



③ Similar neurons extracted in different files should have similar spatial footprint as well as similar temporal traces across files. User-specified correlation threshold is used in this step.

Merge their A. See MergeAC() for detailed merging strategy.

4 Those neurons that cannot be merged will have A's (Each sample file's BigA) weighted and summed based on standard deviation of each A column's corresponding C trace. See ReducingA() for detailed method.

Acommon Aunique

Afinal=[Acommon, Aunique]

Sample data 1

2

For each Sample data

For each A0 mask cell, use it on
background subtracted sample data
to extract C (Each mask cell start
fresh). After extraction of one
neuron, re-estimate it's A and peel
the signal (A\*C) off.

Sample data 2's A0s

1 2 3 4 5 6

Sample data 3's A0s

1 2 3 4 5 6

Each sample file has a BigA

data folder

⑤ Use this A to extract neuron temporal C in all data you are interested in. No initiation and iteration for data. Use background subtraction strategy in the normal cnmf-e to subtract background, then use regression to find C corresponding to A. Save results in neuron.signal and neuron.filelist See more in "Input and Output" in "Getting Started" section.