

CNMF-E Manuel and Flow Chart

Depending on the area of the brain you are analyzing there are several different types of demo's you could choose to run your data through.

demo_endoscope.m: For small objective fields and a small population of neurons. This script will make it so you can trim, delete, and alter neurons that the script has found. You can go through all the cells it finds so in the event your data finds hundreds of cells, this could be time consuming.

demo_large_data_1p.m: This is probably the script most of you would use as it is meant for records with high populations of neurons. It has minimal user interface but with some manual filtered.

demo_large_data_p2.m: This script is designed for 2-photon analysis and this we will only briefly go through as most of us will not use this.

***These scripts take tif files and .mat data files. Before inputting your raw data into any of these scripts make sure you have aligned your videos together if you have multiple, and make sure they are saved as a single tif or mat file. Once you have done this place them in MATLAB directory with CNMF-E.

**make sure if you are using a .mat file that it includes your video data and the size of the video. One way to get this file is by concatenating all your videos together with FIJI(ImageJ) and saving them as a tif file. Then running your tif file through NORMCORRE to align your videos. NORMCORRE once run, will produce variables (M1, M2), for rigid correction or non- rigid correction (you can choose to save either or), and change the name of your chosen M# to Y, and the size of your video as Ysiz. Then in your workspace save these two variables as a single mat file. This is the file you will use to input into CNMF-E

Demo_large_data_1p.m

To run your data in this script, make sure once again that your data is in the current folder directory along with CNMF-E. Open the demo_large_data_1p.m script and at the top you will see:

```
4  %% choose data
5  neuron = Sources2D();
6  nam = get_fullname('./jisooWake.mat'); % this demo data is very small, here we just use it as an example
7  nam = neuron.select_data(nam); %if nam is [], then select data interactively
```

Change variable *nam* on line 6 to whatever your file name is, then click Run.