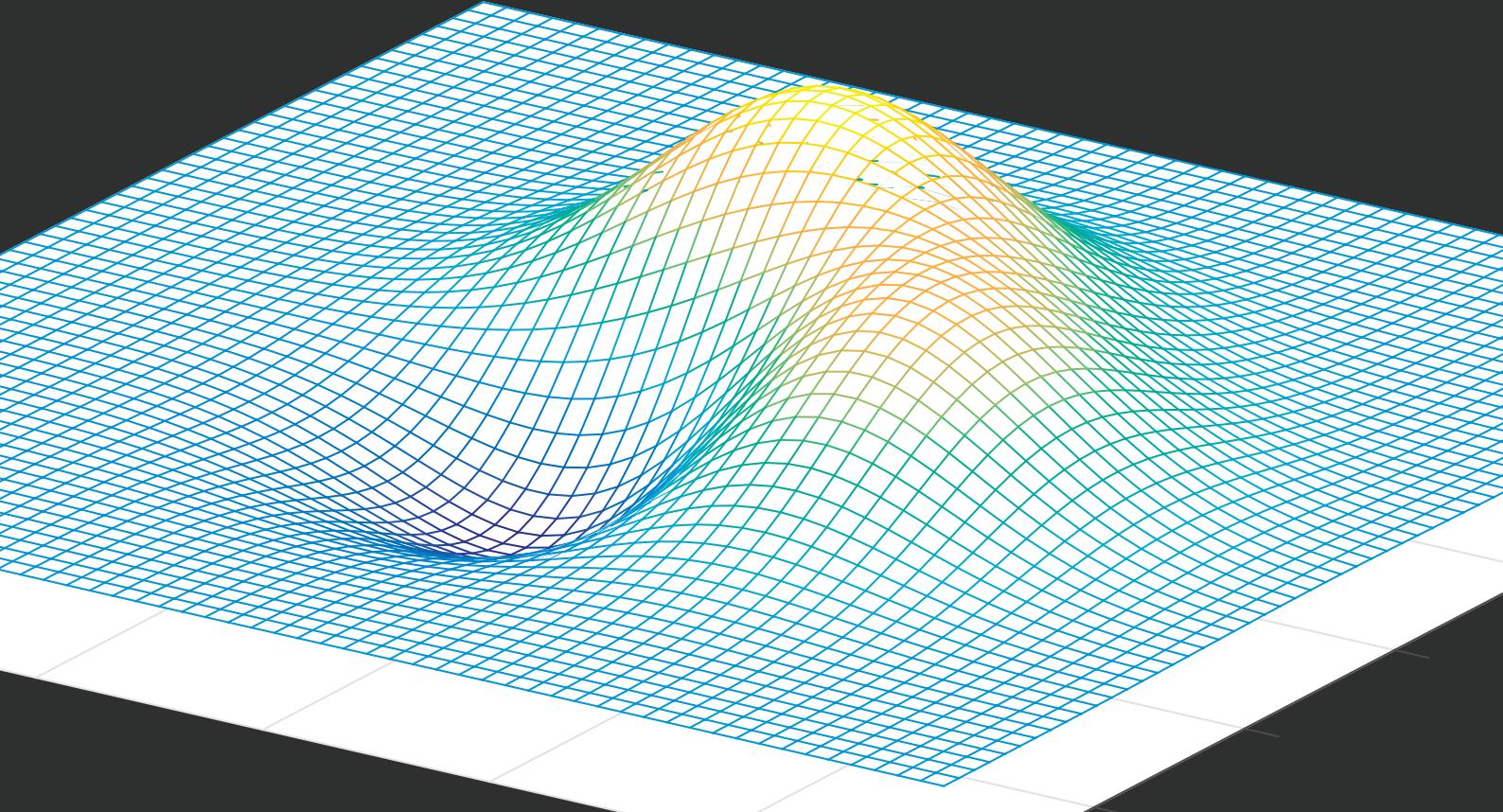


iMap

4

Guidebook



iMap 4: An Open Source Toolbox for the Statistical Fixation Mapping of Eye Movement data with Linear Mixed Modeling

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Please note that the final version of iMap 4 will be released in the next few months (see also page 49).

The philosophy, as well as the rationale of the iMap approach is explained in Caldara & Miellet (2011) and Miellet, Lao & Caldara (2014).

iMap 4 represents a major update of the statistical approach used in the toolbox, but keeps the original spirit that motivates our work:

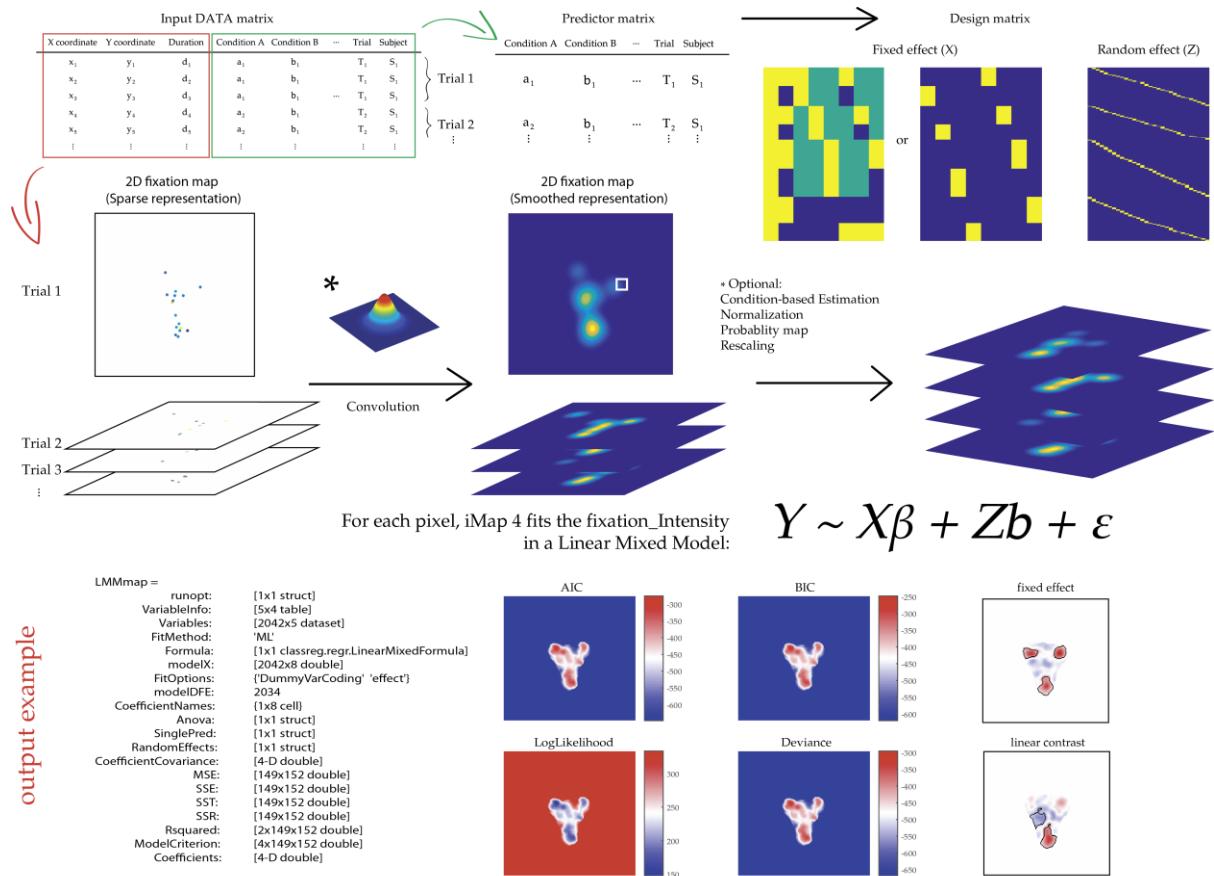
The current application was written in Matlab by Junpeng Lao and Nayla Sokhn. For any enquiries, please contact Junpeng.lao@unifr.ch or nayla.sokhn@unifr.ch

The development of iMap 4 was supported by the Swiss National Science Foundation grant (n° 100014_138627) awarded to Roberto Caldara.

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iMap 4 Overview



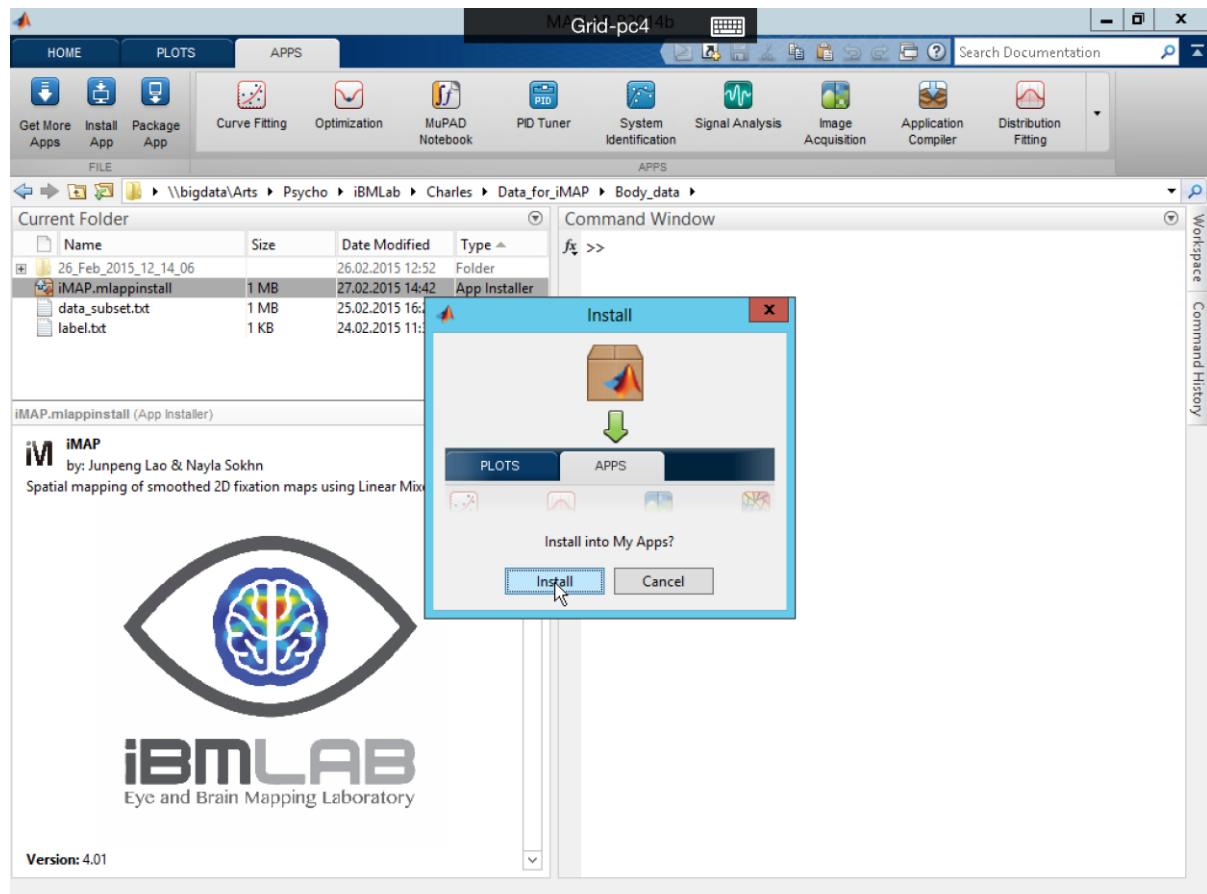
iMap 4 is an open source Matlab toolbox for the statistical fixation mapping of eye movement data, implementing a user-friendly interface that provide straightforward, easy to interpret statistical graphical outputs. iMap 4 matches the standards of the robust statistical analysis implemented in neuroimaging techniques (MEEG, fMRI). iMap 4 applies univariate, pixel-wise Linear Mixed Models (LMM) on the smoothed fixation maps with each subject as one of the random effects, which offers the flexibility to code for multiple between- and within- subject comparisons. Users can perform all possible linear contrasts for the fixed effects (main effects, interactions, etc.). Importantly, it implements a novel spatial cluster test based on bootstrapping to assess the statistical significance of the linear contrasts. We hope that iMap 4 could provide an easy access to the routine use of robust data-driven analyses in spatial fixation mappings.

The methodological details of the spatial mapping using Linear Mixed Models and the validation of the bootstrap clustering method implemented in iMap 4 are not provided in the current guidebook. These statistical features of the toolbox are the core of a scientific publication that is currently in preparation. For a general thoughtful introduction to mixed models, users of the toolbox should refer to Raudenbush & Bryk (2002), McCulloch, Searle & Neuhaus (2011), and Christensen (2011). We recommend iMap 4 users also read Baayen, Davidson & Bates (2008) and Bolker et al., (2009) for some examples on how to perform and report mixed model analysis.

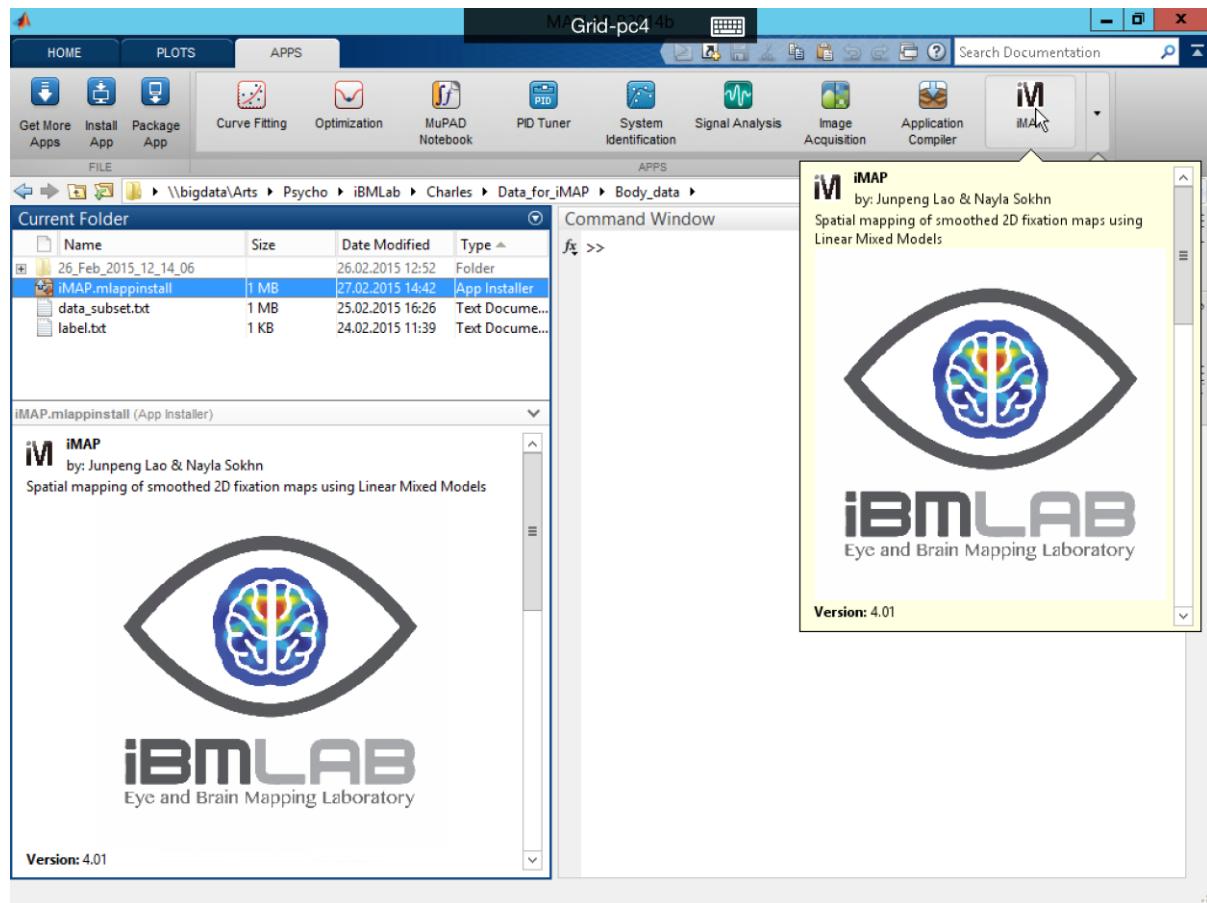
Installation

iMap 4.0 requires Matlab 2013b (version 8.2) or above with the Image Processing Toolbox and the Statistics Toolbox. If your Matlab environment is equipped with the Parallel Computing Toolbox, some function will launch in parallel to speed up the computation.

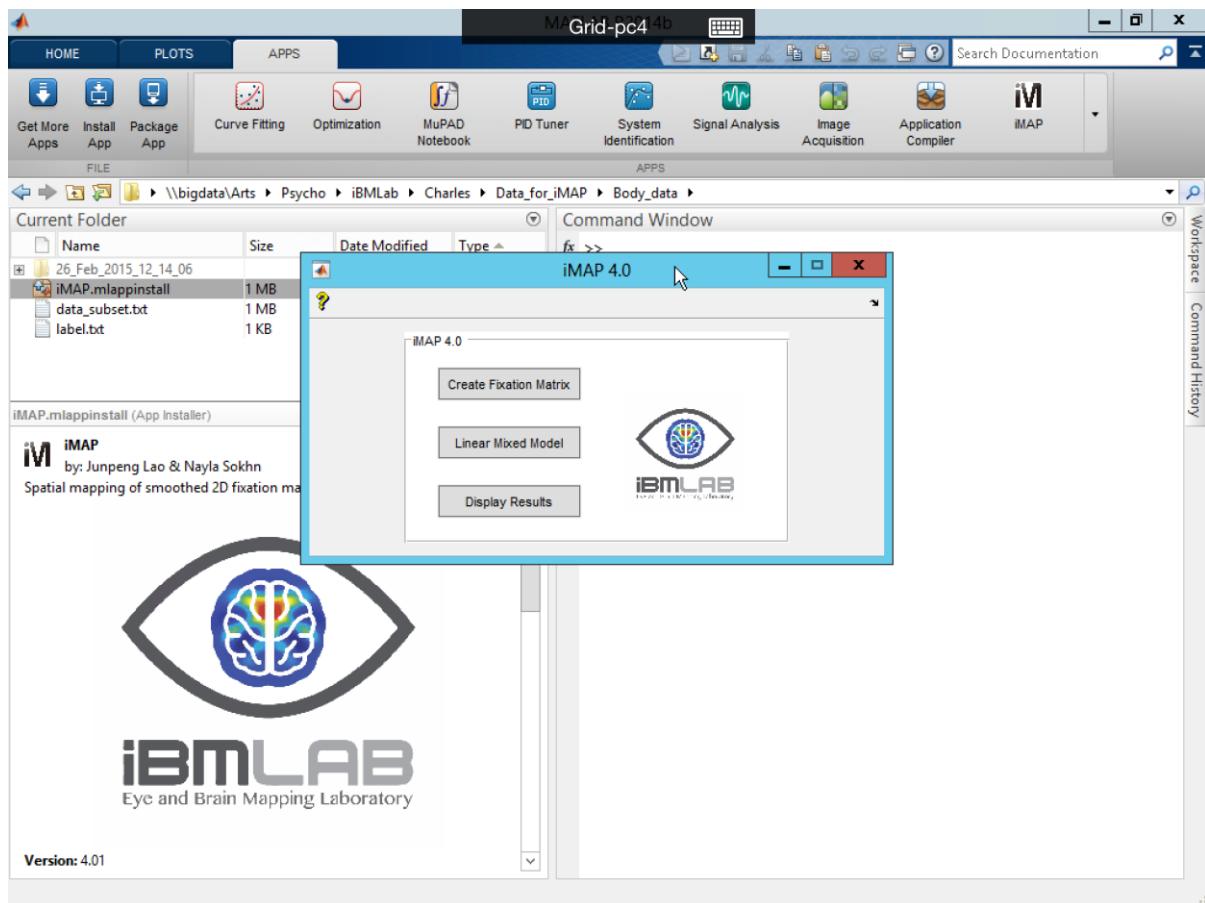
To installation iMap 4, simply unzip the iMap.zip, double click the iMAP.mlappinstall



iMap 4 is then installed on your Matlab software. You can now click on the App tab on Matlab main window to locate the app. You can also find the content of iMap 4 under your default Matlab search path: ./MATLAB/Apps/iMAP



Launch iMap 4 simply by clicking the app or type >>iMAP in your command window



Please note: any time you click on this guidebook will appear.

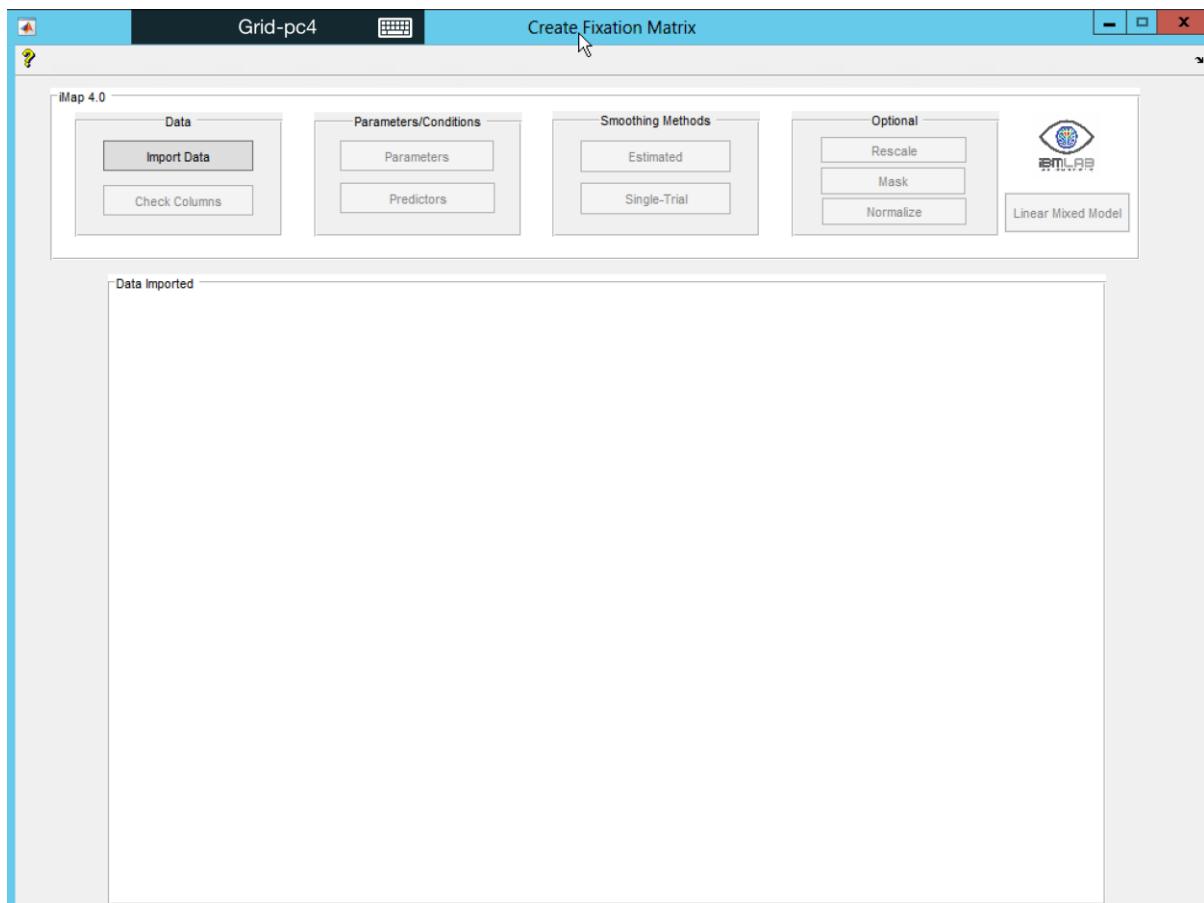
Create the Fixation Matrix and the Predictor Table

The following session will show how to prepare data inputs for Linear Mixed Modeling.

One data file is included in the .zip file as an example; it's a subset of a data set from

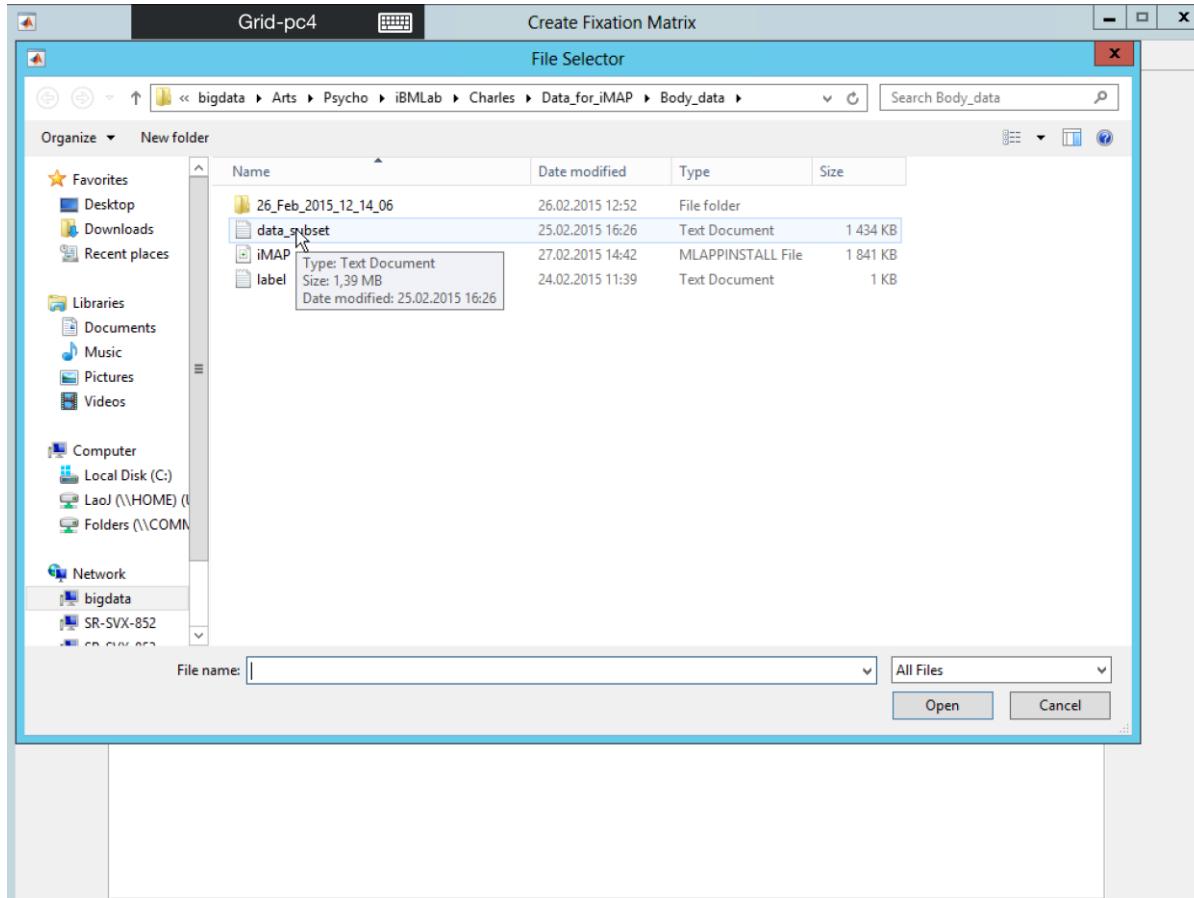
Bovet,J., Lao, J., Bartholomé, O., Caldara, R., and Raymond, M., Mapping females' bodily features of attractiveness (submitted)

Click “Create Fixation Matrix” to start



Import Data

Click “**import data**” to import one or multiple files.



(a) One file

You can import either text files (.txt) or Matlab files (.mat)

1. Text file (.txt)

You need to specify the **number of columns** and the **delimitation of the file**. Four delimitations are treated in this version: space, tabulation, comma and semicolon.

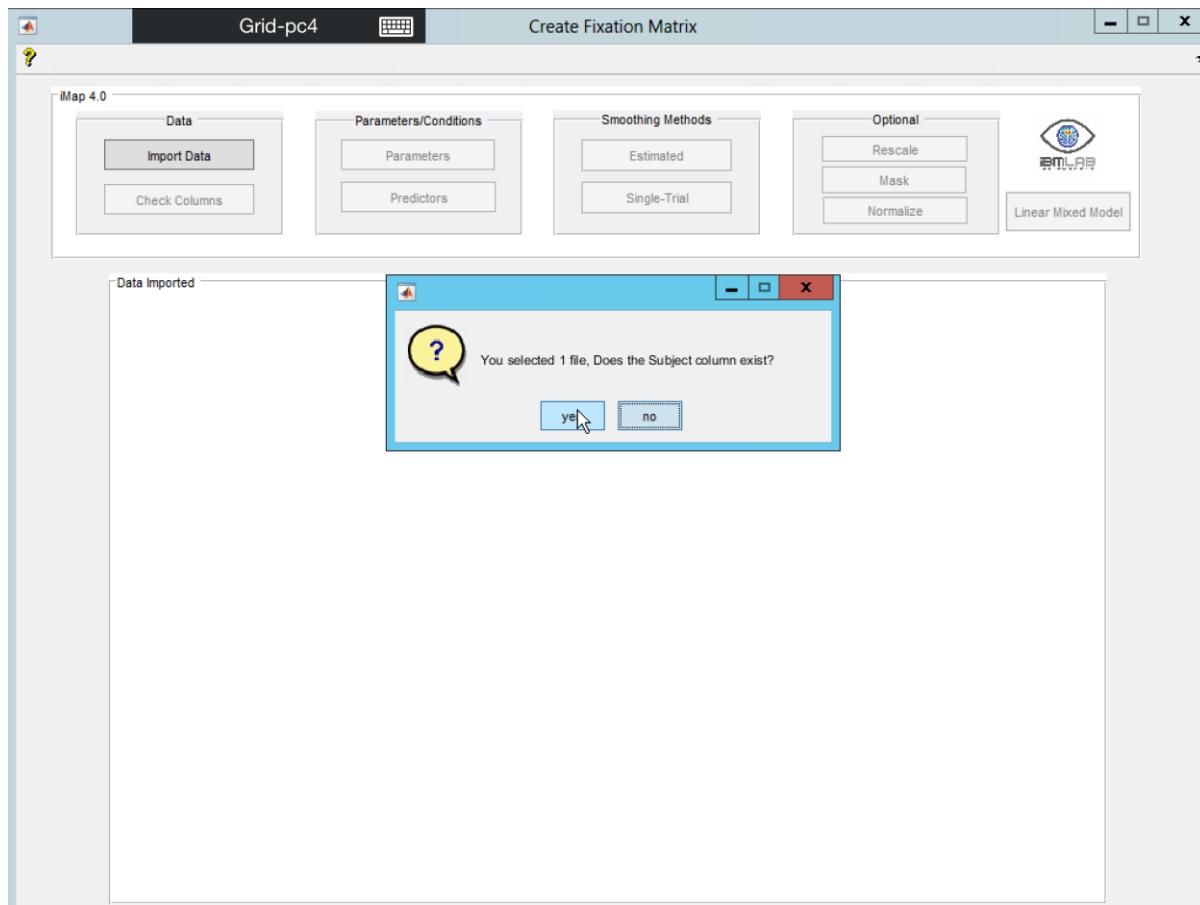
2. Matlab file (.mat)

There should be only one matrix file within your .mat file

(b) Multiple files

You can import multiple files having the same number and type of columns. Moreover, all files should be either .txt or .mat but not a mixture of both.

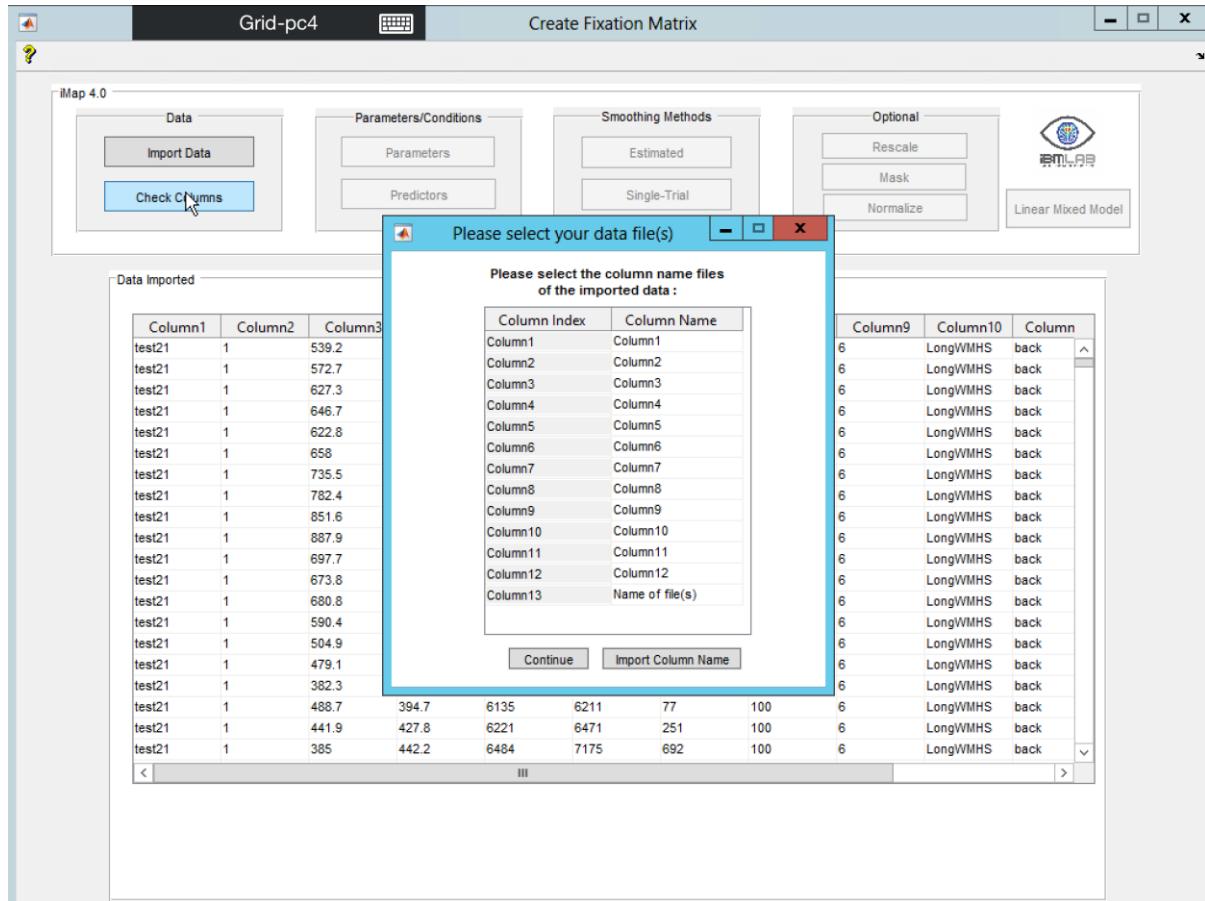
Please note: To be able to proceed to next steps, it is mandatory to have at least Five columns in the file that refer to: **Subject**, **Trial**, horizontal fixation location **X**, vertical fixation location **Y** and the fixation **Duration**. Moreover, **Trial** index should be unique within a subject (i.e., all trials are represented by different number even they are not belonging to the same condition).



When you import one or multiple file(s), a pop-up window will ask you if “**Subject**” information is included in the selected file(s). If you answer “**no**”, a pop-up will appear for you to define subject manually. You need to select the files corresponding to the same subject by clicking on checkboxes.

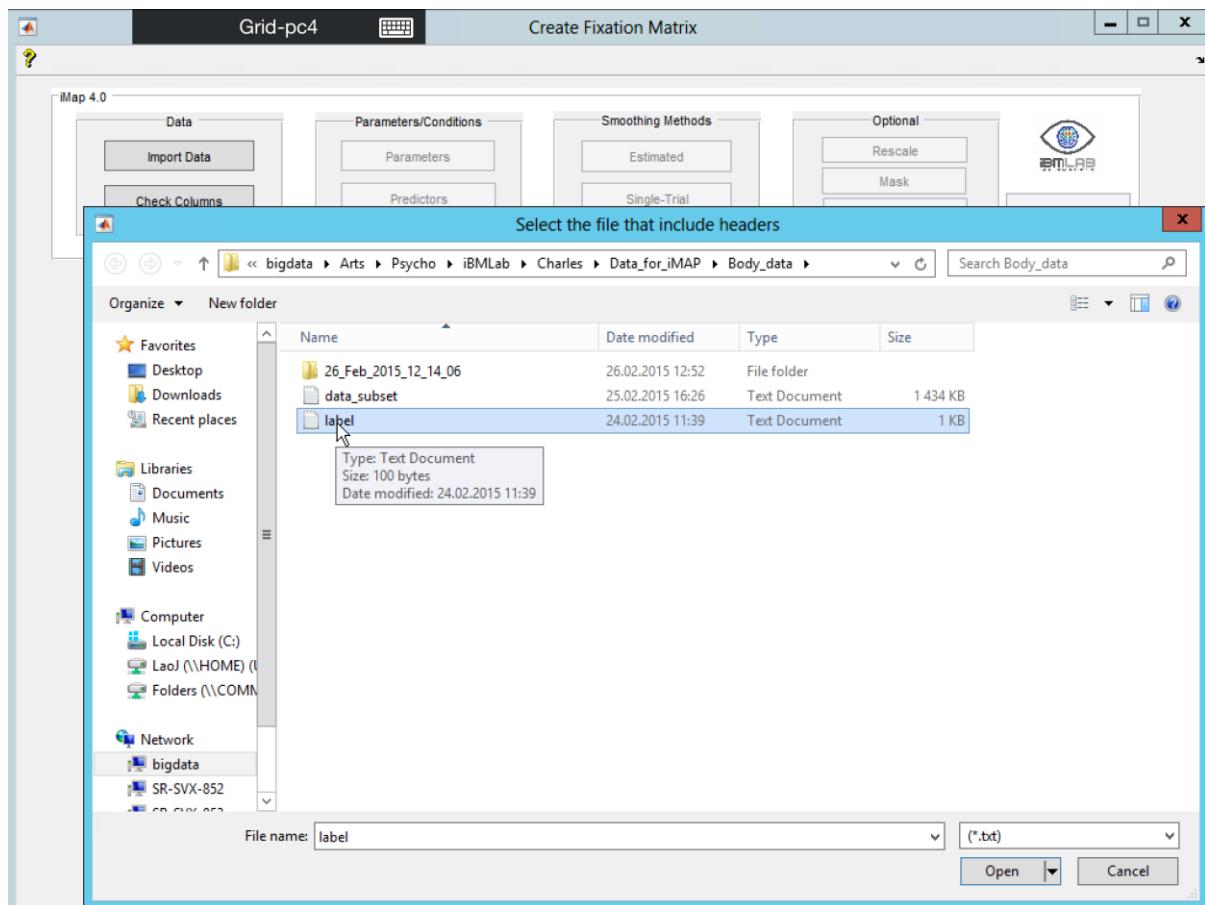
Check Columns

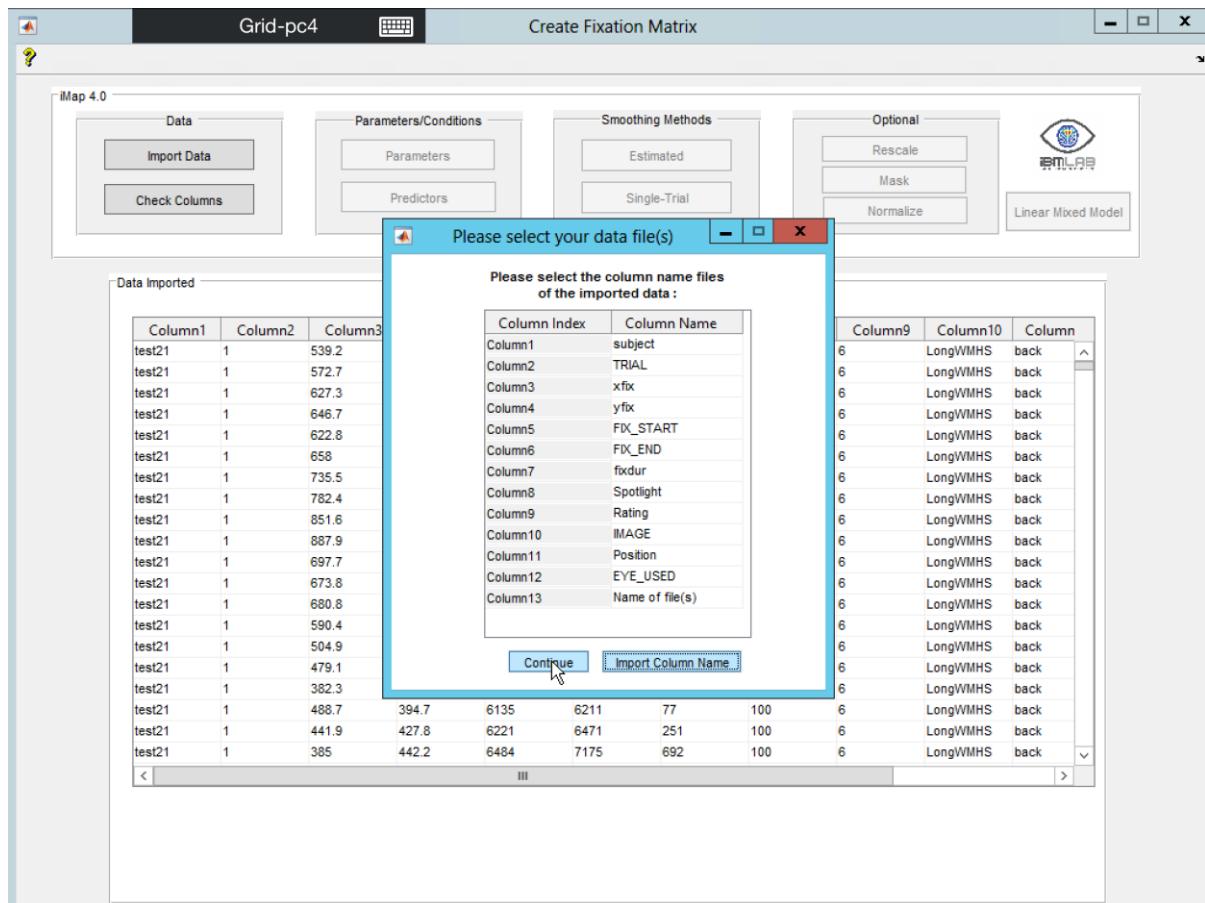
In this step, you can rename the columns and create new predictor from existing predictors.



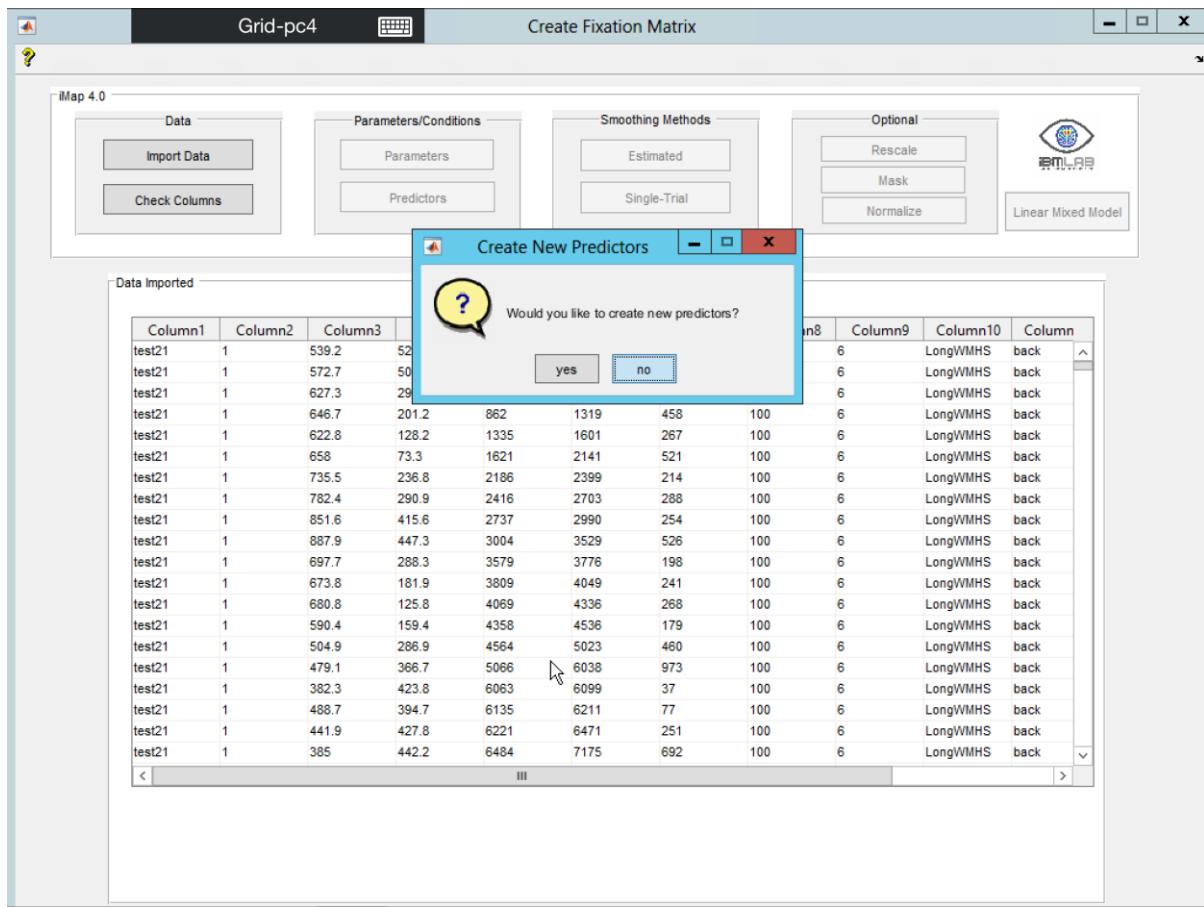
Column name could be changed here by manual input.

You can also import a .txt file with one column name on each line.

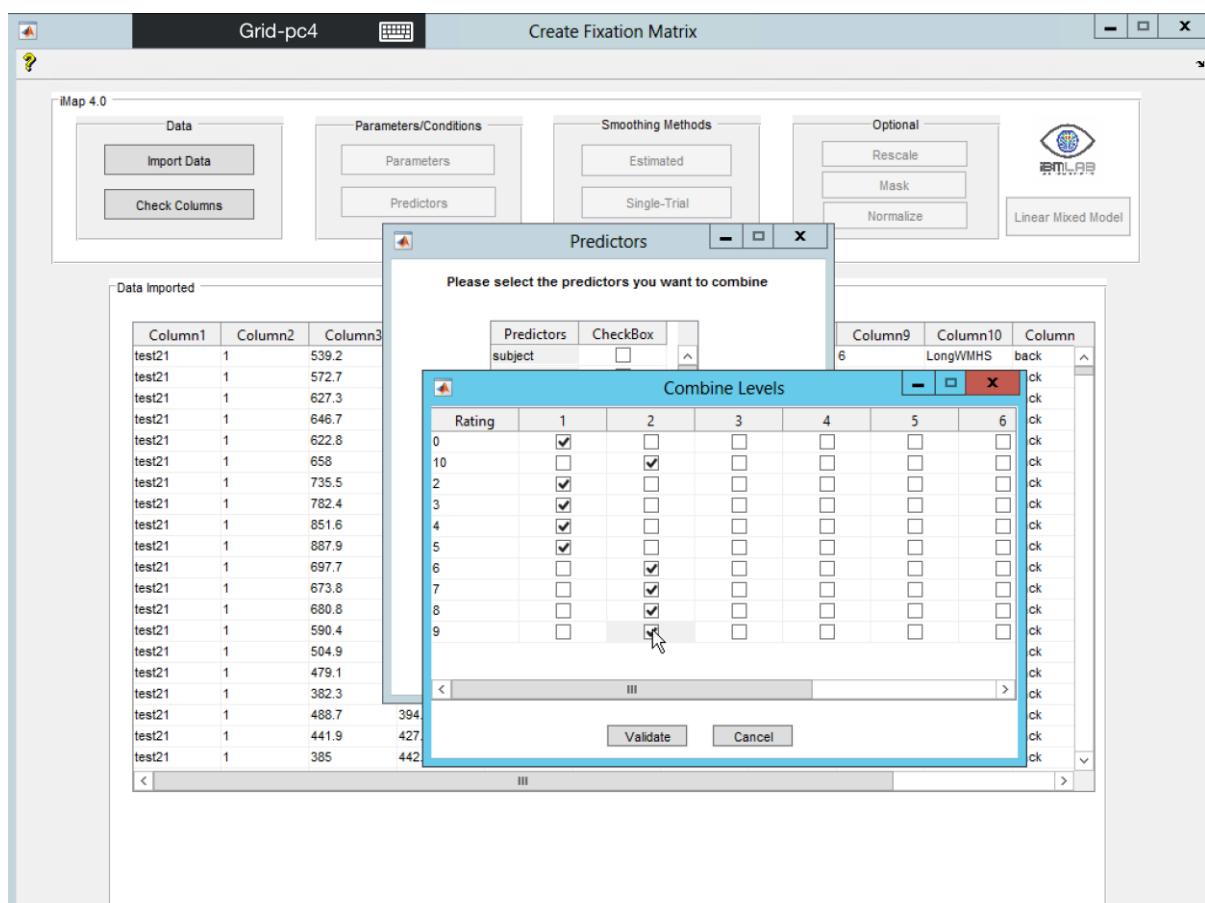
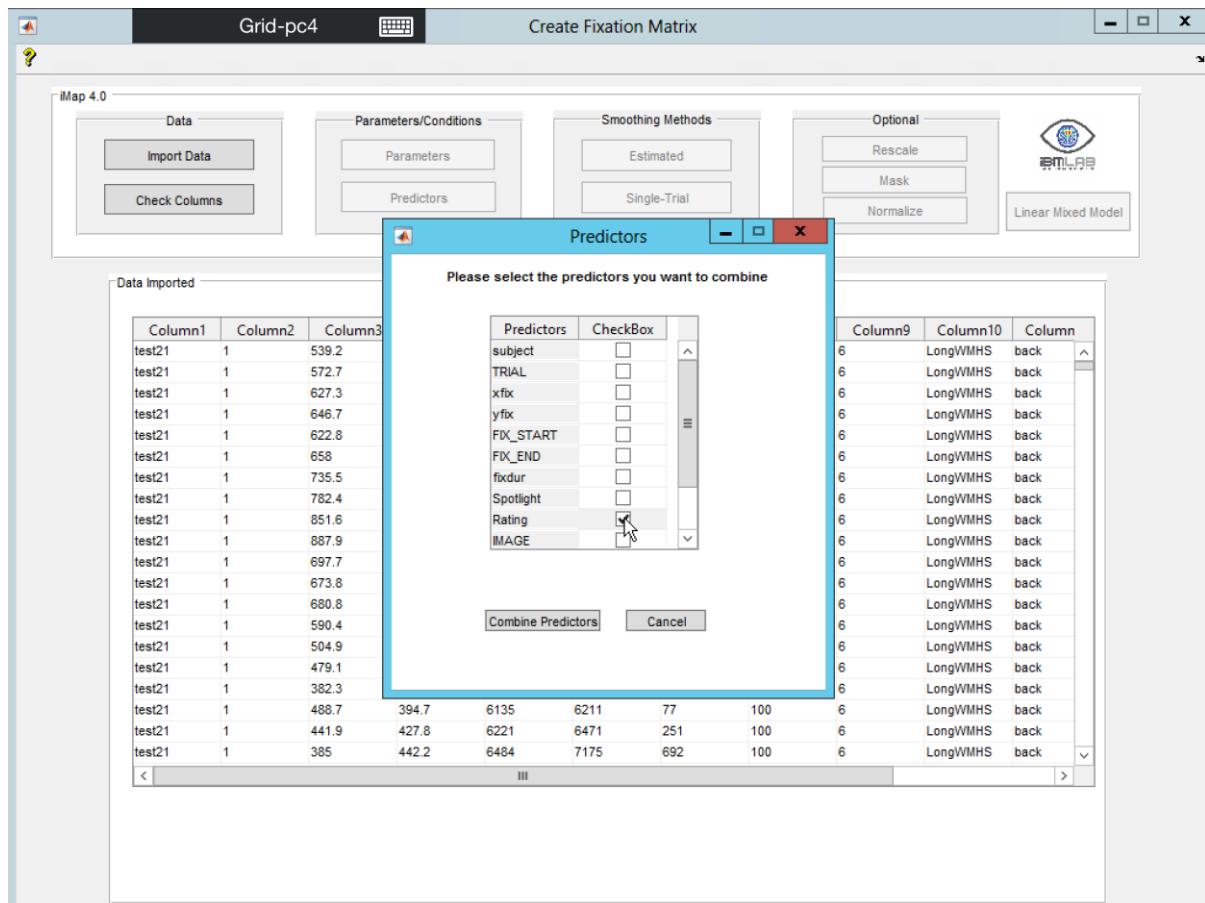




After clicking “**Continue**”, a pop-up will appear for creating new predictors



This is for the cases that user would like to create a categorical predictor from an existing continuous predictor. For example, the following screen shots show how to transfer “**Rating**” into a categorical predictor “**RatingCat**”:



Grid-pc4 Create Fixation Matrix

iMap 4.0

Data Imported

	Column1	Column2	Column3
test21	1	539.2	
test21	1	572.7	
test21	1	627.3	
test21	1	646.7	
test21	1	622.8	
test21	1	658	
test21	1	735.5	
test21	1	782.4	
test21	1	851.6	
test21	1	887.9	
test21	1	697.7	
test21	1	673.8	
test21	1	680.8	
test21	1	590.4	
test21	1	504.9	
test21	1	479.1	
test21	1	382.3	
test21	1	488.7	394
test21	1	441.9	427
test21	1	385	442

Predictors

Please select the predictors you want to combine

Predictors CheckBox

subject											
0	<input type="checkbox"/>										
10	<input type="checkbox"/>										
2	<input type="checkbox"/>										
3	<input checked="" type="checkbox"/>										
4	<input type="checkbox"/>										
5	<input checked="" type="checkbox"/>										
6	<input type="checkbox"/>										
7	<input type="checkbox"/>										
8	<input type="checkbox"/>										
9	<input type="checkbox"/>										

Rating

Enter the name of this new predictor

RatingCat

OK Cancel

Column9 Column10 Column

6	LongWMHS	back	ck
4	<input type="checkbox"/>		ck
5	<input type="checkbox"/>		ck
6	<input type="checkbox"/>		ck
7	<input type="checkbox"/>		ck
8	<input type="checkbox"/>		ck
9	<input type="checkbox"/>		ck

Validate Cancel

Grid-pc4 Create Fixation Matrix

iMap 4.0

Data Imported

fix	FIX_START	FIX_END	fixdur	Spotlight	Rating	IMAGE	Position	EYE_USED	Name of file(s)	RatingCat
7	342	336	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
357	519	163	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
559	840	282	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
862	1319	458	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
1335	1601	267	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
1621	2141	521	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
2186	2399	214	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
2416	2703	288	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
2737	2990	254	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
3004	3529	526	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
3579	3776	198	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
3809	4049	241	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
4069	4336	268	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
4358	4536	179	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
4564	5023	460	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
5066	6038	973	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
6063	6099	37	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
6135	6211	77	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
6221	6471	251	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	
6484	7175	692	100	6	LongWMHS	back	RIGHT	data_subset.txt	10&6&7&8&9	

Parameters

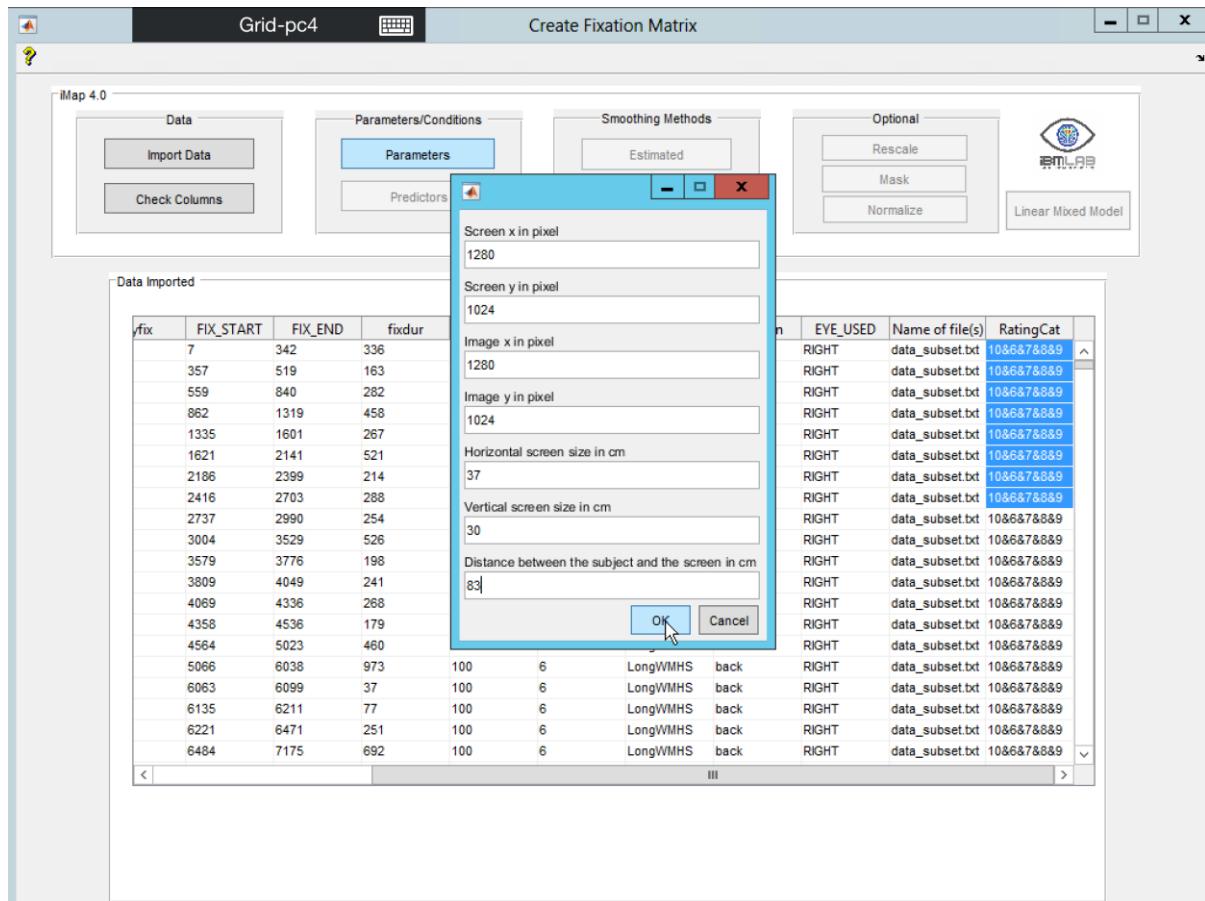
You need to specify the following parameters:

Screen resolution in your experiment (x and y), in the current example is 1280*1024.

The resolution of the presented stimuli during experiment (in pixel), here is also 1280*1024.

Screen size in centimeters, in this case 37*30 cm.

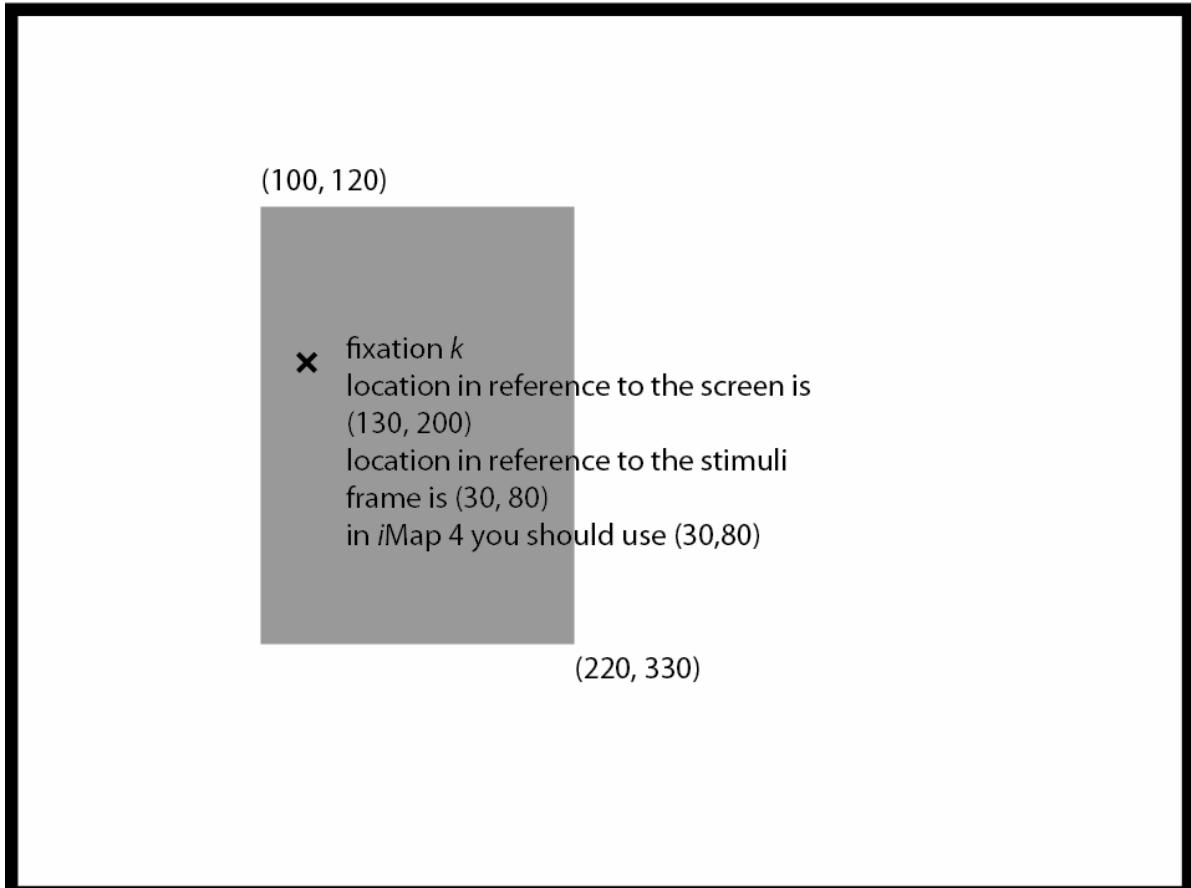
Participant distance to the screen (83 cm).



The parameters are mandatory to be filled before proceeding.

Please note: the fixation X and Y from your input file should be a relative fixation location in reference with the stimuli. See below as an example.

(0, 0)



(100, 120)

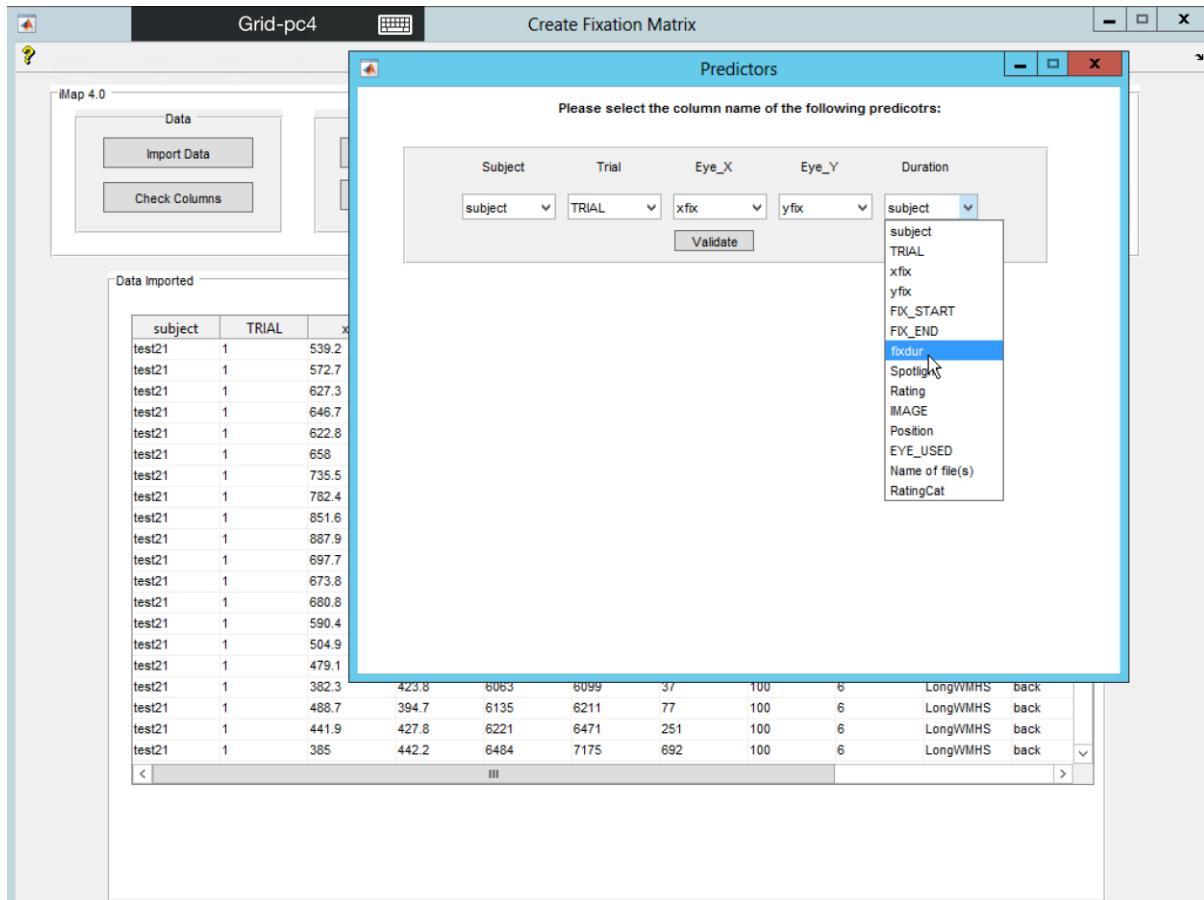
- ✖ fixation *k*
- location in reference to the screen is (130, 200)
- location in reference to the stimuli frame is (30, 80)
- in iMap 4 you should use (30,80)

(220, 330)

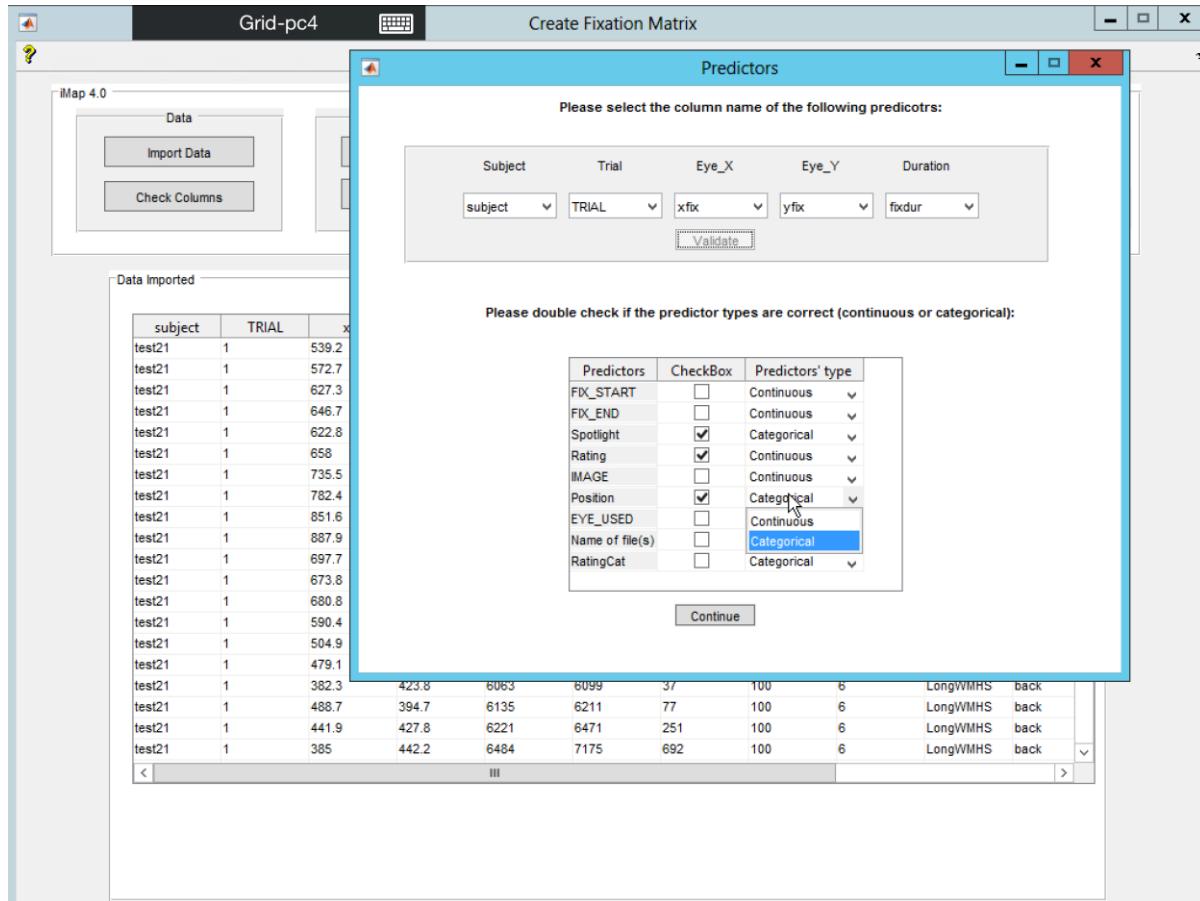
(Screen resolution x and y)

Predictors

First define the columns that refer to Subject, Trial, fixation X, Y and Duration.



Then iMap 4 will then ask for the predictors you would like to include in the modeling (your experiment conditions – fixed effects, and random covariance you would like to control – random effects). The selected variables will be saved in the PredictorM as one of the output files.



Please note: verify carefully whether you would like to treat your predictors as continuous (e.g., subjective rating) or categorical (e.g., gender). By default, the type of predictor is set to categorical if it has less than 5 levels.

A pop-up window will appear for you to specify the fixation map type (the value on the map represents either fixation durations or fixation numbers). Moreover, you could include or exclude specific fixation (e.g., just to model the first fixation).

Grid-pc4 Create Fixation Matrix

iMap 4.0

Data Imported

subject	TRIAL	xfix	yfix	FIX_START	FIX_END	fixdur	Spotlight	Rating	IMAGE	Position
test21	1	539.2	522	7	342	336	100	6	LongWMHS	back
test21	1	572.7	504.5	357	519	163	100	6	LongWMHS	back
test21	1	627.3	292.5	559	840	282	100	6	LongWMHS	back
test21	1	646.7	201.2	862	1319	458	100	6	LongWMHS	back
test21	1	622.8	128.2	1335	1601	267	100	6	LongWMHS	back
test21	1	658	73.3	162					LongWMHS	back
test21	1	735.5	236.8	218					LongWMHS	back
test21	1	782.4	290.9	241					LongWMHS	back
test21	1	851.6	415.6	273					LongWMHS	back
test21	1	887.9	447.3	300					LongWMHS	back
test21	1	697.7	288.3	357					LongWMHS	back
test21	1	673.8	181.9	380					LongWMHS	back
test21	1	680.8	125.8	406					LongWMHS	back
test21	1	590.4	159.4	435					LongWMHS	back
test21	1	504.9	286.9	456					LongWMHS	back
test21	1	479.1	366.7	506					LongWMHS	back
test21	1	382.3	423.8	6063	6099	37	100	6	LongWMHS	back
test21	1	488.7	394.7	6135	6211	77	100	6	LongWMHS	back
test21	1	441.9	427.8	6221	6471	251	100	6	LongWMHS	back
test21	1	385	442.2	6484	7175	692	100	6	LongWMHS	back

Fixation Options

What type of fixation map would you like?

Duration Map Number of Fixation Map

Do you want to use/exclude specific fixations conditions?

Specific Exclude All fixations

Validate

Grid-pc4 Create Fixation Matrix

iMap 4.0

Data Imported

subject	TRIAL	xfix	yfix	Fixations	Checkbox	Spotlight	Rating	IMAGE	Position
test21	1	539.2	522	Fixation 1	<input checked="" type="checkbox"/>	0	6	LongWMHS	back
test21	1	572.7	504.5	Fixation 2	<input type="checkbox"/>	0	6	LongWMHS	back
test21	1	627.3	292.5	Fixation 3	<input type="checkbox"/>	0	6	LongWMHS	back
test21	1	646.7	201.2	Fixation 4	<input type="checkbox"/>	0	6	LongWMHS	back
test21	1	622.8	128.2	Fixation 5	<input type="checkbox"/>	0	6	LongWMHS	back
test21	1	658	73.3	Fixation 6	<input type="checkbox"/>	0	6	LongWMHS	back
test21	1	735.5	236.8	Fixation 7	<input type="checkbox"/>	0	6	LongWMHS	back
test21	1	782.4	290.9	Fixation 8	<input type="checkbox"/>	0	6	LongWMHS	back
test21	1	851.6	415.6	Fixation 9	<input type="checkbox"/>	0	6	LongWMHS	back
test21	1	887.9	447.3					LongWMHS	back
test21	1	697.7	288.3					LongWMHS	back
test21	1	673.8	181.9					LongWMHS	back
test21	1	680.8	125.8					LongWMHS	back
test21	1	590.4	159.4					LongWMHS	back
test21	1	504.9	286.9					LongWMHS	back
test21	1	479.1	366.7					LongWMHS	back
test21	1	382.3	423.8					LongWMHS	back
test21	1	488.7	394.7					LongWMHS	back
test21	1	441.9	427.8					LongWMHS	back
test21	1	385	442.2					LongWMHS	back

Fixations

What type of fixation map would you like?

Duration Map Number of Fixation Map

Do you want to use/exclude specific fixations conditions?

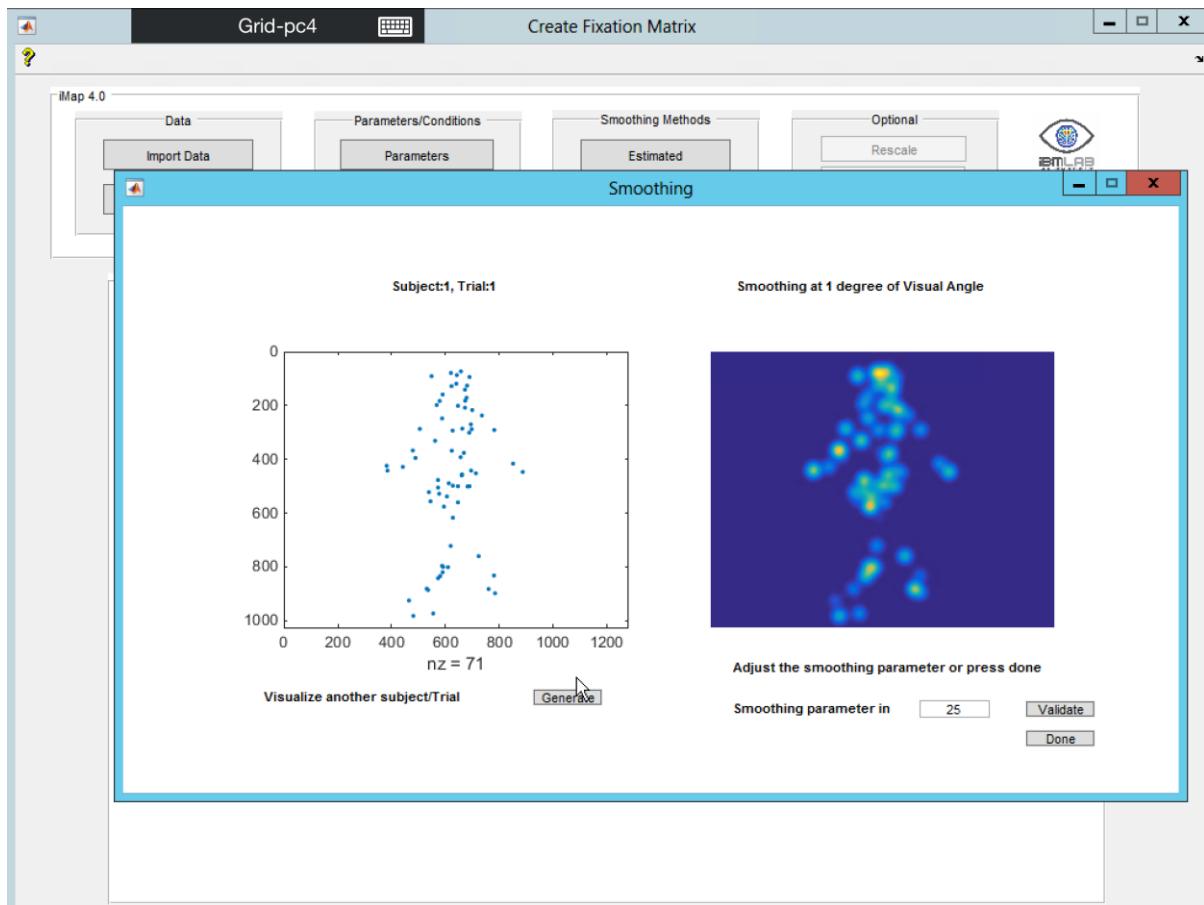
Specific Exclude All fixations

Validate

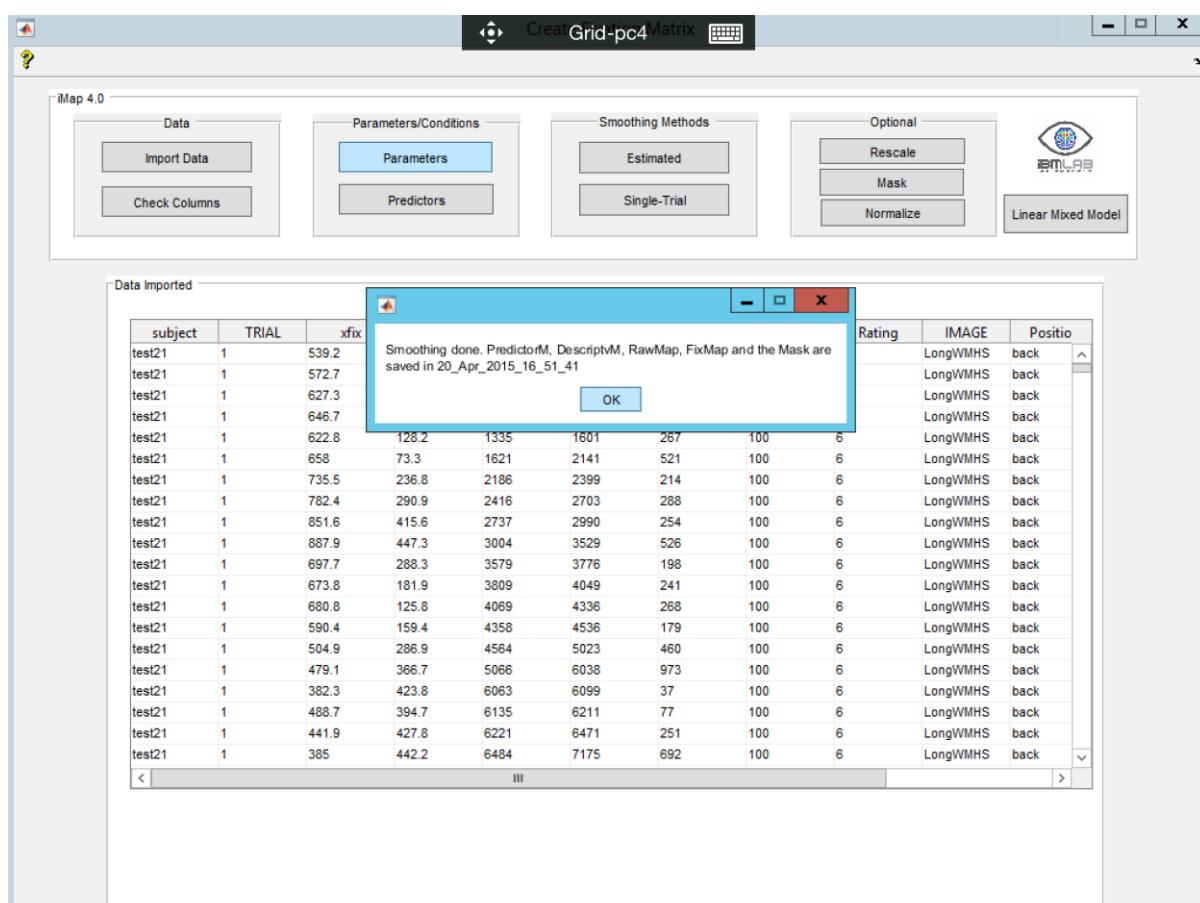
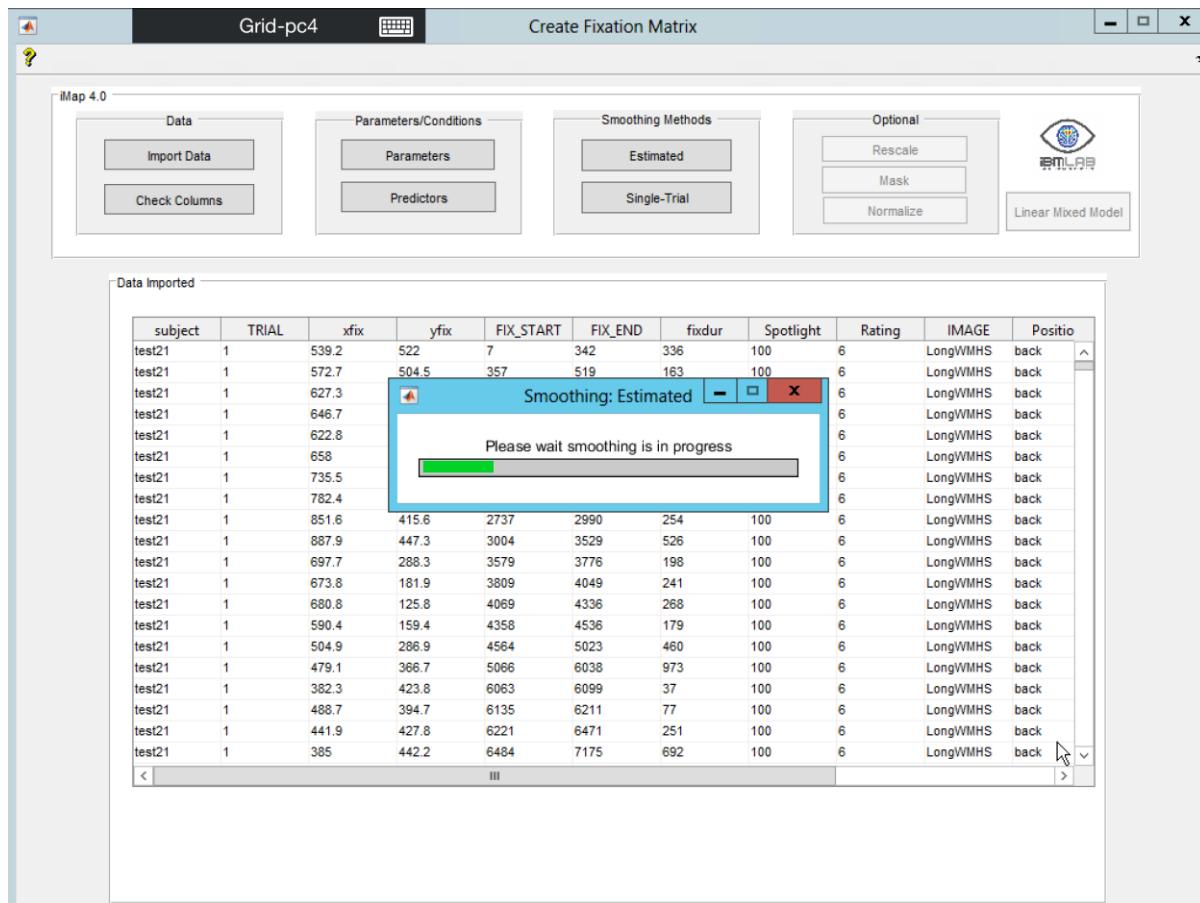
Smoothing

This step produces a 3D smoothed fixation map (size number_of_item * xSize * ySize). Raw fixation map is smoothed by convolve with a Gaussian Kernel in two ways in iMap 4: (a) the estimated method that the first dimension coded for each condition in each participant, (b) Single-trial method that the first dimension coded for each single trial.

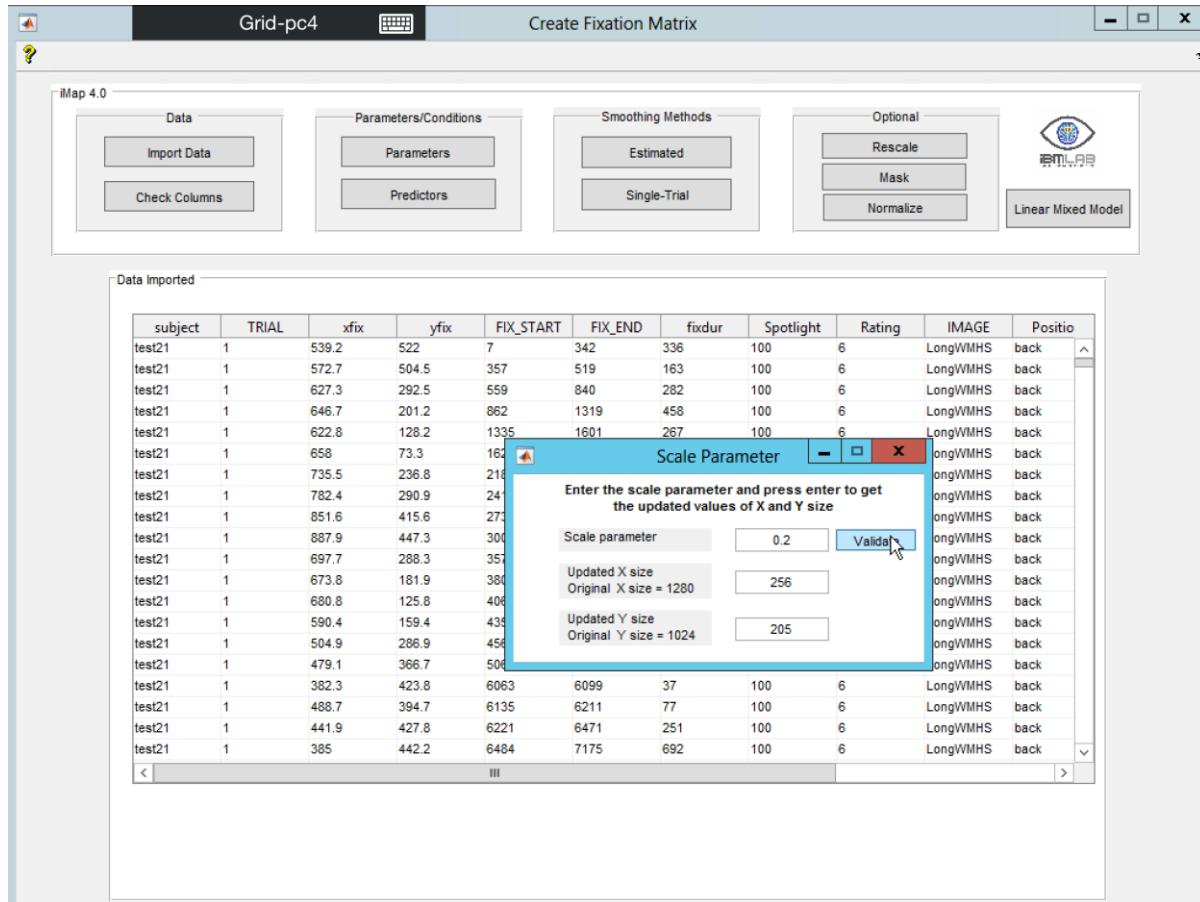
A pop-up will first appear for you to decide the smoothing parameter. The default in iMap 4 is 1° of visual angle. iMap 4 will automatically convert the visual angle into pixel value, notice that here in this example we will set it to 20 pixel.



You can click “**Generate**” on the left to visualize another subject/Trial, or you can change the parameter and click “**Validate**” to see the smoothing effect. The smoothing will begin when you click on “**Done**”. Finally, a pop-up will show you the directory where the resulting matrixes have been saved.



Alternatively, you can select the Single-trial method. It is the most appropriate if you have a continuous predictor variating at single-trial level. You will need to perform rescaling first to reduce memory usage and computational time. A pop-up will lead you to perform rescaling. (It's the same one when you click on “**Rescale**” in Optional). After that, the procedure will be identical to the estimated method.

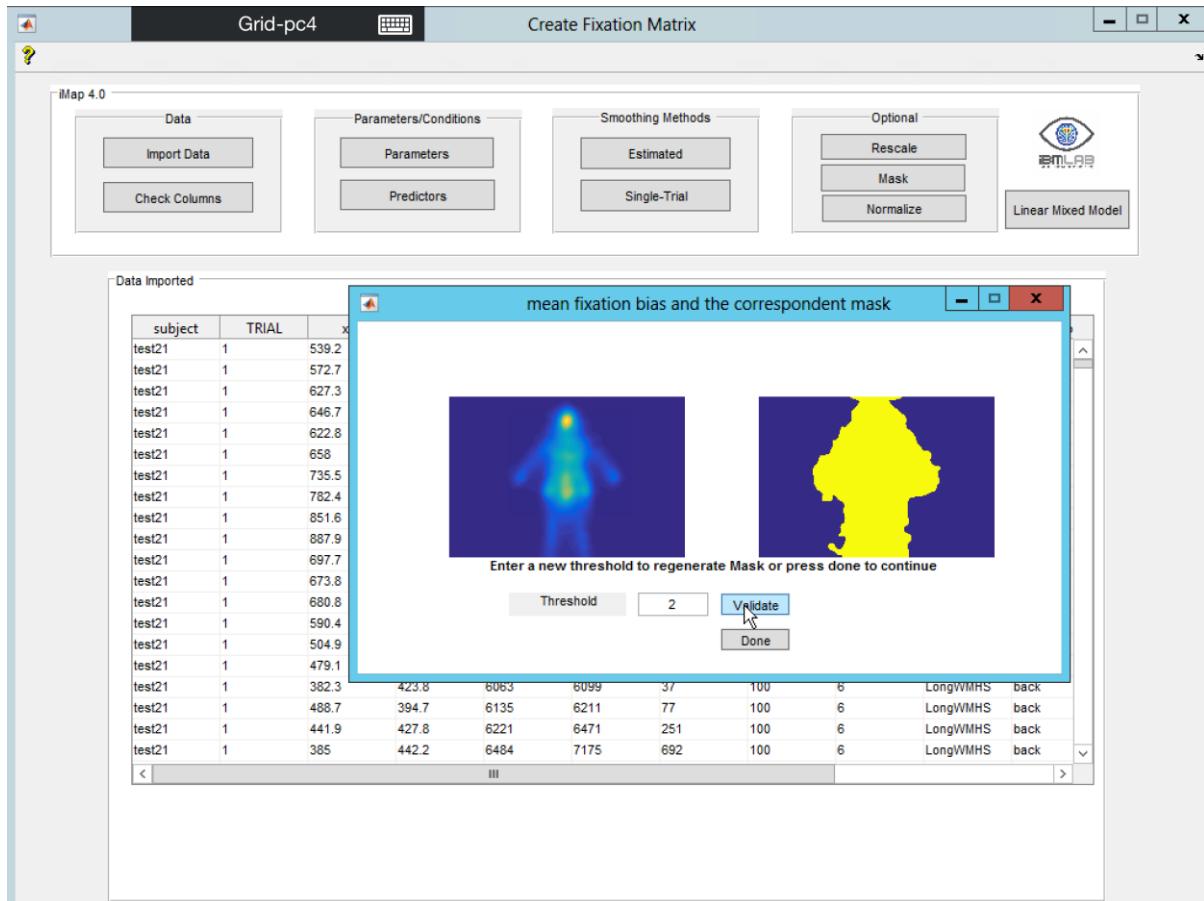


Please note: you can find an example script using the Single-Trial method to analyze a computer generated data in the iMap 4 installation folder.

Optional

Optional features include the aforementioned “**Rescale**”, “**Mask**” generation and spatial “**Normalization**” on the fixation map.

“**Mask**”: In iMAP4, model fitting is only performed within a given mask, as the sparse outliers in 2D fixation map are very likely to generate erroneous estimation. The default threshold is the full width at half maximum (FWHM) for the minimal fixation duration after smoothing.

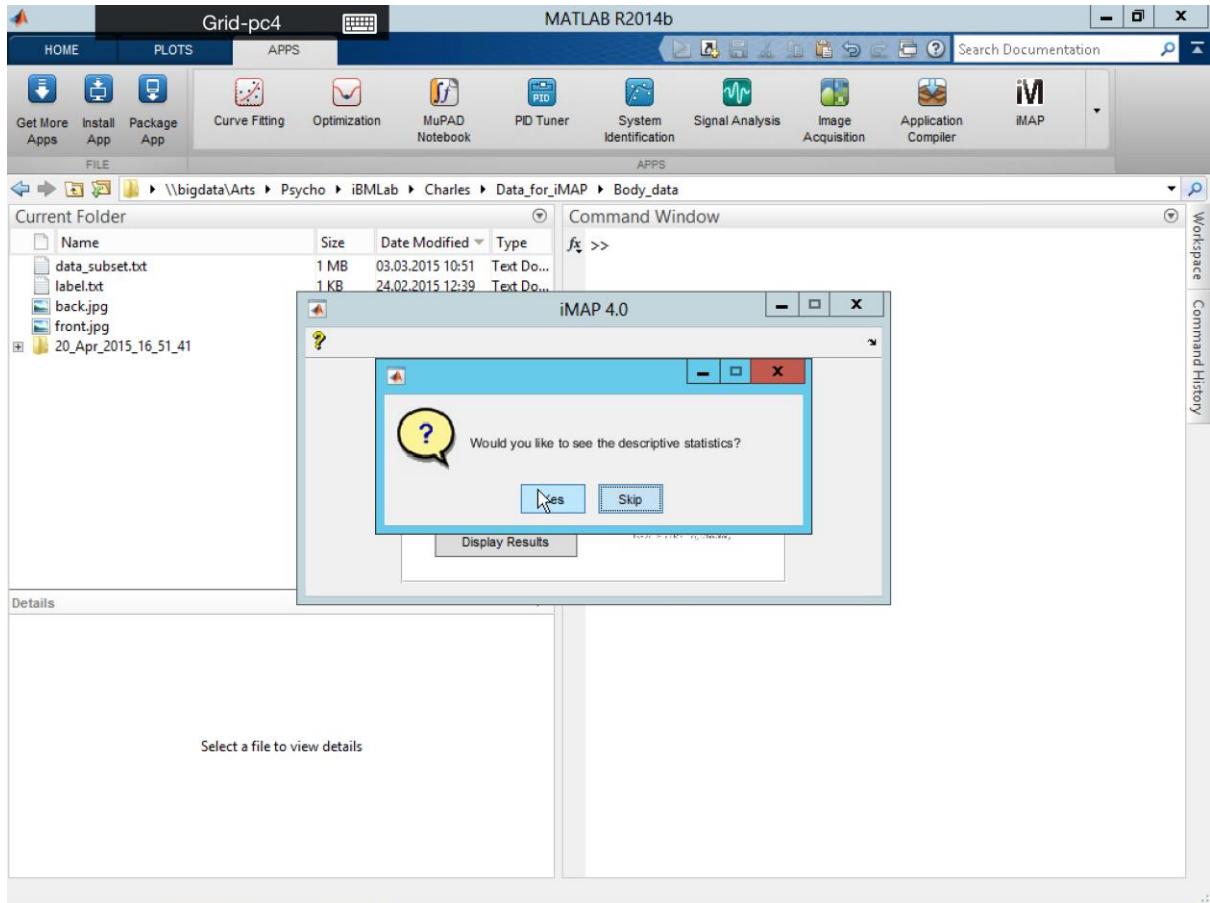


“**Normalization**” (not shown here) could be done either by performing pixel-wise Z-score or divide by total trial/condition duration.

Descriptive Statistics Report

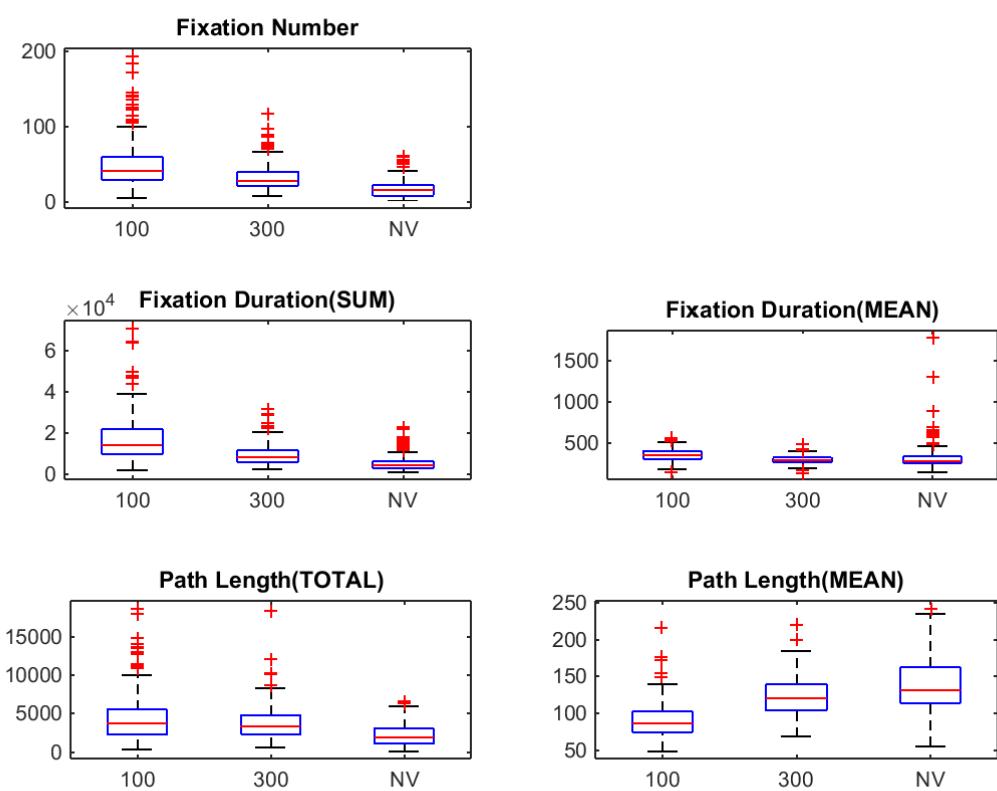
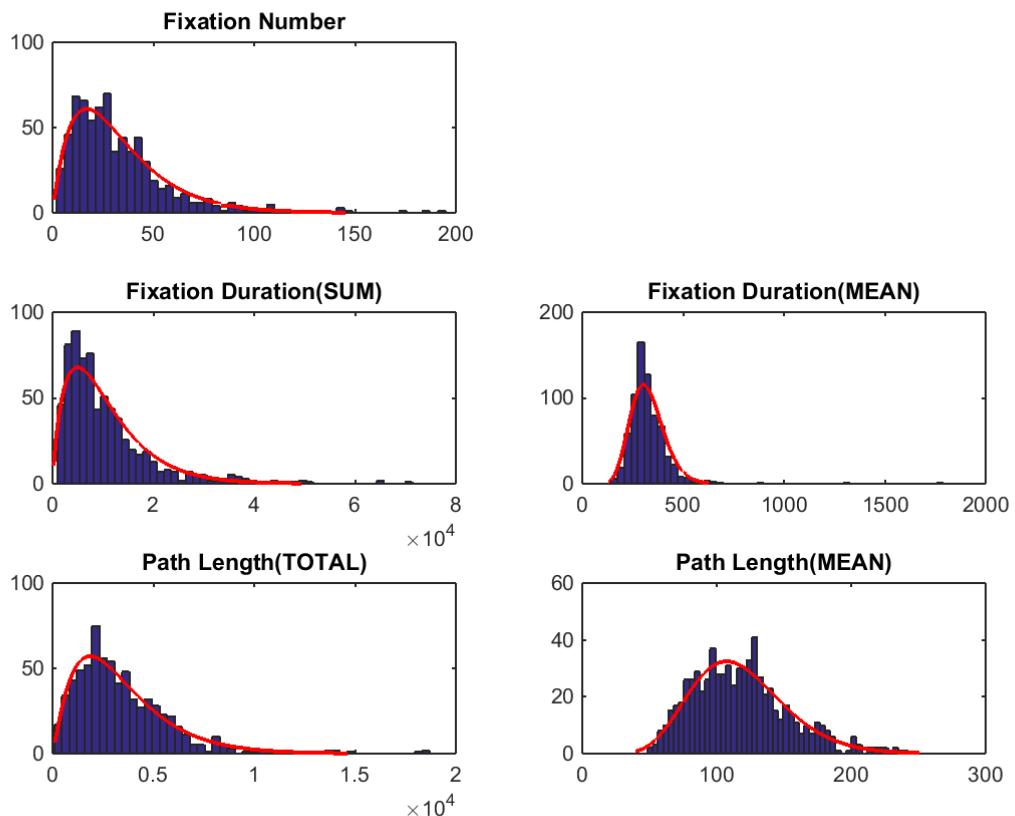
*updated on April 20, 2015

Before proceeding to “**Linear Mixed Model**”, you can get a sense of your dataset by visualizing the descriptive statistics.

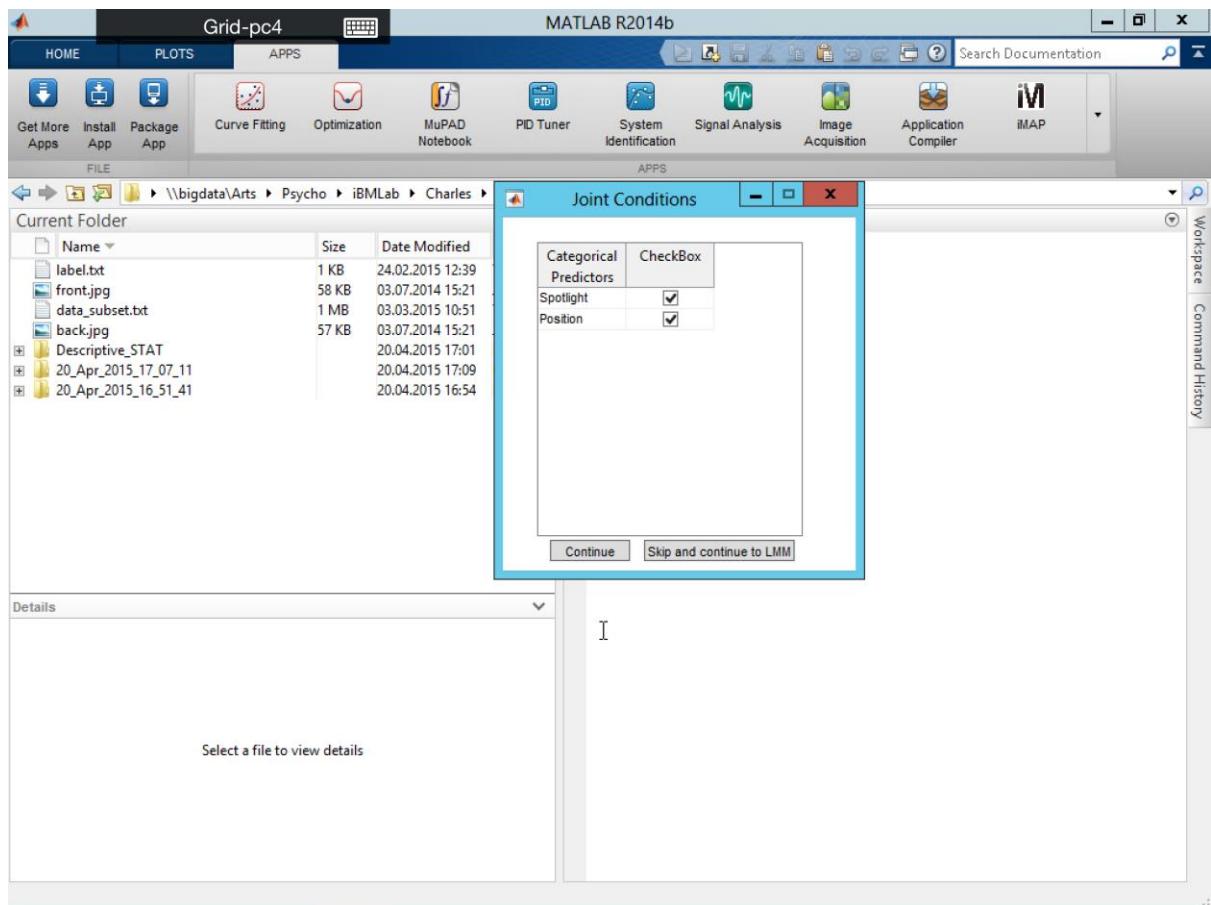


For each of the categorical condition, *iMap4* output the mean fixation map for each level. Descriptive statistics for the following eye movement measurements will be plot in a histogram or boxplot:

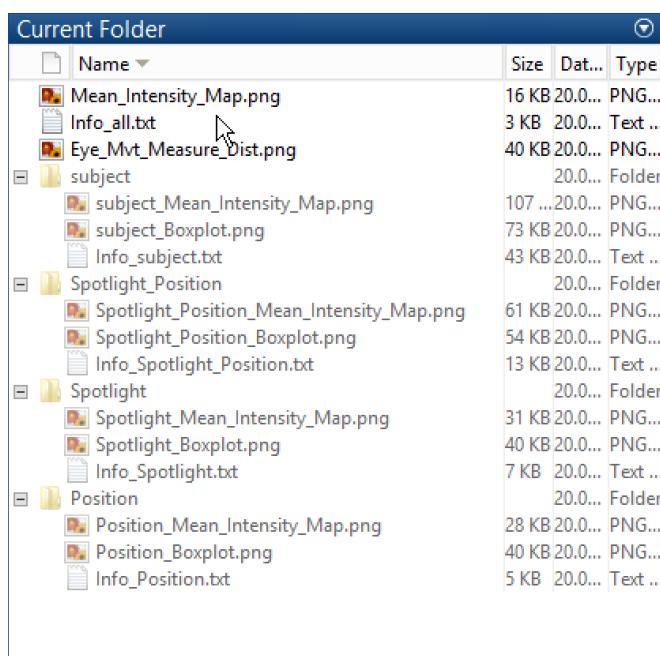
- Number of fixation
- Sum of fixation duration (Total viewing time)
- Mean fixation duration
- Total path length (total eye movement path length in pixel)
- Mean path length



Moreover, you can save the descriptive statistics for all possible combinations of a set of selected conditions.



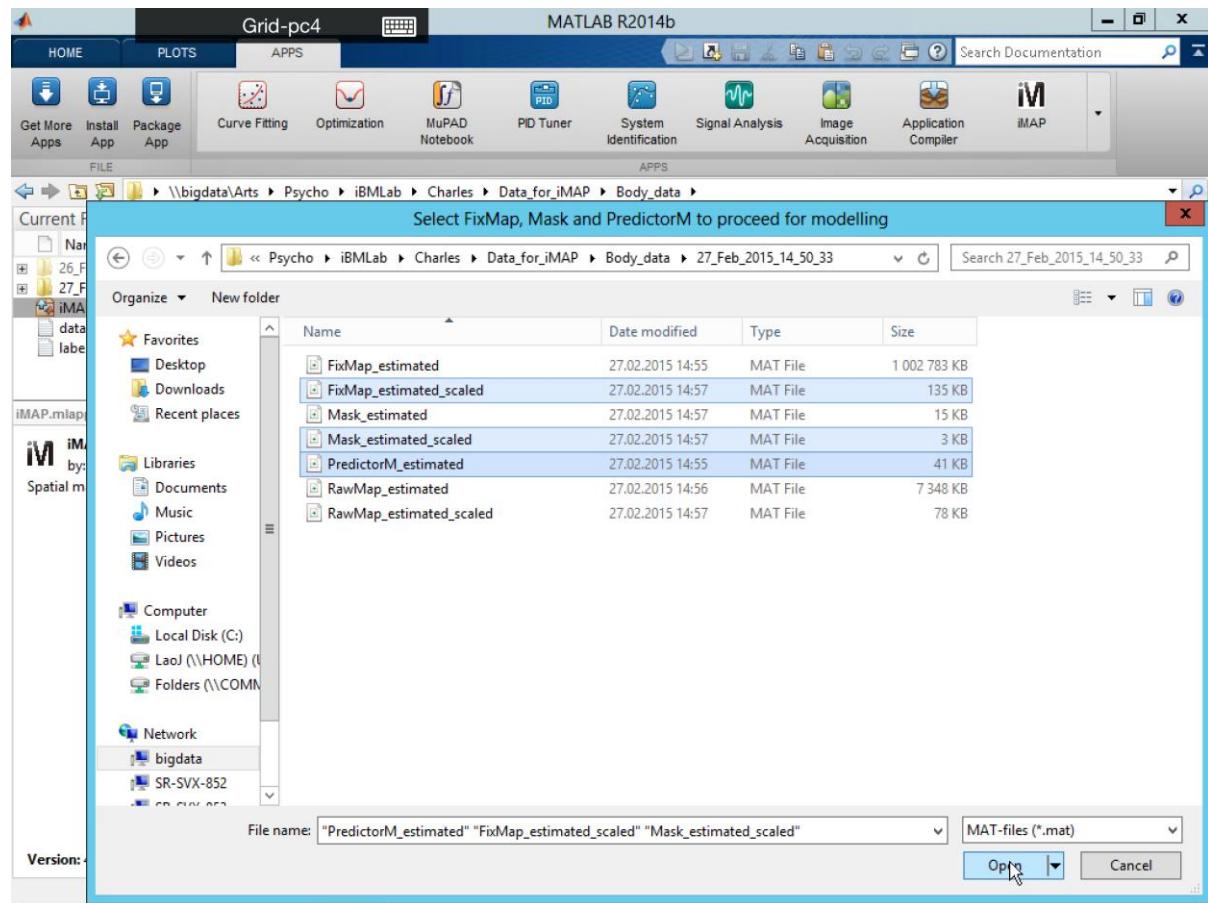
Numeral output and description of the figure could be found in a text file "Info_*.txt". You could find all the saved figure and information under folder './Descriptive_STAT' and its subfolders. Further statistical analysis on these eye movement measurements could be performed by loading the DescriptvM matrix.



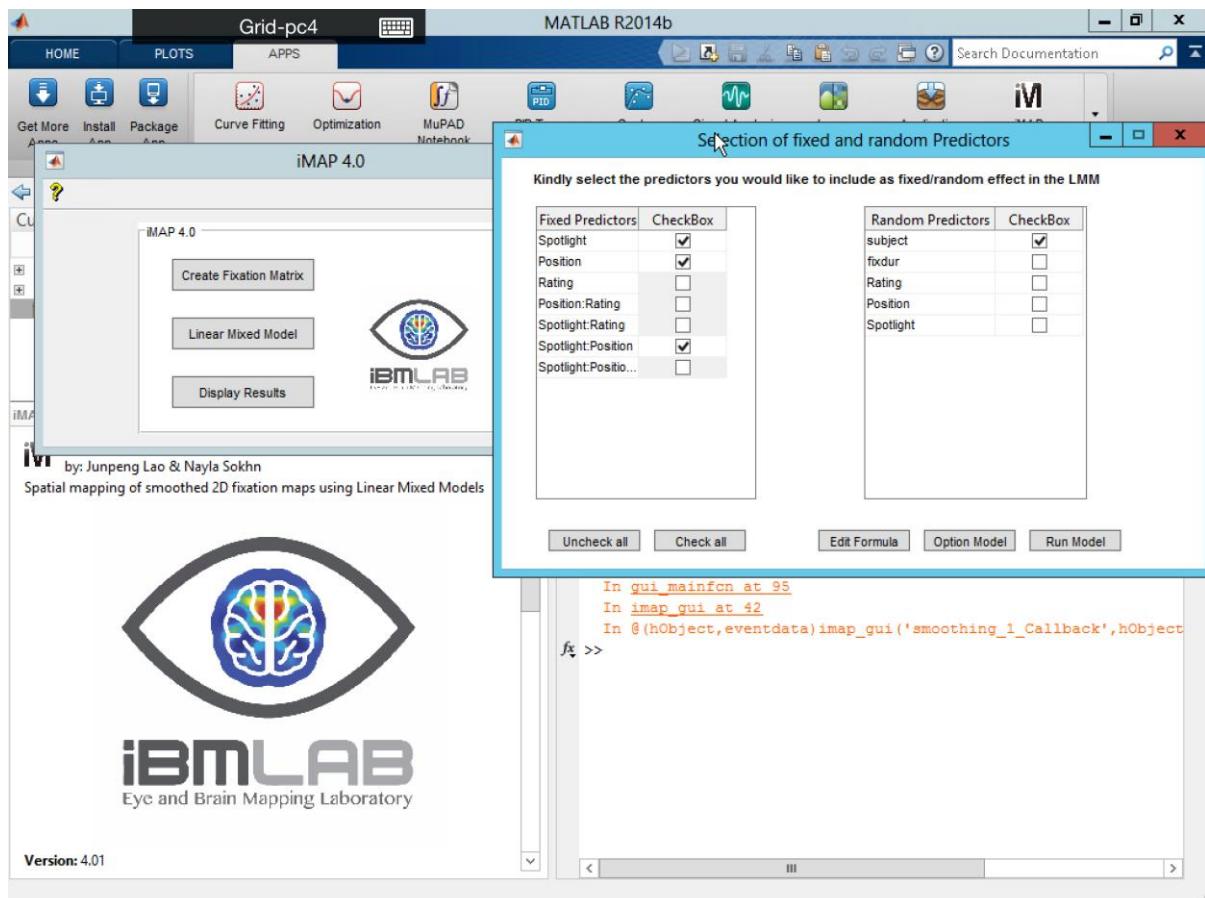
Spatial Mapping Using Linear Mixed Models

The following session will show how to perform the Linear Mixed Modeling, especially how to prepare the syntax inputs.

A pop-up will ask for the already saved FixMap, Mask and PredictorM after you click on the “Linear Mixed Model”.

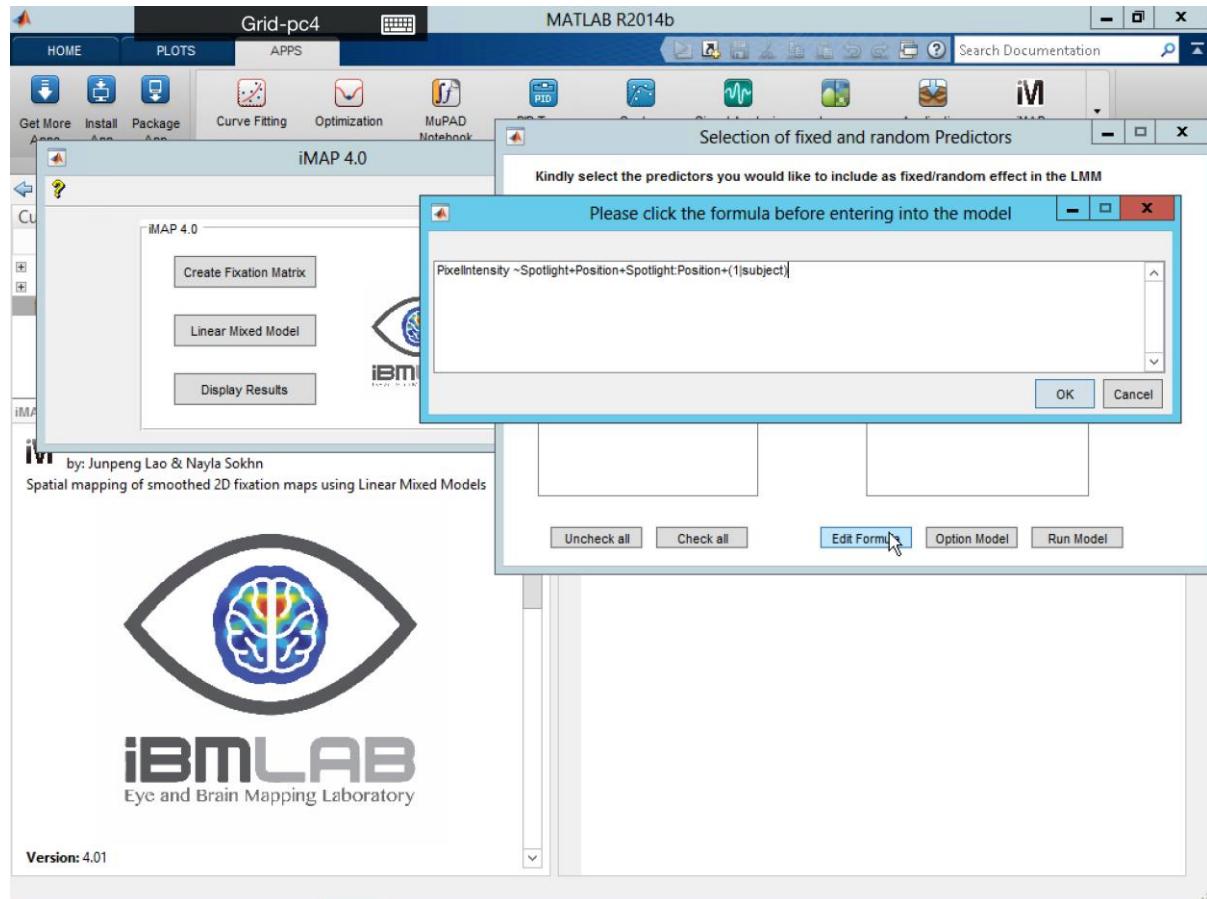


Here you could select your fixed effect (main and/or interaction) and random effect.



The linear formula can be further specified by clicking “**Edit Formula**”. In the following example the formula for the LMM is

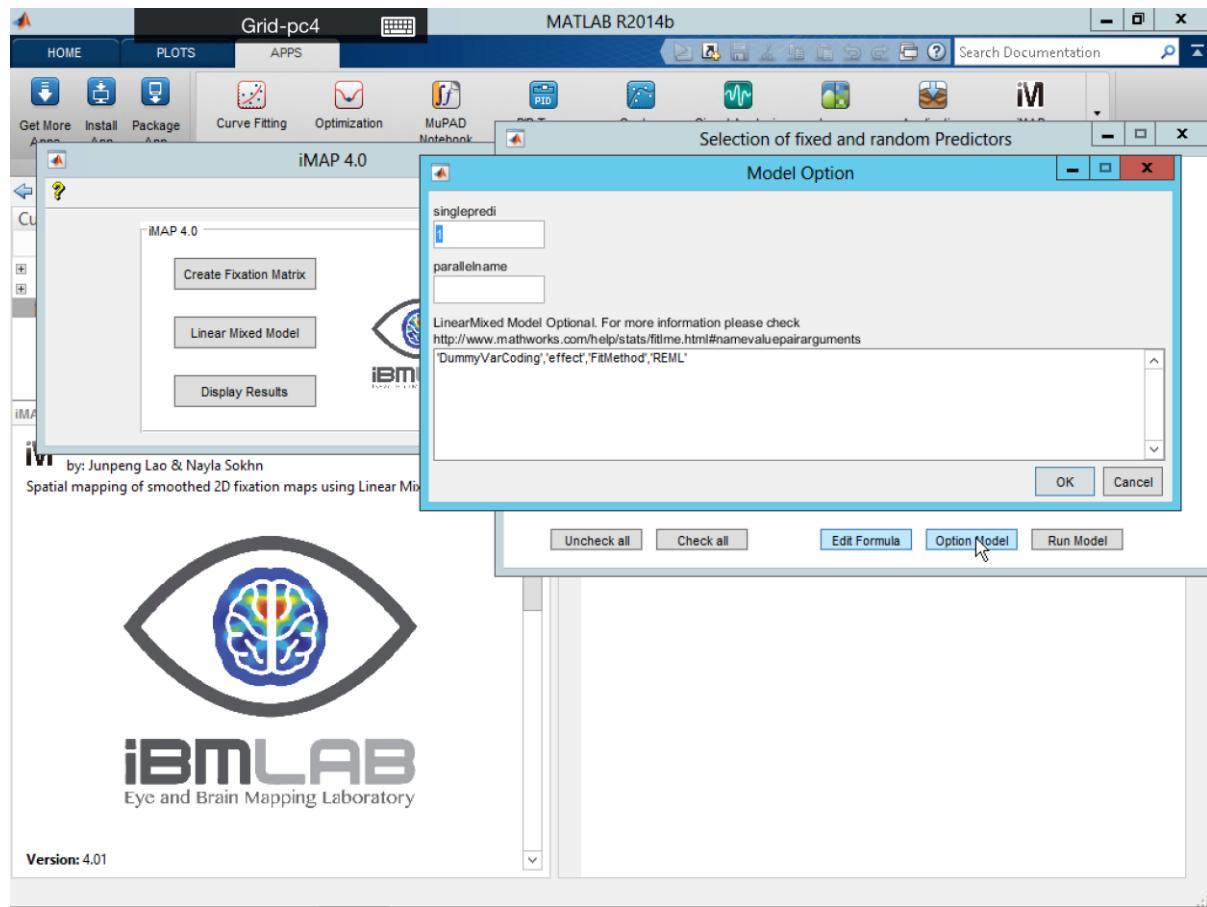
PixelIntensity ~ Spotlight + Position + Spotlight:Position + (fixdur|subject)



If you would like to perform “**Linear Contrast**” later on, set “**singlepredi**” to 1. Also if your machine has access to Distributed Computing Servers you could input the cluster name in “**parallelname**” (*iMap* 4 will connect to local cluster by default if your machine equips with parallel toolbox).

Moreover, you can specify the option for linear mixed model fitting. The input arguments accept by *iMap* 4 is identical to the *LinearMixedModel* class in Matlab. For more information please check:

<http://www.mathworks.com/help/stats/fitlme.html>

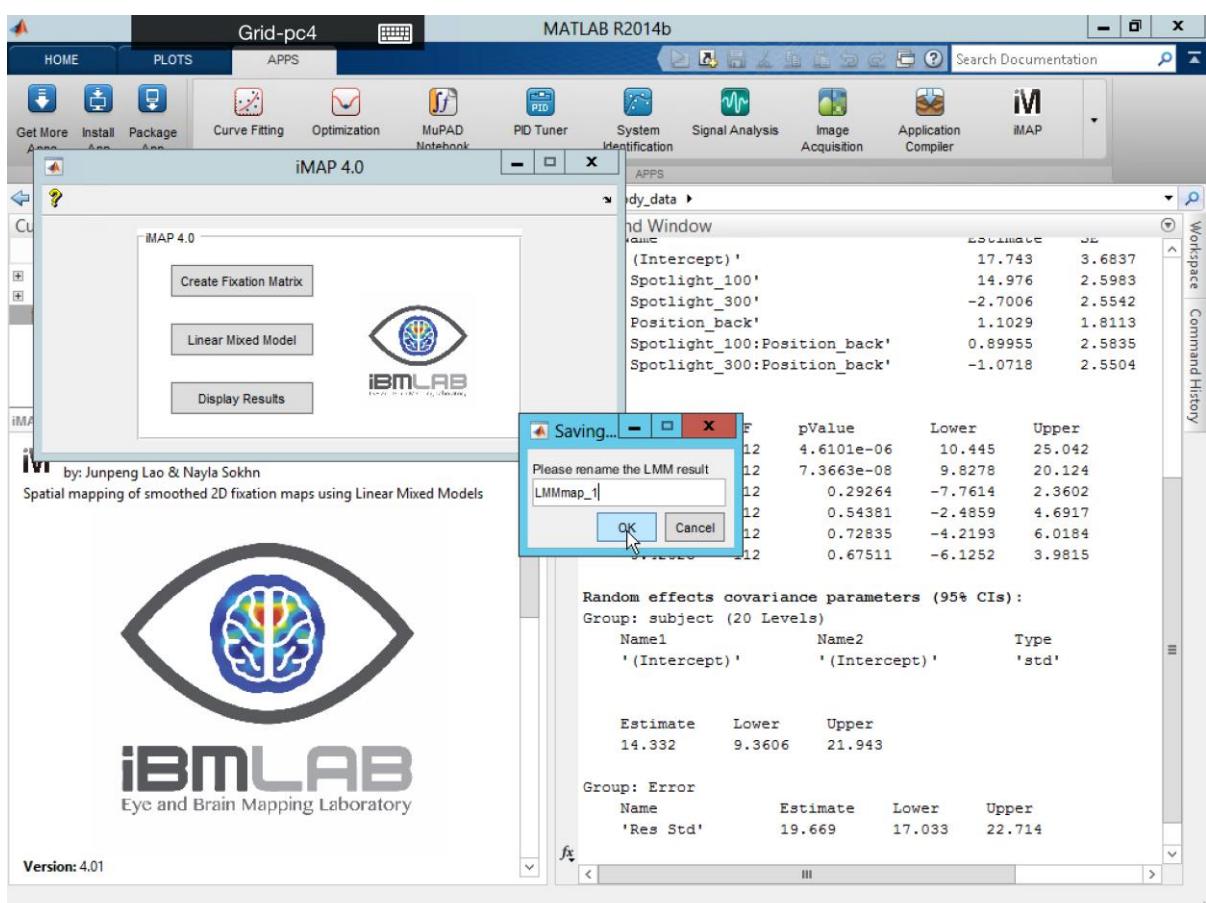
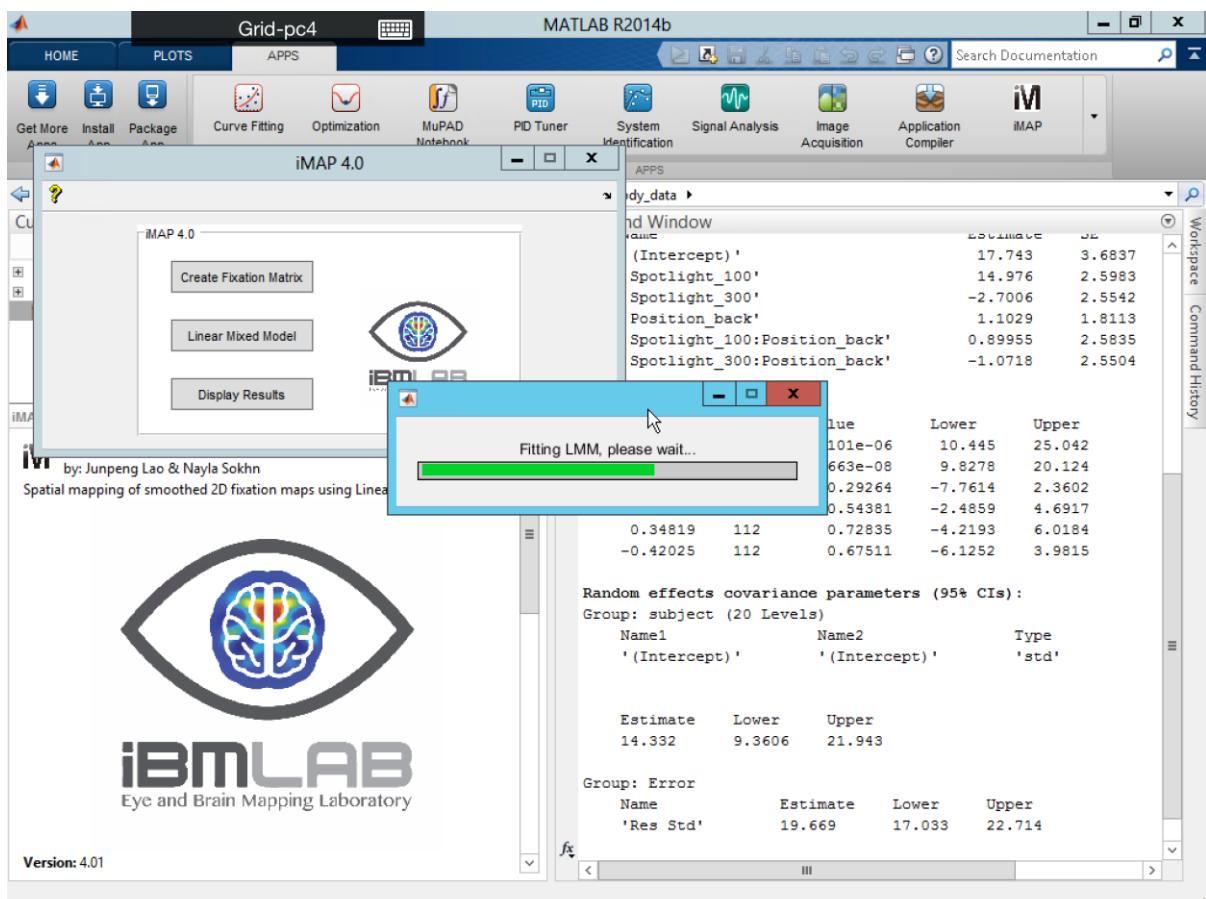


To proceed to the modeling, click “**Run Model**”. A pop-up will prompt you to rename the result for saving when the modeling finishes.

Details on parameter estimation please refer to McCulloch, Searle & Neuhaus (2011) and Pinheiro & Bates (2000) as well as the Matlab help documents

<http://www.mathworks.com/help/stats/estimating-parameters-in-linear-mixed-effects-models.html>

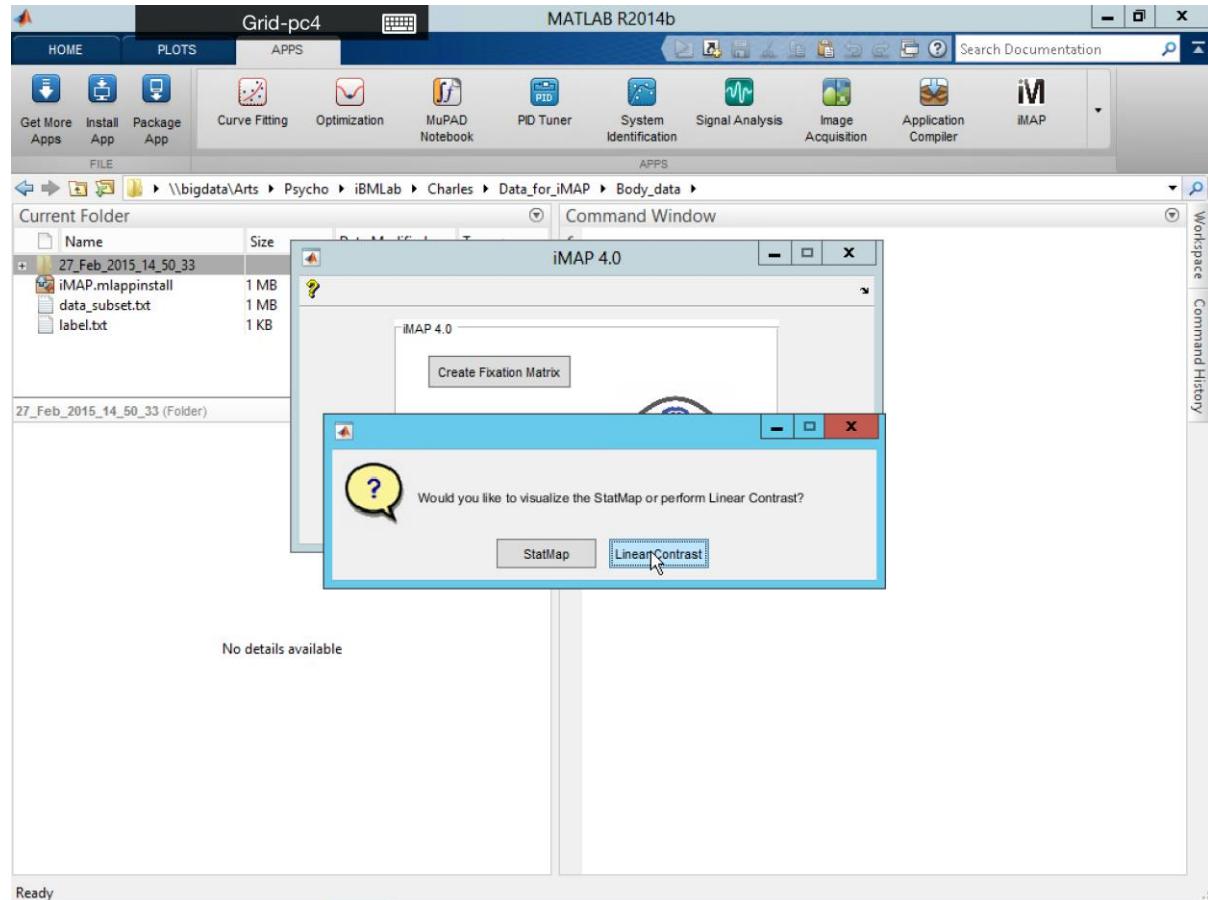
Please note: *iMap* 4 fits a linear mixed model for each pixel within the mask, and it's usually a very slow process. Please be patient when this step is running.

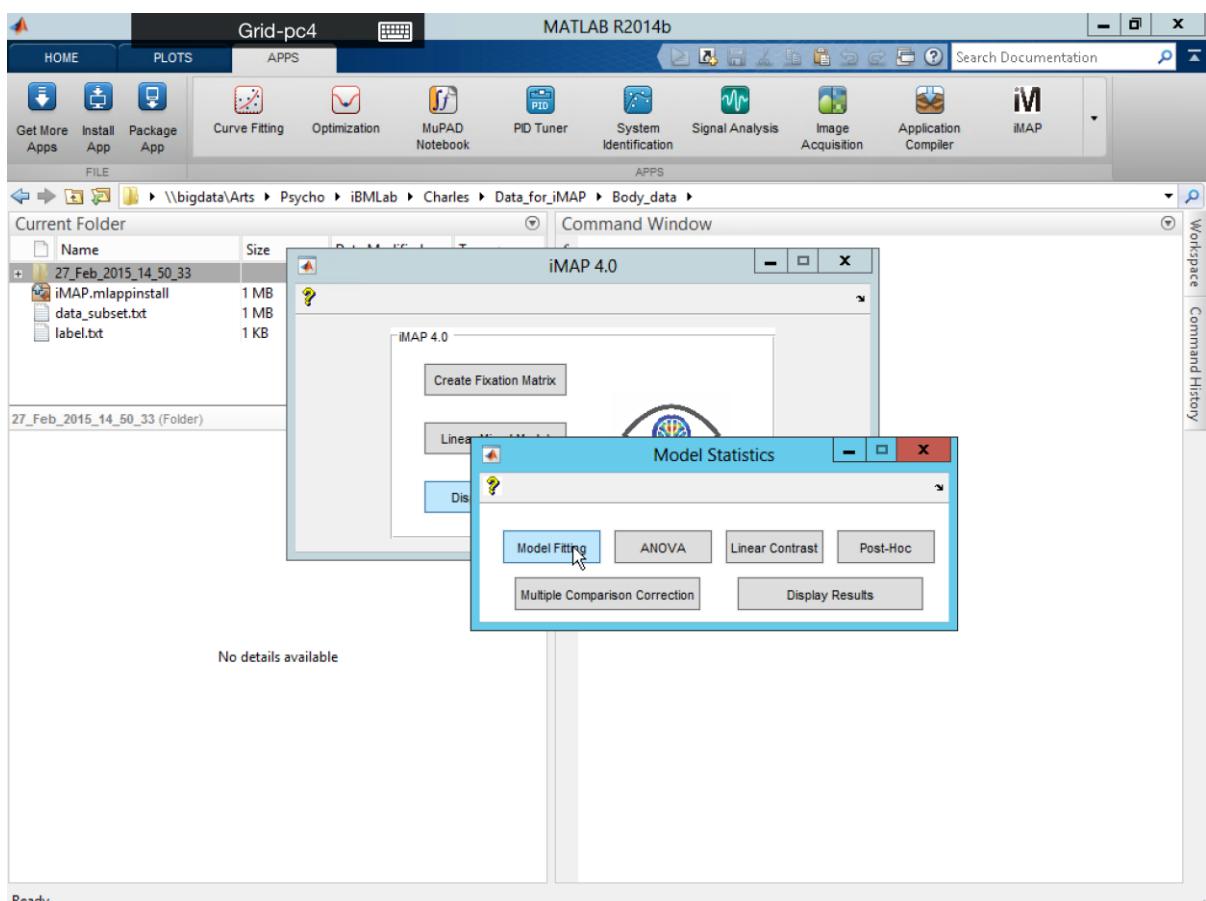
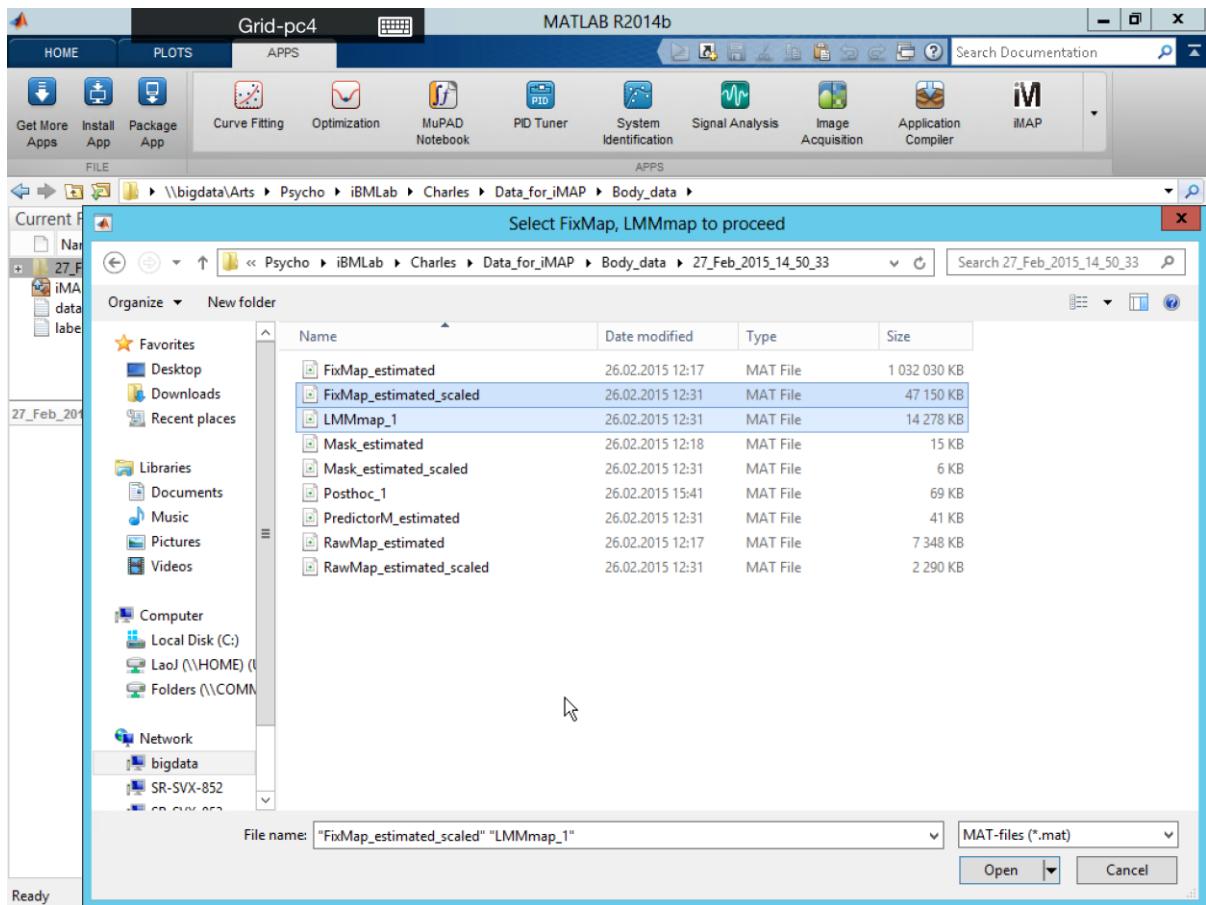


Perform Hypothesis Testings and Display Results

The following session will show how to visualize the Linear Mixed Model result, and how to perform hypothesis testing and multiple comparison correction.

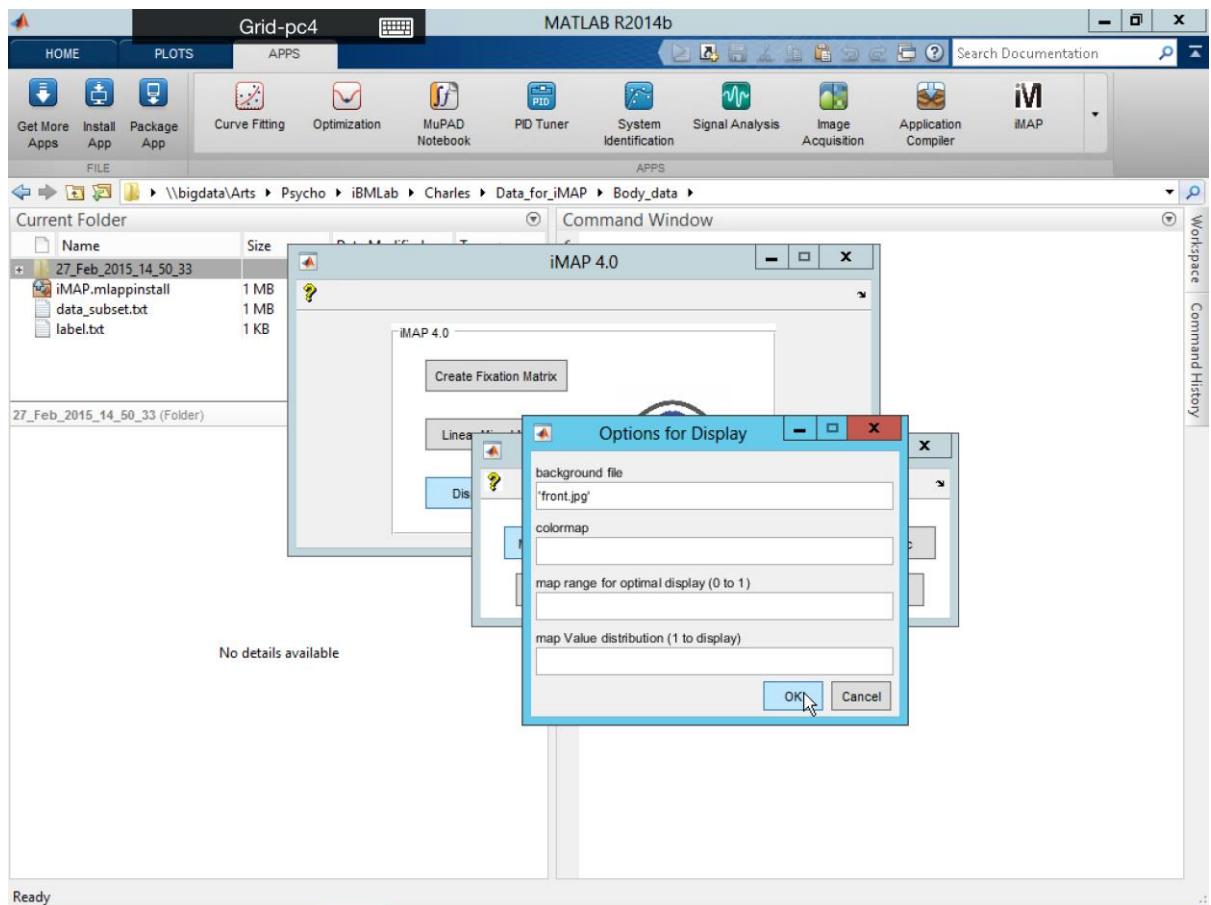
Click “Linear Contrast” and load LMMmap and its correspondent FixMap to continue.

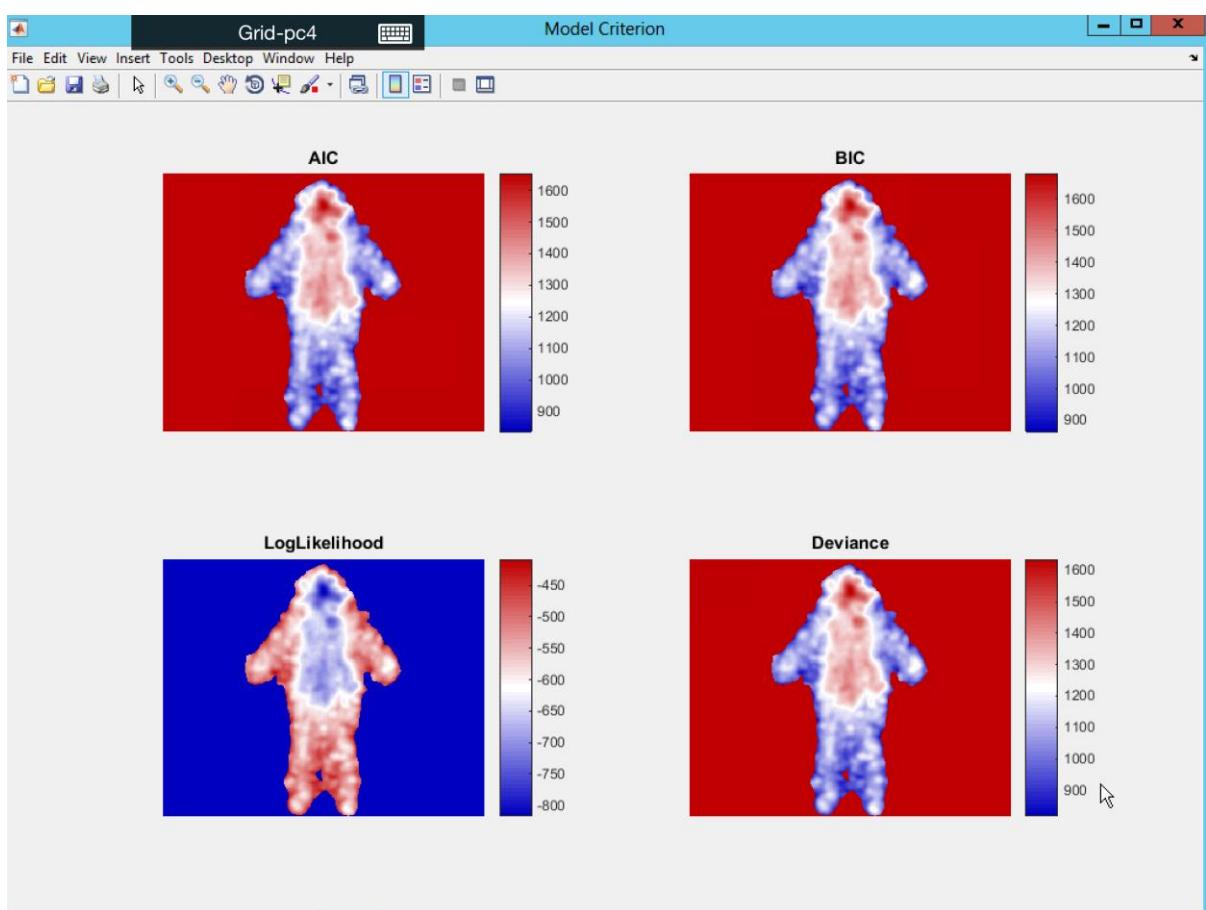
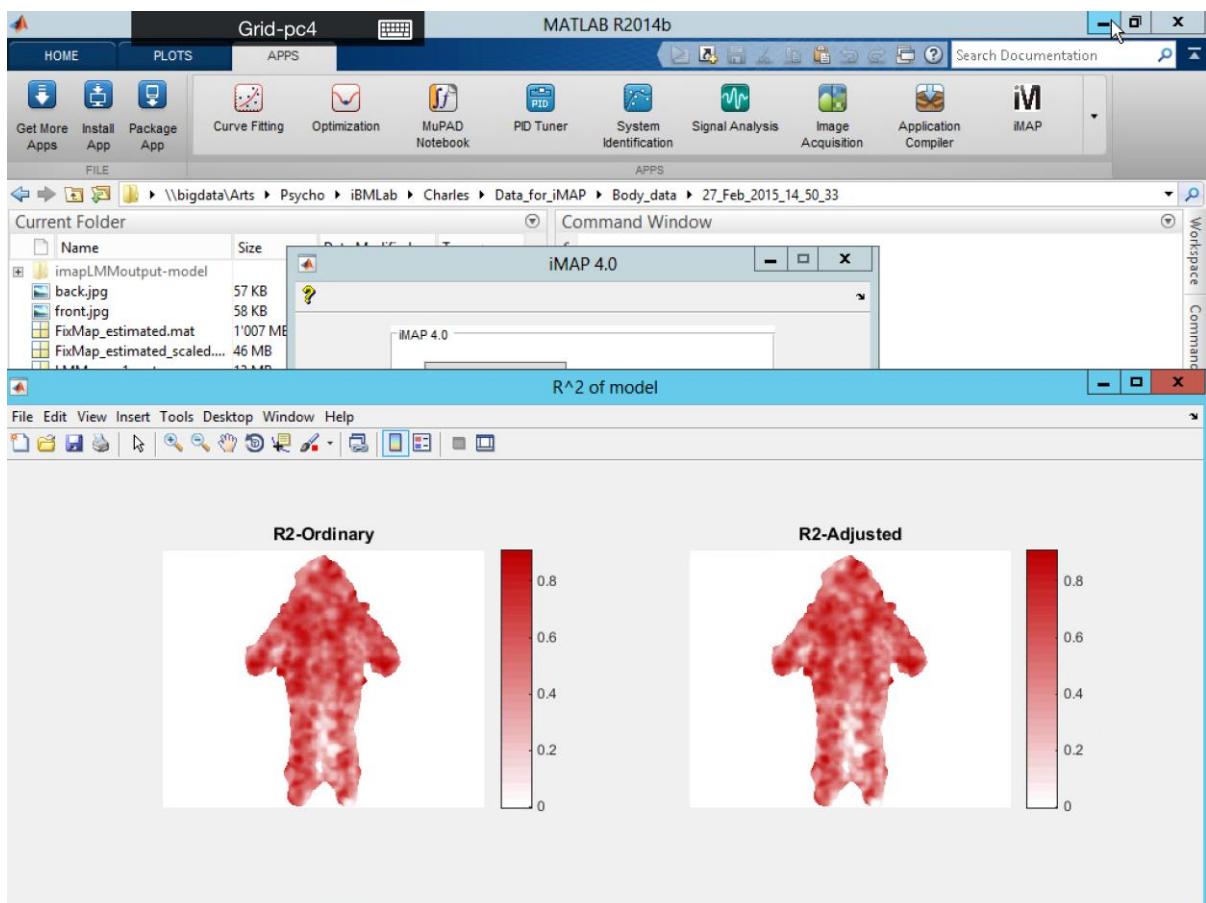




Display Model Fitting

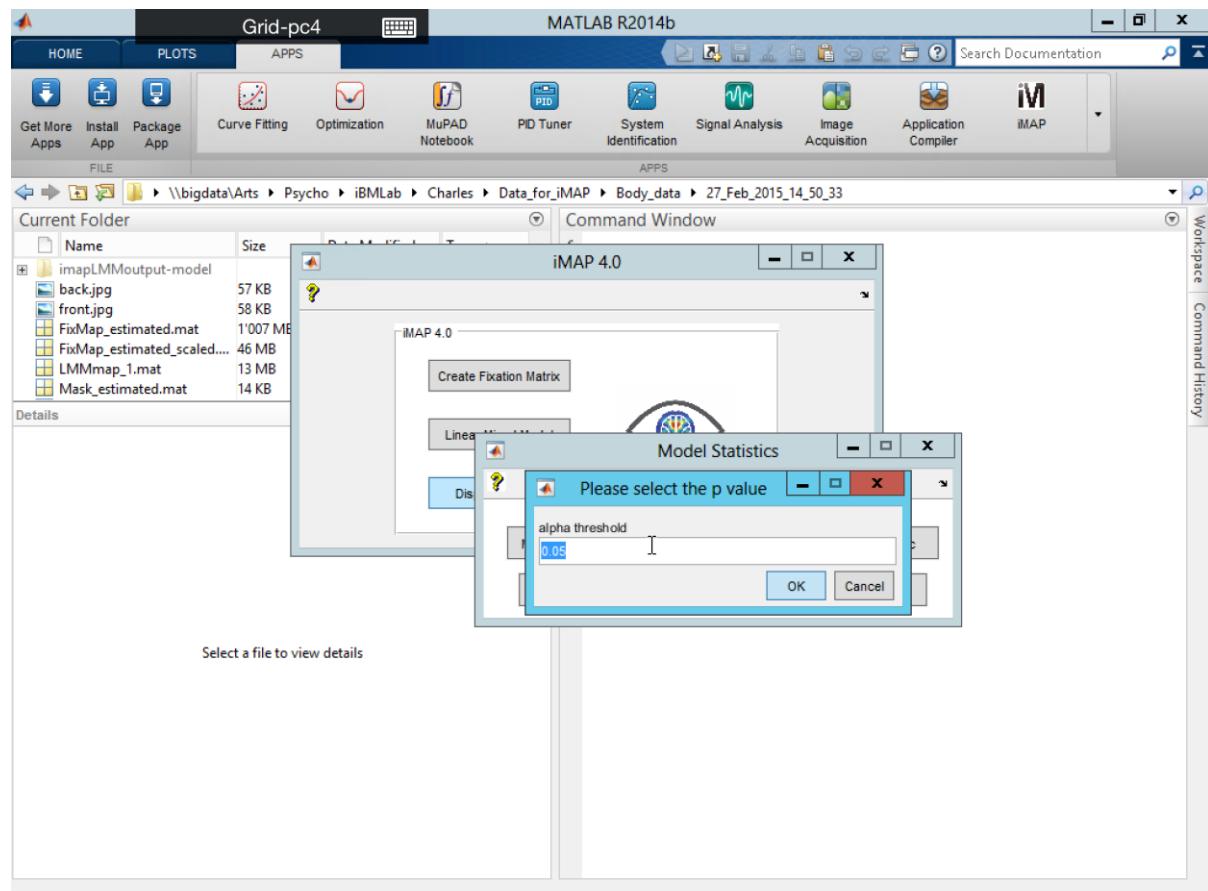
Click “**Model Fitting**” to visualize the R^2 , adjusted- R^2 , AIC, BIC, Log-Likelihood Ratio and Deviance from the model fitting result.





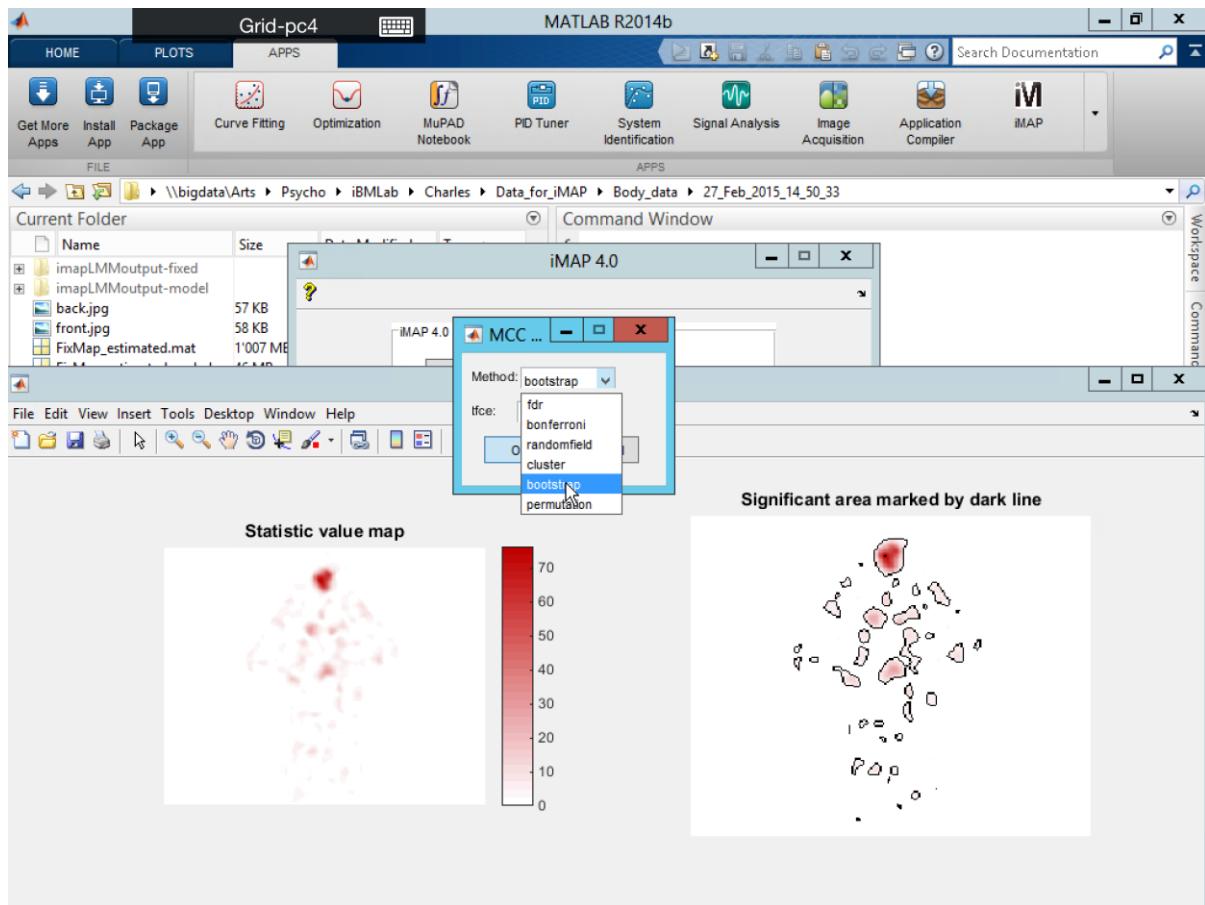
Display ANOVA for Fixed Effects and Perform Multiple Comparison Correction

Click “ANOVA” to visualize the F-test on the main effect and/or interaction of the fixed effects. The result of parametric test will be displayed first, then followed by the multiple comparison correction (MCC).

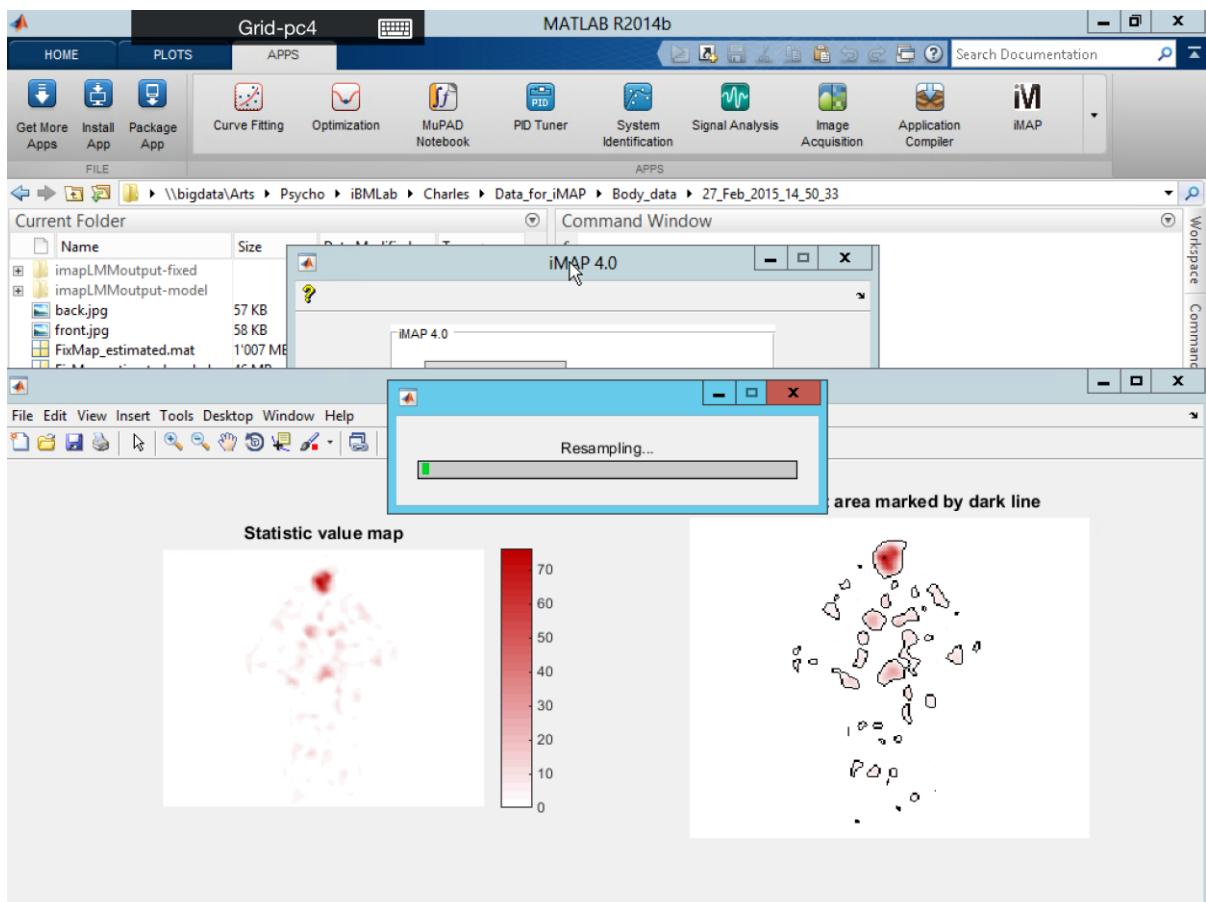
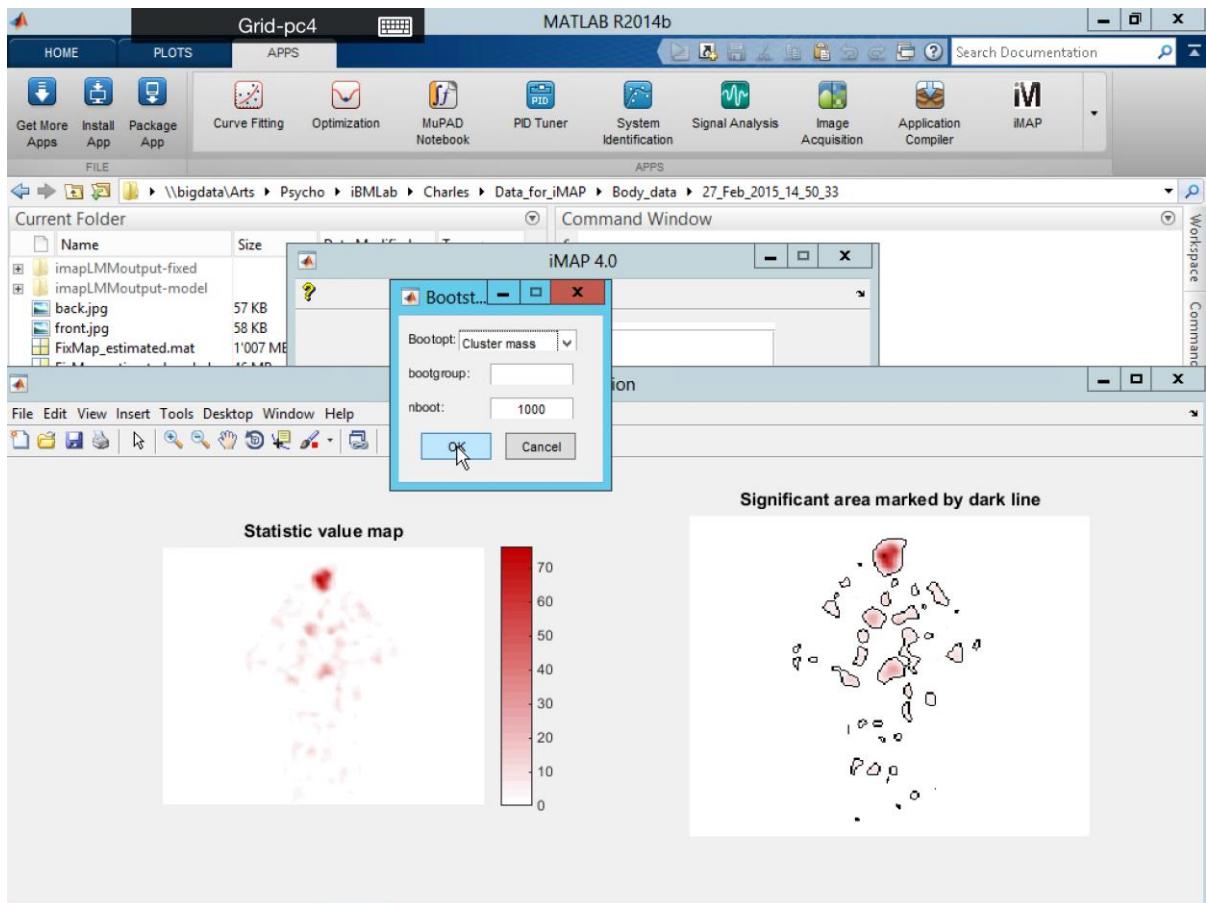


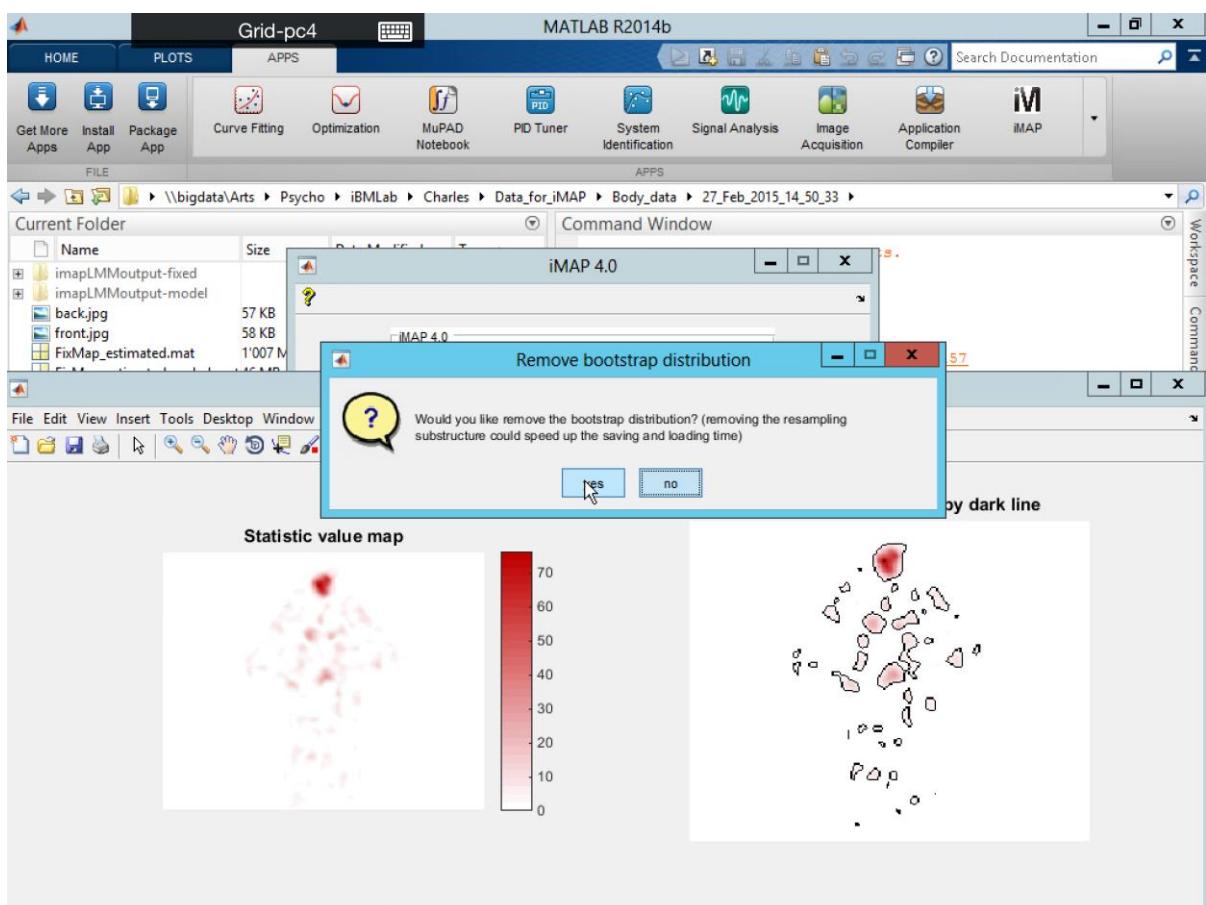
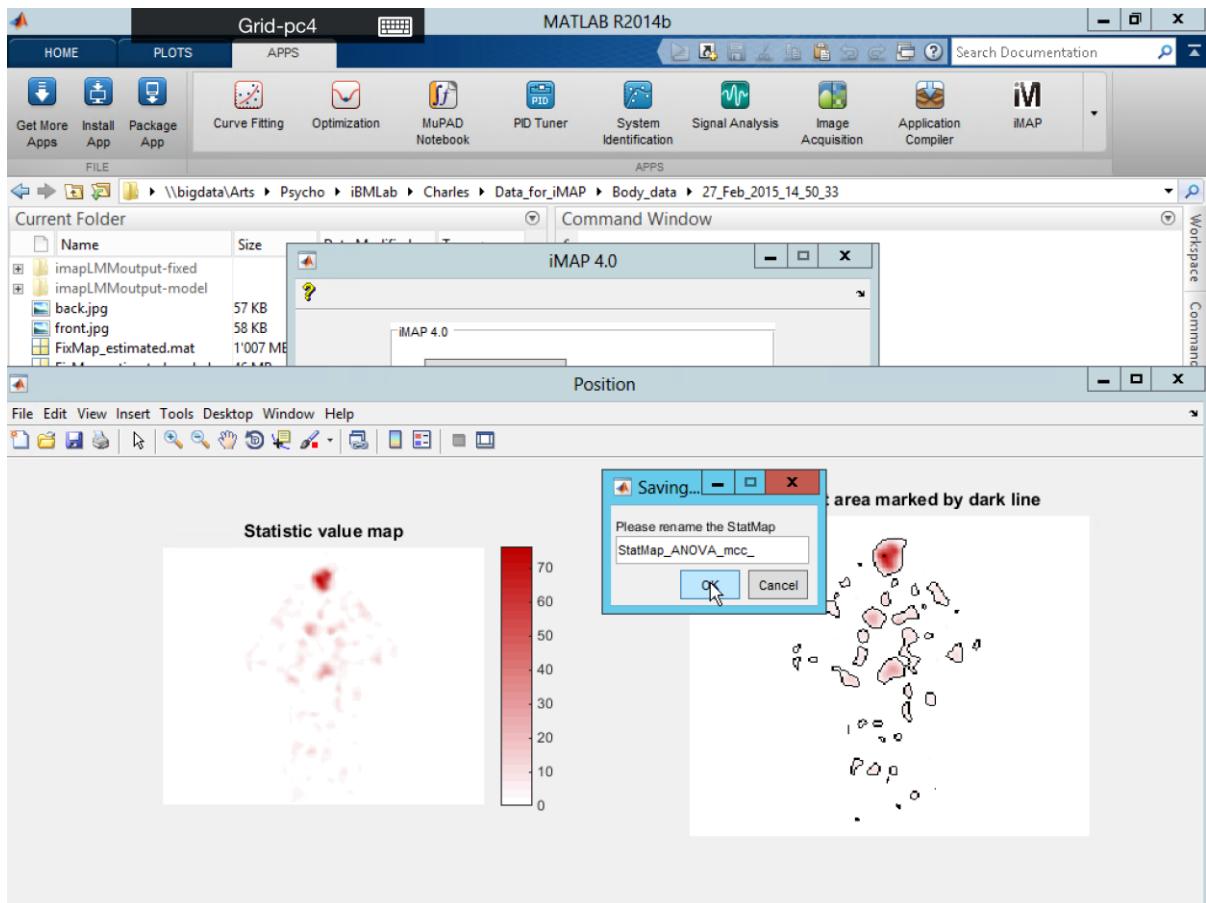
For multiple comparison correction, many options are included in iMap 4: FDR, Bonferroni Correction, Random Field Theory, Bootstrap Clustering and Permutation. Bootstrap Clustering method is the default option, as its familywise error rate (FWER) has already been validated.

You could also perform the multiple comparison correction on the TFCE map instead of the original statistic values (Smith and Nichols, 2009).

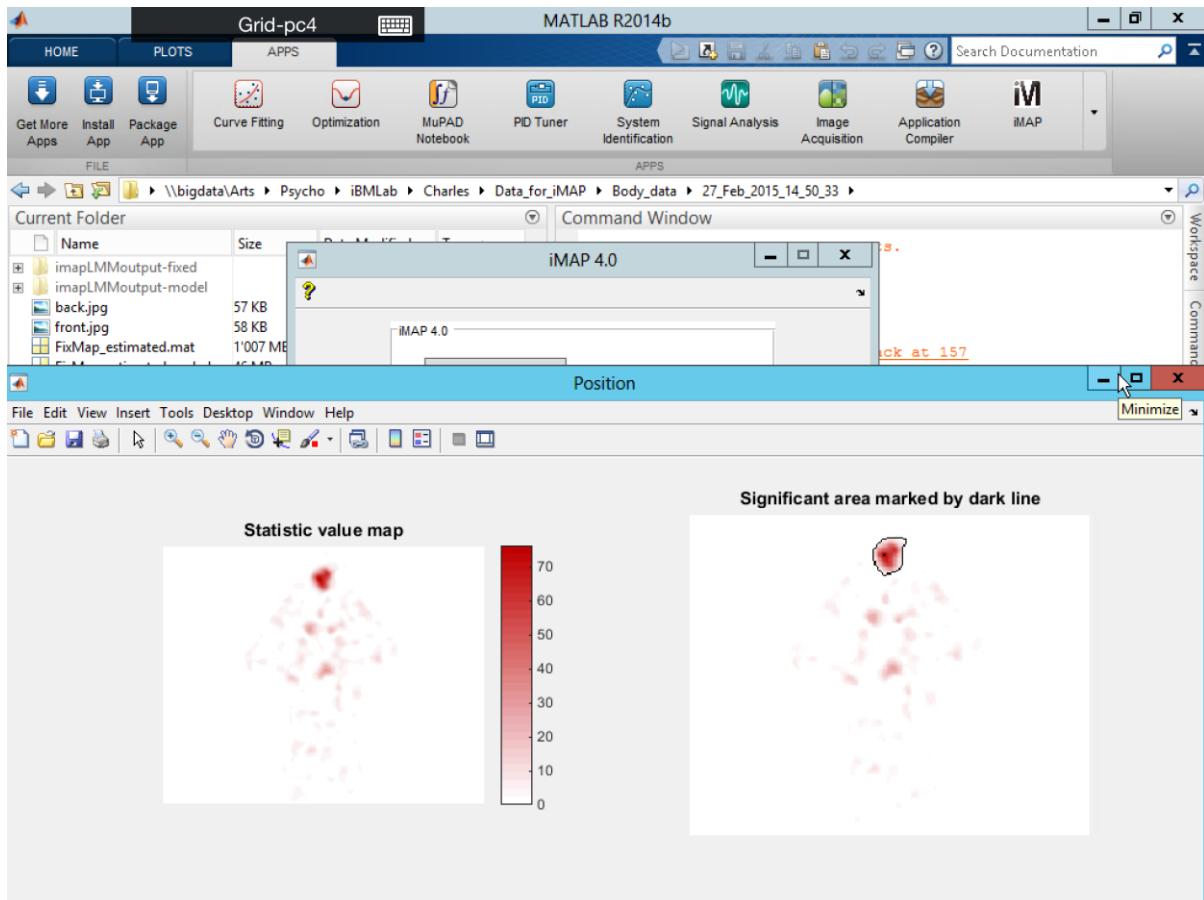


Please note: for Bootstrap Clustering method, if you have a between-subject variable (e.g., gender), you should input it into the bootgroup in the following pop-up window.

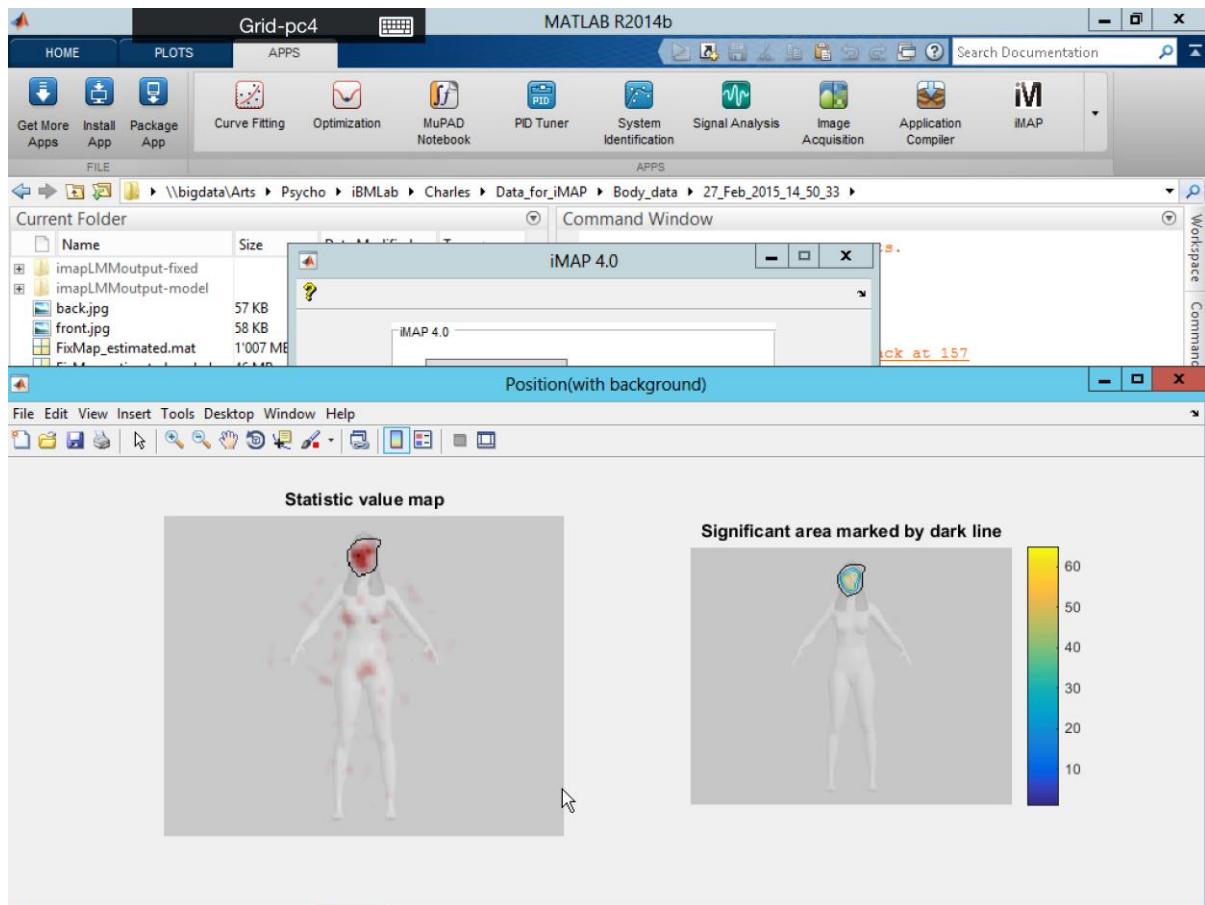




As you can see below the result after MCC, many small significant areas are actually false positive.

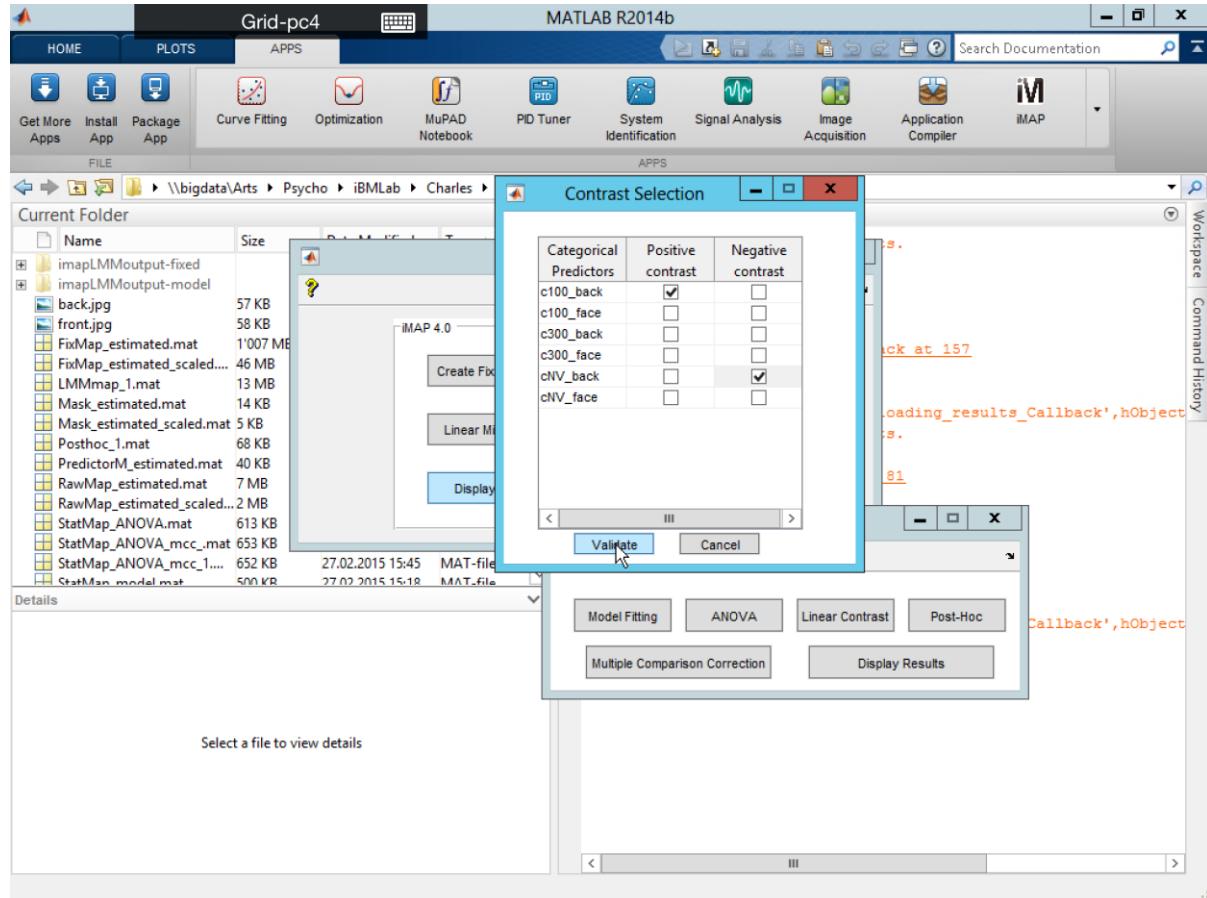


The resulting statistic values and masks are in Matlab Structure format: StatMap (before MCC) or StatMap_c (after MCC). They are saved in the same directory with LMMmap, while the figures are saved under a new folder in .eps format. If a background file is included in display option, the same statistic map will be displayed overlaying on top of the background file.



Perform Linear Contrast on Categorical Predictors

Click “**Linear Contrast**” to proceed. This step is very similar to performing **ANOVA**



In the example above, the following linear contrast will perform:

$$H_0 : c_{100_back} - c_{NV_back} = \mathbf{h} \text{ vs. } H_1 : c_{100_back} - c_{NV_back} \neq \mathbf{h}$$

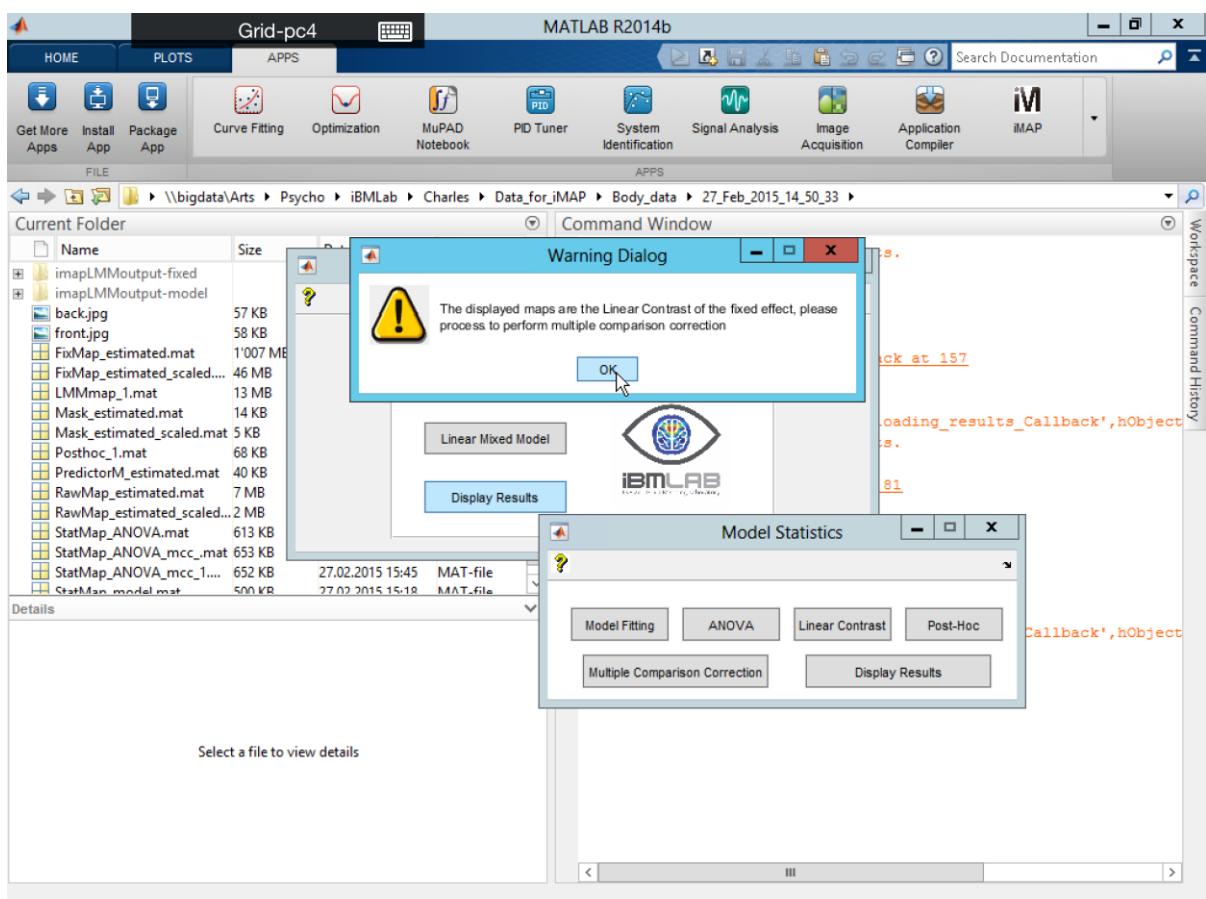
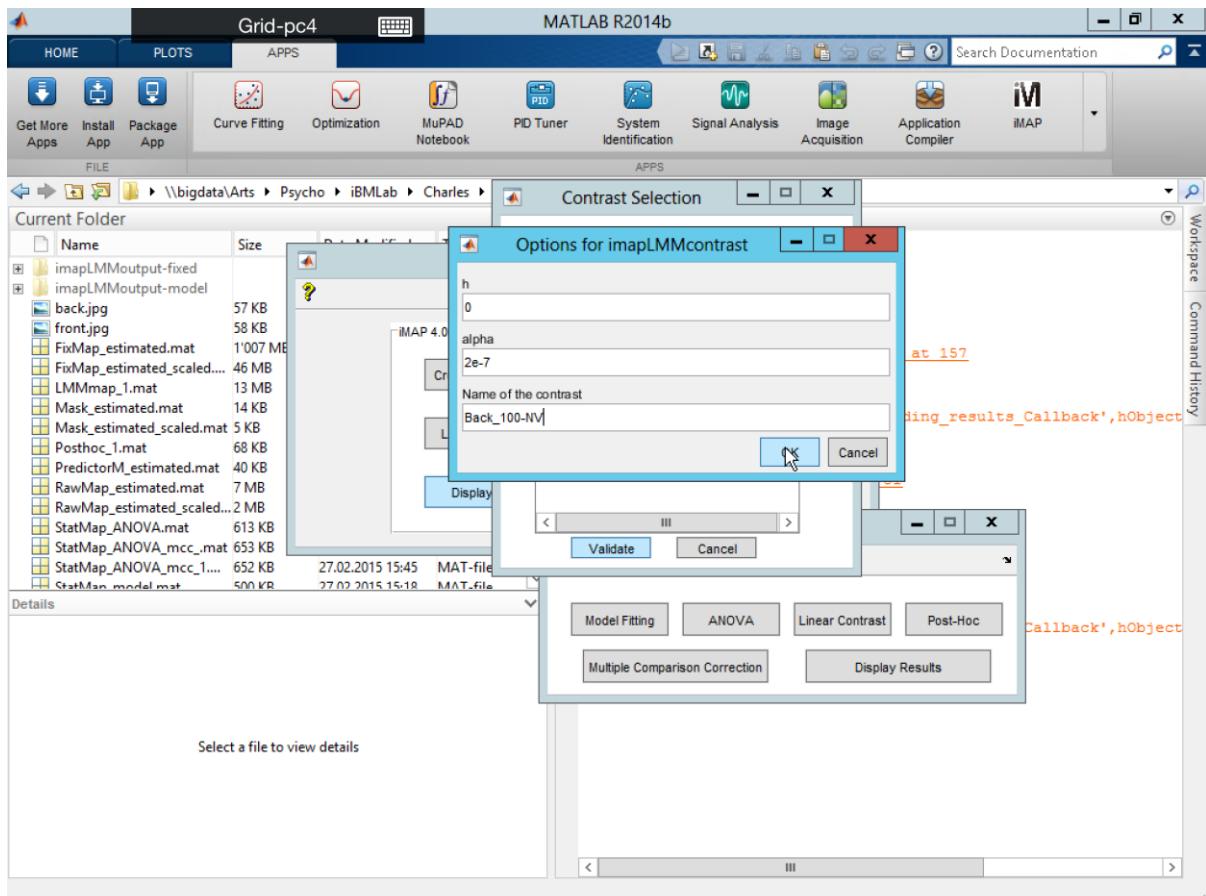
A pop-up will appear for you to specify the hypothesis (\mathbf{h} , usually is 0), p-value threshold (alpha, usually is .05), and the Name of the contrast test.

Please note (1): Here the categorical predictors are estimated with a full model only containing categorical conditions. In another word, iMap 4 removes all the covariance from continuous predictors in the original model and then fits a full model with all interactions on the categorical conditions. In the example showing here the two models are identical.

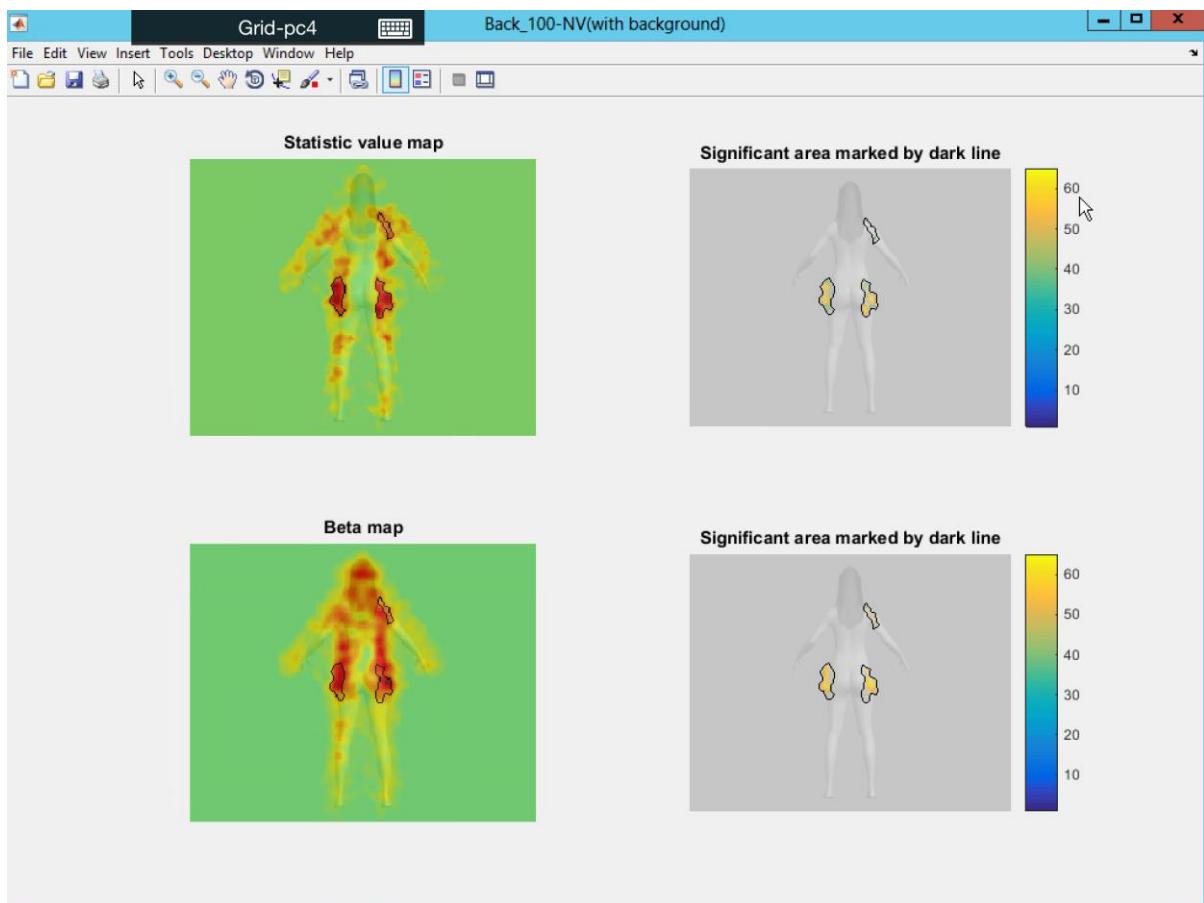
Please note (2): essentially, linear contrast performs the hypothesis testing of

$$H_0 : \mathbf{c} * \boldsymbol{\beta} = \mathbf{h} \text{ vs. } H_1 : \mathbf{c} * \boldsymbol{\beta} \neq \mathbf{h}$$

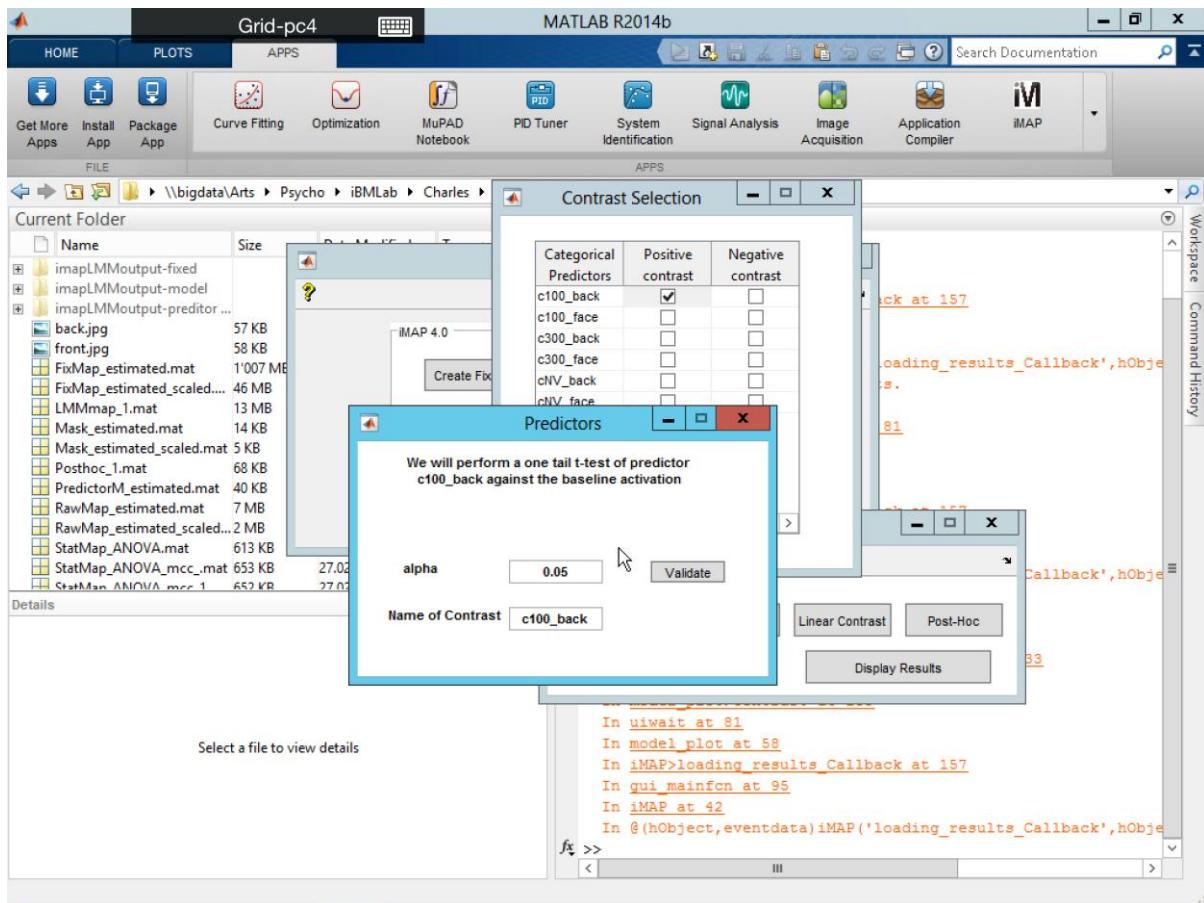
In the example shown above, the $\mathbf{c} = [1 \ 0 \ 0 \ 0 \ -1 \ 0]$ and $\mathbf{h} = [0]$. If you had selected an unbalance contrast (for example $\mathbf{c} = [1 \ 0 \ 0 \ 0 \ -1 \ -1]$), iMap 4 will balances the contrast vector before continue (change the original \mathbf{c} into $\mathbf{c}' = [2 \ 0 \ 0 \ 0 \ -1 \ -1]$).

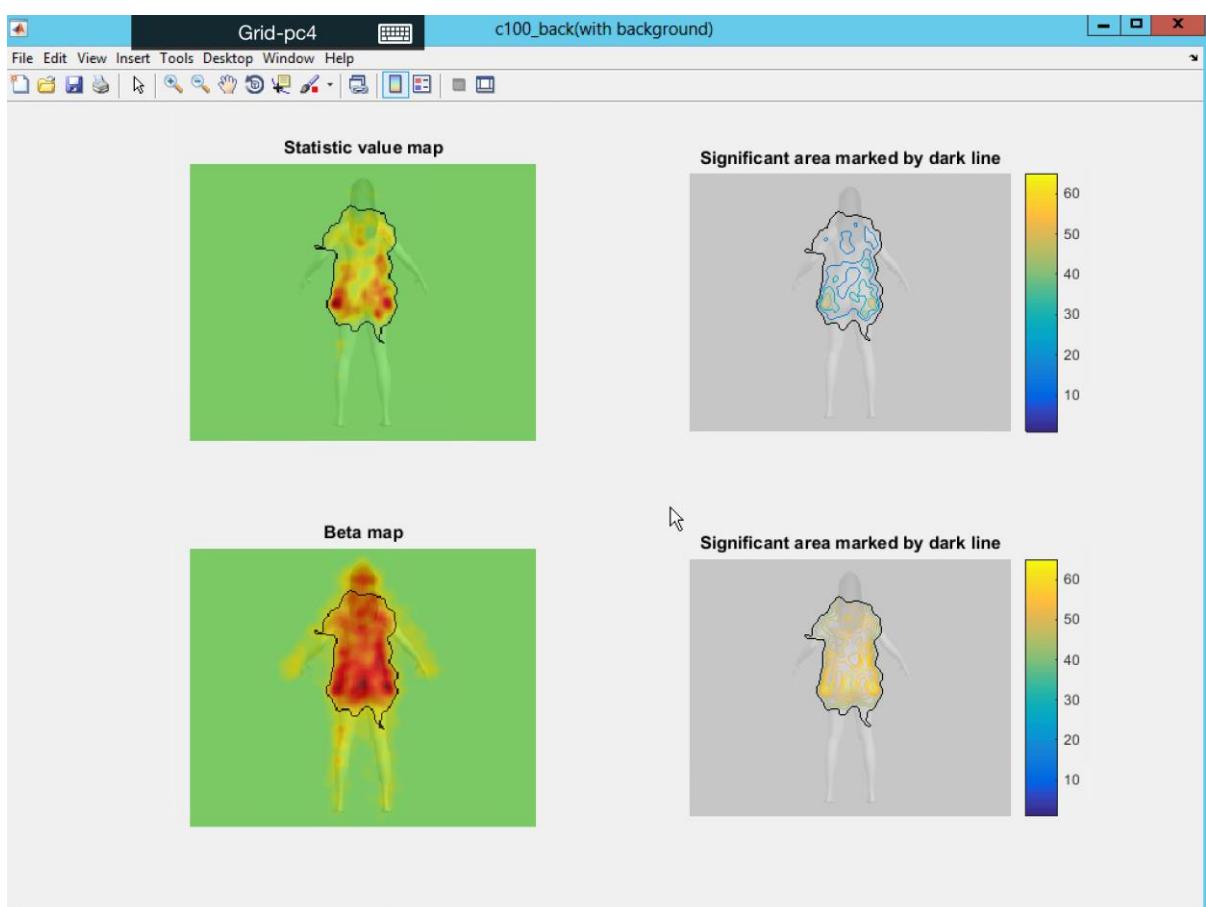
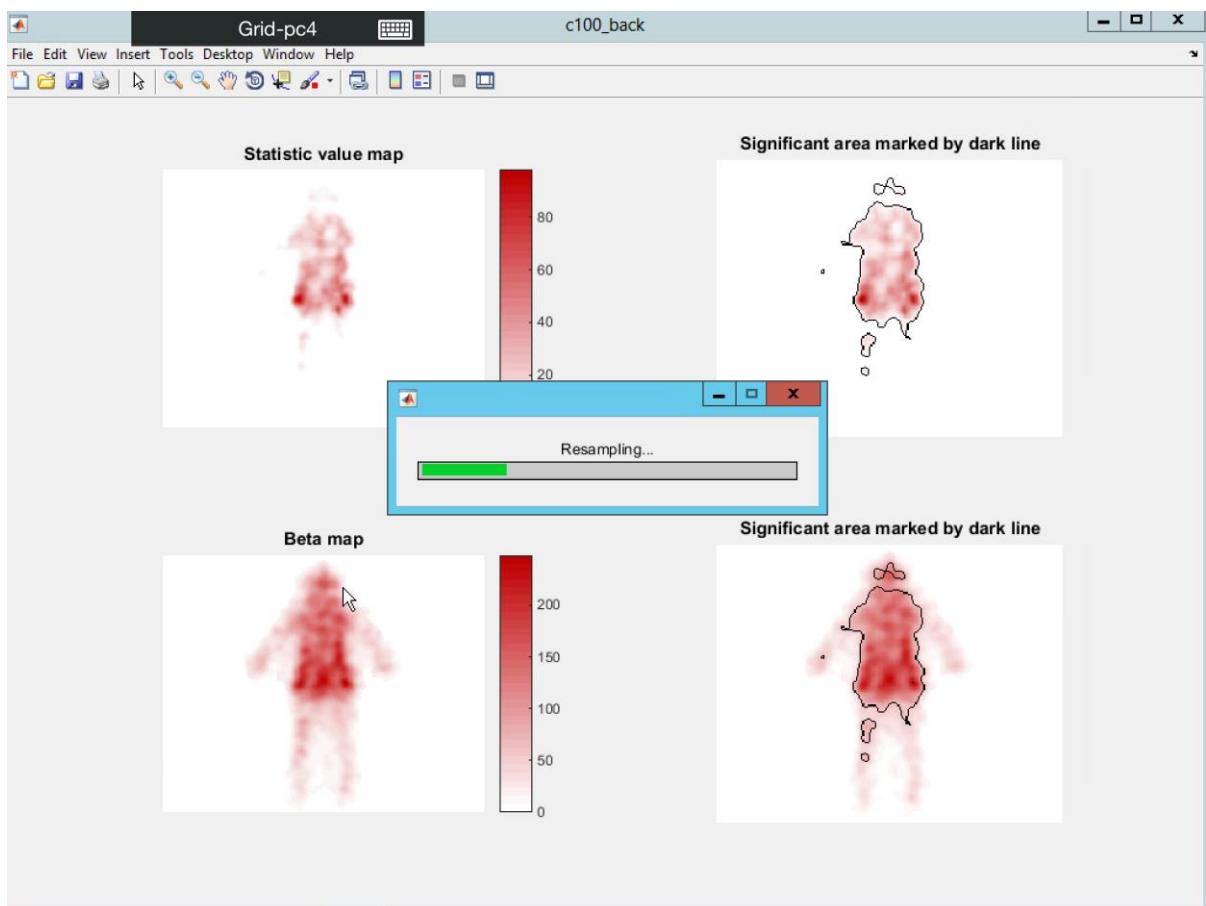


The result below is the figure output after multiple comparison correction using Bootstrap Clustering as MCC and displayed in another colormap setting.

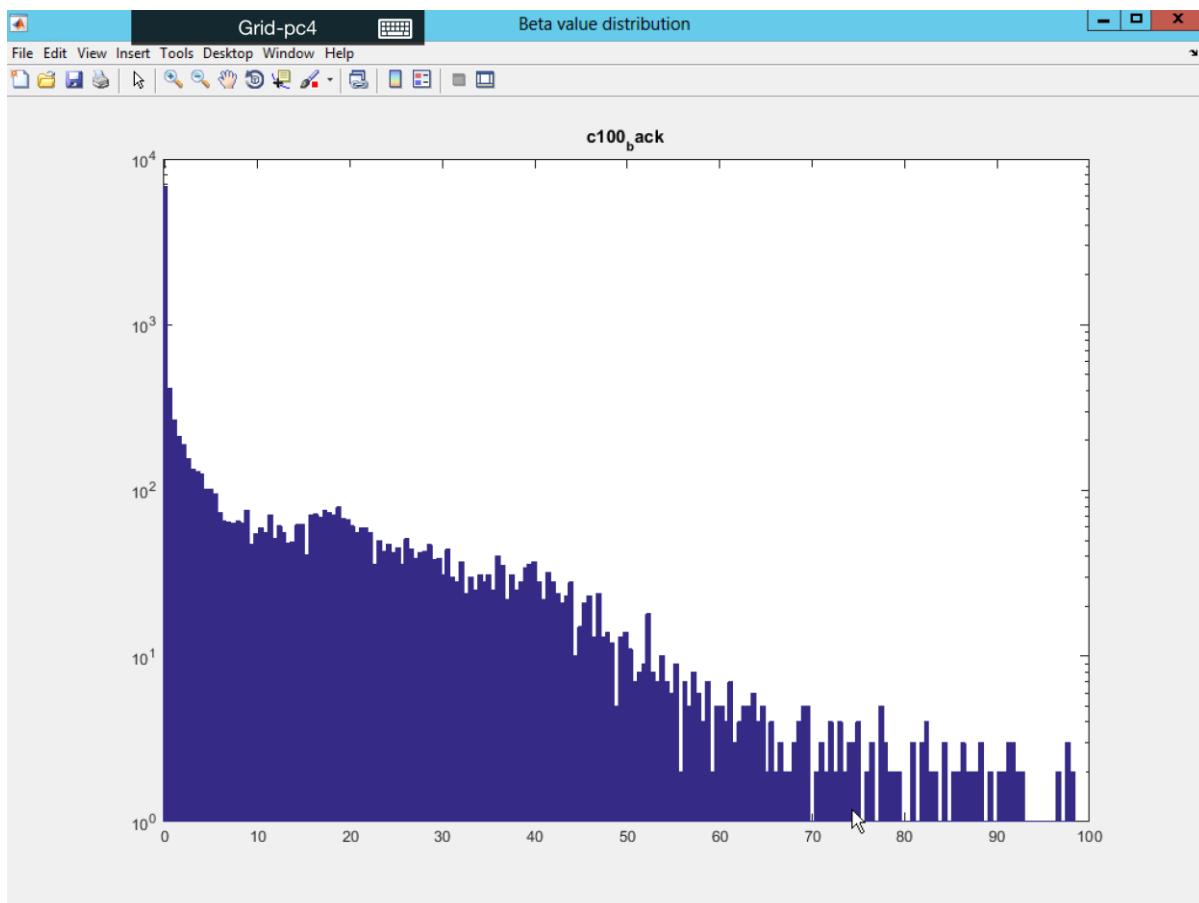


You can also perform a one-tail t-test of a single predictor against the “baseline activation” (the mean fixation intensity within the mask). The result will show the significant above chance fixation region.





In all the above cases, you have the option to visualize the distribution of the statistical value by putting “1” in the relevant display option.

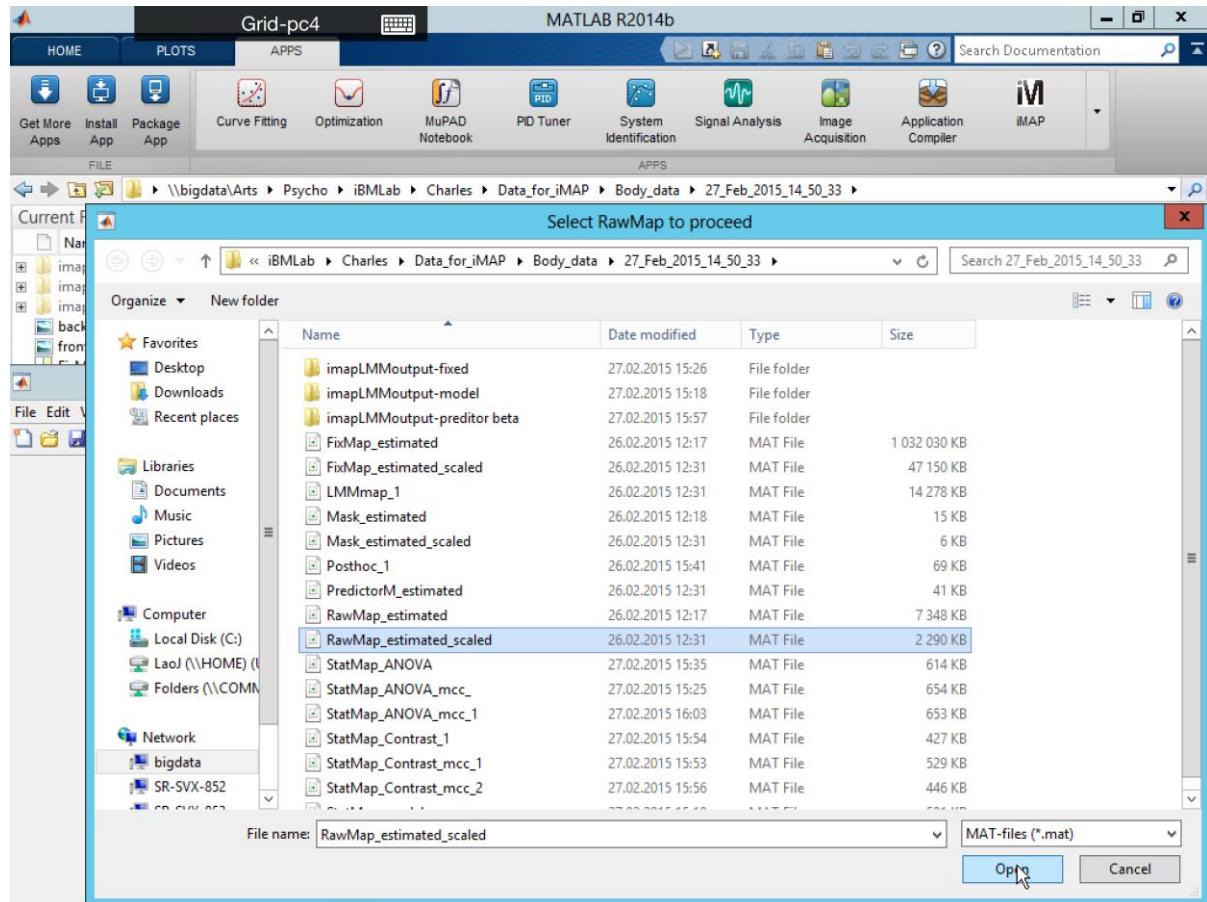


Post-hoc Analysis on Selected Mask

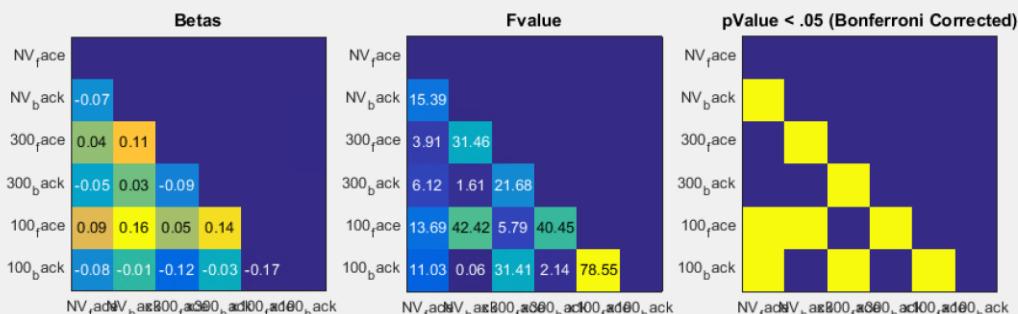
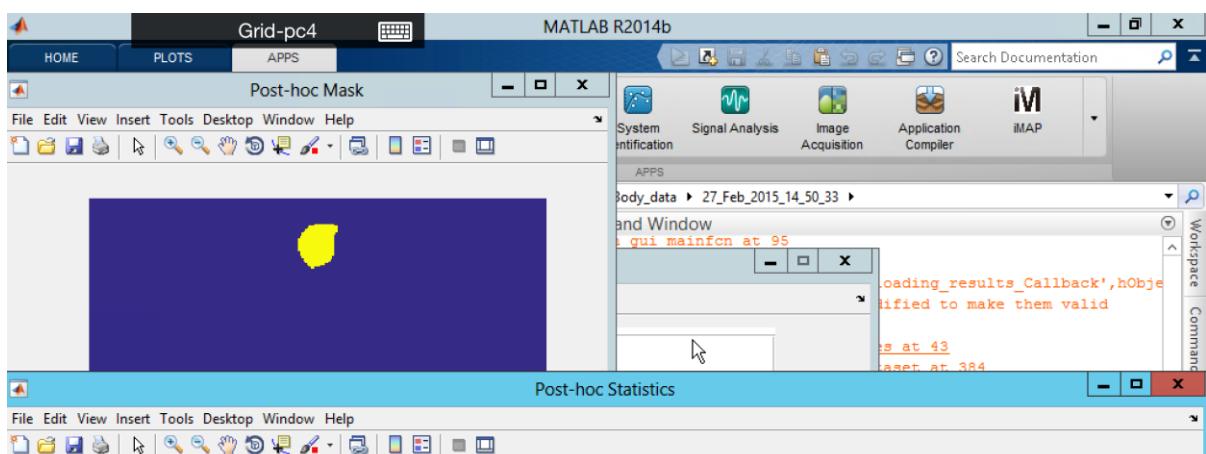
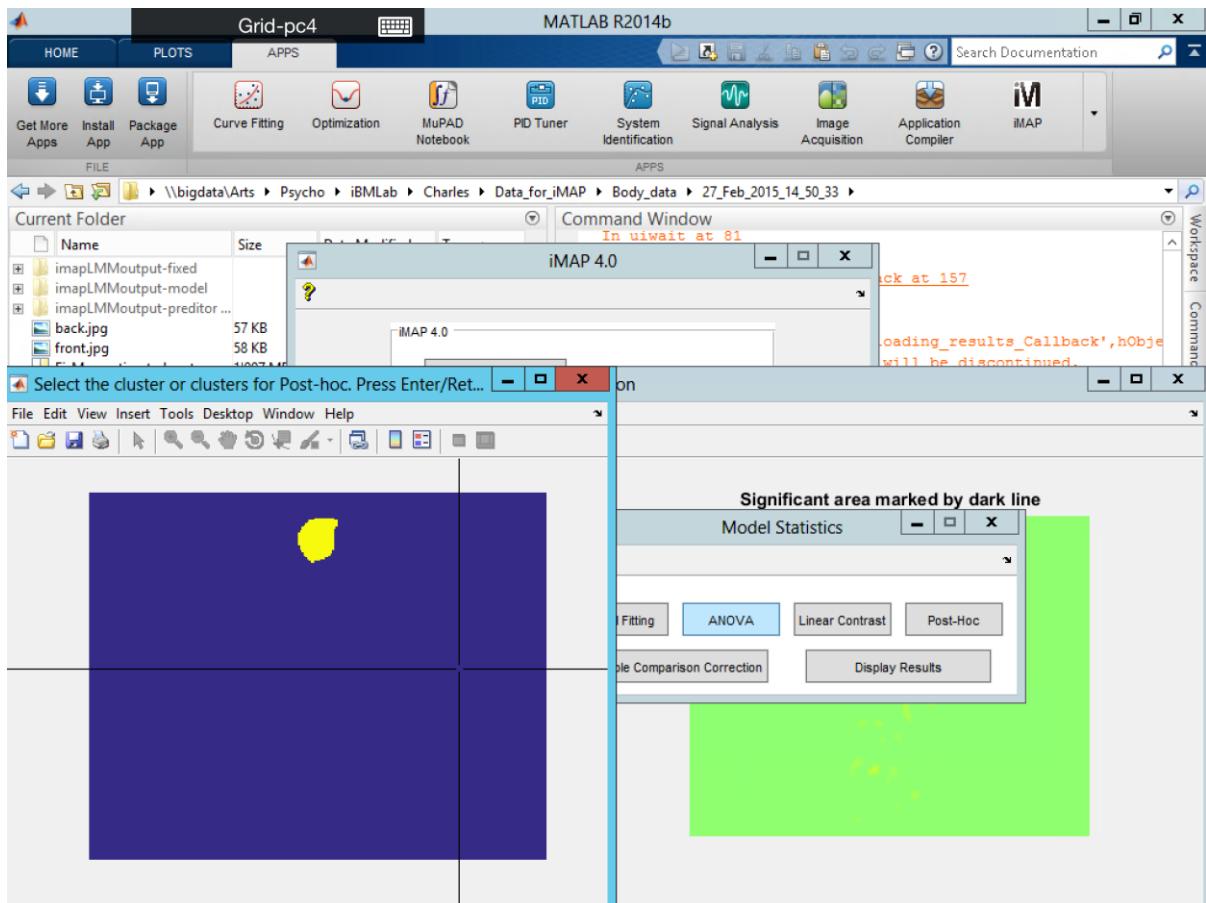
Here we show how to perform a post-hoc analysis after a significant ANOVA result.

After performing ANOVA or linear contrast, one or more masks will be generated. You can then perform post-hoc in these masks (similar idea as the Region or Area of interested).

First selected the correspondent RawMap.

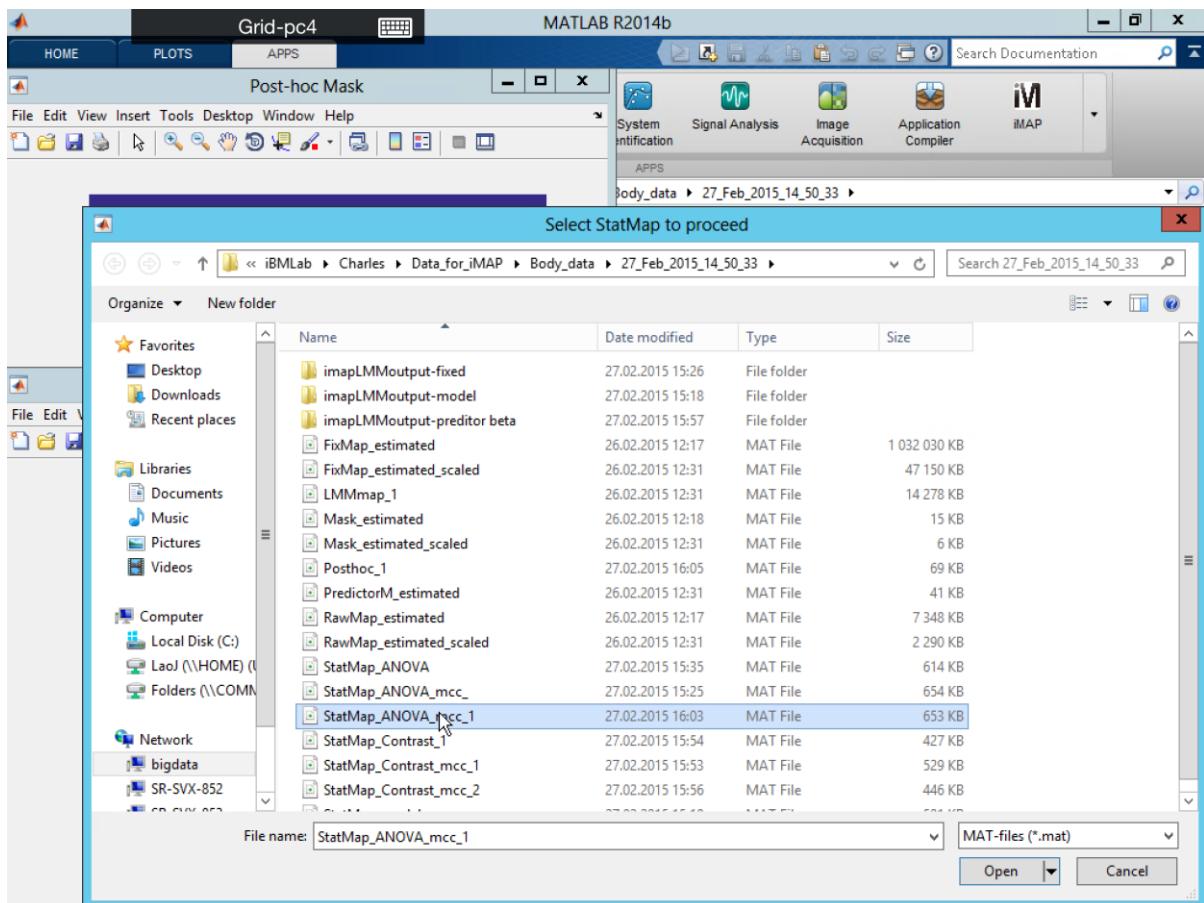


A pop-up will appear for you to select the region. You can select multiple regions and press "Enter" when finish. You can also press "Enter" without selecting anything to skip a mask. Student t-tests of the raw fixation value for all possible pair comparison of the categorical predictors within the mask will be performed.



Display Saved StatMap or StatMap_c

Once the StatMap or StatMap_c has been saved, you can visualize it again by loading them directly.



Example Matlab Script and iMap Utilities Functions

In the *iMap* 4 installation folder, you can find two demo scripts. *imap_DEMO.m* reproduces most of the analysis reported in this guidebook. *imap_DEMO_ST.m* shows an example of using the single-trial method to analyze data. There are also explanations about the structure of the input/output files in the demo scripts.

Some additional utilities functions could be found in the *iMap_utilities* folder after installation:

```
./MATLAB/Apps/iMAP/imap_utilities
```

Future Developments

The following features are part of *iMap* 4 but have not been implemented in the GUI yet:

- The display of random-effects coefficients
- The bootstrap confidence interval of the fixed coefficients
- A robust option by Winsorization of the single-trial FixMap.

The following features are still under development:

- Random-effects related statistics.
- Permutation methods as statistic and multiple comparison correction for fixed effects (Winkler et al., 2014)
- Model comparison while multiple models are tested

Future changes and updates of *iMap* (Caldara & Miellet, 2011) will be announced on the iBMLab website <http://perso.unifr.ch/roberto.caldara/>

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