Overview

EyeTrackerAnalyzer is a tool dedicated to analyzing eye tracking data, that can be interfaced via an API (Application Programming Interface - A bundle of MATLAB functions that constitute EyeTrackerAnalyzer's operations), or via a MATLAB GUI (Graphical User Interface). With EyeTrackerAnalyzer you can extract from the eye tracking data the following elements:

* Saccades - Rapid eye movements. The saccades are extracted using Engbert's algorithm (cite). Calculated variables per saccade:
* onset
* duration
* amplitude
* direction
* velocity
* Fixations - Defined as segments of valid eye samples that are not part of a saccade. Calculated variables per fixation:
* onset
* duration
* position
* Pupils' sizes - As reported directly by eye trackers.
* Blinks - Can be extracted directly as reported directly by eye trackers or based on the pupil sizes data.

EyeTrackerAnalyzer also generates various figures:

* saccadic rate - the chance for a saccade onset on every trial sample
* average saccade amplitude per direction (polar graph)
* saccades number per direction (polar graph)
* main sequence - saccade amplitude as a function of saccade velocity

The usage pipeline with EyeTrackerAnalyzer is as follows:

1. Package the different subjects' data files inside .ETA files with which EyeTrackerAnalyzer operates.
2. Assign data segmentation parameters values - Data segmentation is the process of cutting out data segments during which events of interest have happened.
3. Assign analysis parameters values - these include the saccades extraction algorithms parameters, data pre-processing parameters, etc.
4. Optional: Traverse the data trial-by-trial and inspect the saccades and blinks found by EyeTrackerAnalyzer as well as cancel false findings and manually mark new ones.

The GUI consists of 4 main panes:

1. Analysis Pane - Holds segmentation and analysis parameters controls. Through this pane one starts the analysis.
2. Multiple Data Files Per Subject Packaging Pane - enables to group multiple eye tracker data files for each subject, and create a single .ETA for each.
3. Single Data Files Per Subject Packaging Pane - enables to read a folder containing eye tracking data files and generate a single .ETA per file read.
4. Raw eye tracking data extraction pane - enables generating a MATLAB structure stored in a .mat file that holds the raw eye tracking data as extracted from an eye tracking data file.

Analysis Pane

Subjects' .ETAs Panel

Here one specifies the .ETAs files on which to run the chosen analysis:

* To add files to the panel, press on the folder with spy glass icon to the left of the panel. Multiple files can be added at one time.
* To remove files from the panel, select the files to be removed and click on the red X icon to the left of the panel. Multiple files can be selected by holding the shift or ctrl buttons while clicking on files.

Analysis Output Folder

Here you specify a folder inside which all the analysis output files will be saved. To choose a folder press the 'Browse' button. The full path of the selected folder will appear inside the text box to the left of the button.

Data Segmentation Panel

Here one inputs the segmentation parameters:

* Trials Onset Triggers - These are the messages sent during the eyes' recording that will define the beginning of an analysis segment.

**(!) Important: The different onset Triggers are used to define the** **conditions to which the corresponding segments are assigned.**

* Trials Offset Triggers - These are the messages sent during the eyes' recording that will define the ending of an analysis segment. The offset triggers have no bearing over the assignments of the segments to conditions. A segment is ended once any of the offset triggers is encountered.

**Note: if while scanning a segment, an onset trigger is encountered before an offset trigger, the segment ends and assigned to the onset trigger that started the segment.**

* Trials Rejection Triggers - These are the messages sent during the eyes recording that will signal EyeTrackerAnalyzer to drop a segment during which the message was sent. A segment is dropped once any one of the rejection triggers is encountered.

The interface for inputting triggers is the same:

* adding a trigger - enter the trigger in the field above the corresponding list pane.
* removing triggers - select the triggers to be removed and press 'Delete', found to the left of the corresponding Pane. Multiple triggers can be selected by holding the shift or ctrl buttons while clicking on triggers.
* Multiple-Triggers-One-Condition: It is also possible to have different triggers define the same condition, and thus have their corresponding segments assigned to the same condition. To achieve this goal, we use a regex (regular expression. for more info see: <https://en.wikipedia.org/wiki/Regular_expression> and <https://regexr.com>) to define a messages pattern. All messages that fit this pattern will be counted as corresponding to the same condition.
* Pre-onset-trigger segment duration - An extra period of data to attach to each segment right before the segment's onset.
* Post-offset-trigger segment duration - An extra period of data to attach to each segment right after the segment's offset.
* Analysis segment duration – {TODO: sort this one out}
* Save Parameters button – Enables to save the entered segmentation parameters to a file from which the currently entered values can be retrieved. The save file's extension will be 'ap'.
* Load Parameters button - Enables to load a previously saved segmentation values from an .ap file.

Analyses Start Buttons

* Analyze Movements - Shows up an additional dialogue with parameters for the eyes movements analysis, from which the actual analysis can be started. A description of this dialogue is in the section Analyses Dialogues.
* Analyze Pupils Diameters – Starts the pupils diameters analysis.

Multiple Data Files Per Subject Packaging Pane

In this pane you will find a panel that enables loading eye tracking data files and select an output file folder and name. Files loaded to this panel will be packaged into a single .ETA which will be treated as a single subject's multi-session data. Once at least one file is added to this panel, another empty panel will be added to the pane, ready to load another subject's data files. A maximum of 10 such panels can be displayed at one time. Removing all files from A panel will clear that panel.

Panel's actions:

* Add data files – Press the folder with spy glass icon. Multiple files can be added at one time.
* Remove data files - Press the red X icon. Multiple files can be selected by holding the shift or ctrl buttons while clicking on files.
* Save .ETA folder and file – Press the blue disk with green arrow icon. A dialogue will open up with which you can select a folder to save the .ETA at and a file name for the .ETA.

At the bottom of the pane you will find:

* Experiment screen's Pixels Per Visual Degree – Spatial magnitudes in EyeTrackerAnalyzer are reported in visual degrees while eyetracking data is recorded in pixels. This is the factor EyeTrackerAnalyzer will use to convert from the eye trackers' data to visual degrees for all the .ETAs created in the current screen.
* Clear All – Press this button to clear all the panels.
* Create – Press to start the .ETAs Creation.

Single Data File Per Subject Packaging Pane

In this pane you will find a panel similar to the Subjects' .ETAs Panel on the Analysis Panel:

* To add files to the panel, press on the folder with spy glass icon to the left of the panel. Multiple files can be added at one time.
* To remove files from the panel, select the files to be removed and click on the red X icon to the left of the panel. Multiple files can be selected by holding the shift or ctrl buttons while clicking on files.
* Save Folder - Here you specify a folder inside which the created .ETA files will be saved. To choose a folder press the 'Browse' button. The full path of the selected folder will appear inside the text box to the left of the button.

At the bottom of the pane you will find:

* Experiment screen's Pixels Per Visual Degree – This is the same control described for the Multiple Data Files Per Subject Packaging Pane.
* Create – Press to start the .ETAs Creation.

Extract Eye Data As .MAT Panel

There are two files loading panels in this pane – one for extraction of a Matlab structure out of an .ETA file, and one for extraction out of an .EDF file. In both panels:

* To add files to the panel, press on the folder with spy glass icon to the left of the panel. Multiple files can be added at one time.
* To remove files from the panel, select the files to be removed and click on the red X icon to the left of the panel. Multiple files can be selected by holding the shift or ctrl buttons while clicking on files.

At the bottom of the pane:

* Save Folder - Here you specify a folder inside which the created .MAT files will be saved. To choose a folder press the 'Browse' button. The full path of the selected folder will appear inside the text box to the left of the button.
* Extract - Press to start the .MATs Extraction.

Analyses Dialogues

Eye Movements Analysis Parameters Panel

* Blinks Delta - Duration before the start of a detected blink and after the end of a detected blink to be marked as part of that blink.
* Blink Detection Method:
* Eye Tracker - Taking the blinks detected by the eye tracker.
* Pupil-Based - Detecting blinks via the pupils data.
* Eye Tracker + Pupil-Based - Taking the union of the blinks detected by the eye tracker and of those detected via the pupils data.
* Smoothing Window Length for Saccadic Rate – Relevant to the saccadic rate measure. This measure undergoes a postprocess in which each sample will equal the mean of all the samples in the time frame centered on that sample.

The control will be grayed out if the 'Generate rate graphs' checkbox is unchecked.

* Velocity Threshold – Engbert algorithm parameter.
* Saccade Amplitude Lower / Upper limit – These controls define a range of amplitudes, whereby saccades with amplitudes outside of it are discarded.
* Minimum Time Between Saccades – Defines a time interval after a saccade onset within which any other found saccade is discarded.
* Minimum Duration for A Saccade – Saccades lasting less than this amount of time are discarded.
* Lowpass Filter – The bandpass of the lowpass filter applied to the data prior to the analyses.
* Generate rate graphs – Whether to generate the saccadic rate graphs
* Generate amplitudes graphs – Whether to generate the amplitudes graphs
* Generate directions graphs – Whether to generate directions graphs
* Generate main sequence graphs – Whether to generate the main sequence graphs.
* Generate Single Graphs – generate the marked graphs individually for each subject.
* Generate Group Graphs – generate the marked graphs for the means over all subjects. The control will be grayed out if only one subject .ETA was added to the 'Subjects .ETAs' panel.
* Perform Data Inspection – Whether to manually go over the data and results (further details in the 'Data Inspector' section).
* Data Inspector' display range – Will be explained in the Data Inspector' section.
* Save Parameters button – Enables to save the entered analysis parameters to a file from which the currently entered values can be retrieved. This is the same file where the segmentation parameters are saved.
* Load Parameters button - Enables to load a previously saved analysis parameters values from an .ap file. This is the same file where the segmentation parameters were saved, hence this will load the segmentation parameters that were saved along with these analysis parameters.
* Go – Start the analysis.
* Cancel – cancel the analysis.

Data Inspector

The Data Inspector enables to traverse the data trial-by-trial and inspect the saccades and blinks found by EyeTrackerAnalyzer as well as cancel false findings and manually mark new ones. The trials are displayed by the Data Inspector in a random order and with no regard to the trials' division to conditions.

The Data Inspector pane will fire up automatically after the analyses finish, if the 'Perform Data Inspection' checkbox was marked. This pane consists of 2 axes displays showing the data and the analysis results (Data Panels below), and a controls panel.

Data Panels

There are 2 panels showing the data, one for the eyes' X positions and the other for the eyes' Y positions over trial time. The eyes positions are in visual angles and are baseline corrected to the mean, and the trial time is in milliseconds. Each panel displays 2 plots, one for the left eye and one for the right. The plots' colors to eyes correspondence is according to the legend above the panel. Segments of missing data are marked by dashed lines connecting both ends of the missing data segments. There is also a horizontal dashed line marking the axes' 0. Over the plots themselves you will find green segments which mark the saccades found by EyeTrackerAnalyzer. If you hover over a saccade marking with the mouse, a tool tip will appear indicating the saccade's amplitude and the eyes' peak velocity during the saccade, both in visual degrees.

Controls Panel

* Subject Displayed – currently inspected subject.
* Trial Displayed – currently inspected trial index. As stated above, this is a random index which does not pertain to the trial's position in the experiment.

In both these controls, to display the next or previous subject/trial, press the '<' or '>' buttons respectively. You can also display a specific subject/trial by entering a number directly in the textbox that shows the currently displayed subject/trial, found between the '<' and '>' buttons.

* Center On Saccade – by pressing the '<' or '>' below this label, the data panels axes will center on a saccade to the left or to the right of the current axes center, respectively.
* Refit Graphs – Adjusts the data panels' axes Y axis so that the entire trial's plots are fitted in the axes exactly.

The next controls also have hotkeys associated with them.

* Pan (Hotkey: P) – Press this button to enable dragging the data panels axes with the mouse. The Cursor's icon will change to a hand.
* Select (Hotkey: S)- Press this button to enable discarding and marking saccades on the plots, and to drop segments of data. The Cursor's icon will change to an arrow:
  + To discard a saccade – click on a saccade segment. The saccade segment will change from green to red. To cancel a discard, click on the saccade segment again.
  + To mark a new segment as a saccade – click on the plot at around the middle of the segment that seems to be a saccade. The saccades extraction algorithm will be run with thresholds more and more liberal, until a saccade is found. The new saccade segments will be marked in blue. To cancel the saccade click on the segment.
  + To drop/reinstate a data segment – click on an empty point on a data panel, such that the point's time coordinate is an edge of the segment to be dropped. A blue vertical line will appear, indicating the selected edge, and a second blue vertical line will follow the cursor. Place the second blue vertical line at the other edge of the data segment to be dropped, then click. If you left click – the data segment will be dropped, while if you right click – the data segment will be reinstated. Dropped data segments, along with contained saccades, will change color to pink.
* Undo (Hotkey: ctrl + z) – undo the last action.
* Redo (Hotkey: ctrl + y) – redo the last action.
* Zoom In (Hotkey: Z) – enables to zoom into the data controls axes. The cursor icon will change to a magnifying glass with a plus.
* Zoom out (Hotkey: ) – enables to zoom out of the data controls axes. The cursor icon will change to a magnifying glass with a minus.
* Re-extract Saccades – Enables to run the saccades extraction again with different parameters. Pressing this will fire up a pane holding all the parameters detailed in 'Eye Movements Analysis Parameters Panel' that pertain to the saccades extraction algorithm.
* Reject-Restore Trial – Press to drop an entire trial. Press again to cancel the drop.
* Save – save the changes done with the Data Processor to the corresponding subjects' .ETA files. The save will overwrite previously saved changes found in the .ETAs. This changes will be loaded automatically for the next analysis run with the same parameters.
* Finish – Close the Data Inspector and proceed with the analyses.
* Cancel Analysis – {TODO: Verify this}

Output Folder

After the analysis is done, you will find the following items inside the output folder:

* grouped graphs folder (generated if 'Generate Group Graphs' option was checked) – stores the graphs generated for the means over all subjects
* subject (#) folders (generated if ' Generate Single Graphs' option was checked) – each folder stores the graphs generated individually for the corresponding subject, numbered according to the order of the .ETA files in the Subjects' .ETAs panel. In addition, each folder will store an analysis\_struct.mat (details below) for the corresponding subject if the 'create individual analysis structs' option was checked.
* error\_log.txt – will hold error messages for various errors that raised during the analysis.
* analysis\_struct.mat – holds the analysis results along with the analysis parameters, Data Inspection stats, and the raw eyes positions data. analysis\_struct.mat structure:
  + eye\_movements\_data [struct] – includes the following fields:
    - saccades [struct] – stores the saccades data extracted in the analysis. has a field for each condition. Each field is

a struct:

* number of saccades [vector] – stores in component *t* the number of saccades extracted for trial *t*.
* durations [cell array] – stores in cell *t* a vector of the saccades' durations extracted for trial *t*.
* amplitudes [cell array] - stores in cell *t* a vector of the saccades' amplitudes extracted for trial *t*.
* directions [cell array] - stores in cell *t* a vector of the saccades' directions extracted for trial *t*.
* onsets [cell array] - stores in cell *t* a vector of the saccades' onsets extracted for trial *t*.
* velocities [cell array] - stores in cell *t* a vector of the saccades' velocities extracted for trial *t*.
* logical onset mat [matrix] – has a line per trial and number of columns equals to the duration of the longest segment (in milliseconds) extracted for the corresponding condition. Cell (i,j) holds 1 if on millisecond j of trial i, a saccade has started, and 0 otherwise.
  + - Fixations [struct] – stores the fixations data extracted in the analysis. has a field for each condition. Each field is

a struct:

* onsets [cell array] - stores in cell *t* a vector of the fixations' onsets extracted for trial *t*.
* coordinates\_left [cell array] - stores in cell *t* a vector of the fixations' left eye coordinates extracted for trial *t*.
* coordinates\_right [cell array] - stores in cell *t* a vector of the fixations' right eye coordinates extracted for trial *t*.
* durations [cell array] - stores in cell *t* a vector of the fixations' durations extracted for trial *t*.
  + - eyeballing\_stats [struct] – stores the stats of the operations done in the data inspector. has a field for each condition. Each field is a struct:
* accepted\_saccades\_nr [vector] - stores in cell *t* the number of accepted saccades extracted for trial *t*.
* rejected\_saccades\_nr [vector] - stores in cell *t* the number of rejected saccades for trial *t*.
* user\_generated\_saccades\_nr [vector] - stores in cell *t* the number of saccades manually marked by the user for trial *t*.
* blinked\_out\_saccades\_nr [vector] - stores in cell *t* the number of saccades rejected for trial *t* due to including samples inside a blink that was manually marked by the user.
* was\_trial\_rejected [vector] – stores in cell *t* 'true' if trial *t* was dropped and 'false' otherwise.
  + - raw\_data [struct] – stores the raw data as generated by the eyetracker. Has a field for each condition. Each field is a struct:
      * right\_eye [struct] – holds the data for the right eye:
        + x [matrix] – holds the x coordinates of the right eye's positions. has a line per trial and number of columns equals to the duration of the longest segment extracted (in milliseconds) for the corresponding condition.
        + y [matrix] – holds the y coordinates of the right eye's positions. has a line per trial and number of columns equals to the duration of the longest segment extracted (in milliseconds) for the corresponding condition.
      * left\_eye [struct] - holds the data for the left eye. Has an identical structure as the right\_eye struct.
      * Vergence [struct] – holds the difference in positions between the left eye and the right eye (left eye position minus the right eye position). Has an identical structure as the right\_eye struct.
      * non\_nan\_times – {TODO: Verify this}
  + results [struct] – Holds the output of various analyses requested by the user:
    - saccadic\_rate [struct] – The average number of saccades onsets for every millisecond in an analyzed segment. Has a field for each condition. Each condition field stores the result vector for trials belonging to the corresponding condition.
  + saccades\_analsysis\_parameters [struct] – Holds a field for every parameter of the analysis.