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eyetools: an R package for simplified analysis of eye data

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10 Abstract

- Abstract goes here
- 12 Keywords: eye-tracking; fixations; saccades; areas-of-interest

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Introduction

Eye tracking is a widely used technique in behavioural sciences, such as attention,

learning, and decision making (Orquin & Holmqvist, 2019). By recording the movement of an

individual's gaze during research studies, researchers can quantify where and how long

individual's look at stimuli presented on screen. Eye tracking offers an insight into real-time

6 cognitive processing, allowing researchers to infer mental states and processes with high temporal

precision (Duchowski & Duchowski, 2017). The most common eye tracking systems use infrared

8 light to detect reflections from the eyes enabling the calculation of gaze position on a screen.

Once this data has been collected, it can be classified into fixations and saccades. Fixations are

time periods where the eyes remain relatively stationary which enable focused attention on stimuli

11 (Rayner, 1998). Conversely, saccades are the rapid eye movements between fixations that are

typically too fast to allow for new information processing (Holmqvist et al., 2011).

A core element to utilising eye data effectively is in knowing how to process and analyse
the information gathered, which is often comprised of hundreds of trials from multiple
participants, and so datasets need to have processing stages applied consistently across
participants and trials. Utilising reproducible workflows, such as implementing R-based pipelines
for processing and analysis can offer this consistency as well as confidence in the outputs and
results. Using R enables access to the Comprehensive R Archive Network (CRAN), a repository
of packages containing functions designed to improve and optimise data processing and analysis
workflows. It is here that we introduce eyetools, an R package designed to work with eye data and
streamlines the processing and analysis pipeline.

The aim of this tutorial is to demonstrate the functionality contained within eyetools. It should appeal to researchers unfamiliar with working with eye data, as we detail steps of converting raw data through to the analysis in a reproducible R environment. It should also appeal to researchers accustomed to working with eye data in other environments who wish to transfer to working in R. In using eyetools as the foundation data pipeline, we hope that this tutorial provides

a comprehensive and clear approach to working with eye data.

eyetools is not the only R package available for working with eye data, a recent assessment 28 of available packages on CRAN identified six that offer eye data relevant functions. eyeTrackr offers functionality for experiments from 'Eyelink' trackers, limiting the usability of the package. Similarly, eyelinker and eyelinkReader are constrained to eyelink data. In contrast, eyetools provides a hardware-agnostic design, relying on data being in a given format that is easily managed from any data source. The emov package offers a limited set of functions, including a fixation algorithm that is based upon the same algorithm used in eyetools, however emov is limited in continued functionality, and plotting and data preparation functions are absent. eyeRead is a package exclusively designed for eye tracking on reading exercises and eyetools is designed for attention and intent-based research. Finally, the eyetrackingR is perhaps the most 37 comprehensive alternative package, but it lacks any functions related to fixations and saccades, 38 instead offering a suite of more naive approaches. 39

This tutorial is separated into five distinct sections. In the first section, we briefly describe
the basic methodology of collecting eye data in general, and in regard to the specific dataset we use
to illustrate all the functionality of the eyetools package. The second section covers the process for
getting data from an eye tracker into an eyetools-friendly format. The third section introduces the
foundational functions of the eyetools package, from fixing missing data, smoothing erratic gaze
patterns, to calculating fixations, and detecting time spent in Areas of Interest (AOIs). The fourth
section takes the processed data, and applies basic analysis techniques commonplace in eye data
research. In the fifth and final section, we reflect on the benefits of the eyetools package, including
contributions to open science practices, reproducibility, and providing clarity to eye data analysis.

Data Collection

First describe basic paradigms for collecting eye data. Also purpose etc. @tom

Then describe the specifics of the dataset we are using - I presume this is the HCL dataset

in full? Should make mention of the fact that the workflow can be done either with the full

dataset, or the two participant dataset provided in package.

Converting Raw Data

@matthew, @tom

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Owing to the vast range of eye tracking hardware available, eyetools does not offer much in the way of converting raw data into the eyetools format of participant ID, trial number, timestamp, x, and y coordinates. In this section, we cover the stages of transforming the data from a TOBII eye tracker.

hdf5_to_csv()

When you have data that is in a binocular format, that is you have a set of coordinates for
each eye, it needs to be converted into single x and y coordinates for both eyes combined. Using
eyetools, this can be done in one of two ways, either taking an average of the coordinattes from the
two eyes, or by choosing the eye with the fewest missing samples is used to represent the data. An
averaging of the two coordinates sets is the typical method of combining binocular data, and can
be done using the combine_eyes() function in eyetools. This returns a flattened list of
participant data that has x and y variables in place of the left_* and right_* variables.

Working with eyetools

In the last section, we finished with the data in a format that holds participant ID, trial number, a timestamp, along with x and y coordinates. This is the format expected by eyetools when working with multi-participant data, however if you some reason you are working with a single participant then the participant ID column is superfluous and can be dropped. This basic data format of ID, trial, time, x, and y ensures that eyetools is applicable to a variety of eye data sources and does not depend on specific eye trackers being used.

Counterbalanced designs

Many psychology experiments will position stimuli on the screen in a counterbalanced fashion. For example, in the example data we are using, there are two stimuli, with one of these appearing on the left and one on the right. In our design, one of the cue stimuli is a "target" and one is a "distractor", and the experiment counterbalances whether these are positioned on the left or right across trials.

Eyetools has a built in function which allows us to transform the x (or y) values of the 81 stimuli to take into account a counterbalancing variable: conditional transform(). This 82 function currently allows for a single-dimensional flip across either the horizontal or vertical 83 midline. It can be used on raw data or fixation data. It requires the spatial coordinates (x, y) and a specification of the counterbalancing variable. The result is a normalised set of data, in which the x (and/or y) position is consistent across counterbalanced conditions (e.g., in our example, we can transform the data so that the target cue is always on the left). This transformation is especially 87 useful for future visualisations and calculation of time on areas of interest. Note that conditional transform() is another function that does not discriminate between multi-participant and single-participant data and so no participant ID parameter is required. To transform the data, we require knowledge of where predictive cues were presented. Using this, conditional transform() can align data across the x or y midline, depending on how stimuli were presented. In the experimental design used in our study, cues were presented either on the left or the right, so by applying conditional_transform(), all the predictive cues in the dataset are recorded on the same side.

6 Repairing missing data and smoothing data

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Despite researcher's best efforts and hopes, participants are likely to blink during data collection, resulting in observations where no data is present for where the eyes would be looking. To mitigate this issue, the interpolate() function estimates the path taken by the eyes based upon the eye coordinates before and after the missing data. There are two methods for estimating the path, linear interpolation ("approx", the default setting) and cubic spline ("spline"). The default method of linear interpolation replaces missing values with a line of constant slope and evenly spaced coordinates reaching the existing data. The cubic spline method applies piecewise cubic functions to enable a curve to be calculated as opposed to a line between points.

When using interpolate(), a report can be requested so that a researcher can measure how much missing data has been replaced. This parameter changes the output format of the function, and returns a list of both the data and the report. The report can be accessed easily using

the following code:

pNum missing_perc_before missing_perc_after

110 1 118

0.02314313

0.015838577

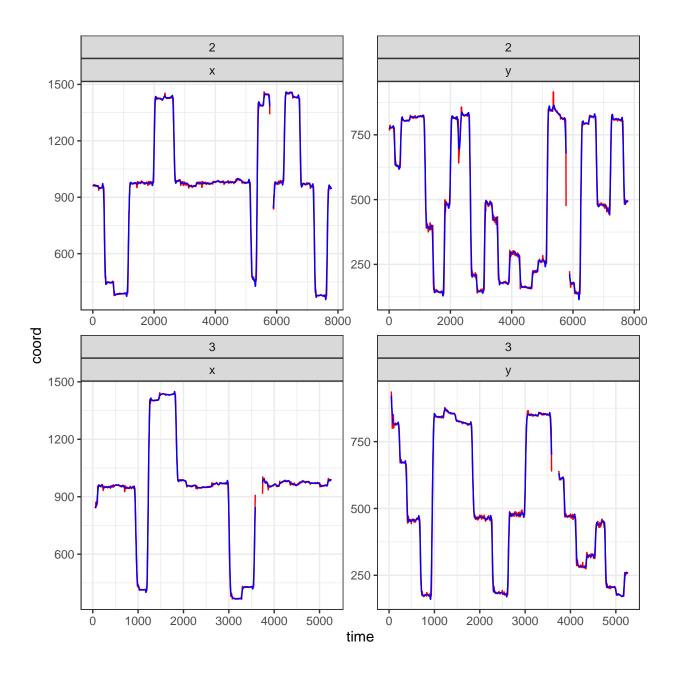
111 2 119

0.01214128

0.005402579

As shown, not all missing data has been replaced, this is because when gaps are larger than
a given size they are kept as missing data due to it being unreasonable to try to estimate the path
taken by the eye. The amount of missing data that will be estimated can be changed through the
maxgap parameter.

Once missing data has been fixed, a common step is to smooth the eye data to remove
particularly jerky eye movements. To do this, smoother() reduces the noise in the data by
applying a moving averaging function. The degree of smoothing can be specified, as well as
having a plot generated for random trials to observe how well the smoothed data fits the raw data.



Fixations

Once the data has been repaired and smoothed, a core step in eye data analysis is to identify fixations (Salvucci & Goldberg, 2000), defined as when the gaze stops in a specific location for a given amount of time. When the eyes are moving between these fixations, they are considered to be saccades. Subsequently, data can be split into these two groups, fixations and saccades. In the eyetools package, there are two fixation algorithms offered; the first algorithm, fixation_dispersion() employs a dispersion-based approach that uses spatial and temporal

data to determine fixations. By using a maximum dispersion range, the algorithm looks for
sufficient periods of time that the eye gaze remains within this range and once this range is exceed,
this is termed as a fixation. The second algorithm, fixation_VTI() takes advantage of the idea
that data is either a fixation or a saccade and employs a velocity-threshold approach. It identifies
data where the eye is moving at a minimum velocity and excludes this, before applying a
dispersion check to ensure that the eye does not drift during the fixation period. If the range is
broken, a new fixation is determined. Saccades must be of a given length to be removed,
otherwise they are considered as micro-saccades [@CITATION_NEEDED_HERE?].

Once fixations have been calculated, they can be used in conjunction with Areas of Interest (AOIs) to determine the sequence in which the eye enters and exits these areas, as well as the time spent in these regions. When referring to AOIs, these often refer to the cues presented and the outcome object. In our example, the two cues at the top of the screen are the cues, and the outcome is at the bottom. We can define these areas in a separate dataframe object by giving the centrepoint of the AOI in x, y coordinates along with the width and height (if the AOIs are rectangular) or just the radius (if circular).

In combination with the fixation data, the AOI information can be used to determine the sequence of AOI entries using the AOI_seq() function. This function checks whether a fixation is detected within an AOI, and if not, it is dropped from the output, and then provides a list of the sequence of AOI entries, along with start and end timestamps, and the duration.

Time spent in AOIs can also be calculated from fixations or raw data using the AOI_time() function available. This calculates the time spent in each AOI in each trial, based on the data type given, in our case fixation data.

If choosing to work with the raw data, there is also the option of using AOI_time_binned() which allows for the trials to be split into bins of a given length, and the time spent in AOIs calculated as a result.

Analysing eye data

@tom

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155 Discussion

In the present tutorial, we began by identifying the current gap in available tools for working with eye data in open-science pipelines. We then provided an overview of the general data collection process required for eye tracking research, before detailing the conversion of raw eye data into a useable eyetools format. We then covered the entire processing pipeline using functions available in the eyetools package that included the repairing and normalising the data, and the detection of events such as fixations, saccades, and AOI entries.

@SOMETHING_ON_THE_ANALYSIS_GOES_HERE.

From a practical perspective, this tutorial offers a step-by-step walkthrough for handling eye data using R for open-science, reproducible purposes. It provides a pipeline that can be relied upon by novices looking to work with eye data, as well as offering new functions and tools for experienced researchers. By enabling the processing and analysis of data in a single R environment it also helps to speed up data analysis.

Advantages of Open-Source Tools

eyetools offers an open-source toolset that holds no hidden nor proprietary functionality.

Data Availability

The data required for reproducing this tutorial is available at: @URL. A condensed version of the dataset (starting with the combine_eyes() function) is a dataset in the eyetools package called HCL.

Code Availability

The code used in this tutorial is available in the reproducible manuscript file available at:

176 References

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