

Neuron count

Sometimes can be interesting to calculate number of objects in an image.

The basic idea is to obtain binary image, and then to count the white objects, that represent the cells. Is clear that is not necessary to have a perfect binary image, because is enough to count the soma. Even, may be useful to have only soma in the image, so we don't count several times the various parts of the cell, which may can be separated during thresholding.

There are two editor to perform it:

- For fluorescent cells
- For no-fluorescent cells

Making distinction is necessary. In fact, fluorescent cells are brighter than the background, and so, after thresholding, the result is objects white against black background. Instead, no fluorescent cells, are darker than the background, so there shall be a reversal of the binary image after thresholding.

Neuron count algorithm is like image processing algorithm, so the first steps are filter, uniform background and grayscale conversion.

Above all for fluorescent cells, soma is more brighter than the other parts of the cell, so is not implemented the contrast enhancing. In this way, dendrites are not put in emphasis: for this type of calculation, dendrites are not important.

After thresholding, is necessary performing some morphological operations on binary image, to remove dendrites and axons and to isolate soma. These are:

- Erosion, with a structuring element of appropriate shape and size;
- Opening, that allows to remove small object;
- Removal spur pixels, performed with an other specific Matlab command.

Doing this, is performed a label operation, just explained in "Select objects". The largest number used to label objects is the number in which they are in the image.

These steps are repeated for all the slice image, photographed in different days, and the results of each processing are saved in a folder, named "Count" as a vector. This folder is automatically created by the software, in the same directory of the slice

images. Instead, the vector is automatically named taking into account the number of the culture and of the slice.

After the processing, the user can plot the vector. There are two modalities:

- Separate plot
- Unique plot