VisME – Visual Microsaccades Explorer

Usage Guide

1 Introduction

VisME is a visual analytics system to explore high-frequency eye tracking data with a special focus on **microsaccades**. The exploration can take place on different levels, for fixations, participants, trials, and test conditions using data of individuals as well as groups of participants. The system provides multiple views, eye movement filters, visibility filters and further options to support users in their exploration.

This document describes the features of the system and how the system can be used to explore eye tracking data visually.

2 Overview

The general workflow to use this system is as follows:
First, data needs to be converted into the appropriate file formats. Next, files for each participant and test condition have to be loaded into the system. If not already included in the input file, both fixations and microsaccades can be detected. Then, the data for analysis can be specified: this can be one trial or multiple trials of multiple participants and/or test conditions. The specified trials will be used for all visualizations.

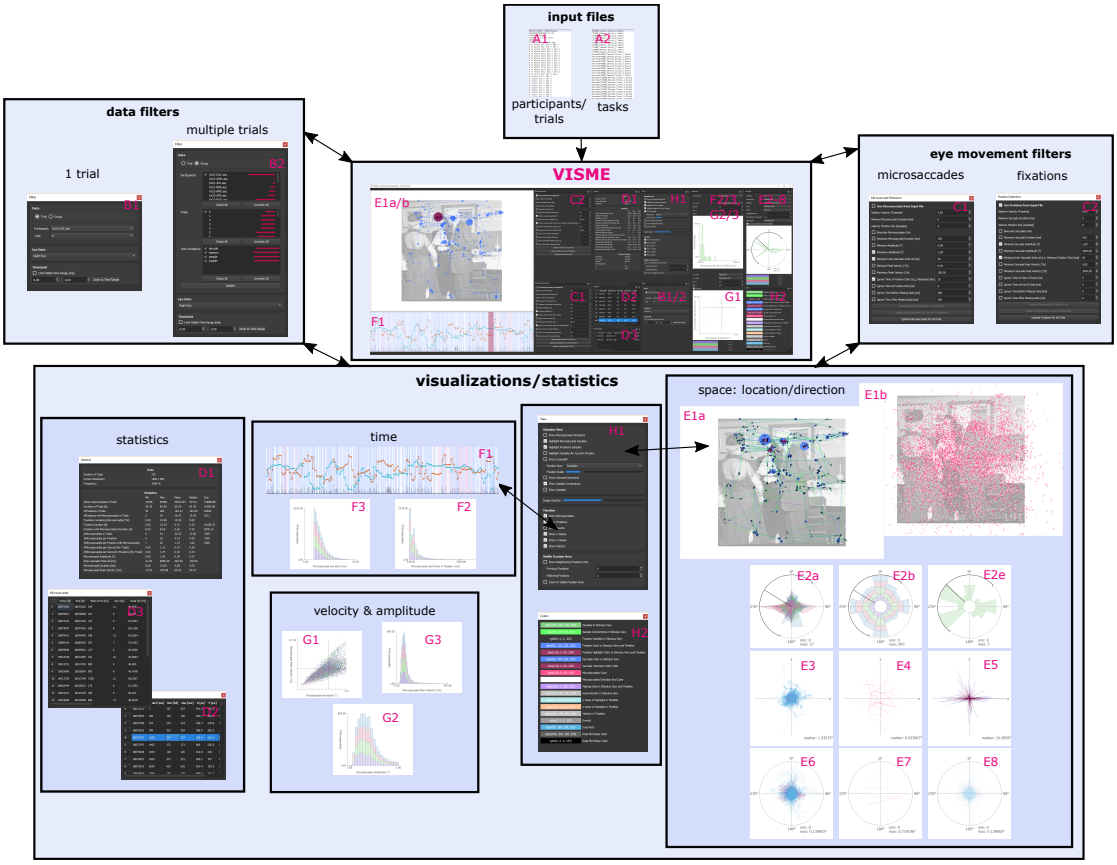
If just **one trial** is selected, in the **stimulus view** the eye tracking data is visualized on top of the stimulus. Here, it is possible to highlight fixations and microsaccades and a scanpath can be shown. In the **timeline view**, the x and y positions, as well as the velocity over time, is shown together with areas marked as fixations and microsaccades. These views are linked and a user can select fixations in one of them and will be able to see its location on the other one. In **polar plots**, **histograms** and **scatterplots** it is possible to explore properties (direction, amplitude, duration, velocity, ...) of microsaccades, gaze samples and saccades.

If **multiple trials** are selected, the stimulus view shows the image of the first trial as background and microsaccade directions on top of it; the timeline view is disabled. The remaining plots show the summarized information of all trials. If test conditions are loaded, a different color value for each test condition is used in scatterplots, histograms and polar plots. For polar plots, it is possible to stack data of different trials on top of each other or to visualize the aggregated data.

By **changing the parameter values** for the eye movement event filters all visualizations are updated to the newly detected fixations/microsaccades.

2.0.1 Main features and visualizations of the system

This graph summarizes the elements of the system grouped by categories:



A1 – **Input file** with eye tracking data for **participants/trials** (**.maf**) (3.0.1)

A2 – **Input file** for **test conditions** (**.mtf**) (3.0.2)

B1 – Data **filter** for **one trial** (4.1.1)

B2 – Data **filter** for **multiple trials/participants/test conditions** (4.1.2)

C1 – **Microsaccades filter** with many adaptable parameters (4.2.1)

C2 – **Fixation (saccade) filter** with many adaptable parameters (4.2.2)

D1 – **General statistics** on data specified in B1/2 (4.2.3)

D2 – **Fixation list** of current trial (if one trial is defined in B1) (4.2.6)

D3 – **Microsaccades list** of current selected fixation (if one trial is defined in B1)(4.2.7)

E1a – **Stimulus View** for one trial: samples, fixations, microsaccades and scanpath can be shown (4.2.4)

E1b – **Stimulus View** for multiple trials: all microsaccade direction lines are shown (4.2.4)

E2a – **Direction** of (micro)saccades or gaze positions as **polar plot** (multiple plots on top of each other for multiple trials) (4.2.11)

E2b – Same as E2a as **rose plot**: data for different trials is stacked and grouped according to test conditions (4.2.11)

E2e – Direction of (micro)saccades or gaze positions as polar plot; data of one trial; also available for data aggregated for multiple trials; also available as rose plot (4.2.11)

E3 – **Fixation samples** with highlighted microsaccade samples (center of fixations is located at center of plot) (4.2.12)

E4 – **Microsaccade directions** and location in relation to fixation center (4.2.12)

E5 – **Saccade directions** (i.e. vectors between two fixations) in relation to previous fixation center (4.2.12)

E6 – **Directional lengths** between neighboring **gaze samples**; all samples which belong to the same fixation are connected; samples which belong to microsaccades are highlighted in pink; plot without connections also available (4.2.13)

E7 – **Directional lengths of microsaccades**; all samples which belong to the same fixation are connected; plot without connections also available (4.2.13)

E8 – **Directional lengths of saccades** (4.2.13)

F1 – **Timeline View** (4.2.5)

F2 – **Start time of microsaccades** within fixations plotted as histogram (4.2.14)

F3 – **(Micro)saccade duration** histogram (4.2.14)

G1 – Scatterplot for **Peak Velocity - Amplitude** relationship of (micro)saccades (4.2.15)

G2 – **Amplitude** histogram for (micro)saccades (4.2.14)

G3 – **Peak velocity** histogram for (micro)saccades (4.2.14)

H1 – **Visibility filter**: specifies what is visible in the stimulus view (E1) and timeline view (F1)

H2 – **Colors**: specifies many colors used in visualizations (4.2.9)

3 Data Preparation and Data Import

For each participant, a separate file is required, which can contain multiple trials; a second file type can contain test condition information.

3.0.1 Eye Tracking Data File (maf)

High-frequency eye tracking data is required as input, with a minimum frequency of 200 Hz in order to detect microsaccades.

If data is not already given as maf file, in a preprocessing step, you will need to transform your data into the appropriate file format with the file extension ".maf".

Each file has to contain all data that belongs to one participant; this can be data for multiple trials.

In the first line a name for the participant has to be provided and a value for pixels per degree in the second line:

```
PARTICIPANT <participantName>
PIXELSPERDEGREE <pixelsPerDegree>
```

Pixels per degree (ppd) can be determined from the distance to the screen (d), the width (or height) of the screen (w) and the horizontal (or vertical) resolution of the screen (p):

$$ppd = \frac{p \cdot \pi}{360 \cdot atan(\frac{w}{2d})}$$

Then, for each trial (specified with a name) the screen coordinates, the frequency, the stimulus (optional) and eye positions have to be given.

Each trial starts with `TRIAL <trialName>` and ends with `ENDTRIAL`

`<trialName>` should be the same for multiple participants in order to detect that the same trial is meant (e.g. if the same stimulus was used).

At the beginning of a trial screen coordinates, the frequency of the recording and a stimulus file path are specified (images are displayed on the center with its original resolution):

```
COORDS <xMin> <yMin> <xMax> <yMax>
FREQ <frequency>
STIMULUS <filePath>
```

The eye tracking data has to be separated for fixations, microsaccades and gaze positions. Microsaccades and fixations are optional as they can be computed by the system, but gaze positions are required (for at least one eye). The order of the different eye movement types (gaze points, fixations, microsaccades) is not important.

Gaze positions, Microsaccades and Fixations can be specified with `R` for the right eye, `L` for the left eye or `B` for averaged values between both eyes.

Samples start with the eye type, followed by a timestep index and the x and y position:
`<eye> <index> <xPos> <yPos>`

If data for a timestamp is not available, there will be no entry for that specific timestamp index.

Fixations start with an `F` followed by the eye type, a timestep index, the duration (given in timesteps), x and y position, which specify the center of the fixation:
`F <eye> <startIndex> <durationIds> <xPos> <yPos>`

Microsaccades start with a `M` followed by the eye type, a start index, the duration, peak velocity, horizontal and vertical component and horizontal and vertical amplitude (these values can be obtained by the algorithm by Engbert and Kliegl):
`M <eye> <startIndex> <durationIds> <peakVelocity(deg/s)> <horizontalComp(deg)> <verticalComp(deg)> <horizontalAmpl(deg)> <verticalAmpl(deg)>`

Additionally, events (which do not contain eye movements but specify a time span with a description) start with an `E` and can be specified with a start index, duration and a description:
`E <startIndex> <durationIds> <name/description>`

Note, that `<startIndex>` has to be a value of the `<index>` values and `durationIds = endIndex - startIndex + 1` (number of samples from start to end of a fixation/saccade).

General format:

```
PARTICIPANT <participantName>
PIXELSPERDEGREE <pixelsPerDegree>

# first trial
TRIAL <trialName>
COORDS <xMin> <yMin> <xMax> <yMax>
FREQ <frequency>
STIMULUS <filePath>

# gaze points
<eye> <index> <xPos> <yPos>
...
# fixations
F <eye> <startIndex> <durationIds> <xPos> <yPos>
...
# microsaccades
M <eye> <startIndex> <durationIds> <peakVelocity(deg/s)> <
    horizontalComp(deg)> <verticalComp(deg)> <horizontalAmpl(deg)> <
    verticalAmpl(deg)>
```

```
...
# events
E <startIndex> <durationIds> <name/description)>
...
ENDTRIAL

# optionally further trials
...
```

Data can also be exported using this format – currently available data (imported or calculated) for gaze positions, fixations, microsaccades and events can be exported for the current trial, participant or all participants.

3.0.2 Eye Tracking Test Condition File (mtf)

The test condition file needs to be loaded after or together (drag and drop) with the maf files. If a further maf file is added to the project, the test condition file needs to be reimported in order to set the test conditions for the new participant as well.

A test condition file is a csv file with each line is the following format:

```
<participantName>,<trialName>,<testConditionName>
```

with `<participantName>` and `<trialName>` as specified in the maf files.

For each test condition, an individual color value will be assigned. Especially when exploring multiple trials, this feature can be helpful. The different color values are available in the data plots, histograms and scatterplots.

3.0.3 File import

```
PARTICIPANT VISME_Tester
PIXELSPERDEGREE 33.33
TRIAL Trial_0
COORDS 0 0 1920 1080
FREQ 600
STIMULUS testImage.jpg
F B 41199 141 973.0 464.0
F B 41349 552 976.0 534.0
F B 41976 1327 963.0 559.0
F B 43305 1492 964.0 560.0
F B 44875 2582 962.0 559.0
F B 47522 4923 960.0 557.0
F B 52526 2814 963.0 565.0
F B 55423 3331 962.0 560.0
F B 58865 3383 963.0 565.0
F B 62296 2225 962.0 563.0
F B 64597 3723 962.0 564.0
F B 68388 2279 963.0 565.0
F B 70733 6012 962.0 568.0
F B 76767 442 958.0 565.0
R 41199 971.0 469.0
R 41200 972.0 469.0
R 41201 971.0 468.0
R 41202 972.0 468.0
R 41203 971.0 468.0
R 41204 971.0 468.0
R 41205 973.0 468.0
R 41206 972.0 468.0
R 41207 971.0 468.0
```

```
VISME_Tester,Trial_0,Task1
VISME_Tester,Trial_1,Task1
VISME_Tester,Trial_2,Task2
VISME_Tester,Trial_3,Task2
VISME_Tester,Trial_4,Task1
VISME_Tester,Trial_5,Task1
VISME_Tester,Trial_6,Task2
VISME_Tester,Trial_7,Task2
VISME_Tester,Trial_8,Task1
VISME_Tester,Trial_9,Task1
SecondVISME_Tester,Trial_0,Task1
SecondVISME_Tester,Trial_1,Task1
SecondVISME_Tester,Trial_2,Task1
SecondVISME_Tester,Trial_3,Task1
SecondVISME_Tester,Trial_4,Task1
SecondVISME_Tester,Trial_5,Task2
SecondVISME_Tester,Trial_6,Task2
SecondVISME_Tester,Trial_7,Task2
SecondVISME_Tester,Trial_8,Task2
SecondVISME_Tester,Trial_9,Task2
AnotherVISME_Tester,Trial_0,Task2
AnotherVISME_Tester,Trial_1,Task2
AnotherVISME_Tester,Trial_2,Task1
AnotherVISME_Tester,Trial_3,Task1
AnotherVISME_Tester,Trial_4,Task2
AnotherVISME_Tester,Trial_5,Task2
AnotherVISME_Tester,Trial_6,Task1
AnotherVISME_Tester,Trial_7,Task1
AnotherVISME_Tester,Trial_8,Task2
```

All supported file formats can be imported either by drag and drop onto the settings/data tabs or the window title bar (multiple files and file types can be imported simultaneously) or by selecting the appropriate import option in the menu. If you open a new file all

previously opened trials will be removed from the project; if you chose to add a file the previous ones will be kept in the project; if you use drag and drop you will be asked what to do with the previously loaded data.

Supported shortkeys for file import/export:

Open file (this removes already loaded data from the project): Ctrl + O

Add file (this keeps already loaded data in the project): Ctrl + A

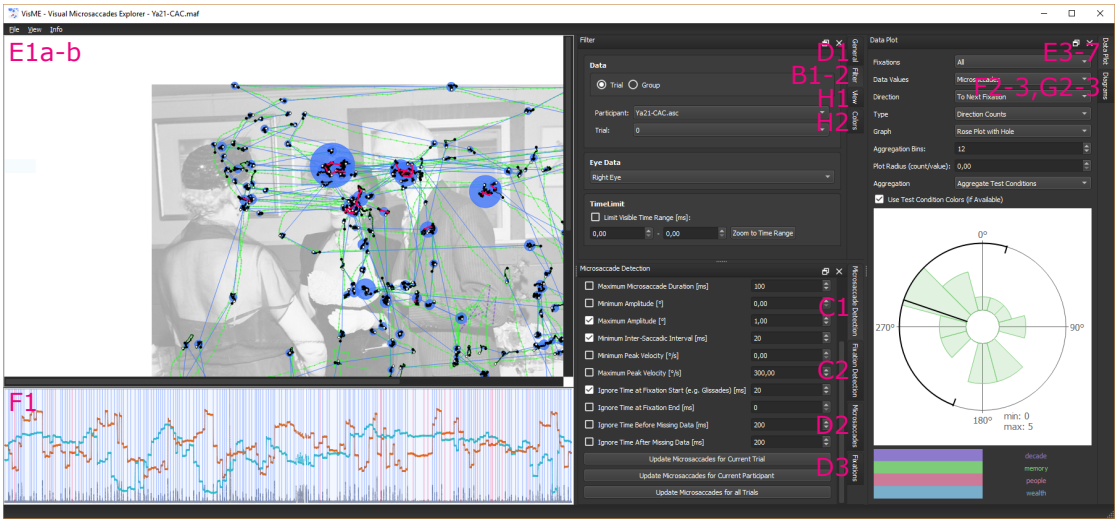
Open Trial Test Condition File (test conditions are applied to already loaded data): Ctrl + Shift + O

4 Visual Analytics System

The visual analytics system has three main areas: a stimulus view, a timeline view and multiple settings/data tabs for further visualizations, filter options and settings.

Data/Settings tabs can be detached from the main window (to move them for example to another screen) and their arrangement inside the main window can be arbitrary: In the overview picture, we moved all tabs in a way that all of them are visibly; by default, most of them are stacked on top of each other. The current arrangement of these tabs is saved in the settings.ini file (located in the directory of the executable file), which is updated every time you close the application.

Default window layout:



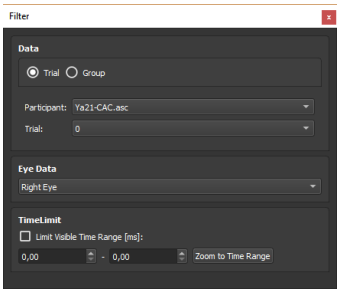
4.1 Select Data

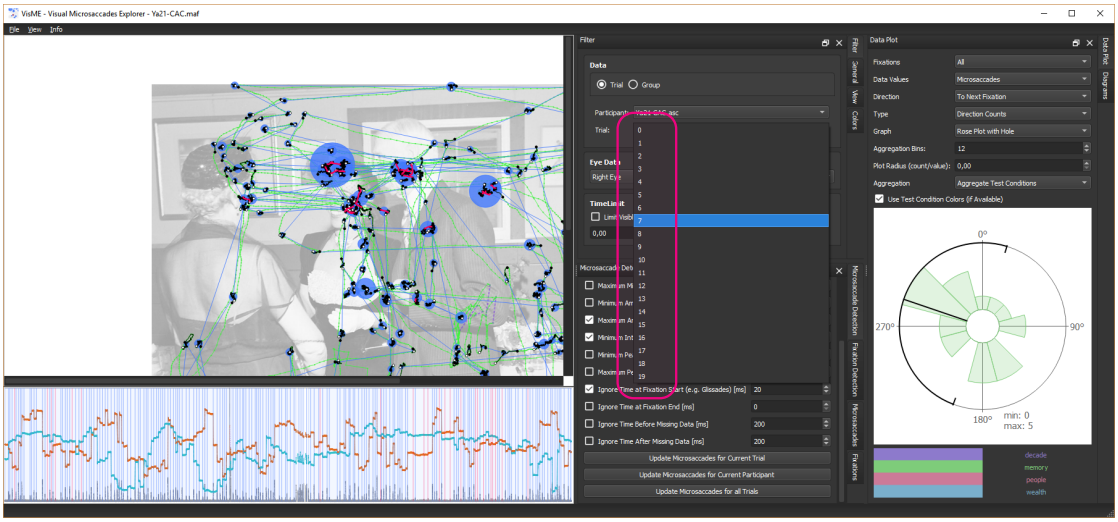
For data selection trials have to be specified as well as the eye type (right/left/average; default: average) and a time range (default: entire trial time ranges). If a time range is

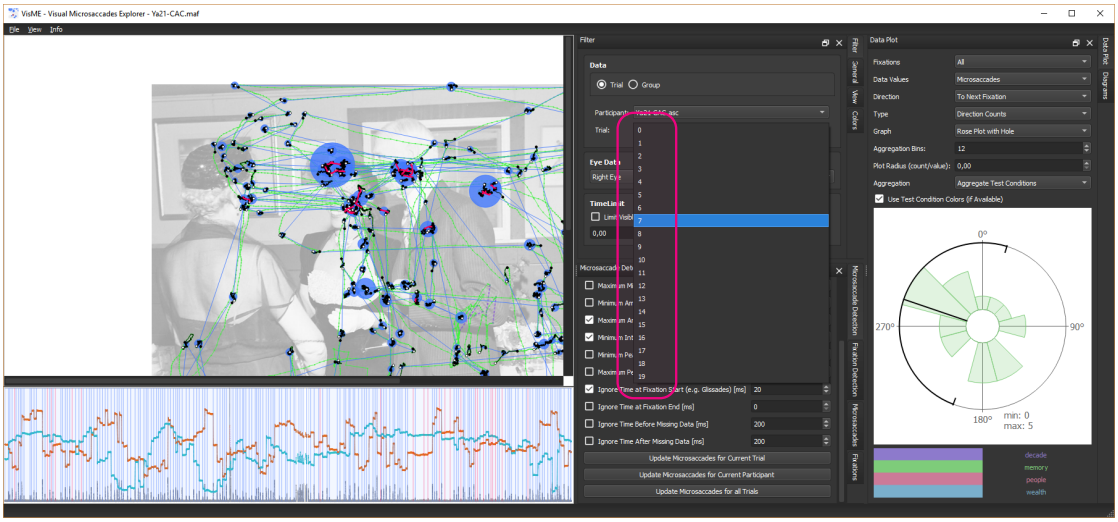
selected only fixations within this time range are used for the analysis; the specified time range is used for all trials.

4.1.1 Trial Mode (B1)

In the default exploration mode for one trial, it is possible to select a participant and a trial and create visualizations for this specific selection. Especially the stimulus view and timeline view can be used to explore one trial visually.



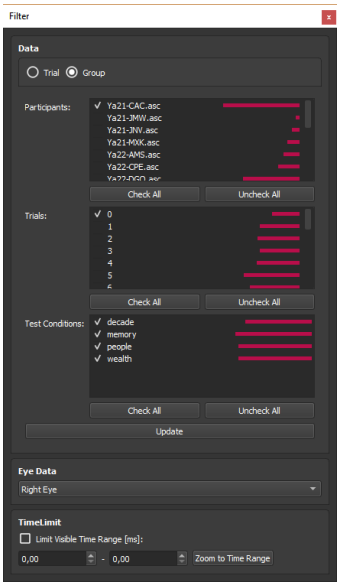


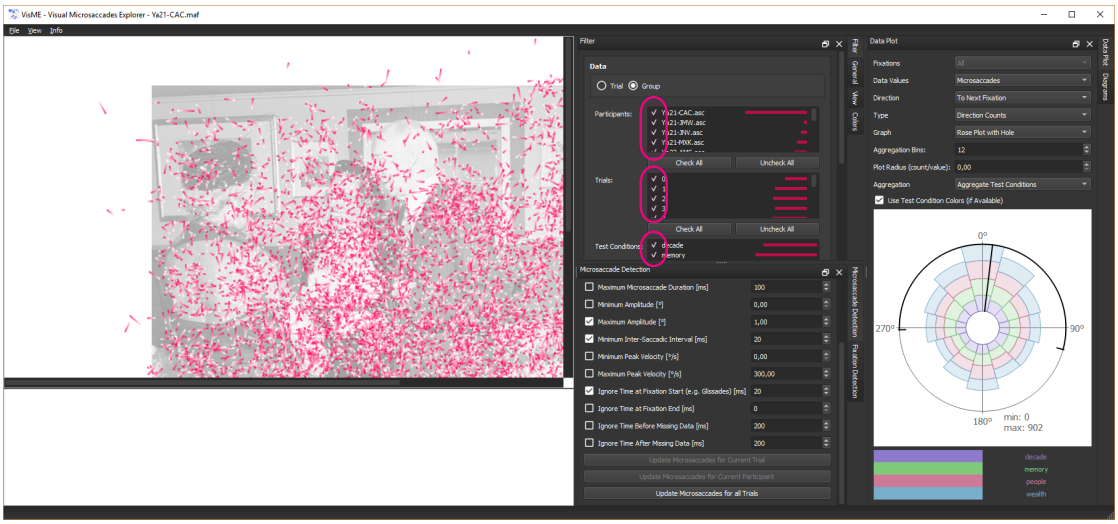


4.1.2 Group Mode (B2)

In group mode, it is possible to select a set of participants, trials, and test conditions. The selection areas show the number of appearances of microsaccades for participants, trials and test conditions in relation to the other participants, trials and test conditions. It is possible to select participants/trials/test conditions with a high or low number of microsaccades. You can select for example all trials of one participant, one specific trial of all participants, all trials of all participants for a specific test condition or any other combination of participants, trials and test conditions.

In group mode, not all features of the trial mode are available: as a large number of data samples must be handled and due to visual clutter in the stimulus and timeline view, we decided to disable most of the related visualizations except for plotting the directional lines of microsaccades in the stimulus view. The polar plots (which are created based on trials) can be plotted either on top of each other or as sum in one plot. The histogram and scatter plot do not change in their behavior except for using all available data instead of one trial.





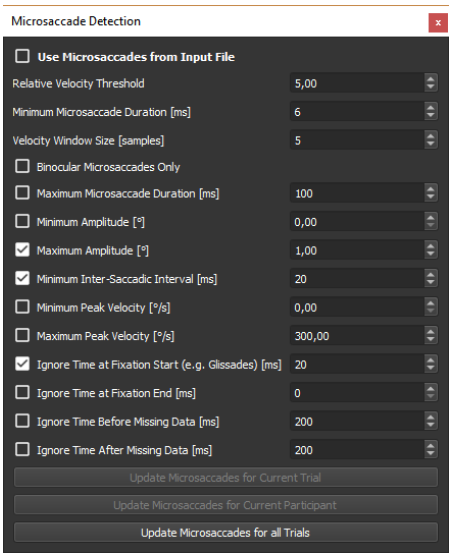
4.2 Eye movement Filters

Fixations and Microsaccades can be defined in the input file or determined with the built-in fixation and microsaccade filter. Both filters allow the specification of multiple parameters and use the same base algorithm introduced by [Engbert and Kliegl, 2003] with additional optional filter settings.

4.2.1 Microsaccade Filter (C1)

The microsaccade filter is a key element of this system. Fixations have to be defined first (either in the input file or with the application). For every fixation, the algorithm

is applied separately; if fixations contain missing data, multiple subsequences might be passed to the algorithm and microsaccades are determined for each subsequence.



Following parameters are available:

Relative velocity threshold: This value was introduced by Engbert and Kliegl (2003) as λ and is used to calculate the velocity thresholds

Minimum microsaccade duration [ms]: This value was introduced by Engbert and Kliegl (2003) to specify the minimum length of a microsaccade

Velocity window size [samples]: Specifies the window size used to determine the velocity

Binocular microsaccades only: optional; only microsaccades that overlap for the left and right eye at least at one sample are considered as binocular microsaccades

Maximum microsaccade duration [ms]: optional; microsaccades with a larger duration are ignored

Minimum amplitude [deg]: optional; microsaccades with a smaller amplitude are ignored

Maximum amplitude [deg]: optional; usually saccades with an amplitude up to one degree are considered as microsaccades

Maximum saccadic interval [ms]: optional; specifies the duration that should be at least between two microsaccades; if microsaccades are closer together only the first one will be considered

Minimum peak velocity [deg/s]: optional; microsaccades with a peak velocity smaller than this value are ignored

Maximum peak velocity [deg/s]: optional; microsaccades with a peak velocity larger than this value are ignored

Ignore time at fixation start [ms]: optional; this value can be used to ignore the first part of a fixation e.g. to ignore glissades

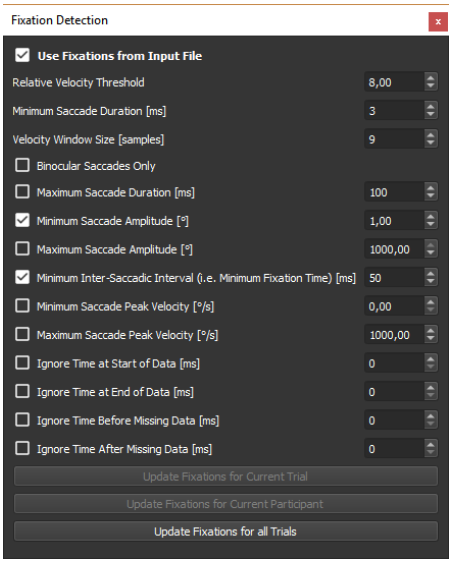
Ignore time before missing data [ms]: optional; this value can be used to ignore the time before missing data as it might contain errors

Ignore time after missing data [ms]: optional; this value can be used to ignore the time after missing data as it might contain errors

This filter can be applied to the current trial, all trials of the current participant or all available trials. Additionally, it is possible to switch back to microsaccades already available in the input data.

4.2.2 Fixation Filter (C2)

The fixation filter (which is actually a saccade filter), uses the areas between two detected saccades as fixations. The same algorithm available for microsaccade detection is used. The default parameter values are different compared to the microsaccades filter. After detecting saccades, the areas between two sequential saccades are used as fixations. We advise to preprocess your data in order to avoid small sections of missing data samples. Only sequences without any missing data can be used with this filter, i.e. fixations that contain missing samples are not detected as fixation; fixations need to be surrounded by saccades or may start at the beginning of the data and end at the end.



Following parameters are available:

Relative velocity threshold: Used to calculate the velocity thresholds

Minimum saccade duration [ms]: Specifies the minimum length of a saccade

Velocity window size [samples]: Specifies the window size used to determine the velocity

Binocular saccades only: optional; only saccades that overlap for the left and right eye at least at one sample are considered as binocular saccades

Maximum saccade duration [ms]: optional; saccades with a larger duration are ignored

Minimum saccade amplitude [deg]: optional; saccades with a smaller amplitude are ignored

Maximum saccade amplitude [deg]: optional; saccades with a larger amplitude are ignored

Minimum saccadic interval [ms]: optional, specifies the duration that should be at least between two saccades; if saccades are closer together only the first one will be considered, i.e. this has the side-effect for minimum fixation duration

Minimum saccade peak velocity [deg/s]: optional; saccades with a peak velocity smaller than this value are ignored

Maximum saccade peak velocity [deg/s]: optional; saccades with a peak velocity larger than this value are ignored

Ignore time at start of data [ms]: optional; the beginning of a trial can be excluded from the detection

Ignore time at end of data [ms]: optional; the end of a trial can be excluded from the detection

Ignore time before missing data [ms]: optional; this value can be used to ignore the time before missing data as it might contain errors

Ignore time after missing data [ms]: optional; this value can be used to ignore the time after missing data as it might contain errors

4.2.3 General Information (D1)

Here, statistical values about especially microsaccades and fixations are shown (minimum/maximum/mean/median values and a sum if appropriate).

Following values are provided:

Number of trials that are currently activated for analysis

Screen Resolution of the monitor used in the experiment

Frequency of the recorded data

#Raw data samples in trials

Duration of trials [s]

#Fixations in Trials

#Fixations with Microsaccades in Trials

Fixations containing Microsaccades [%]

Fixation duration [s]

Fixation (with microsaccades) duration [s]

#Microsaccades in trials

#Microsaccades per fixation

#Microsaccades per fixation with microsaccades

#Microsaccades per second (for trials)

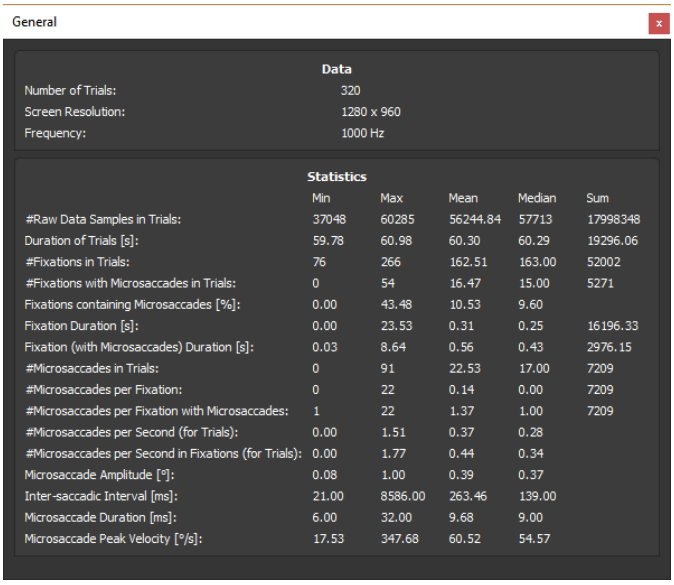
#Microsaccades per second in fixations (for trials)

Microsaccade amplitude [deg]

Intersaccadic interval [ms]

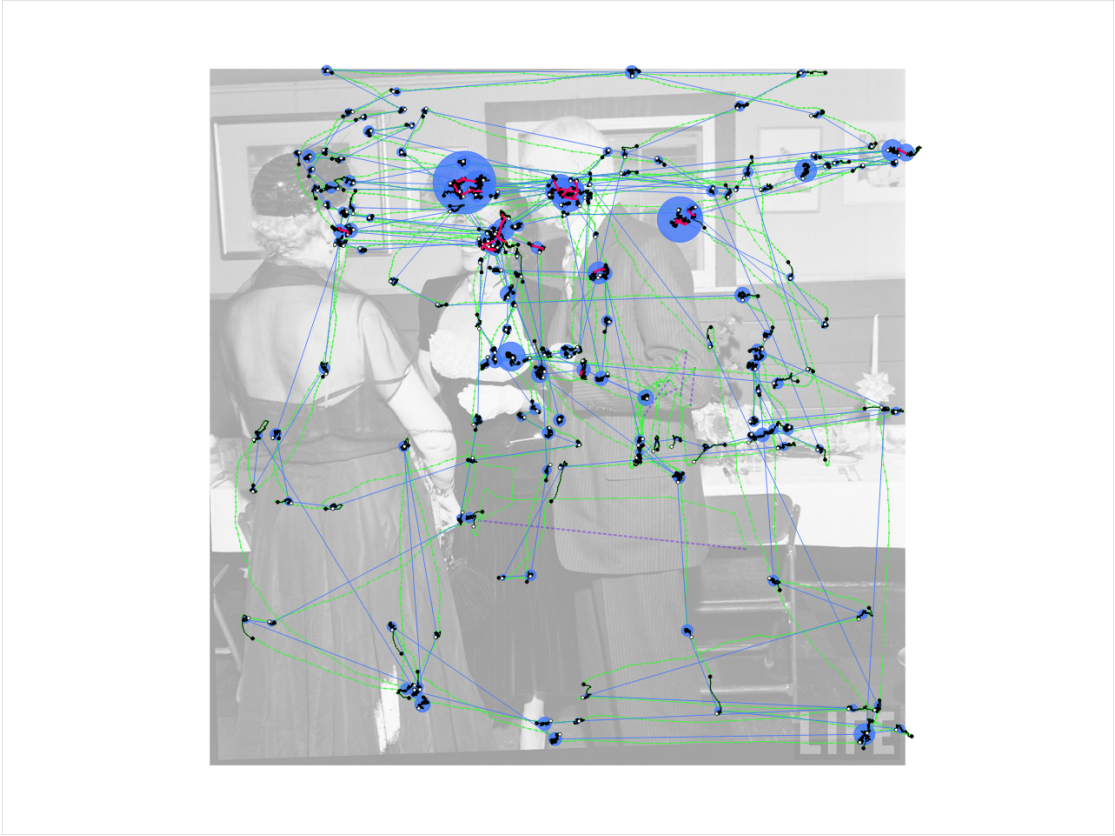
Microsaccade duration [ms]

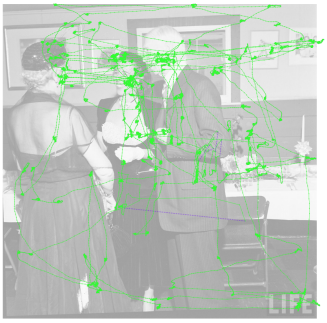
Microsaccade peak velocity [deg/s]

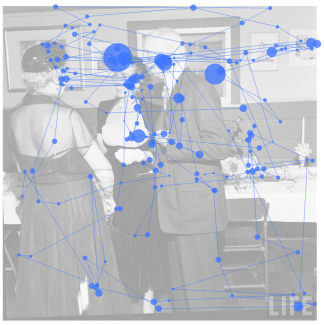


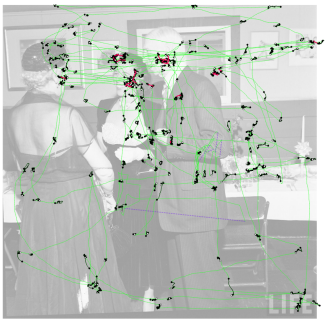
4.2.4 Stimulus View (E1/2)

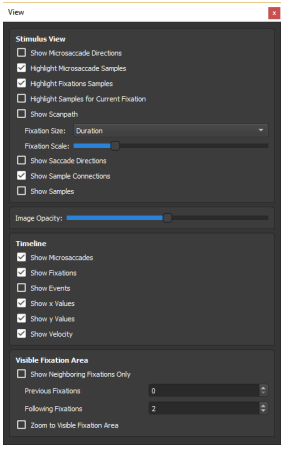
The *Stimulus view* is the main view to verify the detected microsaccades in relation to the whole eye movement for single trials or the overall microsaccade directions for multiple trials.











Filter options:

The opacity of the stimulus can be controlled as well as the visibility of raw data samples, their connections, saccade directions, scanpath (with scalable fixation size; their size can be equal, related to their duration or to the microsaccade count), highlighted fixation samples and microsaccade samples and directions. Highlighted samples can be limited to the currently selected fixation. Hovering over fixation circles shows a tooltip with its index.

In the scanpath, a color gradient is indicating the direction of the eye movement: from pink to blue if saccade directions are enabled. If not enabled, just for the selected fixation, the line with a larger amount of pink points towards the next fixation and the other one towards the previous one. When highlighting fixation samples, the first sample of a fixation is highlighted by a black circle and the last one by a white circle to indicate its movement direction.

The visible fixation range can be limited in relation to the selected fixation and its neighbors. It is possible to scroll through all fixations using the keyboard to get to the next and previous fixations. This will update the selected fixation in both the stimulus and the timeline view.

Supported shortkeys and mouse events:

Reset size of view: Ctrl + 0

Zoom in: Ctrl + + or *mouse wheel*

Zoom out: Ctrl + - or *mouse wheel*

Panning: *mouse click* on view and move mouse

Show fixation index: *hover* over fixation

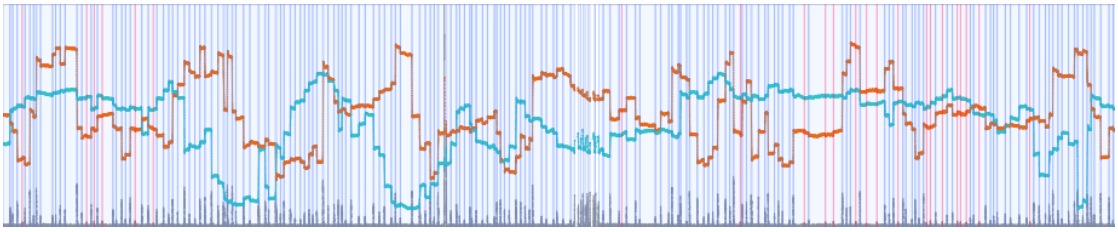
Select fixation: *mouse click* on fixation

Unselect all fixations: *mouse double click* on view at a position without fixations

Next fixation: → or N

Previous fixation: ← or P

4.2.5 Timeline View



The *Timeline view* shows the x and y position, as well as the velocity over time, for a trial. Additionally, fixations and microsaccade areas can be highlighted. Fixation areas can be used interactively to detect them in the Stimulus View and to update data plots. Further, additional events (e.g. special temporal incidents) can be shown in a similar way. Hovering over fixation in both the timeline and stimulus view shows a tooltip with its index. Hovering over event areas in the timeline shows the name of the event.

Supported shortkeys and mouse events:

Reset size of view: Ctrl + Alt + 0

Zoom in: Ctrl + Alt + + or *mouse wheel*

Zoom out: Ctrl + Alt + - or *mouse wheel*

Panning: *mouse click* on view (additionally, use Ctrl if you want to click on fixation areas) and move mouse

Show fixation index: *hover* over fixation

Select fixation: *mouse click* on fixation

Select time range: press Alt and select area with mouse

Next fixation: → or N

Previous fixation: ← or P

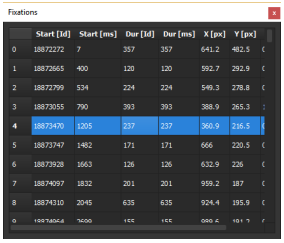
Filter options similar to the stimulus view:

Velocity, x and y values, fixations and microsaccades can be shown in this view.

The timeline can be zoomed to the currently visible fixations specified in *Visible Fixation Area*.

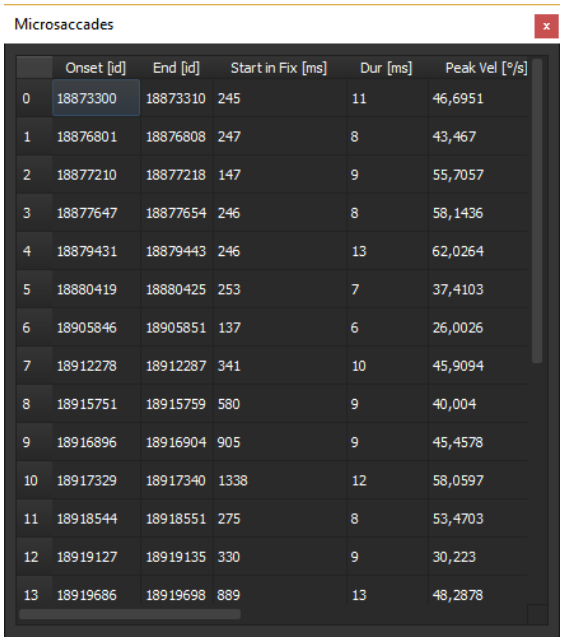
4.2.6 Fixation list

A list containing all fixations of the current trial (with some properties) sorted in temporal order can be used to select one fixation and to highlight it in the other views.



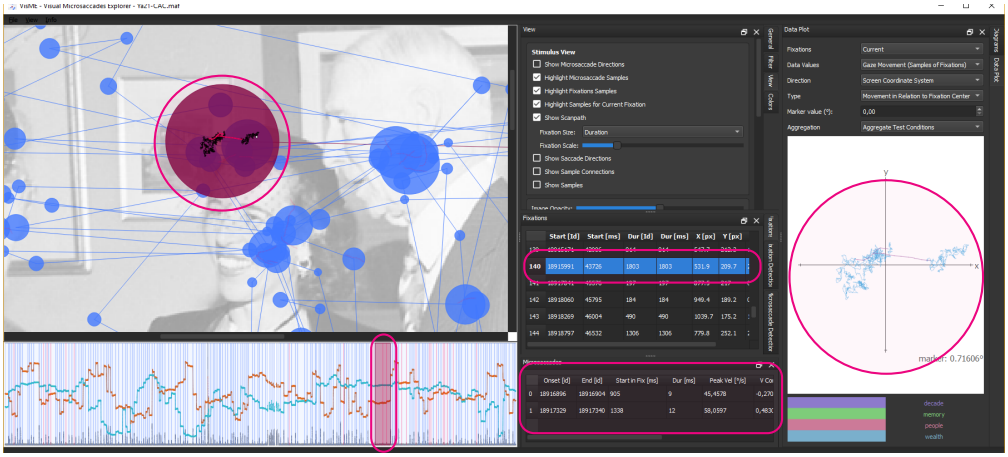
4.2.7 Microsaccades list

If a fixation is selected, its microsaccades are shown in this list along with some properties.



4.2.8 Trial: Fixations in Stimulus View, Timeline View and Data Plots

Following image shows the areas which will be updated when the currently selected fixation changes:



4.2.9 Color Settings

If you want to change colors used in the visualizations, you can do this in the color tab. In order to reuse the color values in other sessions, they can be exported and reimported into the system.

4.2.10 Data Plots

Multiple data plots can be created for microsaccades, saccades and gaze samples. When using saccades the connections between two fixations are used and when using gaze samples only the ones within fixations get analyzed. The plots can be oriented according to different directions: as visible on the view, towards the next fixation and towards the previous fixation. In the following the different types of data that is visualized is described.

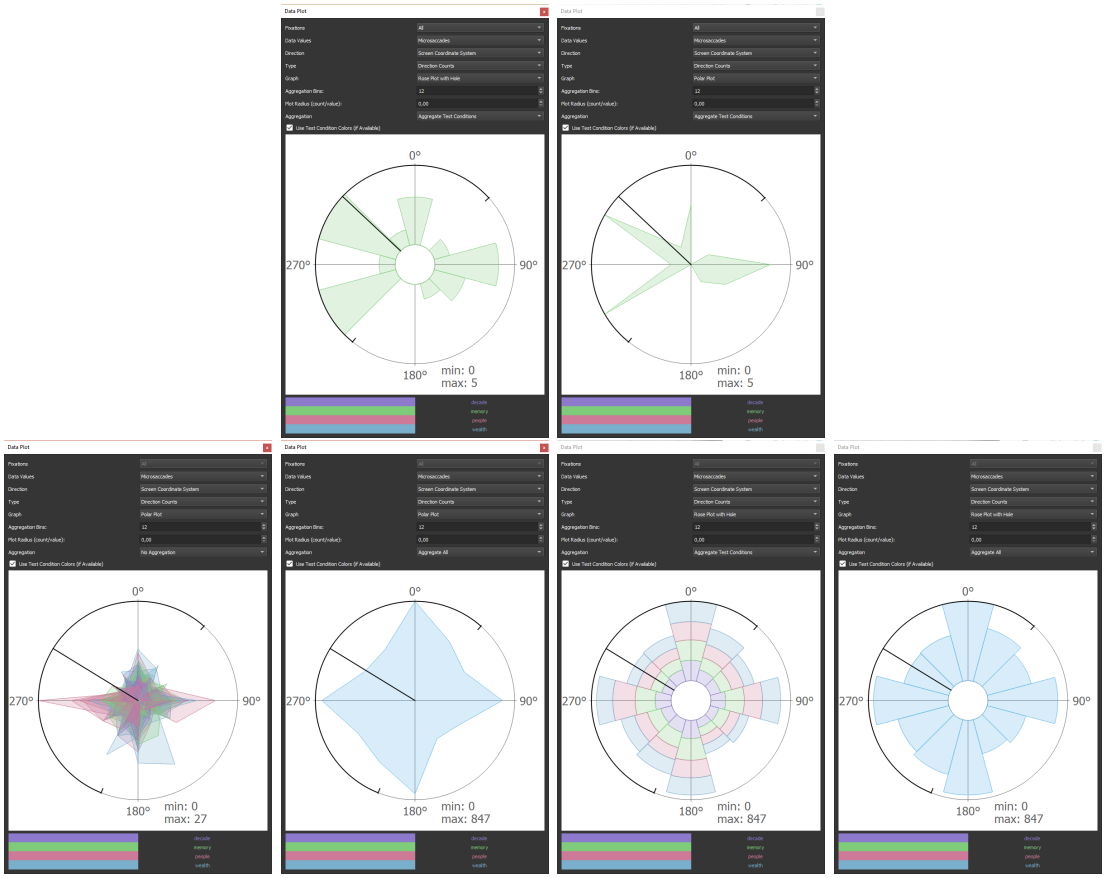
4.2.11 Data Plots – Directional Counts

A common visualization to explore microsaccades are directional plots (usually polar plots or rose plots) to explore the direction count towards each direction (Directional Counts): The direction of (micro)saccades or gaze samples can be visualized either in relation to neighboring saccades (the next one or the previous one) or as oriented on the stimulus. It can be used for all available fixations, the current one or all visible ones.

It is possible to switch between polar plots (which use overplot to compare multiple trials) and rose plots (stacking is used for multiple trials). Color can be used to differentiate between multiple test conditions, and it is possible to create an aggregated plot of all directional values (i.e. the visualization is performed as if there was only one large trial), aggregated for test conditions, participants and trials. By default, each trial is handled separately. By default, the axes are scaled to the maximum value in the graph but can be changed to a fixed value as well.

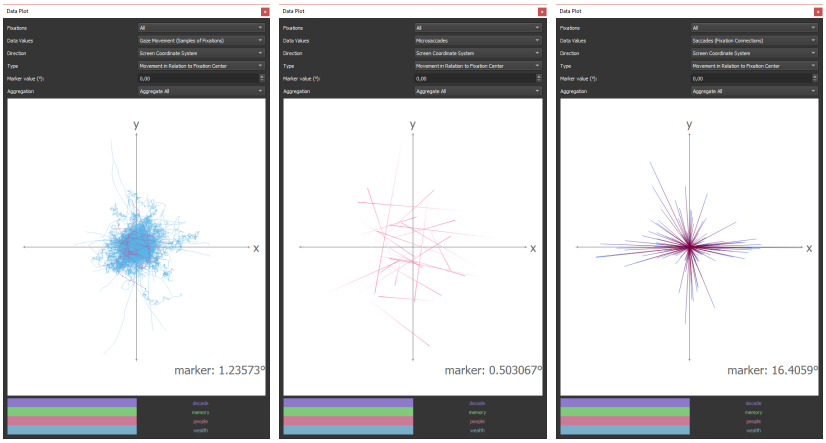
For all radial plots, the black line shows the mean direction and the arc the standard deviation.

Some examples:



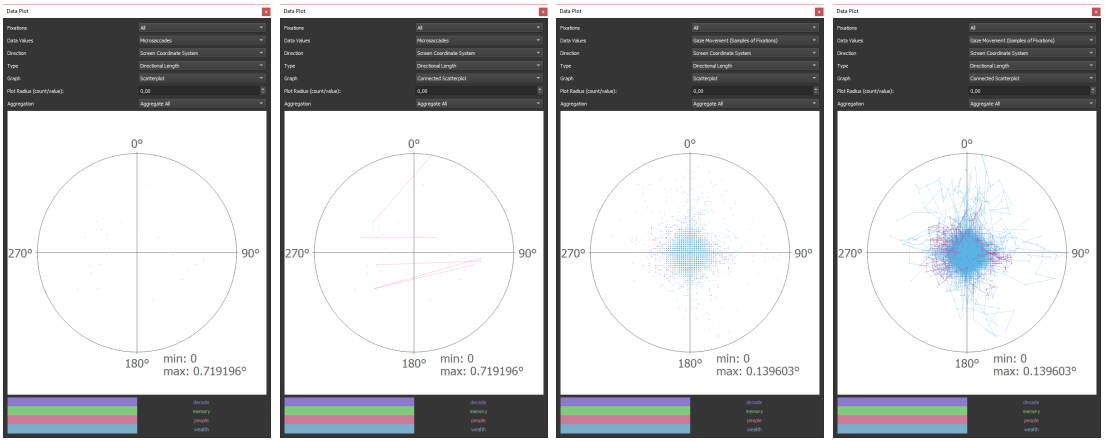
4.2.12 Data Plots – Movement Directions

The movement direction, amplitude and position of gaze samples, microsaccades and saccades in relation to the fixation center can be explored (Movement in Relation to Fixation Centre). For gaze data, this is a close-up visualization of fixation samples plotted on top of each other with highlighted microsaccades. For microsaccades, the start and end positions are connected by a line, and a color gradient is used for the direction: from pink to white. Saccades indicate the direction and distance to the next fixation; a color gradient from pink to blue is used.

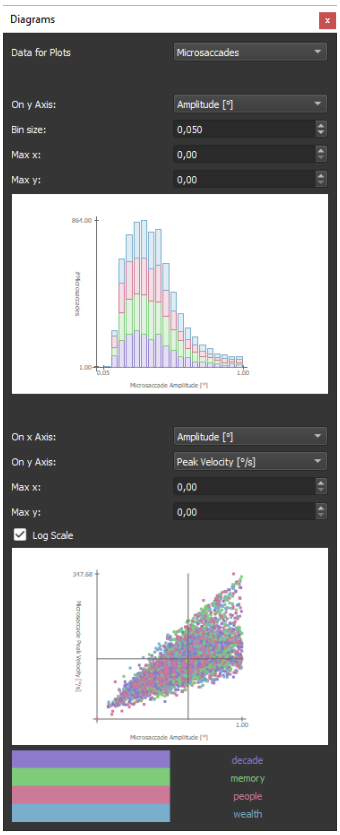


4.2.13 Data Plots – Directional Lengths

The directional length plots can be common scatterplots or connected scatterplots for data samples which belong to the same fixation. For microsaccades, saccades and sequential gaze positions, the eye movement direction and the length/distance is determined and plotted. If gaze samples are shown, samples of microsaccades are highlighted; this plot can also be seen as a directional velocity plot.

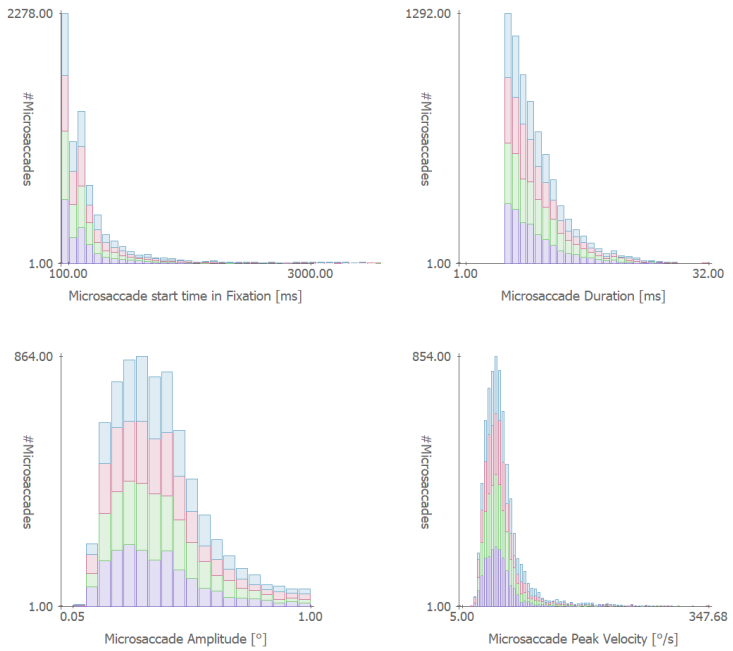


4.2.14 Histograms



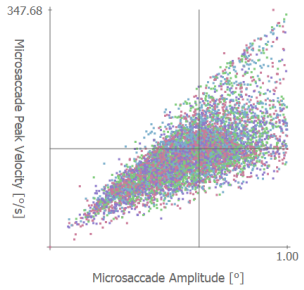
The histogram in the diagram tab can be used to visualize the start position of microsaccades within fixations as well as the duration, amplitude and peak velocity of (micro)saccades.

If test conditions are used, the bars are separated for each test condition with different colors.



4.2.15 Scatterplot

Scatterplots can be used to visualize the relationship between amplitude, velocity and duration of (micro)saccades. Especially the relationship between velocity and amplitude is a common visualization to verify microsaccades. If test conditions are used, the samples are colored according to the corresponding test condition. Both a linear and a logarithmic scale can be selected.

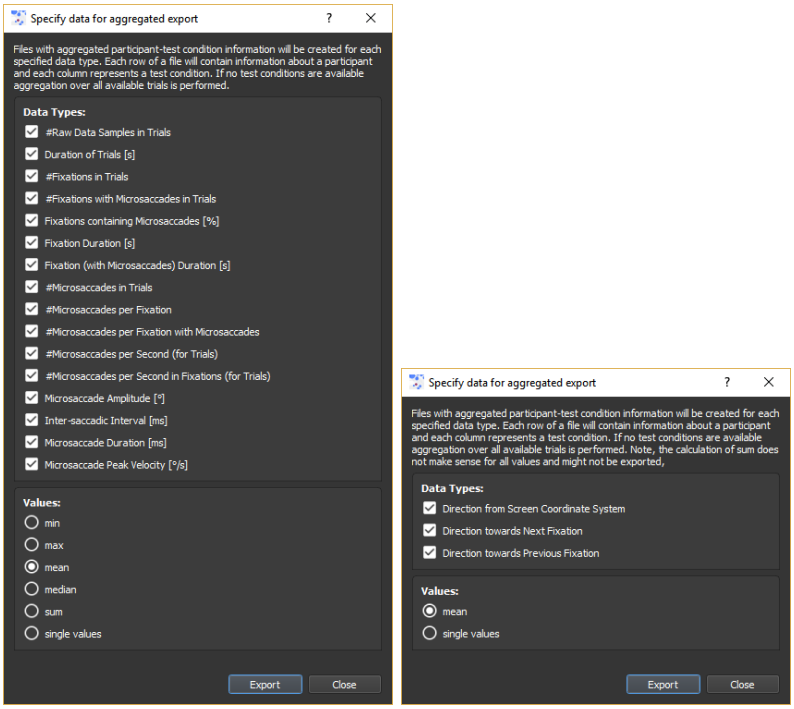


5 Data Export

Data can be exported to further explore it with other statistical software such as *R*, *Python* or *Matlab* and for later import into VisME. It is possible to export data of the current trial/participant or of all loaded participants in the format, which is also used for

importing into the system. Further, images of all views can be exported; these contain meta data about some of the current filter settings to recreate results in the system.

Some aggregated statistics can be exported for further analysis in other applications. This can be done for different properties of fixations and microsaccades. The files will contain data for each participant and test condition. Each participant is represented by a row and each test condition by a column. If no test conditions are specified, one aggregated value for each participant will be exported. For angular values (direction of microsaccades), a mean value or all values separately can be exported. For further properties of fixations/microsaccades minimum, maximum, mean, median, sum and all values separately can be exported. As the sum does not make sense for all data types, their export might be skipped.



Additionally, some further settings can be saved:

5.0.1 Microsaccades Parameter File (mpf)

This file contains parameter settings for the microsaccade filter; it can be exported and imported with the system. Values can be changed in a text editor manually and in the user interface.

5.0.2 Fixation Parameter File (fpf)

This file contains parameter settings for the fixation filter; it can be exported and imported with the system. Values can be changed in a text editor manually and in the user

interface.

5.0.3 Color Settings File (csf)

This file contains color values for the visualizations; it can be exported and imported with the system. Color values can be changed in a text editor manually and in the user interface.
Supported shortkeys:

Export Data for all Participants: Ctrl + D
Export Stimulus View as PNG file: Ctrl + Shift + E
Export Stimulus Scene as PNG file: Ctrl + E

5.1 Final Remarks

We tested the system with 1000 Hz and 500 Hz eye tracking data.

Our system was developed as a research project and may contain bugs and behave in unexpected ways.

Please feel free to contact us if you want to give feedback or have any issues using the system.

References

[Engbert and Kliegl, 2003] Engbert, R. and Kliegl, R. (2003). Microsaccades uncover the orientation of covert attention. *Vision Research*, 43(9):1035 – 1045.