# User Manual

# for

# T.E.A.R.S. - 1.0

***Developed by:***

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**for making this project possible!**

**For more information, visit our web-page at:**
**https://www.math.lsu.edu/courses/capstone_course/Summer2015**

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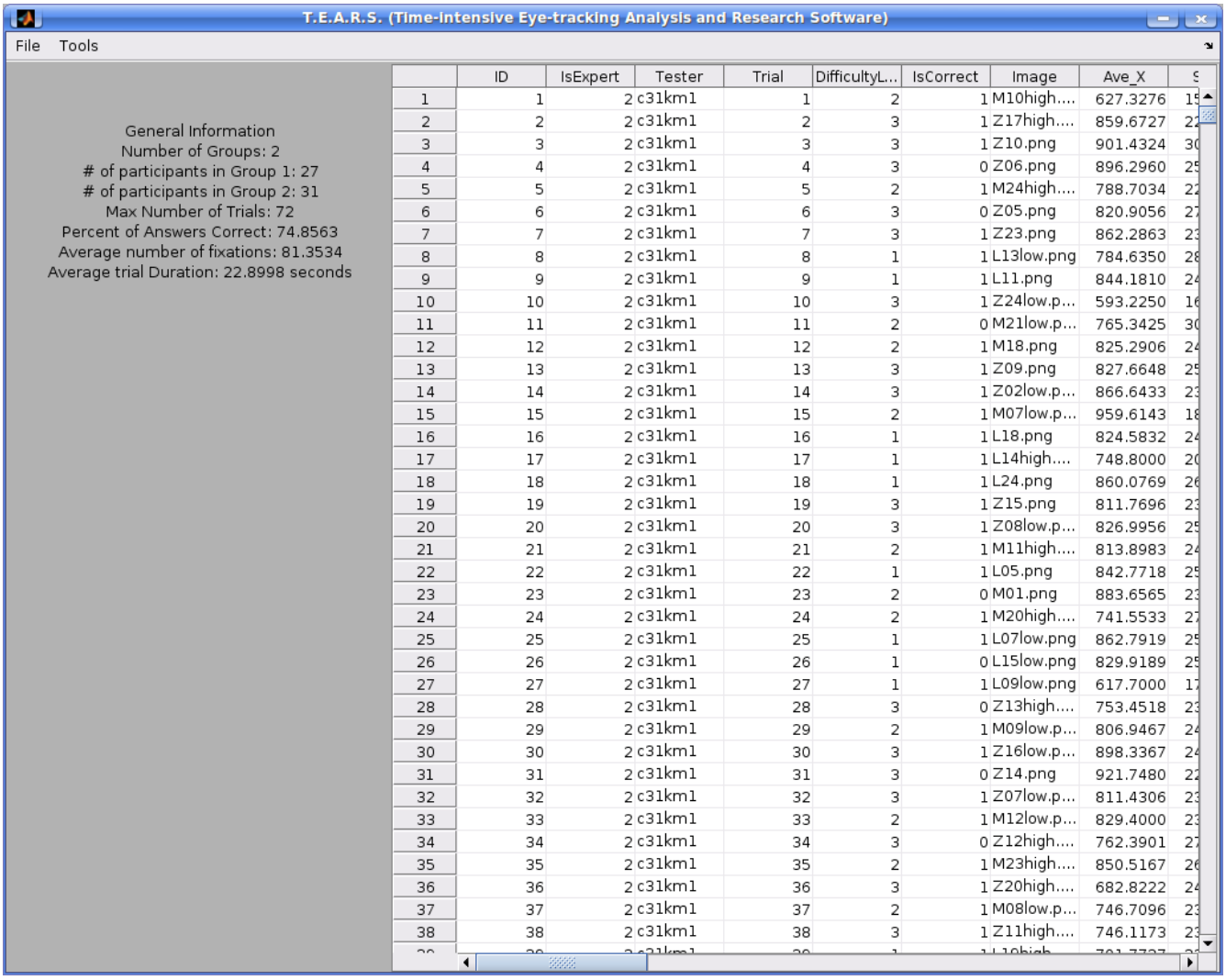
# Introduction




| | ID | IsExpert | Tester | Trial | DifficultyL... | IsCorrect | Image | Ave_X | S |
|---|---|---|---|---|---|---|---|---|---|
| 1 | 1 | 2 | c31km1 | 1 | 2 | 1 | M10high.... | 627.3276 | 15 |
| 2 | 2 | 2 | c31km1 | 2 | 3 | 1 | Z17high.... | 859.6727 | 22 |
| 3 | 3 | 2 | c31km1 | 3 | 3 | 1 | Z10.png | 901.4324 | 30 |
| 4 | 4 | 2 | c31km1 | 4 | 3 | 0 | Z06.png | 896.2960 | 25 |
| 5 | 5 | 2 | c31km1 | 5 | 2 | 1 | M24high.... | 788.7034 | 22 |
| 6 | 6 | 2 | c31km1 | 6 | 3 | 0 | Z05.png | 820.9056 | 27 |
| 7 | 7 | 2 | c31km1 | 7 | 3 | 1 | Z23.png | 862.2863 | 23 |
| 8 | 8 | 2 | c31km1 | 8 | 1 | 1 | L13low.png | 784.6350 | 28 |
| 9 | 9 | 2 | c31km1 | 9 | 1 | 1 | L11.png | 844.1810 | 24 |
| 10 | 10 | 2 | c31km1 | 10 | 3 | 1 | Z24low.p... | 593.2250 | 16 |
| 11 | 11 | 2 | c31km1 | 11 | 2 | 0 | M21low.p... | 765.3425 | 30 |
| 12 | 12 | 2 | c31km1 | 12 | 2 | 1 | M18.png | 825.2906 | 24 |
| 13 | 13 | 2 | c31km1 | 13 | 3 | 1 | Z09.png | 827.6648 | 25 |
| 14 | 14 | 2 | c31km1 | 14 | 3 | 1 | Z02low.p... | 866.6433 | 23 |
| 15 | 15 | 2 | c31km1 | 15 | 2 | 1 | M07low.p... | 959.6143 | 18 |
| 16 | 16 | 2 | c31km1 | 16 | 1 | 1 | L18.png | 824.5832 | 24 |
| 17 | 17 | 2 | c31km1 | 17 | 1 | 1 | L14high.... | 748.8000 | 20 |
| 18 | 18 | 2 | c31km1 | 18 | 1 | 1 | L24.png | 860.0769 | 26 |
| 19 | 19 | 2 | c31km1 | 19 | 3 | 1 | Z15.png | 811.7696 | 23 |
| 20 | 20 | 2 | c31km1 | 20 | 3 | 1 | Z08low.p... | 826.9956 | 25 |
| 21 | 21 | 2 | c31km1 | 21 | 2 | 1 | M11high.... | 813.8983 | 24 |
| 22 | 22 | 2 | c31km1 | 22 | 1 | 1 | L05.png | 842.7718 | 25 |
| 23 | 23 | 2 | c31km1 | 23 | 2 | 0 | M01.png | 883.6565 | 23 |
| 24 | 24 | 2 | c31km1 | 24 | 2 | 1 | M20high.... | 741.5533 | 27 |
| 25 | 25 | 2 | c31km1 | 25 | 1 | 1 | L07low.png | 862.7919 | 25 |
| 26 | 26 | 2 | c31km1 | 26 | 1 | 0 | L15low.png | 829.9189 | 25 |
| 27 | 27 | 2 | c31km1 | 27 | 1 | 1 | L09low.png | 617.7000 | 17 |
| 28 | 28 | 2 | c31km1 | 28 | 3 | 0 | Z13high.... | 753.4518 | 23 |
| 29 | 29 | 2 | c31km1 | 29 | 2 | 1 | M09low.p... | 806.9467 | 24 |
| 30 | 30 | 2 | c31km1 | 30 | 3 | 1 | Z16low.p... | 898.3367 | 24 |
| 31 | 31 | 2 | c31km1 | 31 | 3 | 0 | Z14.png | 921.7480 | 22 |
| 32 | 32 | 2 | c31km1 | 32 | 3 | 1 | Z07low.p... | 811.4306 | 23 |
| 33 | 33 | 2 | c31km1 | 33 | 2 | 1 | M12low.p... | 829.4000 | 23 |
| 34 | 34 | 2 | c31km1 | 34 | 3 | 0 | Z12high.... | 762.3901 | 27 |
| 35 | 35 | 2 | c31km1 | 35 | 2 | 1 | M23high.... | 850.5167 | 26 |
| 36 | 36 | 2 | c31km1 | 36 | 3 | 1 | Z20high.... | 682.8222 | 24 |
| 37 | 37 | 2 | c31km1 | 37 | 2 | 1 | M08low.p... | 746.7096 | 23 |
| 38 | 38 | 2 | c31km1 | 38 | 3 | 1 | Z11high.... | 746.1173 | 23 |

**T.E.A.R.S.** (Time-intensive Eye-tracking Analysis and Research Software) is a toolkit for analyzing arbitrary subsets of fixation data, and uses several powerful comparison algorithms to find patterns and recurrences within these data sets. In order to run **T.E.A.R.S.** the user must have a copy of **MATLAB 2014** and must also have the **Image Processing toolbox**. As the software name suggests, many of the processes run in T.E.A.R.S. are rather time consuming. To avoid possible errors, the programmers suggest reading and/or referring to this user guide when using any tool within **T.E.A.R.S.**

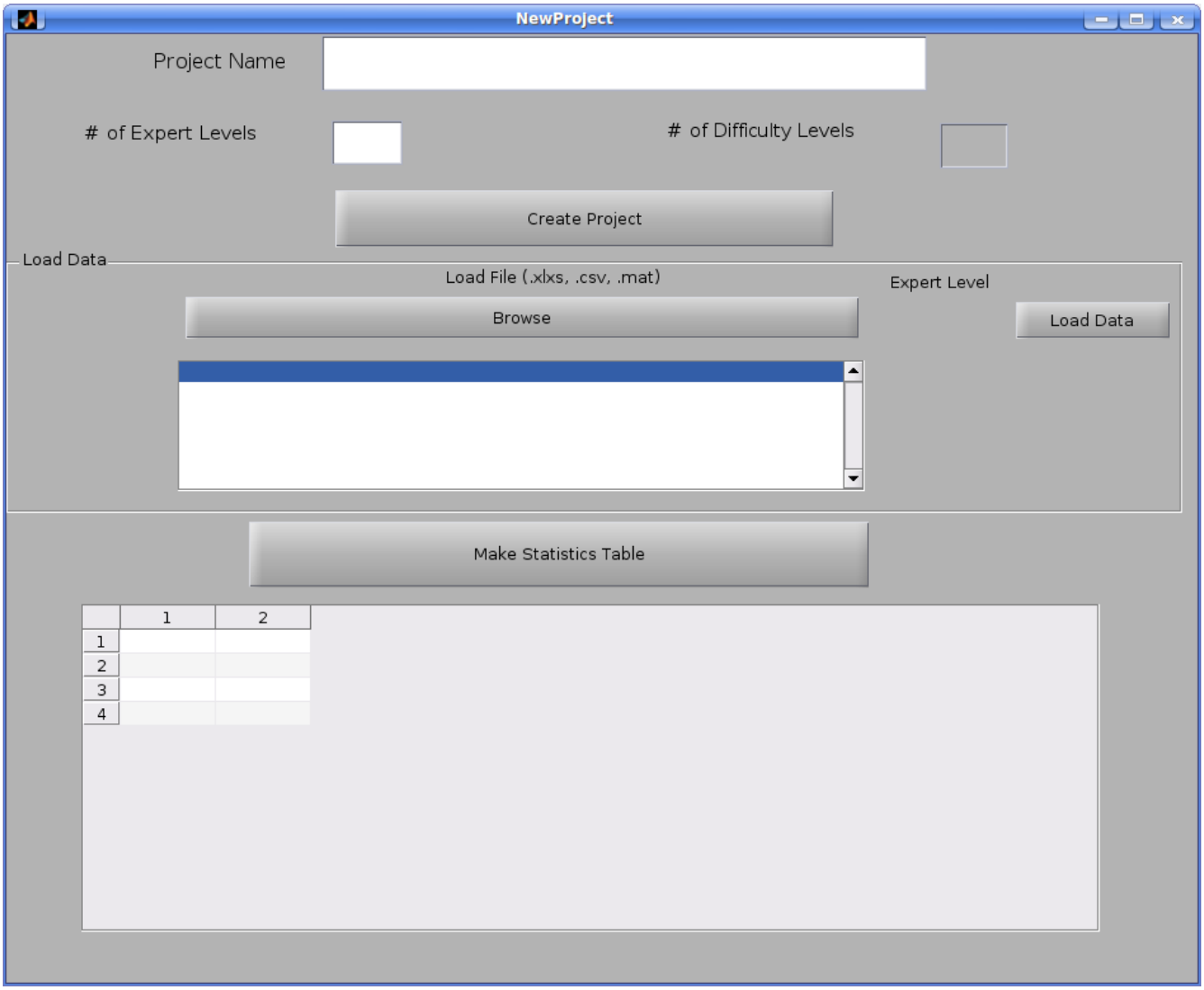
To run **T.E.A.R.S.**, first open **MATLAB** and select (double-click) the folder-path in the '**Current Folder**' panel on the left containing '**tears.m**'. Then, simply enter '**tears**' into the command window of MATLAB.

Please note that all of the data outputted by **T.E.A.R.S.** Is completely dependent on what is contained within the files inputted into the '**New Project**' menu. Blank cells and other unspecified inaccuracies in the data fed to our GUI may cause errors beyond the scope of this guide, and could possibly invalidate outputs given by any and/or all tools within **T.E.A.R.S.** Additionally, all fixation data should be scaled to a resolution of **740x580** for accurate results.
Excel files must be formatted in a particular manner, described in detail in the section dedicated to the '**New Project**' menu.

The comparison methods used in this GUI are as follows :
Levenshtien Distance, ScanMatch, MultiMatch, and Cross-Recurrence.

We hope your experience with our software is fantastic! If there are features you would like to see in future versions of **T.E.A.R.S.** please let us know. Thank you.

# New Project




The '**New Project**' menu requires first that you enter a name for your project and the number of groups being compared in your study. If applicable, you may also input the number of difficulty levels present in the trials. Once all of the information is added, select the '**Create Project**' option.

Now it is time to read in the data from your study. Hit the '**Browse**' button to search through your computer and add the relevant files either from the comma-separated-value (**.csv**) or Excel (**.xlxs**) file type. The labels necessary for reading the data are as follows, all fields case-sensitive:

**RECORDING_SESSION_LABEL** : The identifier of each subject
**TRIAL** : The number of the trial
**CORRECT** : Whether the subject gave a correct (**denoted by 1**) or incorrect (**denoted by 0**) response

**CURRENT_FIX_DURATION** : Fixation duration data
**CURRENT_FIX_INDEX** : The index of each fixation
**CURRENT_FIX_X** : The X coordinate value of each fixation
**CURRENT_FIX_Y**: The Y coordinate value of each fixation
**DIFFICULTY_LEVEL** : The difficulty of each trial

If your study uses image files, you will also need the column :

**IMAGE** : Identifier for the image used in each trial

**Additionally, many of this project's functions REQUIRE that your fixation data is SCALED. The resolution of your fixation data, for accurate results, should be 740x580.**
Additionally, if you are using images, you will be prompted to copy any image files (**.png** files give the best results of the common image file types) into the '**images**' folder within the '**Project Name**' folder.

Each data file you upload should contain the data of at most ONE group that you are testing. For example, if you are testing three different groups, you will need at least three different Excel files.

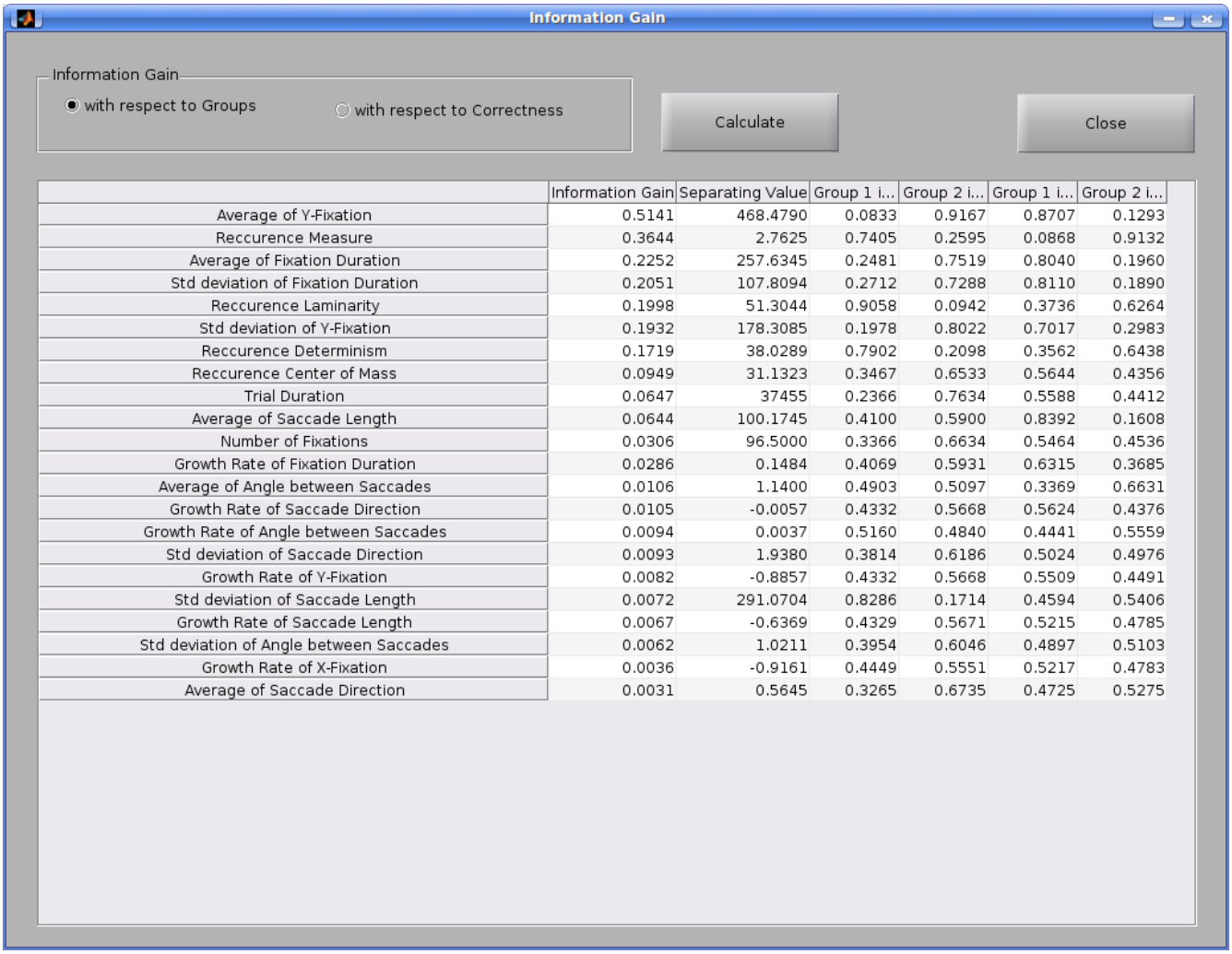
The '**Group Number**' drop-down menu allows you to select the Group that each set of data is being added to. For example, suppose that all of the data for Group 1 is split amongst three Excel Files. You could load each of these into the Group 1 selection.

Every time you want to add a data file into the folder, select it along with the group number, then hit the '**Load File**' button.

Now, you're all ready. Hit the '**Make Statistics Table**' button, and go out and get a cup coffee; this feature can take a significant amount of time to complete, especially for larger data sets.

Once this process has finished, close the '**New Project**' window. Your project is now saved and can be opened by the '**Open Project**' function whenever you need it!

# Information Gain

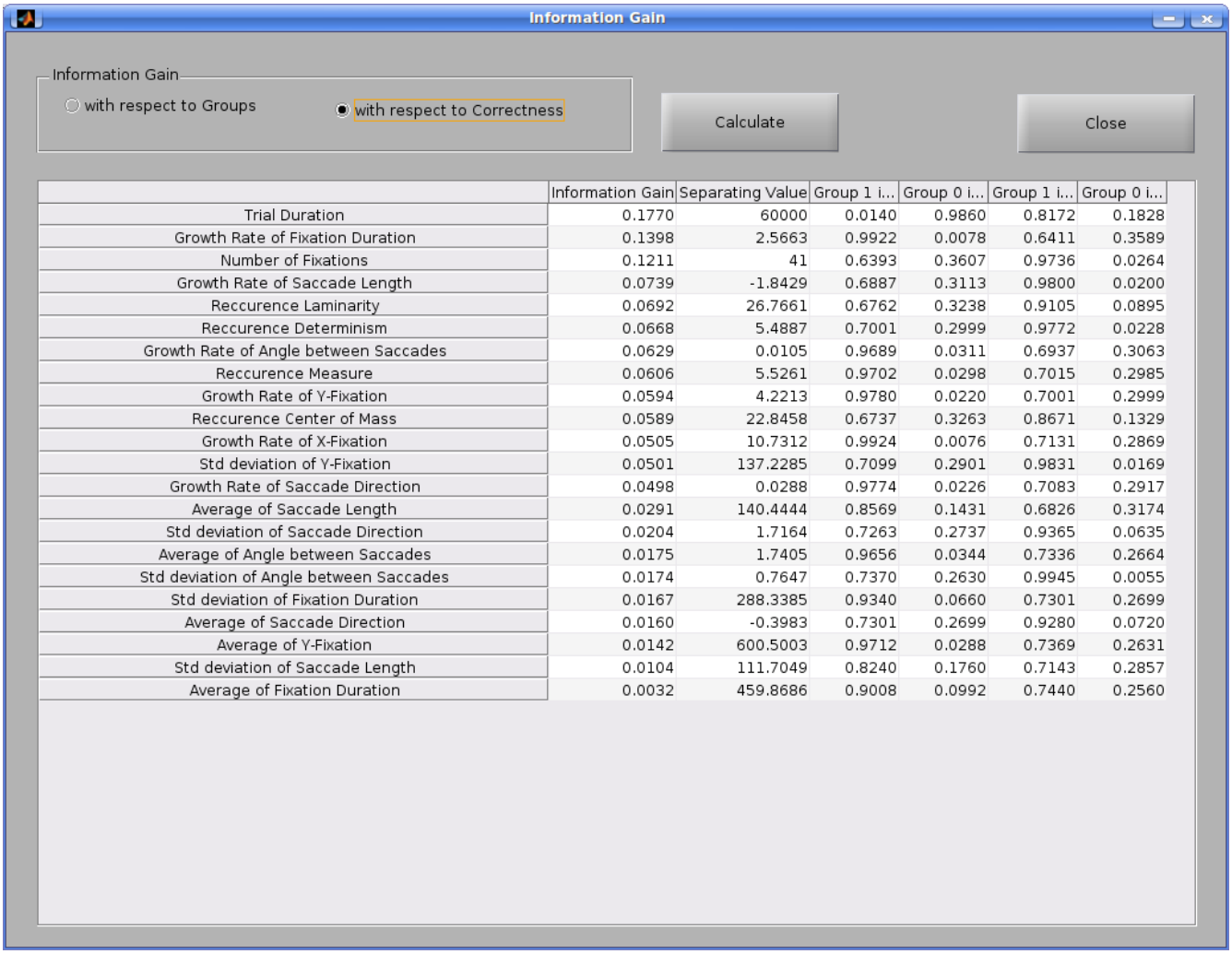



| | Information Gain | Separating Value | Group 1 i... | Group 2 i... | Group 1 i... | Group 2 i... |
|---|---|---|---|---|---|---|
| Average of Y-Fixation | 0.5141 | 468.4790 | 0.0833 | 0.9167 | 0.8707 | 0.1293 |
| Reccurence Measure | 0.3644 | 2.7625 | 0.7405 | 0.2595 | 0.0868 | 0.9132 |
| Average of Fixation Duration | 0.2252 | 257.6345 | 0.2481 | 0.7519 | 0.8040 | 0.1960 |
| Std deviation of Fixation Duration | 0.2051 | 107.8094 | 0.2712 | 0.7288 | 0.8110 | 0.1890 |
| Reccurence Laminarity | 0.1998 | 51.3044 | 0.9058 | 0.0942 | 0.3736 | 0.6264 |
| Std deviation of Y-Fixation | 0.1932 | 178.3085 | 0.1978 | 0.8022 | 0.7017 | 0.2983 |
| Reccurence Determinism | 0.1719 | 38.0289 | 0.7902 | 0.2098 | 0.3562 | 0.6438 |
| Reccurence Center of Mass | 0.0949 | 31.1323 | 0.3467 | 0.6533 | 0.5644 | 0.4356 |
| Trial Duration | 0.0647 | 37455 | 0.2366 | 0.7634 | 0.5588 | 0.4412 |
| Average of Saccade Length | 0.0644 | 100.1745 | 0.4100 | 0.5900 | 0.8392 | 0.1608 |
| Number of Fixations | 0.0306 | 96.5000 | 0.3366 | 0.6634 | 0.5464 | 0.4536 |
| Growth Rate of Fixation Duration | 0.0286 | 0.1484 | 0.4069 | 0.5931 | 0.6315 | 0.3685 |
| Average of Angle between Saccades | 0.0106 | 1.1400 | 0.4903 | 0.5097 | 0.3369 | 0.6631 |
| Growth Rate of Saccade Direction | 0.0105 | -0.0057 | 0.4332 | 0.5668 | 0.5624 | 0.4376 |
| Growth Rate of Angle between Saccades | 0.0094 | 0.0037 | 0.5160 | 0.4840 | 0.4441 | 0.5559 |
| Std deviation of Saccade Direction | 0.0093 | 1.9380 | 0.3814 | 0.6186 | 0.5024 | 0.4976 |
| Growth Rate of Y-Fixation | 0.0082 | -0.8857 | 0.4332 | 0.5668 | 0.5509 | 0.4491 |
| Std deviation of Saccade Length | 0.0072 | 291.0704 | 0.8286 | 0.1714 | 0.4594 | 0.5406 |
| Growth Rate of Saccade Length | 0.0067 | -0.6369 | 0.4329 | 0.5671 | 0.5215 | 0.4785 |
| Std deviation of Angle between Saccades | 0.0062 | 1.0211 | 0.3954 | 0.6046 | 0.4897 | 0.5103 |
| Growth Rate of X-Fixation | 0.0036 | -0.9161 | 0.4449 | 0.5551 | 0.5217 | 0.4783 |
| Average of Saccade Direction | 0.0031 | 0.5645 | 0.3265 | 0.6735 | 0.4725 | 0.5275 |

The **'Information Gain'** window calculates the information gain with respect to **Groups** (Level of Expertise) or **Correctness**.

*Group Number* is assigned during the creation of a project for each uploaded Excel file. It is aimed to reflect the Expertise Level. For instance, Group 1 may refer to Novices while Group 2 refers to Experts. *Correctness* reflects whether or not the trial is correct (referred as Group 1) or incorrect (referred as Group 0).

If you open the window at the first time, you need to choose one of the options **'with respect to Groups'** or **'with respect to Correctness'**. Then click on **'Calculate'** button. The calculating will take several minutes, after which you will see a table similar to the one on the figure. The result is saved into a file named **'gainWrtGroups.csv'** or **'gainWrtCorrect.csv'**.




| | Information Gain | Separating Value | Group 1 i... | Group 0 i... | Group 1 i... | Group 0 i... |
|---|---|---|---|---|---|---|
| Trial Duration | 0.1770 | 60000 | 0.0140 | 0.9860 | 0.8172 | 0.1828 |
| Growth Rate of Fixation Duration | 0.1398 | 2.5663 | 0.9922 | 0.0078 | 0.6411 | 0.3589 |
| Number of Fixations | 0.1211 | 41 | 0.6393 | 0.3607 | 0.9736 | 0.0264 |
| Growth Rate of Saccade Length | 0.0739 | -1.8429 | 0.6887 | 0.3113 | 0.9800 | 0.0200 |
| Reccurence Laminarity | 0.0692 | 26.7661 | 0.6762 | 0.3238 | 0.9105 | 0.0895 |
| Reccurence Determinism | 0.0668 | 5.4887 | 0.7001 | 0.2999 | 0.9772 | 0.0228 |
| Growth Rate of Angle between Saccades | 0.0629 | 0.0105 | 0.9689 | 0.0311 | 0.6937 | 0.3063 |
| Reccurence Measure | 0.0606 | 5.5261 | 0.9702 | 0.0298 | 0.7015 | 0.2985 |
| Growth Rate of Y-Fixation | 0.0594 | 4.2213 | 0.9780 | 0.0220 | 0.7001 | 0.2999 |
| Reccurence Center of Mass | 0.0589 | 22.8458 | 0.6737 | 0.3263 | 0.8671 | 0.1329 |
| Growth Rate of X-Fixation | 0.0505 | 10.7312 | 0.9924 | 0.0076 | 0.7131 | 0.2869 |
| Std deviation of Y-Fixation | 0.0501 | 137.2285 | 0.7099 | 0.2901 | 0.9831 | 0.0169 |
| Growth Rate of Saccade Direction | 0.0498 | 0.0288 | 0.9774 | 0.0226 | 0.7083 | 0.2917 |
| Average of Saccade Length | 0.0291 | 140.4444 | 0.8569 | 0.1431 | 0.6826 | 0.3174 |
| Std deviation of Saccade Direction | 0.0204 | 1.7164 | 0.7263 | 0.2737 | 0.9365 | 0.0635 |
| Average of Angle between Saccades | 0.0175 | 1.7405 | 0.9656 | 0.0344 | 0.7336 | 0.2664 |
| Std deviation of Angle between Saccades | 0.0174 | 0.7647 | 0.7370 | 0.2630 | 0.9945 | 0.0055 |
| Std deviation of Fixation Duration | 0.0167 | 288.3385 | 0.9340 | 0.0660 | 0.7301 | 0.2699 |
| Average of Saccade Direction | 0.0160 | -0.3983 | 0.7301 | 0.2699 | 0.9280 | 0.0720 |
| Average of Y-Fixation | 0.0142 | 600.5003 | 0.9712 | 0.0288 | 0.7369 | 0.2631 |
| Std deviation of Saccade Length | 0.0104 | 111.7049 | 0.8240 | 0.1760 | 0.7143 | 0.2857 |
| Average of Fixation Duration | 0.0032 | 459.8686 | 0.9008 | 0.0992 | 0.7440 | 0.2560 |

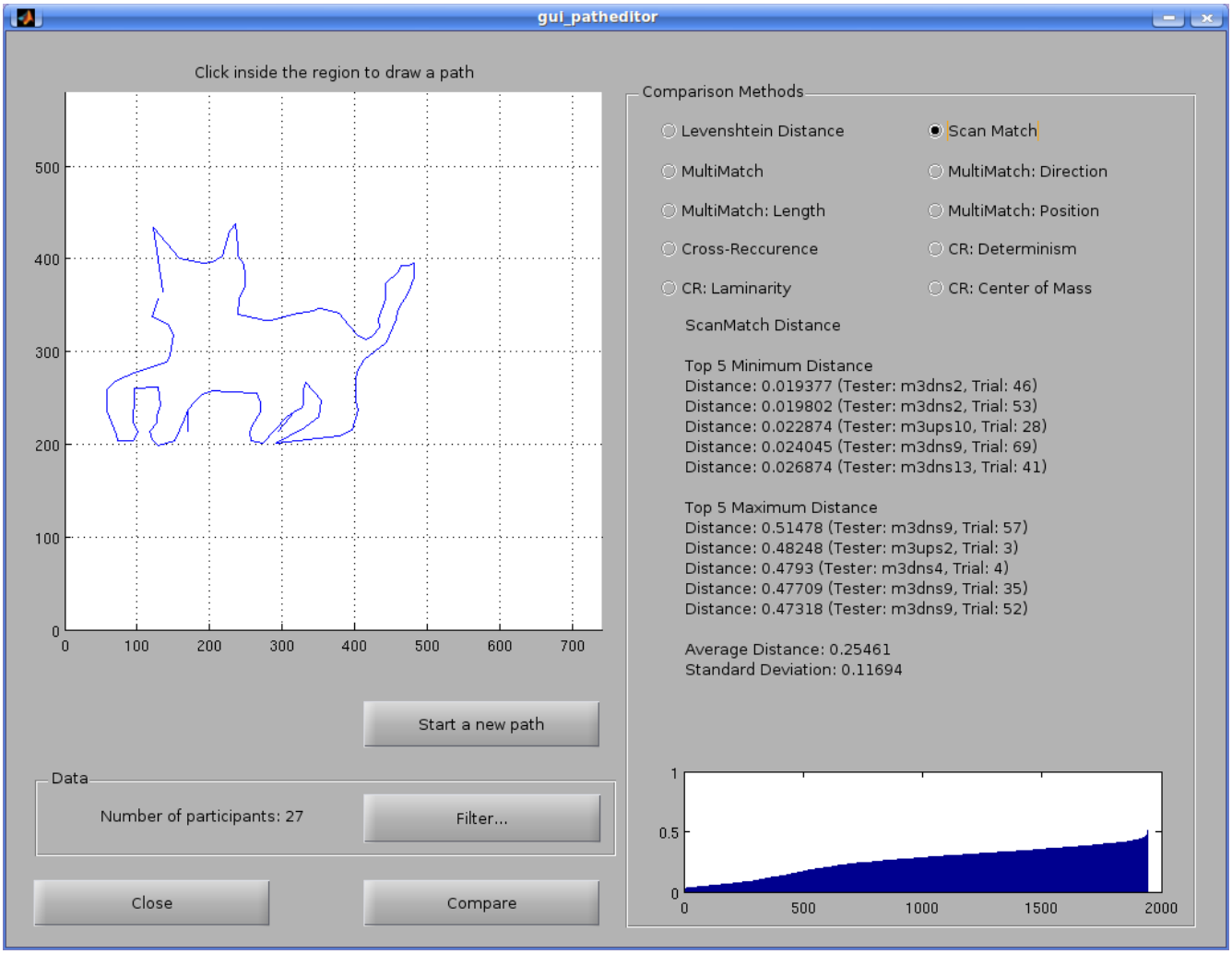
In the table, each row corresponds to one of the characteristics of a path. The meaning of the columns is following:

- **Information Gain**: (takes values from 0 to 1) the bigger information gain the more significant the characteristic in distinguishing trials between Groups or between Correct and Incorrect answers.
- **Separating Value**: while calculating Information gain, whole range of values of a characteristic are divided into two intervals. For instance, all values of **Average of Y-Fixation** are divided into those with the average greater then **468.4790** and those with the average less then **468.4790**.

- Meaning of the next column will depend on the selection of **Information Gain**:
- If **'with respect to Groups'** is selected
  - **Group 1 in (C > V)**: fraction of the trials among the total number of trials with the characteristic greater then the separating value, that are performed by participants from Group 1. For instance, **8.33%** of the trials with **Average of Y-Fixation** greater then **468.4790** are performed by participants from Group 1.
  - **Group 2 (C > V)**: fraction of the trials among the total number of trials with the characteristic greater then the separating value, that are performed by participants from Group 2. For instance, **91.67%** of the trials with **Average of Y-Fixation** greater then **468.4790** are performed by participants from Group 2.
  - **Group 1 in (C < V)**: fraction of the trials among the total number of trials with the characteristic less then the separating value, that are performed by participants from Group 1. For instance, **87.07%** of the trials with **Average of Y-Fixation** less then **468.4790** are performed by participants from Group 1.
  - **Group 2 in (C < V)**: fraction of the trials among the total number of trials with the characteristic less then the separating value, that are performed by participants from Group 2. For instance, **12.93%** of the trials with **Average of Y-Fixation** less then **468.4790** are performed by participants from Group 2.
- If **'with respect to Correctness'** is selected
  - **Group 1 in (C > V)**: fraction of correct trials among the total number of trials with the characteristic greater then the separating value. For instance, **1.4%** of the trials with **Trial Duration** greater then **60** seconds are correct.
  - **Group 0 in (C > V)**: fraction of incorrect trials among the total number of trials with the characteristic greater then the separating value. For instance, **98.6%** of the trials with **Trial Duration** greater then **60** seconds are incorrect.
  - **Group 1 in (C < V)**: fraction of correct trials among the total number of trials with the characteristic less then the separating value. For instance, **81.72%** of the trials with **Trial Duration** less then **60** seconds are correct.
  - **Group 0 in (C < V)**: fraction of incorrect trials among the total number of trials with the characteristic less then the separating value. For instance, **18.28%** of the trials with **Trial Duration** less then **60** seconds are incorrect.

***Remark**: the information gain value can be misleading. Notice that* **Trial Duration** *has a high information gain with separating value of* **60** *seconds because* **60** *seconds is the time limit for a trial. The high information gain on* **Average of Y-Fixations** *can be a result of that fixation coordinates are not scaled or not aligned properly.*

# Group Path Comparison

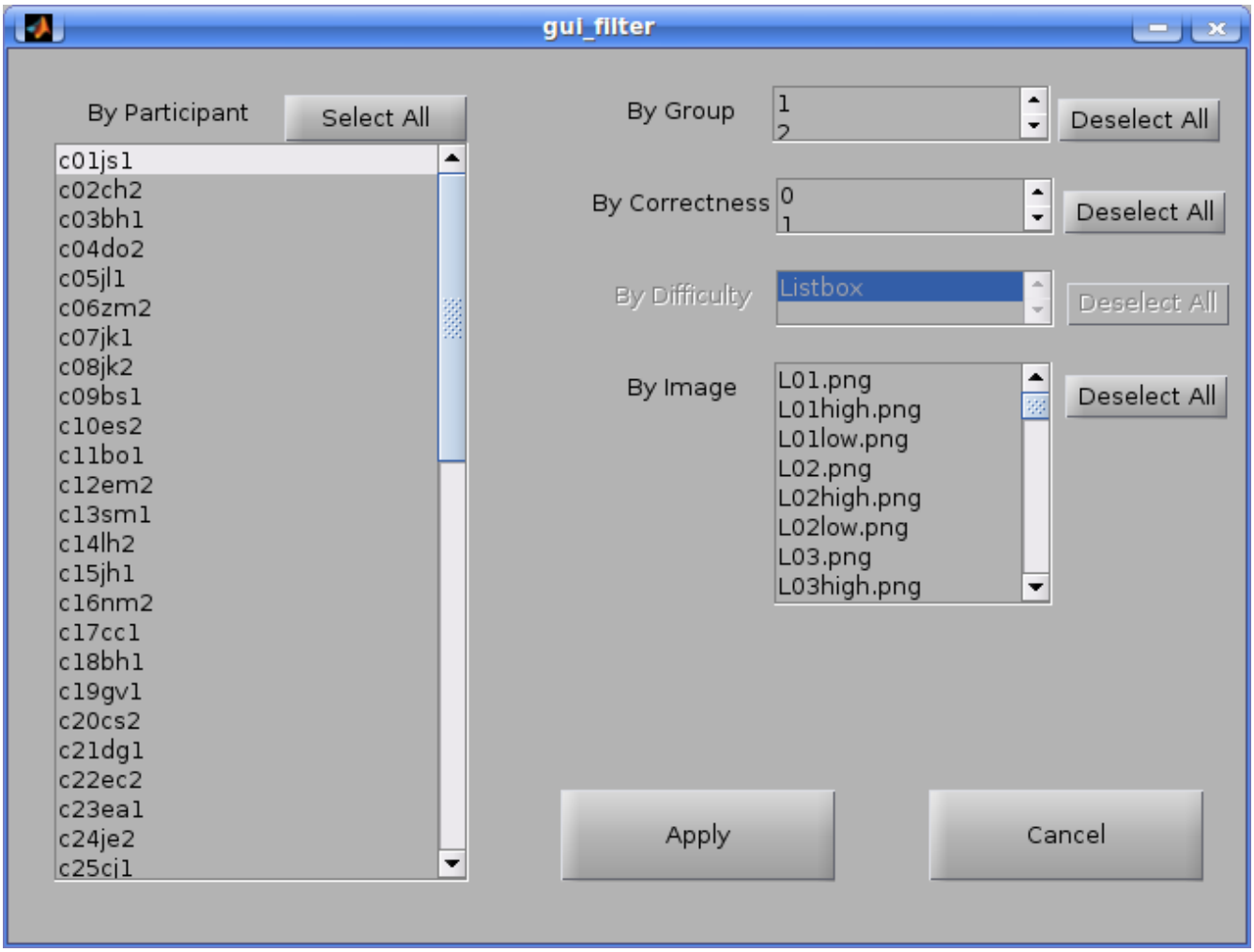



The '**Group Path Comparison**' tool allows one to draw a path on the provided grid and compare it to the eye-tracking fixation data.

To begin, click on the given grid. This will create an initial point to begin the drawn path. Subsequent clicks will draw a line between the point being clicked on and the previous point. The world is your oyster; no matter how simple or complex your path, our software will work. For the rest of this demonstration, our feline friend will be used as an example path.

At any time, one can hit the '**Start a new path**' button, which will clear the grid and allow you to start anew.

After drawing a path, select the '**Filter**' button. From here, one is able to determine the subset of data to be compared to the drawn path.




Remember, the '**Ctrl+Click**' function allows the selection of multiple elements.

As you can see in the above image, data can be filtered by individual participants, group number, correctness of responses, and images.

**When using the filter, ALWAYS select which participants are being filtered, otherwise, the system defaults to a single participant.**

When you are happy with your filter, hit the '**Apply**' button to save your settings.

Now you are ready to start the comparison algorithms! Hit the '**Compare**' button button. This can also take quite a bit of time, depending on the size of the subset of data being considered.

Once this process is done, one can select the type of comparison method being used, and **T.E.A.R.S.** Will display the top 5 minimum and maximum distances (trial number and participant), as well as the average distance and standard deviation. On the next page, we will describe each of the comparison methods in detail.

**Levenshtien distance** : A metric for determining the 'distance' between two strings. In the case of eye-tracking data, this string is a sequence of fixations. The distance is given by the number of single character insertions, deletions, and substitutions to change one string into another. Of course, for computational feasibility in this instance, the space on which fixation information is plotted MUST be discretized by a large-enough mesh.

**ScanMatch** : This is an improvement on using Levenshtien distance for fixation data, implementing the Needleman-Wunsch algorithm to compare eye-movement sequences. In general, ScanMatch is robust in measuring sequence deviation, where it becomes more inaccurate with respect to wild geometric deviation. (Scaling is very important here.)

**MultiMatch** : Compared to ScanMatch, most implementations of MultiMatch are more geometrically robust, whereas it is not as good at measuring sequence deviations. There are four implementations of MultiMatch used in **T.E.A.R.S**., each measuring different aspects of the data. Unlike in ScanMatch, areas of interest are not used.

*Shape* : Vector distance between aligned saccade pairs, measure of scanpath shape similarity.

*Length* : Measures similarity in saccadic amplitude by finding the length between vector endpoints.

*Direction* : A measure of angular distance between saccade vectors, useful for determining shape similarity when amplitudes are wildly different.

*Position* : Measures scan path similarity based on Euclidean distance.

**Cross-recurrence** : In general, Cross-recurrence is a good tool for the analysis of temporal dynamics of fixation data. **T.E.A.R.S.** makes use of four different CR methods, described below.

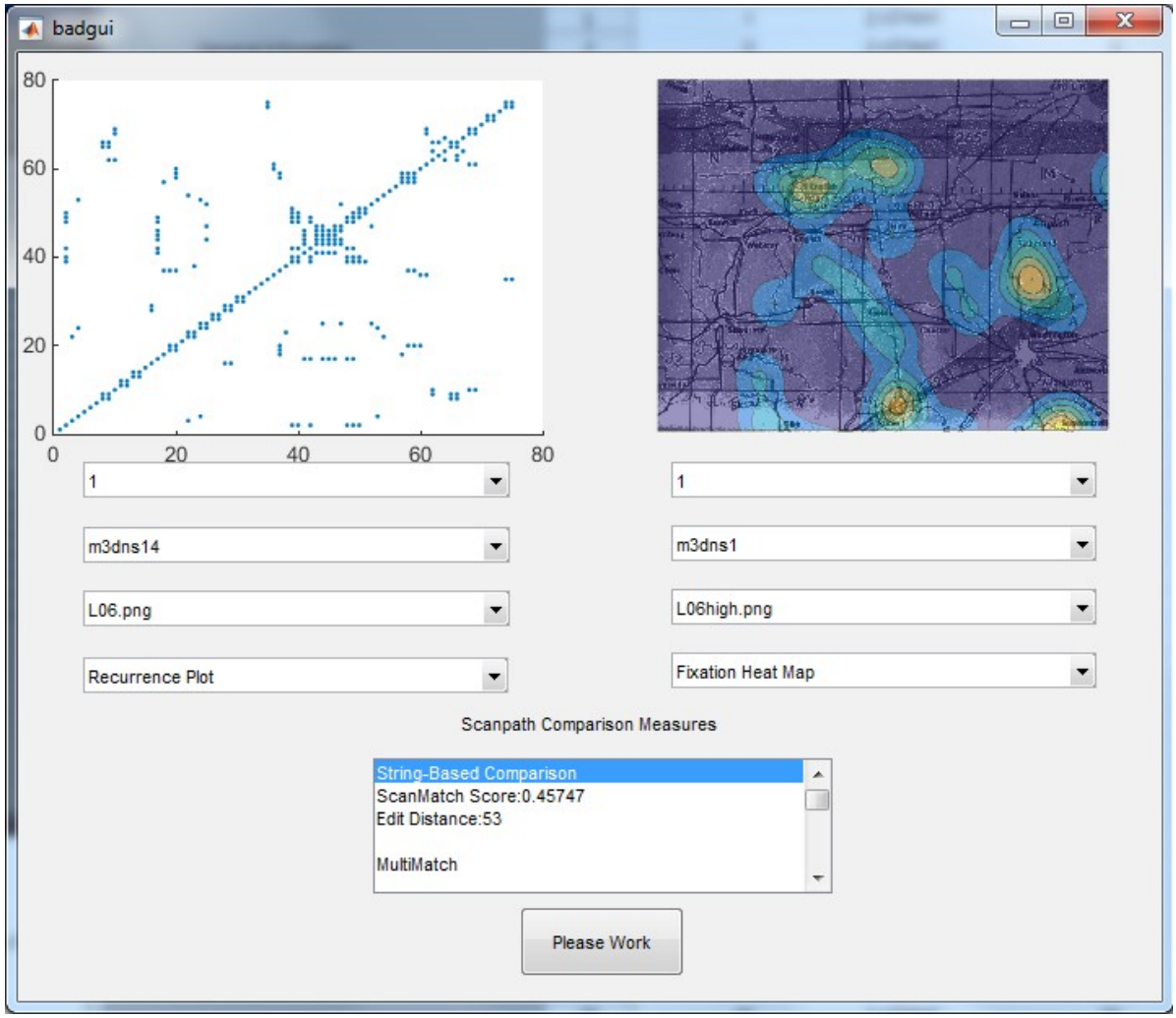
*Recurrence* : Good at measuring how often observers return to previously fixated image positions

*Determinism* : Measures the proportion of recurrent points forming diagonal lines and represents repeating gaze patterns in the recurrence diagram.

*Laminarity* : Generally indicates that specific areas of a scene are repeatedly fixated.

*Center of recurrence mass* : Measure that indicates approximately where in time most of the recurrent points are situated.

# Pairwise Path Comparison




The **'Pairwise Path Comparison'** window calculates various scanpath comparison measures, given two trials selected by the user.

To choose the trials you wish to compare, you must select the group, subject and mapid (trial), in the first, second and third drop down menus respectively. The names listed in each drop-down menu are taken from the raw data (Excel files). In the fourth drop-down menu you can choose which visual representation of the scanpath you wish to view. To compute the various scanpath comparison measures, click the '**Please Work**' button at the bottom of the GUI.

In the example above, the data was grouped in “pilots” and “students” labeled ‘1’ and ‘2’ respectively. Each member (subject) of a group was given a unique name, in this case we have selected “m3dns14” and “m3dns1”. The trials themselves are labeled by the image files that the subject viewed, in this case “L06.png” and “L06high.png”. Finally, we have chosen to display the recurrence plot and fixation map.

# Scanpath Visualization

## Fixation Maps

To generate the fixation maps, we place a 2-D Gaussian (bump) centered on each fixation in the scanpath. By doing this we create a surface on our 780x540 plot, where the height at a given point represents the attention given to that point on the image. We then can generate a contour plot of this surface and impose on it the original map (if one exists).

For the scaled fixation maps, the height of each Gaussian bump was scaled by the duration of the corresponding fixation. The unscaled maps treats each fixation equally.

## Scan Path

For the scan path plot, we simply place a line plot of the scan path over the original image (or a blank plot window if no image exists)

## Recurrence Plot

The recurrence plot is an n-by-n scatter plot, where n is the length of the fixation sequence (scanpath) in question. A filled-in circle is placed at the point (i,j) if fixation i and fixation j are “recurrent” in the sense described in the “Cross-Recurrence analysis” section below. Essentially, two fixations are recurrent if they are close based on Euclidean distance. These are the diagrams from which the recurrence measures are derived.

# Scanpath Comparison

## String-Based Comparisons

For string-based comparisons, each scanpath is first encoded as a string. Usually this is done by superimposing a grid onto the image and assigning each fixation a character based on which grid element it is contained in. One can also use areas of interest (AOIs) for creating strings.

**Edit Distance:** The distance is given by the number of single character insertions, deletions, and substitutions to change one string into another. This distance is given by a non-negative integer, a distance of 0 indicates two identical strings and a distance of n indicates the minimal number of "edits" required to transform one string into another.

Edit distance can also be computed using AOIs for trials which use the same image. See **Areas of Interest**.

**ScanMatch** : This is an improvement on using Levenshtien (edit) distance for fixation data, implementing the Needleman-Wunsch algorithm (used for comparing DNA sequences) to compare eye-movement sequences. ScanMatch scores returns a number in the interval (0,1], where 1 indicates the same string and increasing string dissimilarity as the score gets closer to 0.

**MultiMatch** : MultiMatch returns several scores based on various geometric and temporal aspects of the given scanpaths. MultiMatch first simplifies both scanpaths (by combining some pairs of successive saccades/fixations), then uses a graph-theoretic path minimization algorithm to align the two paths. Given the simplification/alignment, MultiMatch then computes five different measures by comparing paired saccades/fixations (the pairing given by the alignment). Scores are given by a real number between 1 and 0, here 1 indicates maximal similarity and 0 indicates maximal dissimilarity. If any fixations are outside of the range (assuming 780x540 image), MultiMatch returns nothing.

**Shape:** Measure of overall scanpath shape similarity, based on aligned saccades

**Length:** Measures similarity in saccadic amplitude of two scanpath.

**Direction:** A measure of angular distance between saccade vectors, useful for determining shape similarity when amplitudes are wildly different.

**Position:** Measures scan path similarity based on Euclidean distance.

**Duration:** Compares aligned fixations based on duration

**Cross-Recurrence:**

For cross-recurrence analysis (CRQA), two scanpaths are reduced to a sequence of fixations and truncated so that both sequences have the same length. Given two fixations from two sequences we wish to compare, we can say these fixations are recurrent if their Euclidean distance is less than 64 pixels. Based on this definition of recurrence, we can define several measures. **T.E.A.R.S.** makes use of four different CR methods, described below.

**Recurrence:** Measures total percentage of recurrence over all pairs of fixations. A value of 100 indicates maximal possible recurrence. In this case, both fixation sequences would lie with the *same* 64 pixel radius ball. A value of 0 indicates no recurrence, meaning for both sequences, no given fixation from sequence 1 is within 64 pixels of a fixation in sequence 2 and vice versa.

**Determinism:** Measures the percentage of recurrent points forming diagonal lines and represents repeating gaze patterns in the recurrence diagram. High determinism indicates recurrences between two scanpath occur in sequential order in both scan paths.

**Laminarity:** Measures the percentage of recurrent points forming horizontal or vertical lines in the recurrence diagram. High laminarity indicates that for some fixations there are recurrent fixations which appear in sequential order.

**Center of Recurrence Mass:** Measure that indicates approximately where in time most of the recurrent points are situated.

**Fixation Position Based Measure:** These scanpath comparison methods essentially use only the coordinates of the fixations comprising each scanpath.

**Mannan Distance:**

"Analyzes the overall similarity between two scanpaths by computing the linear distances between two scanpaths by computing the linear distance between the fixations in the first scanpath and the nearest neighbor in the second scanpath [and vice versa]"

The following two scanpath comparison measures are based on the data used to generate the fixation maps. To generate the fixation maps, we place a 2-d unit Gaussian (bump) centered on each fixation in the scanpath. By doing this we create a surface on our 780x540 plot, where the height at a given point represents the attention given to that point on the image.

Several methods of comparison were developed for these surfaces. For the **KullBeck Liebler Distance** and the **Correlation Coefficient**, we treat these surfaces as probability density functions (PDFs) on the 780x540 space and use methods from probability theory to compare various PDFs.

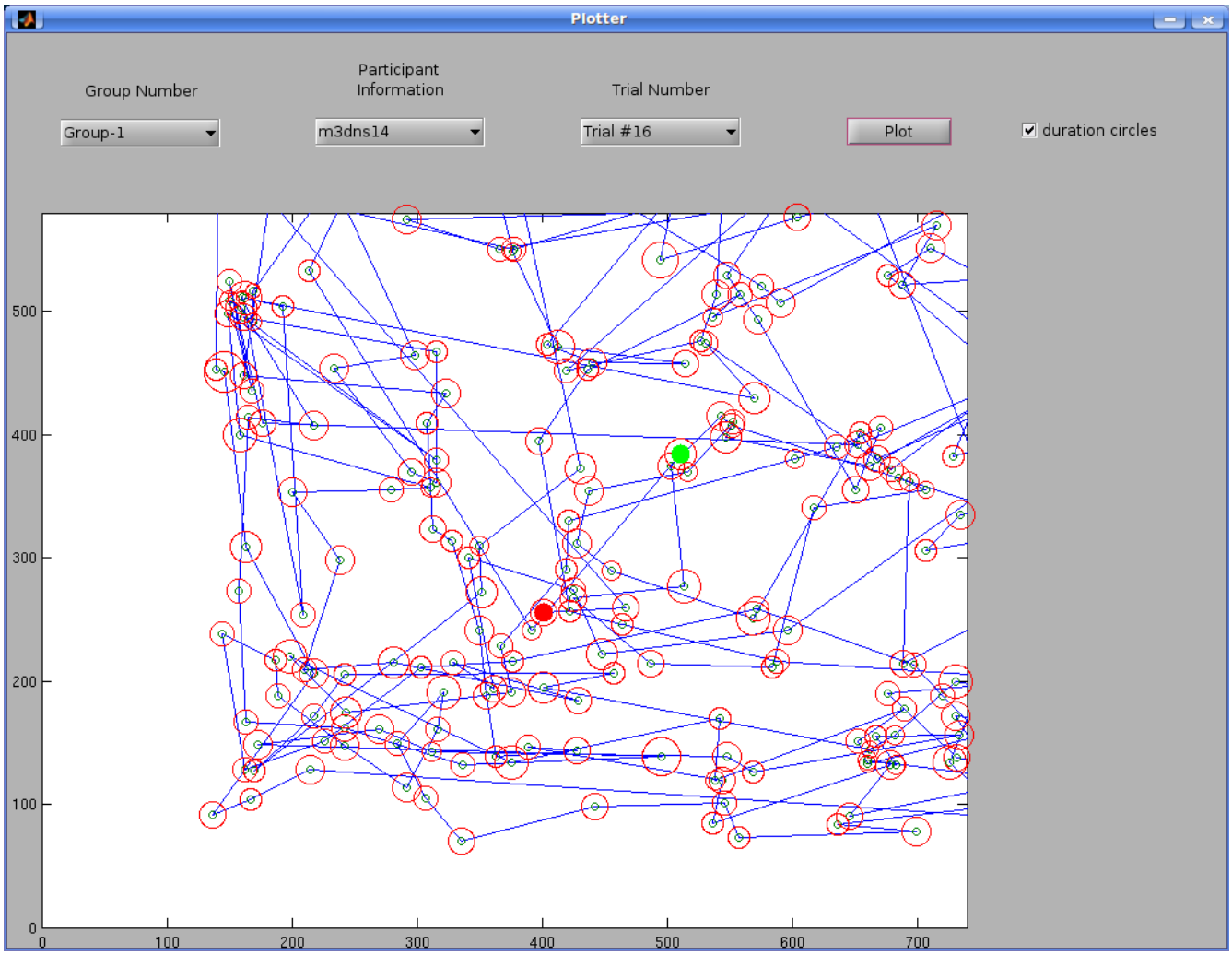
**KullBeck Liebler Distance:**

Returns a non-negative real value. A value of 0 indicates maximal similarity (both PDFs are the same) a value greater than 0 indicates increasing dissimilarity

**Correlation Coefficient:**

Returns a real number in the interval [-1,1]. A value approaching 0 indicates increasing dissimilarity and a value with absolute value approaching 1 indicates increasing similarity.

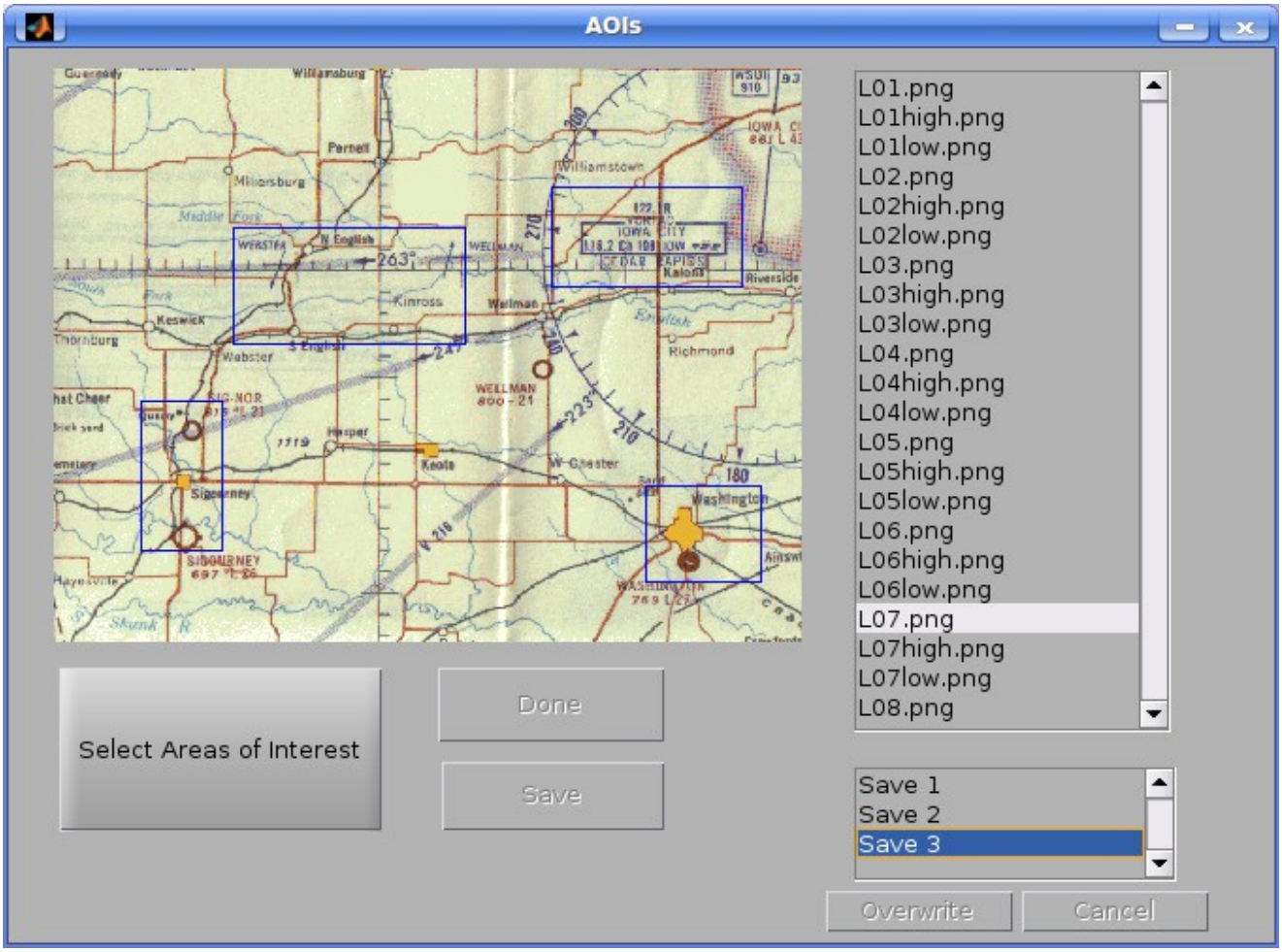
# Fixation Plotter




The '**Plotter**' is a very simple tool to use! First, select the Group Number from the leftmost drop-down menu. This will populate the '**Participant**' drop-down menu directly to its right. Select one of these, and the '**Trial**' drop-down menu will be populated. Select one of these, and hit the '**Plot**' button. This will plot the fixation data for that trial, with the filled-in green circle representing the first fixation, and the filled-in red circle representing the final fixation.

The check-box '**duration circles**' will create a representation of how long each spot is being fixated on; the larger the radius of the open circle, the longer that fixation-duration.

# Areas of Interest




**T.E.A.R.S** provides analyses based on user-input '**Areas of Interest (AOIs)**' for images used in a Project (see **Pairwise Path Comparison**). The Areas of Interest menu is where the user can draw and save these AOIs.

The names of the images saved in the '**images**' folder of the current Project will be listed on the left side of the Areas of Interest window. Select an image's name to display it. Any existing AOIs saved for the selected image will appear in the smaller listbox; clicking on these will show the saved AOIs on the current image.

To draw AOIs for an image, select that image's name and then click '**Select Areas of Interest**'. This will allow you to draw AOIs on the image until pressing '**Done**'. (**MATLAB** may report an "Interruption during mouse selection" error when '**Done**' is pressed, which can be safely ignored.) To erase the AOIs you have just drawn and select new AOIs, click '**Select Areas of Interest**' to draw new AOIs for the current image, or select a new image. To save the AOIs you have just drawn, click '**Save**'. You will see a new Save added to the save list for the current image.

**Each image holds a maximum of three Saves.** If you click '**Save**' for an image with three existing Saves, you will be prompted to overwrite an existing Save, or '**Cancel**'. If you click '**Yes**' at the overwrite prompt, you will be able to select the existing Save you wish to overwrite. Clicking '**Overwrite**' will permanently overwrite the selected Save with the current AOI data. Clicking '**Cancel**' here or at the overwrite prompt will return you to the option of saving current AOIs or selecting new ones.

AOIs can be used in **Pairwise Path Comparison** to compute **edit distance** for associated trials. In contrast to the edit distance which is reported automatically, where characters are assigned to each fixation based on their location in a 5x5 grid, fixations under the AOI edit distance are assigned to characters based which AOI they fall in. For instance, a trial with three AOIs and fixations falling in the following order:

1 – 1 – No AOI – No AOI – No AOI – 2 – 3 – 3 – 3

would be given the string ' aadddbccc'. Note that the smaller alphabet will tend to make AOI edit distances much smaller than standard edit distance.

To compute AOI edit distance, go to the **Pairwise Path Comparison** menu and select the same image for both trials. If there is saved AOI data for this image, AOI edit distance for each Save will be reported at the end of the **Scanpath Comparison Measures**.

# References


1. Anderson, N. C., Anderson, F., Kingstone, A., & Bischof, W. F. (2014). A comparison of scanpath comparison methods. *Behavior research methods*, 1-16.

2. Anderson N. C., Bischof W. F., Laidlaw K. E., Risko E. F., Kingstone A. (2013). Recurrence quantification analysis of eye movements. Behav. Res. Methods 45, 842–856

3. Beck, Melissa R., Michael Trenchard, Amanda van Lamsweerde, Rebecca R. Goldstein, and Maura Lohrenz. (2012). Searching in Clutter: Visual Attention Strategies of Expert Pilots.

4. Dewhurst, R., Nystrom, M., Jarodzka, H., Foulsham, T., Johansson, R. & Holmqvist, K. (in press). It depends on how you look at it: scanpath comparison in multiple dimensions with MultiMatch, a vector based approach. Behaviour Research Methods

5. Mitchell, Tom M. *Machine Learning*. New York: McGraw-Hill, 1997. Print.

6. Scanmatch: http://seis.bris.ac.uk/~psidg/ScanMatch/

7. MultiMatch: http://wiki.humlab.lu.se/dokuwiki/doku.php?id=public:useful_links#scanpath_comparison