

Instructions for using the MixGE toolbox

Add the directory of the MixGE toolbox to the MATLAB path.

In the Command Window, type “mixge” to launch the MixGE toolbox. You should see the MixGE main window (window 1) as shown below.

Window 1: MixGE main window

The screenshot shows the MixGE main window interface. It is divided into three main sections: Phenotype, Gene, and Others. The Phenotype section has radio buttons for 'Matrix' (selected) and 'Images', and a 'Matrix' dropdown menu set to 'Not selected'. The Gene section has dropdown menus for 'Genotype', 'Characteristic', and 'Weight', all set to 'Not selected'. The Others section has dropdown menus for 'Covariate' and 'Environment', both set to 'Not selected', and an 'Output Directory' field with a 'Browse' button. At the bottom, there are five buttons: 'Load data file' (labeled B), 'Load batch file' (labeled C), 'Save batch file' (labeled D), 'Display past results' (labeled E), and 'Begin computation' (labeled F). A red letter 'A' is placed in the top left corner of the window.

Fill in the fields in **A**. Click **F** to begin computation based on what is filled in **A**. The output would be stored as an “out.mat” file in the output directory specified in **A**.

Click **B** and select a .mat file, to load data into the MATLAB workspace. Variables loaded into the MATLAB workspace will be made available for selection in the dropdown menus in **A**.

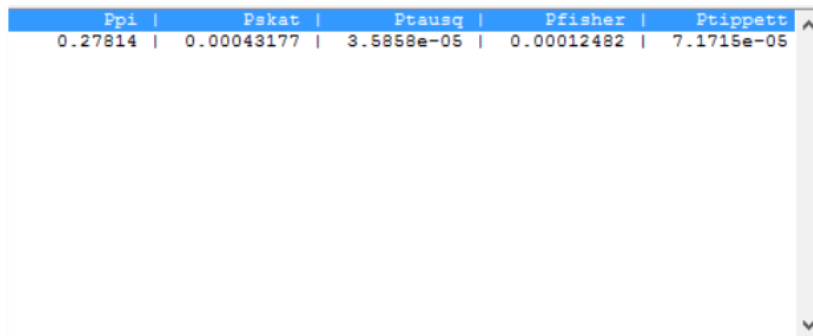
Click **D** to save a batch file. Batch files store information on what is filled in **A**, that can be loaded using **C** at a later time, if for example you wish to rerun the computation with modifications.

Two examples are provided with the toolbox. For the first example, “Genotype” is the single nucleotide polymorphisms of the EPHA1 gene, “Covariate” is intracranial volume and education in years, “Environment” is the first principal component of six cardiovascular disease risk factors (age, gender, body mass index, systolic blood pressure, current smoking status and diabetes), and “Phenotype” is hippocampal volume. To load the first example, make sure that the “Matrix” radio is selected, and click **C** and select “example_Matrix_batch.m” in the “example_Matrix” folder. For the second example, “Genotype”, “Covariate” and “Environment” are the same as for the first example, but “Phenotype” is

tensor-based morphometry (TBM) images. Also, only the data for the first 10 subjects are provided due to space constraints. To load the second example, make sure that the “Images” radio is selected, and click **C** and select “example_Images_batch.m” in the “example_Images” folder. However, before running the second example, run “install.m” in the “example_Images” folder to properly initialise the paths of the TBM images.

Click **E** and select an “out.mat” file to display past results. The “out.mat” file must have been created by the MixGE toolbox. The results for the two examples mentioned above are provided with the toolbox, except that for the second example, the result provided is based on all 697 subjects. The “out.mat” files for the two examples can be found in the respective folders of the two examples.

Window 2: Display result for matrix-based “Phenotype”



Ppi	Pskat	Ptausq	Pfisher	Ptippett
0.27814	0.00043177	3.5858e-05	0.00012482	7.1715e-05

This is an example of the window you would see when displaying result for matrix-based “Phenotype”. This particular window is the result for the first example provided with the toolbox.

Window 3a: Display result for image-based “Phenotype”

P value map:
Fisher

Atlas:

Orientation:
RAS

Significant cluster(s):

Buttons: Threshold, Browse, Save cluster, View cluster

This is the window you would see when displaying result for image-based “Phenotype”. Select the P value map you are interested in from the dropdown menu, and click the “Threshold” button. This will perform FDR correction on the P values and thresholding of the corrected P values at a significance level of 0.05. Significant clusters (if any) will be displayed in the list at the bottom of the window.

P value map:
Fisher

Atlas:
MixGE toolbox\example_images\atlas.img

Orientation:
RAS

Significant cluster(s):

- Cluster 1 (Size: 2089)
- Cluster 2 (Size: 508)
- Cluster 3 (Size: 163)
- Cluster 4 (Size: 79)
- Cluster 5 (Size: 12)
- Cluster 6 (Size: 6)
- Cluster 7 (Size: 3)

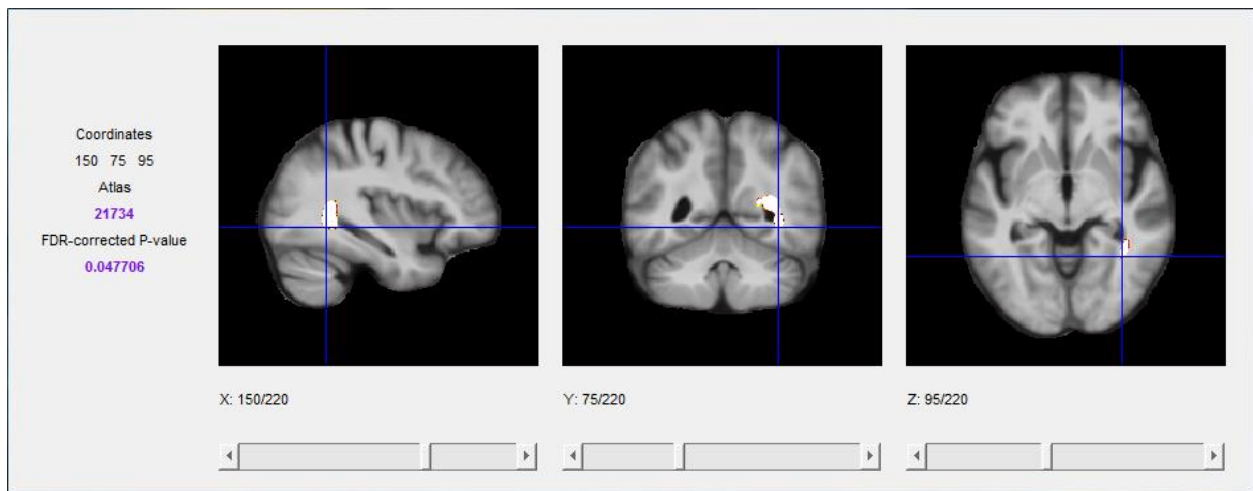
Buttons: Threshold, Browse, Save cluster, View cluster

This particular window is the result for the second example provided with the toolbox after the “Threshold” button has been clicked and an atlas has been selected.

Select a cluster you are interested in from the list, and click the “Save cluster” button to save a .img/.nii file as well as a .mat file for the selected cluster.

Select a cluster you are interested in from the list, select an atlas, define the orientation of the images, and click the “View cluster” button to view the selected cluster. You should see the display cluster window (window 3b) as shown below.

Window 3b: Display cluster for image-based “Phenotype”



This is an example of the window you would see when displaying a cluster for matrix-based “Phenotype”. This particular window is cluster 1 for the second example provided with the toolbox.