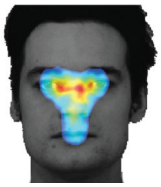
*i*Map3



*i*Map toolbox for eye-tracking data analysis - Version 3

http://perso.unifr.ch/roberto.caldara/index.php?page=4

Sébastien Miellet, Cyril R. Pernet, Junpeng Lao, Guillaume A. Rousselet, Luca Vizioli, & Roberto Caldara (2013). University of Fribourg
Junpeng Lao (2012) for the indtorgb function. Cyril Pernet & Guillaume Rousselet (2013) for the tfce2d function
sebastien.miellet@unifr.ch

CITATION

If you use *i*Map, please cite us. You could use the following sentence:

Eye movement data were analysed with *i*Map3 (Caldara and Miellet, 2011), which implements a novel statistical approach to correct for multiple comparisons (Pernet, Chauveau, Gaspar, Rousselet, 2011; Smith and Nichols, 2009).

References:

Caldara, R., & Miellet, S. (2011). *i*Map: A Novel Method for Statistical Fixation Mapping of Eye Movement data. Behavior Research Methods, 43(3), 864-78

Pernet, C.R., Chauveau, N., Gaspar, C.M., & Rousselet, G.G. (2011). LIMO EEG: A Toolbox for Hierarchical LInear MOdeling of ElectroEncephaloGraphic Data. Computational Intelligence and Neuroscience. Article ID 831409, doi:10.1155/2011/831409

Smith S.M., & Nichols, T.E. (2009). Threshold-free cluster enhancement: addressing problems of smoothing, threshold dependence and localisation in cluster inference. Neuroimage, 44(1), 83-98. doi: 10.1016/j.neuroimage.2008.03.061.

PLEASE REFER TO **SECTION 7** FOR THE STATISTICAL DETAILS OF THE NEW VERSION OF IMAP

Table of Contents

1. Update details

version 3

1- New "statistical engine". *i*Map3 now uses t-tests and bootstrapped TFCE transformed scores to correct for multiple comparisons (TFCE: threshold-free cluster-enhancement; Smith & Nichols, 2009), instead of being based on the Random Field Theory (used in previous versions up to *i*Map2.1).

The associated benefits are: a) a more appropriate and direct estimate of data variability, b) specific tests for independent and paired samples, c) a better control for false positives.

Many thanks to Cyril R. Pernet and Guillaume A. Rousselet for their help with the implementation of this approach.

We are also grateful to Chris McManus for the careful reading of the original version of iMap, which stimulated our development of the new version of this toolbox.

2- A bug due to the impossibility of calculating effect sizes when there is no effect has been fixed.

3- This version includes an option to generate the raw fixation maps.

4- This version no longer creates temporary working files.

5- A normalization of the individual maps is done across the search space in order to represent the individual fixation bias.

6- Improved appearance of the statistical fixation maps.

7- Possibility to set the transparency of the background image and the statistical maps.

Previous versions

Version 2.1

1- This version solves potential problems when the dimensions (x, y) of the search space are not an even number of pixels

Version 2

1- The setting of the parameters is now done via a configuration structure (see examples), which allows more flexibility in calling iMap, but also gives the user flexibility in inserting his own parameters.

2- New parameters have been added for: setting the colorbar scaling, setting the sigma (kernel for the statistical smoothing), and setting the significance of the threshold.

3- The "clicking step" used to generate the maps is no longer necessary. Many thanks to Junpeng Lao who wrote the 'indtorgb' function.

4- The one-tailed and two-tailed critical values (found in Zcrit.txt or displayed in the Matlab command window) are defined from the value of the significance threshold set as one of the parameters.

5- The contours for significant areas are now displayed in white for all the fixation maps. It should improve the view of the significant areas.

6- A mistake in the data preparation code for the scenes example has been fixed.

Version 1.1

1- Fixes potential problems with floating point in the calculation of the search-space size

2- Creates a Zcrit.txt file indicating the size of the search-space, the default critical value of a one-tailed Z for alpha = .05 (significance threshold for the individual maps), the default critical value of a two-tailed Z for alpha = .05 (significance threshold for the difference map). This information is also displayed in the Matlab command window.

3- The CiVol and STAT_THRESHOLD functions have been modified to avoid the display of confusing information in the Matlab command window.

2. Input data

An input data file is a matrix with a fixation per line. The only crucial data are the coordinates (x and y) and duration of the fixations and the trial numbers. Any other column can be used for specifying your conditions.

Typically the data files are .mat files (called data1.mat, data2.mat,...) containing matrices called "summary". This can be obtained from any txt file (e.g. fixation report from EyeLink, Data Viewer, custom preprocessing code,…).

3. How to use *i*Map3

Copy *i*Map3 and its support functions in the folder containing the data file (or alternatively set paths for input and output data).

Set the parameters (see configuration structure section) in a configuration structure (e.g. cfg.xSize=400). Default values will be used for non-specified parameters.

Call the *i*Map3 function with the configuration structure (e.g. imap3(cfg)).

See examples at the end of this document and the example folders for more specific explanations.

Please keep in mind that running *i*Map3 takes a bit of time due to the use of bootstrapping and TFCE. We included wait bars so the user can keep track of the analysis progression.

Some analyses with small stimulus size can be performed on a 4 Go RAM computer. Please note that you might encounter some “Out of Memory” issues when using a 32bits OS and/or Matlab; or depending on memory allocation settings in Matlab. However, we strongly recommend using a 8 or even better 16 Go RAM computer.

We recommend using *i*Map3 at first with the default settings to have a general view on the results. Then, in a second step for the final analysis, we advise to use a higher number of bootstraps (1000 or more for better estimate) and, if necessary, to set the color scale and transparency of the maps.

4. Configuration structure

VARIABLES that can be set in the cfg structure

e.g. cfg.xSize=400. See examples at the end of this document.

1- **xSize** and **ySize**: stimulus size in pixels (e.g. 382, 390)

IMPORTANT: Please keep in mind that the stimuli dimensions (xSize and ySize) might be inverted depending on whether the user considers them in graph coordinates (abscissa/ordinate, bottom left origin), screen coordinates (top left origin) or matrices (number of lines first, number of columns second). Here we consider matrix coordinates.

2- **columnx**, **columny**, **columnduration**, **columnitem**: specify the column number for x, y coordinates, fixation durations and item number. This allows flexible data format. By defaults these columns are 1, 2, 3 and 4

3- **dataset1** and **dataset2**: specify the data .mat files that will be tested/compared. For example [1:20], [21:40] to compare data1 to data20 with data 21 to data40. The second data set is optional. If only one dataset is tested, iMap produces a statistical map and eye-tracking indexes for this dataset. If two datasets are specified, iMap provides the statistical maps and eye-tracking indexes for both dataset and the difference map and indexes.

4- **twosampletest**: 1=paired or 2=independent

5- **smoothingpic**: Standard deviation in pixels of the Gaussian used for the data map smoothing. The default value is 10 pixels.

IMPORTANT: Please note that the smoothing should take into account the actual viewing conditions (resolution, size, distance of the screen) and spatial resolution of the eye tracker. Therefore, this parameter varies from experiment to experiment.

6- **maptype**: 1 for fixation duration maps, 2 for number of fixations maps. The default value is 1.

7- **firstfix**: This option allows you to ignore the first fixation of each trial. This is particularly useful if the stimuli are centred and a central fixation cross is presented before the trials. 1 (default option) keeps all the fixations, 2 ignores the first fixation of each trial.

8- **backgroundfile**: e.g. 'facebackground.tif'. This option allows you to add a background picture to the statistical fixation maps.

9- **specificfix**: To select one or several specific fixations. e.g. [3 3] or [1 3]. This value is optional.

10- **searchspace**: By default the stimulus space, xSize * ySize. The search space size can be specified with a logical mask, i.e. by entering the file name of a black and white picture (e.g. "facemask.tif") where the white part indicates the search space.

11- **scaledownup**: To be specified as a 2 value vector ([scaledown scaleup]). This allows you to set the color coded scale. It has the advantage of allowing the same scale to be used for the individual (specific to datasets) maps and the contrast map. We recommend running *i*Map3 at first without setting this parameter in order to get an idea of the range of the t-values and then to set this parameter for the final analysis.

12- **sigthres**: Significativity threshold. One-tailed for the individual maps, two-tailed for the difference map. By default .05 (.025 for the contrast map)

13- **nboot**: Number of resamples for the multiple comparisons correction (default 500).

14- **rawmaps**: Generates tiff images (called rawfix1 and rawfix2) of the raw (without normalization and smoothing) fixation locations and durations. 1 = no, 2 = yes (default)

15- **transpim**: Set the transparency of the background image from 0 to 1 (default = 1)

16- **transpmap**: Set the transparency of the statistical map from 0 to 1 (default = .65)

17- **mindatapoints**: Minimal number of data points required to include a pixel in the analysis (default = 10). Obviously, *i*Map3 cannot compute the pixel-wise t-values without (enough) data. Hence, in order to obtain reliable variability and central tendency indices, a minimal number of data points per pixel is necessary. Please see the face processing example for details on this variable.

18- **logicalmask**: Generates tiff images (called logicalmask1, logicalmask2 and logicalmaskcontrast) representing the pixels included in the analysis in function of the number of data points threshold. 1 = no (default), 2 = yes

5. Output

1- **Fixation maps**: *i*Map3 creates .tif pictures of the single and difference fixation maps merged with a background picture. It displays the significant areas (displayed heat maps) after correction for multiple comparisons. The color coding of the heat maps indicates the t-values. It also provides the options to create .tif pictures with normalized scales and raw (without smoothing and normalization) fixation maps. Please see examples.

2- **Global eye-tracking measures**. *i*Map3 creates .txt files with global eye-tracking measures for both datasets (called eyebasicdataset1.txt and eyebasicdataset2.txt). The columns are: the number of fixations, the total fixation duration, the mean fixation

duration, the path length and the mean saccade length). The lines correspond to the raw data files (participants, sessions).

Number of Fixations	Total Fixation Duration	Mean Fixation Duration	Path Length	Mean Saccade Length
29.09677	7.483355	0.2343271	1,539.18	48.12055
27.87097	5.932745	0.2136969	1,699.69	61.15729
27.67742	7.76056	0.2542954	1,674.231	54.56829
28.41935	7.174361	0.2308422	1,353.442	43.39324
27.87097	4.96008	0.1603119	2,130.377	69.2846
27.32258	7.850284	0.2606777	1,726.404	57.04416

3- **Z-scores**: *i*Map3 creates a text file called Zscore.txt that includes the mean Z-scores in the significant area for (respective columns) dataset 1 in the area 1 and area 2 (areas in which the fixation durations are significantly longer for dataset 1 and 2 respectively), dataset 2 in the area 1 and area 2. Please refer to the code for the exact output structure that might vary depending on the observed significant effects.

Single Maps		Difference Map			
Dataset 1	Dataset 2	Dataset 1, Area 1	Dataset 1, Area 2	Dataset 1, Area 1	Dataset 1, Area 2
4.483855	4.909454	4.646505	2.261218	1.699236	5.669345

4- **Effect sizes**: It also creates a .txt file with the Cohen's d between both datasets for area 1 and 2 (areas in which the fixation durations are significantly longer for dataset 1 and 2 respectively). The file is called cohend.txt.

5- **Eye-tracking measures in significant areas**: *i*Map3 creates .txt files with the eye-tracking data in both the significant areas and the rest of the picture. The files are called eyeareadataset1.txt and eyeareadataset2.txt and are organised the following way: mean fixation duration for area 1 then for area 2 then for the rest of the picture. In the same format are: path length, total fixation duration and number of fixations. Please refer to the code for the exact output structure that might vary depending on the observed significant effects.

Mean Fixation Duration (s)			Path Length (pixels)			Total Fixation Duration (s)			Number of Fixations		
Area 1	Area 2	Rest	Area 1	Area 2	Rest	Area 1	Area 2	Rest	Area 1	Area 2	Rest
0.3178	0.2506	0.2521	135	47	65	0.8901	0.2753	7.1256	2.79	1.00	28.46
0.1881	0.2297	0.2128	63	117	90	0.1566	0.4580	5.3216	0.87	1.87	25.16
0.3166	0.2829	0.2778	300	71	89	1.4285	0.3257	6.8447	4.75	1.18	24.75
0.2904	0.2448	0.2540	108	53	82	0.7069	0.3226	6.9384	2.50	1.39	27.61
0.1808	0.1693	0.1775	89	59	63	0.2640	0.1710	5.0603	1.46	1.00	28.43
0.3323	0.3189	0.2759	266	113	86	1.5321	0.6282	6.5381	4.64	1.96	23.68

6- **Raw maps**: Raw (without normalization and smoothing) fixation locations and durations for each data set. The raw maps are generated by default.

6. Examples

Please note that these data are only provided in order to illustrate how to use the toolbox. We do not intend to prove the validity of the method or to run simulations from these examples.

Also note that you might observe slightly different results when trying these examples. This is due to the imperfect convergence with 500 random replacement bootstraps. We recommend using 500 bootstraps to have a quick look at the output but to use a higher number of bootstraps in order to obtain the final results.

6.1. Face processing example

Subsample of data from Miellet, Vizioli, He, Zhou & Caldara (2013) and Miellet, He, Zhou, Lao & Caldara (2012).

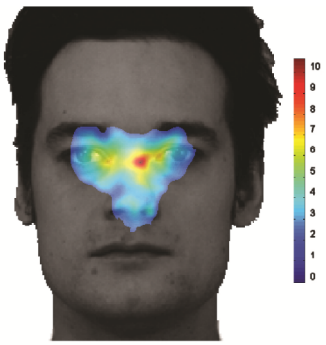
East-Asian (EA, 15 observers) and Western-Caucasian (WC, 15 observers) participants performed an old-new task on EA and WC faces.

The data in this example are in .mat files (called data1.mat, data2.mat,...), the matrices are called "summary". The stimulus presentation was using the Psychophysic Toolbox. The raw data have been recorded in Matlab using the EyeLink Toolbox. The eye position was recorded every 8ms then we computed fixations and saccades (with a custom algorithm), and centered them in the stimulus space. There was a central fixation cross before each trial then the 382x390 stimulus was randomly placed on a 800x600 screen.

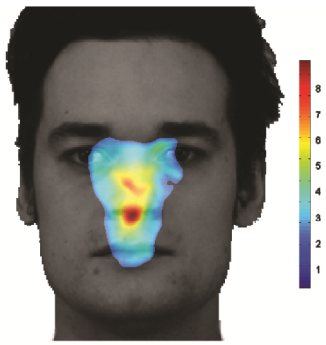
Western Caucasian [1:15] vs East Asian [16:30] participants (WC and EA faces stimuli for both groups). This example shows an eye bias for WC observers (warm colors on the contrast map) and a center of the face bias for EA participants (cold colors on the contrast map).

```
clear all
cfg=[];
cfg.xSize=382;
cfg.ySize=390;
cfg.dataset1=1:15;
cfg.dataset2=16:30;
cfg.rawmaps=2;
cfg.twosampletest=2; % twosampletest: 1=paired or 2=independant
cfg.backgroundfile='facebackground.tif';
imap3(cfg)
```

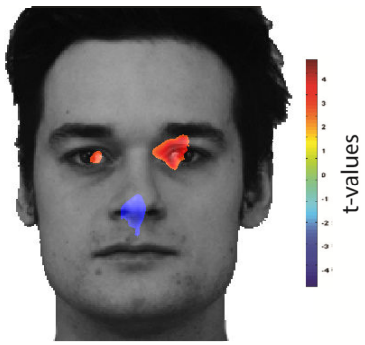
We could run the analysis in this example on a regular laptop with 4 Go RAM.



Significant area for WC

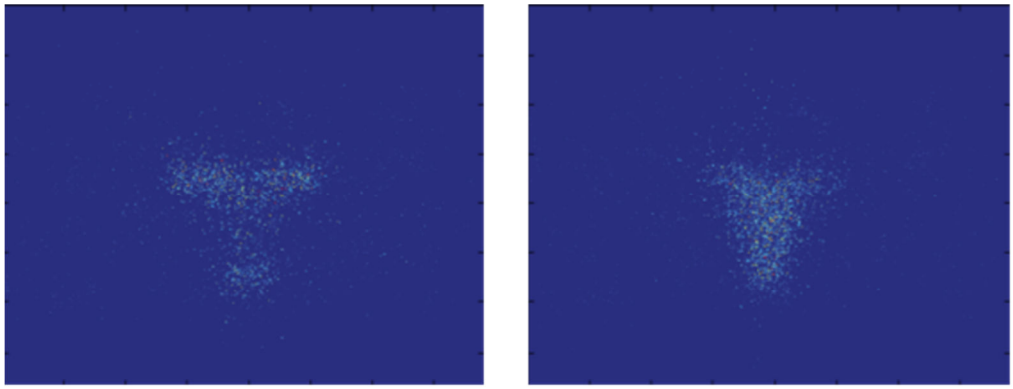


Significant area for EA

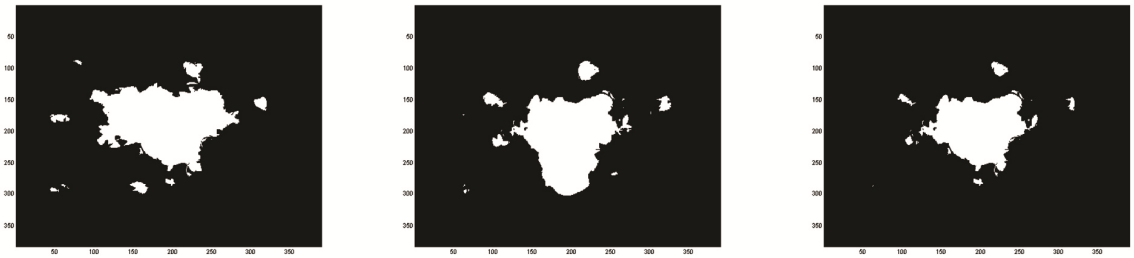


Significant fixation biases
WC in red and EA in blue

Setting cfg.rawmaps=2 allows us to inspect the fixation locations and durations before smoothing and normalization.



In this example, we used the default settings, including the default minimal number of data points per pixel (mindatapoints = 10 which represents two thirds of each group size). Setting cfg.logicalmask = 2 allows us to visualize the areas of the stimulus space that are included in the analysis for each of the 3 analyses (dataset 1, dataset 2, contrast). The white parts show the pixels included in the analysis.



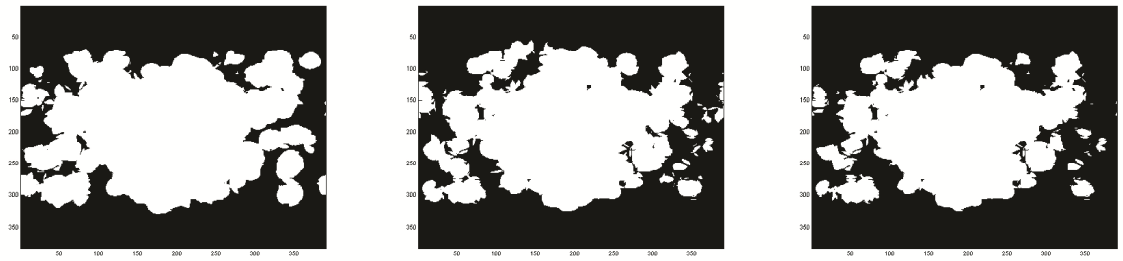
Dataset 1 Dataset 2 Contrast

Pixels included in the analysis with mindatapoints=10

It is important to examine these logical masks together with the raw maps to ensure that the right number-of-data-points threshold is used. Indeed, the optimal threshold might vary according to the task, stimuli, participants, vision conditions… Too small a number of data points would lead to unreliable variability and central tendency indices. An extreme case

would be to include pixels with only 1 data point for which the t-values would be infinite. In contrast, a too high threshold might exclude from the analysis pixels showing a genuine effect.

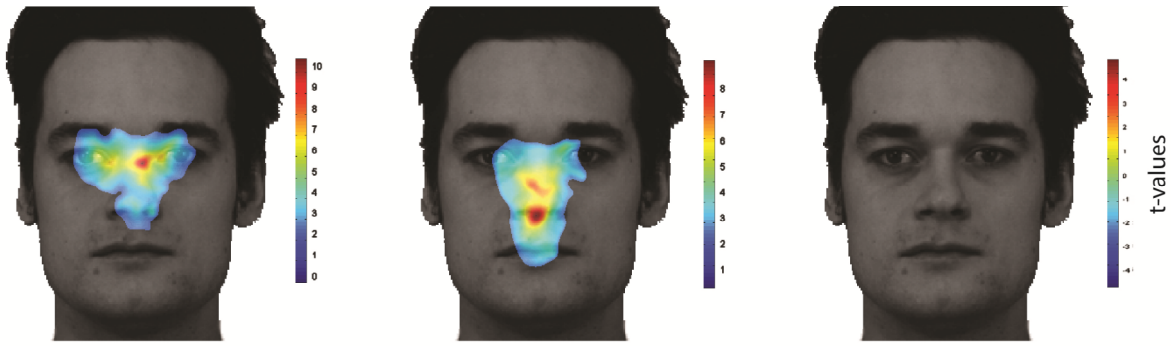
In the following, the 2 most extreme case scenarios for this example (mindatapoints = 2 and 14) will be considered.



Dataset 1 Dataset 2 Contrast

Pixels included in the analysis with mindatapoints=2

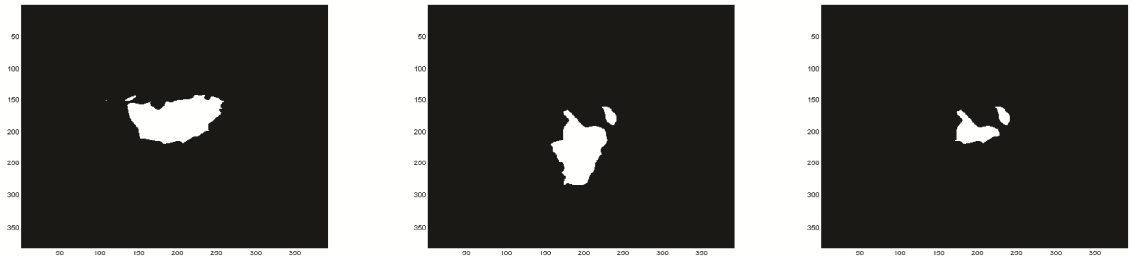
The analysis masks include, as expected, more pixels when the minimum-data-points threshold is lower (here mindatapoints = 2). This lead to the following results:



Significant area for WC Significant area for EA Significant fixation biases WC in red and EA in blue

Computing t-values from 2 data points is of course an extreme case scenario that cannot be recommended and that is used here only to illustrate the effect of the mindatapoints parameter. Including pixels with such a small number of observations produce unreliable variability and central tendency indices and lower the signal to noise ratio; hence reducing the sensitivity of the method.

A higher mindatapoints parameter, close to the samples size, produces better estimates of the fixation distributions but in turn reduces the overlapping analysis areas, hence reducing the likelihood to observe significant effects. The analysis masks below show the most extreme situation for the present example (mindatapoints 14, sample size-1), including in the analysis only the pixels for which almost all the participants have values (mindatapoints = 15 was leading to empty masks).



Dataset 1 Dataset 2 Contrast

Pixels included in the analysis with mindatapoints=14

This parameter is too restrictive, leaving only few pixels to be analysed in the contrast mask and thus restricting areas that could be significant. Importantly, a mindatapoints value too close to the samples size might lead to *i*Map3 crashing. Indeed, in order to ensure a reliable bootstrapped threshold in the multiple comparisons correction procedure, the resampling with replacement considers only samples containing at least mindatapoints unique values.

In summary, we recommend to use the highest mindatapoints value as possible in order to obtain reliable pixel-wise fixation distributions. With our datasets, two-thirds of the samples size proved to be an appropriate trade-off. The analysis logical masks and raw fixation maps allow ensuring that the meaningful parts of the stimulus space are included in the analysis. If these 2 conditions cannot be met (enough observations per pixel AND enough pixels included in the analysis), larger samples are necessary.

As clearly shown in this example an absolute threshold cannot be set as the optimal mindatapoints parameter depends on the sample size and fixation distributions. It is important to note that in the worst case scenario, a suboptimal mindatapoints parameter might reduce the sensitivity of *i*Map3 but will not lead to false positives.

Any input on how to determine this parameter with a strictly data-driven approach would be highly appreciated.

6.2. Scene processing example

The data for this example are a subsample from Miellet, S., Zhou, X., He, L., Rodger, H., & Caldara, R. (2010). Investigating cultural diversity for extrafoveal information use in scenes. . *Journal of Vision*, *10*(6):21, 1-18.

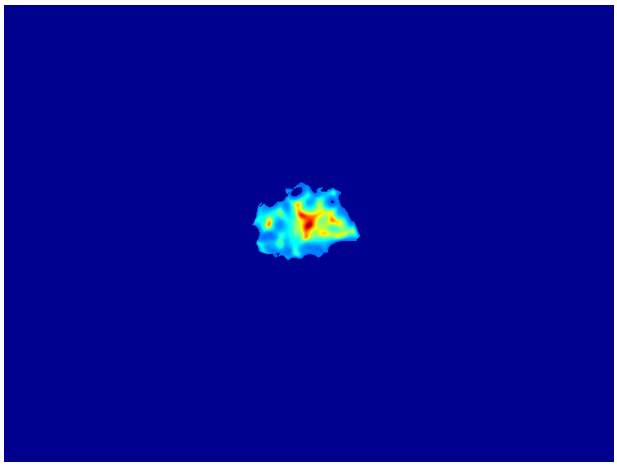
In this experiment, the participants had to detect and identify an animal in a natural visual scene (full-screen, colour pictures). The two main manipulations were the size of the target and the size of a gaze contingent central scotoma (*Blindspot*). The target and the *Blindspot* sizes could be 0, 2, 5 or 8 degrees of visual angle.

The target position was randomly distributed in the scene so, in order to make the fixation maps, one can normalize the fixation positions relatively to the target position and make a new fixation space where all the targets are centered.

See an example with normalizedscenes.m

```
clear all
cfg=[];
cfg.xSize=600;
cfg.ySize=800;
cfg.dataset1=[1:10]; imap3(cfg)
```

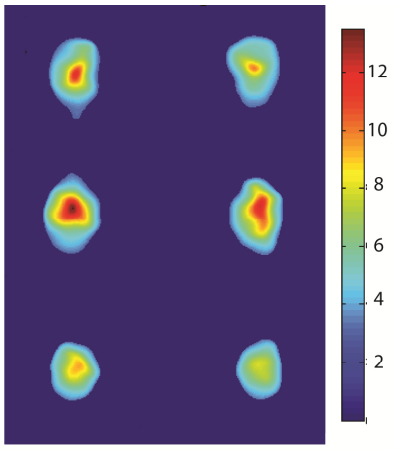
Due to the larger search space (600*800), this analysis necessitated the use of a 8 Go RAM computer.



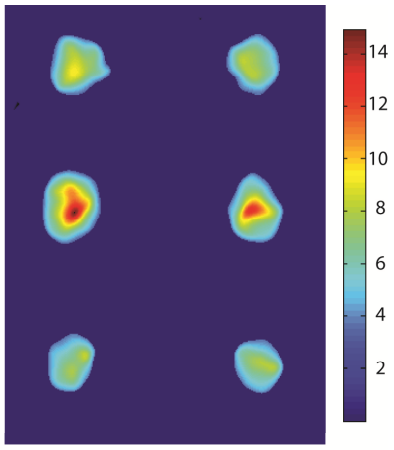
6.3. Memory task

The data from this example are a subsample from Harkin, B., Miellet, S., & Kessler, K. (2012). What checkers actually check: An eye tracking study of working memory and executive control. PLoS ONE, 7(9): e44689. doi:10.1371/journal.pone.0044689.

The code memorytask.m prepares the data and run imap. The eye-tracking data are in text files that will be converted in matrices. The screen based coordinates are also centered on the stimulus. The raw data come from a fixation report generated by DataViewer (SR-Research). The experiment was presented with E-Prime.



Significant areas for High-checkers



Significant areas for Low-checkers

From this dataset there is no significant general difference between the 2 groups of observers (High- and Low-checkers). Note that the original study, focusing on the specific information displayed at each location, revealed that checkers fixate more often and for longer when misleading information is presented than non-checkers. Specifically, checkers spend more time checking stimulus locations as well as locations that had actually been empty during encoding.

7. Approach description

*i*Map offers a free, open-source, flexible and user friendly toolbox to analyze eye movement data with a robust data-driven approach that generates statistical fixation maps.

Importantly, *i*Map does not require the a-priori segmentation of the experimental images into Regions Of Interest.

With *i*Map, fixation data are first smoothed by convolving Gaussian kernels (this procedure embodies eye-tracker accuracy) to generate three-dimensional fixation maps. The individual smoothed fixation maps are then Z-scored in the stimulus space in order to represent the individual fixation bias.

7.2.1. Statistical maps

In contrast with previous versions, *i*Map now simply computes independent- and paired-samples t-values on each pixel across datasets. A signal enhancement method is then applied on the t-maps. And finally a bootstrap procedure is used to correct for multiple comparisons.

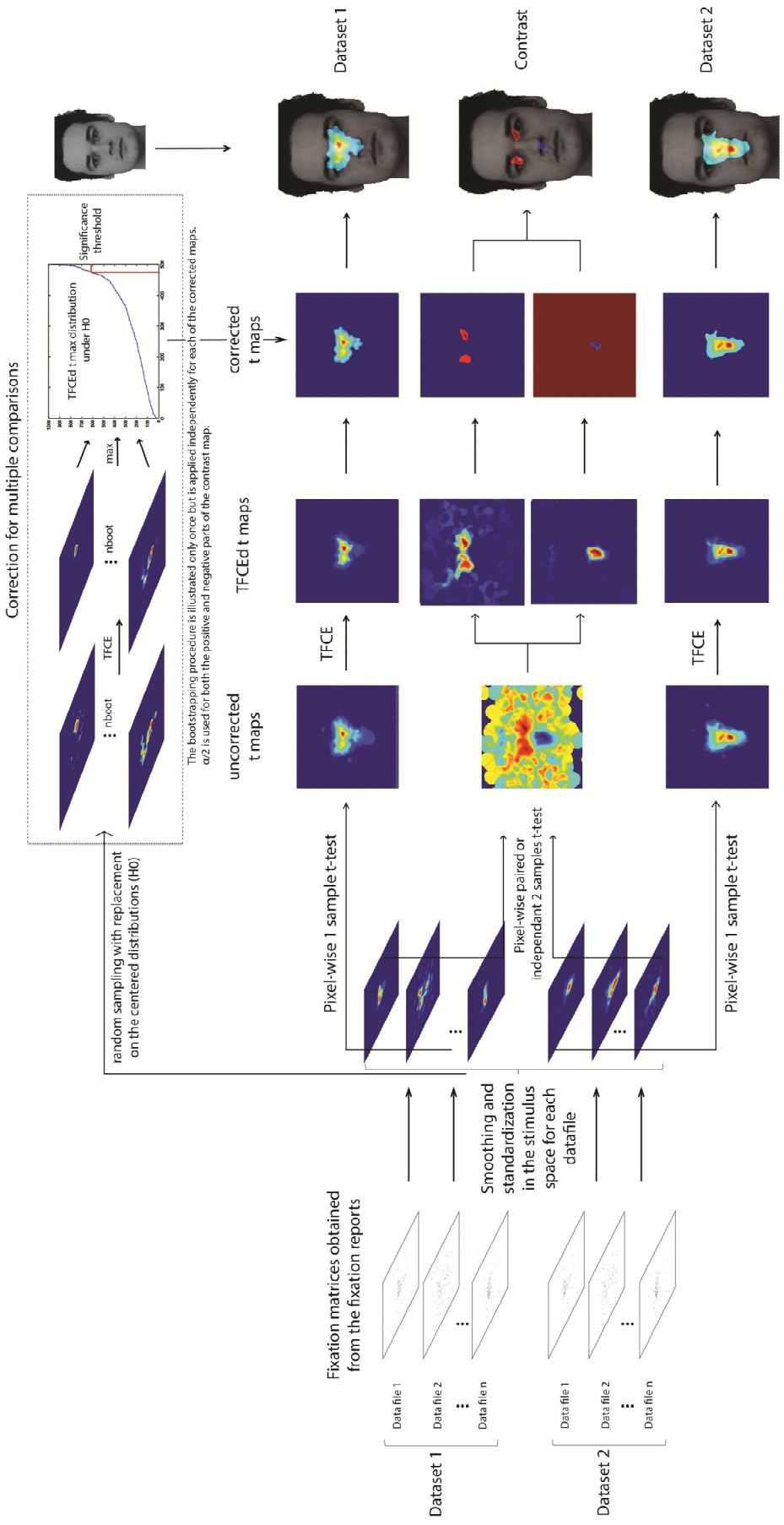
7.2.2. Threshold-Free Cluster-Enhancement

The t-maps are then TFCE transformed, using a function derived from LIMO-EEG (Pernet et al., 2011). The “threshold-free cluster-enhancement” (TFCE) approach (Smith & Nichols, 2009) takes into account both amplitude and extent of the signal. The TFCE approach aims to enhance areas of signal that exhibit some spatial contiguity without relying on hard-threshold-based clustering. The image is passed through an algorithm, which enhances the intensity within cluster-like regions more than within background (noise) regions. The output image is therefore not intrinsically clustered / thresholded, but after TFCE enhancement, thresholding will better discriminate between noise and spatially-extended signal. This generic form of non-linear image processing boosts the height of spatially distributed signals without changing the location of their local maxima. Hence, it optimises the detection of both diffuse, low-amplitude signals and sharp, focal signals. Strong control over family-wise error is obtained by using a bootstrap threshold of the maximum TFCE scores expected by chance.

7.2.3. Nonparametric multiple comparisons correction

In order to avoid false positives in the statistical maps due to multiple comparisons, we implemented a nonparametric multiple comparisons correction. A bootstrap procedure (cfg.nboot parameter, 500 resamples by default) is performed under H0. H0 is obtained by centering each dataset, hence retaining the real data variability (Wilcox, 2012). The maximum value of each bootstrapped TFCE enhanced map (pixel with the largest TFCE intensity) is kept in order to create a distribution of the max intensities. The max intensities are then sorted and the 95th percentile obtained to yield a one-sided 95% confidence interval. The intensity of each pixel in the statistical map of the original data is then compared to the maximum pixel intensity 95% confidence interval just obtained. Any significant pixel of the true data smaller than the pixel intensity threshold of the maximum pixel intensity distribution (α) is eliminated from the statistical map. The pixel intensity threshold is set to be .05 by default (cfg.sigthres parameter).

7.1. Flow chart of *i*Map3 processing pipeline



7.2. New statistical engine for iMap3

Regarding the contrast, it should be noted that our TFCE implementation produces only positive values. In the bootstrap procedure, taking the maximum value would confound the biases for dataset 1 and dataset 2. For instance, in the case of independent samples, the distribution of maximum values could originate from only one of the two samples. For this reason, the positive and negative parts of the t-value maps are considered independently and the pixel intensity threshold is set to α/2 for both. Note that a similar approach is used in Fieldtrip (Maris & Oostenveld, 2007).

7.3. Limitations of previous versions using the pixel-test (up to iMap2.1)

Previous versions of *i*Map (up to *i*Map2.1; Caldara & Miellet, 2011), relying on the pixel-test based on the Random Field Theory (see Chauvin et al., 2005), tended to be over-sensitive, particularly with small samples leading to peaky distributions. Moreover, the inter-individual variability was not directly taken into account.

The pixel-test based on the Random Field Theory (see Chauvin et al., 2005) is required to be run on Z-scored maps (normalized across the stimulus space). This is not a problem with the individual dataset maps, which show relative fixation biases in the stimulus space. Hence previous data sets and simulations do not seem to reveal spurious significant effects with such individual dataset maps. In contrast, the Z-scoring in the stimulus space of the contrast maps, while preserving genuine effects also exaggerates smaller differences that might then reach the significance threshold. Therefore, these differences should be interpreted with great caution. From our point of view, this is the main reason why depending on particular data distributions it is possible to obtain spurious significant effects in contrast fixation maps when analysed with the pixel test; despite its good sensitivity and the fact that it takes into account the spatial correlation inherent to the data set and the multiple comparisons issue.

The pixel test is based on the maximum of a random field and this is best adapted for focal signal with high Z-scores. With eye movement data, depending on the experimental stimuli and conditions, the signal is not necessarily focal. For example, different observers could all look preferentially at the centre of gravity of a target or diagnostic area, producing a focal and intense signal in the group map. Alternatively, the observers could all look at different specific points of the target, leading to a less intense and more extended signal.

For all these reasons, we decided to apply a different approach in *i*Map3, taking directly into account the inter-observer variability and using TFCE for an optimised detection of both diffuse, low-amplitude signals and sharp, focal signals.

8. Credits

tfce2d is adapted from **LIMO-EEG**.

Pernet, C.R., Chauveau, N., Gaspar, C.M., & Rousselet, G.G. (2011). LIMO EEG: A Toolbox for Hierarchical LInear MOdeling of ElectroEncephaloGraphic Data. Computational Intelligence and Neuroscience. Article ID 831409, doi:10.1155/2011/831409

9. Disclaimer

*i*Map3 is free software; you can redistribute it and/or modify it.
We cannot be held responsible for any damage that may (appear to) be caused by the use of iMap. Use at your own risk.
This program is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE.
Please cite us and let us know if you have any comments or suggestions.
Thank you to all the users who have sent us feedback.
Any comments, suggestions, constructive criticisms are very welcome. Any offer for code optimisation as well!!!

References:

Caldara, R., & Miellet, S. (2011). iMap: A novel method for statistical fixation mapping of eye movement data. *Behavior Research Methods*, *43*(3), 864-878.

Chauvin, A., Worsley, K. J., Schyns, P. G., Arguin, M., & Gosselin, F. (2005). Accurate statistical tests for smooth classification images. *Journal of Vision*, *1*, 659–667. 5(9).

Harkin, B., Miellet, S., & Kessler, K. (2012). What checkers actually check: An eye tracking study of working memory and executive control. *PLoS ONE*, *7*(9): e44689. doi:10.1371/journal.pone.0044689.

Kriegeskorte, N., Simmons, W. K., Bellgowan, P. S. F., and Baker, C. I. (2009). Circular analysis in systems neuroscience – the dangers of double dipping. *Nature Neuroscience*, *12*, 535–540.

Maris, E., & Oostenveld, R. (2007). Nonparametric statistical testing of EEG- and MEG-data. *Journal of Neuroscience Methods*, *164*(1), 177–190.

Miellet, S., He, L., Zhou, X., Lao, J. & Caldara, R. (2012). When East meets West: gaze-contingent Blindspots abolish cultural diversity in eye movements for faces. *Journal of Eye Movement Research*, *5*(2):4, 1-12.

Miellet, S., Vizioli, L., He, L., Zhou, X., & Caldara, R. (2013). Mapping face recognition information use across cultures. *Frontiers in Perception Science*, *4* :34. doi: 10.3389/fpsyg.2013.00034.

Miellet, S., Zhou, X., He, L., Rodger, H., & Caldara, R. (2010). Investigating cultural diversity for extrafoveal information use in scenes. *Journal of Vision*, *10*(6):21, 1-18.

Pernet, C.R., Chauveau, N., Gaspar, C.M., & Rousselet, G.G. (2011). LIMO EEG: A Toolbox for Hierarchical LInear MOdeling of ElectroEncephaloGraphic Data. *Computational Intelligence and Neuroscience*. *Article ID 831409*, doi:10.1155/2011/831409

Smith S.M., & Nichols, T.E. (2009). Threshold-free cluster enhancement: addressing problems of smoothing, threshold dependence and localisation in cluster inference. *Neuroimage*, *44*(1), 83-98. doi: 10.1016/j.neuroimage.2008.03.061.

Wilcox, R. R. (2012). *Introduction to robust estimation and hypothesis testing. Statistical modeling and decision science* (3rd ed., pp. xxi–690 p.). Amsterdam ; Boston: Academic Press.