Code used for microglia surveillance as in Madry, Kyrargyri, Arancibia-Cárcamo, Jolivet, Kohsaka, Bryan & Attwell (2017) Neuron

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This code requires the following files (all found in this repository)

* Surveillance.m
* SurveillanceGUI.m
* Surveillance.fig

All images should be saved as 1 movie for each cell for a period of imaging, and preprocessed to create binary images.

Data should be saved in folders within a directory to be analysed, this directory containing sub-folders, each containing a sub-set of the data that should be pooled in the analysis: e.g. one folder for all the WT cells and one for all the KO cells. Inside each sub-folder there should be a sub-subfolder called ‘binarised’ containing the timelapse movies (as .tif files). The program will analyse as many treatments (i.e. sub-folders) are there are in the directory to be analysed.

A ‘Results.mat’ file, which can be opened in MATLAB, will be generated with the data.

### Installing

Clone or copy the directory to any location. Add the directory to the MATLAB path.

### Run

From MATLAB right click on SurveillanceGUI.m and select Run

A graphical user interface should open.

*Timeline* – Input the min and max timepoints to be analysed

*Baseline-* Input the time range over which to normalise the surveillance

*Max number of cells-* Input the maximum number of cells to be analysed for a given condition (this number may be overestimated, but not underestimated)

*GO* Run the program

### How to run the Example.

Clone or copy the directory “Example cells” from GitHub to any location.

From MATLAB right click on SurveillanceGUI.m and select Run

In the graphical user interface keep the default settings as they are and click on GO

A pop up window will appear asking for the directory to analyse

Select the folder called “Example cells” and click Open

The data will be displayed in 5 graphs (see Example\_Graphs.png):

* Surveillance index against Time (min)
* Normalised surveillance index against Time (min)
* Ramification index against Time (min)
* Pixels surveyed (cumulative surveillance) against Time (min)
* Initial slope of cumulative surveillance for each genotype.

A file (“Results.mat”) will appear in the “Example cells” directory.