as fixation 'f', saccade 's', unknown 'u' or NA

#### 2. x-coordinates

List of length number of trials with vectors of the x-coordinates of each trial

#### 3. y-coordinates

List of length number of trials with vectors of the y-coordinates of each trial

#### 4. Method

single value indicating what method was used to classify fixations and saccades

5. Robustness     Vector containing the mean durations of usable data segments per trial in milliseconds. Higher values indicate better data quality
6. Precision     Vector containing the mean differences in pixels between raw data points and a smoothed version of the data. Higher values indicate poorer data quality
7. Velocity thresholds  
      Vector with the velocity thresholds of each trial (methods: gazePath, Mould, MouldDur) in deg/s, or a single value when a single velocity threshold is used (methods: velocity, Mould.all, dispersion)
8. Duration threshold  
      Vector with the duration thresholds of each trial (method: Mould) in milliseconds, or a single value when a single duration threshold is used (methods: gazePath, MouldDur, Mould.all, velocity and dispersion)
9. Speed         List of length number of trials with vectors containing the speed at each sample
10. Samplerate   The samplerate
11. Head target distance  
      List of length number of trials with vectors containing the distance to the screen in mm for each sample
12. Height in pixels  
      Vector of length number of trials with the stimuli heights in pixels
13. Height in mm  
      Vector of length number of trials with the stimuli heights in mm
14. Width in pixels  
      Vector of length number of trials with the stimuli widths in pixels
15. Width in mm  
      Vector of length number of trials with the stimuli widths in mm
16. Fixations and saccades per trial  
      List of length number of trials with dataframes containing the fixations and saccades, see also summary()

### Author(s)

Daan van Renswoude & Ingmar Visser

### References

- van Renswoude, D. R., Raijmakers, M. E. J., Koornneef, A., Johnson, S. P., Hunnius, S. and Visser, I. (2018). GazePath: An eye-tracking analysis tool that accounts for individual differences and data quality. *Behavior Research Methods*, 50(2), 834-852. [doi:10.3758/s1342801709093](https://doi.org/10.3758/s1342801709093)
- Mould, M. S., Foster, D. H., Amano, K. and Oakley, J. P. (2012). A simple nonparametric method for classifying eye fixations. *Vision Research*, 57, 18-25.

### Examples

```
#### Example
data(screen)
data(eye_dat)
example <- gazePath(eye_dat, x1 = 1, y1 = 2, d1 = 4, trial = 3,
```

```
height_px = screen[,1], height_mm = screen[,2],
width_px = screen[,3], width_mm = screen[,4],
method = 'gazeopath', samplerate = 500)

## Use different i's to check the estimated fixations per trial
i <- 1
plot(example, trial_index = i)

## The estimated fixations, ordered per trial
s <- summary(example, complete_only = FALSE)
```

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GUI

*Graphical User Interface (GUI) for gazeopath implemented in Shiny*

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### Description

This function is a wrapper around gazeopath and provides a graphical user interface (GUI) in shiny to parse raw eye-tracking data into fixations and saccades. The GUI functions opens a browser that serves as GUI to parse and visualize eye-tracking data

### Usage

```
GUI()
```

### Arguments

no arguments

### Details

no details

### Value

nothing is returned

### Author(s)

Daan van Renswoude & Ingmar Visser

### References

van Renswoude, D. R., Raijmakers, M. E. J., Koornneef, A., Johnson, S. P., Hunnius, S. and Visser, I. (2018). Gazeopath: An eye-tracking analysis tool that accounts for individual differences and data quality. *Behavior Research Methods*, 50(2), 834-852. [doi:10.3758/s1342801709093](https://doi.org/10.3758/s1342801709093)

Mould, M. S., Foster, D. H., Amano, K. and Oakley, J. P. (2012). A simple nonparametric method for classifying eye fixations. *Vision Research*, 57, 18-25.

**Examples**

```
## Not run:  
GUI()  
  
## End(Not run)
```

---

screen

*Screen Dimensions*

---

**Description**

Screen and stimuli dimensions in pixels and mm, belonging to the dataset 'eye\_data'.

**Usage**

```
data(screen)
```

**Format**

A dataframe with 4 variables (the height and width of stimuli in pixels and mm)

**Source**

S. P. Johnson

**References**

S. P. Johnson

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