Install UOBRAINFLEX python env from sjara github page

Min python 3.7.2 (3.8.5 also works), matplotlib 3.1.3 or 3.3.2, skimage 0.19.1

Need to update matplotlibrc.template file from github?

Open spyder 4.15 or newer from inside anaconda browser after selecting uobrainflex environment while in “home”

Select wrench icon at top in spyder, set python interpreter as envs/uobrainflex/python.exe

Select ipython console/graphics and set graphics backend to by Qt5

Run Rotate\_CCF.py to create areas, CCF, masks, and outlines.npy files in folder named after rotation degree (22deg for A1V1M2 – thus positive is view angle rotated right to look at rt ctx)

Run ccf\_alignment.py. Use output of kaufman and saxena matlab multimodal map protocol (see other instructions) as mmm and the output of rotate\_ccf (see above) as the ccf. These input image files should end in “\_MMM.png”.

Select one mmm pt then corresponding ccf pt, then next mmm pt then corresponding ccf pt, etc.. First four pts should be external bounding box. Select at least 5 internal pts.

The output of this step is: STD\_ccf\_points.npy, and STD\_mmm\_points.npy. These files are put in the same folder as the mmm image.

Load data in suite2p and create mean image png output in corresponding target session analysis folder (top level). Add “\_MMM.png” suffix.

Next, run analyze\_WF\_session\_meso\_Feb1022.py. First image input is CCF, second image input is mmm, and third image input is target session image (can do unrotated…if pre-rotated, may need to change border threshold cutoff from 0.001 back to 0.01.

Output is masks w/o overlap corrected, masks w/ overlap corrected, and border map (also shown as figs); also output are npy files containing session\_mmm and session\_vessel alignment / warping points.

Can change color of each mask to indicate mean arousal correlation, arousal correlation variance, arousal correlation spatial heterogeneity factor, etc….

For each cell detected in Suite2p, get (x,y) position. Then, loop through all masks. For each mask, check to see if (x,y) position of each mask pixel matches that of cell. If yes, add region ID to cell dictionary, update arousal correlation summary stats (see above) for that mask region.

Awesome!...!