# Preparing the data

The preprocessing is summarized in the sDavid object. This object can be calculated using the function **Run\_all\_folders.m**.

## Run\_all\_folders.m:

INPUT and ASSUMPTIONS:

Running the code from the directory "Brain project".

This directory includes:

* currDataList.txt – a list of session names. Example is avilable.
* CelltypeClassification.mat – Eran's file.

OUTPUT: updated sDavid

We will state that in line **56** the path to the data is constructed and it may differ on a different computer.

this function calls **get\_data\_mich.m** that saves a mean for every relevant entry (for sessions with file names in the currDataList.txt file) according to the pre-determined heuristic.

## Correlation.m:

Using this function the ACH curve is computed. This function is not automated. To use this function for a specific session name i.e. 'es25nov11\_3'the user must state this folder name explicitly in line 13 of this script.

## morphological\_scattering.m

saves all the morphological features and generates a plot of the PDFs and pairwise scatterings. Assumes work from the directory in which 'sDavid' is saved in.

## morpho­logical\_POC.m

generate sample plots for each feature, demonstrating the ROIs and values. Better if run section by section (section are separated by %%).

## Temporal\_scattering.m

same for temporal feature.

## temporal\_POC.m

same for temporal feature.

## save\_data\_for\_python.m

saves the needed file for the python code in its place. The user must run both scattering functions before running this function for proper functionality.