

delete samples with empty A. Concatenate A's, altogether K neurons.

AOs 1 2 3 4 5 6

1 Normal CNMF-E for each sample file i individually Output: A0s(i), File(i)

A0s' mask

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.

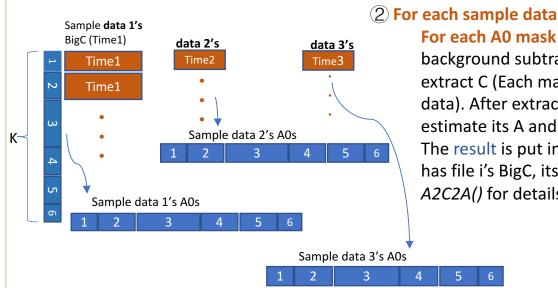
Merge their A. Only neurons that are found at least twice are kept, ie, only neurons merged are kept into Afinal. See *MergeAC()* for detailed merging strategy.

Output: Afinal, MC, newIDs, merged ROIs

- ACS

Afinal

④ 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_batch.neuron. See more in key variable table: neuron batch.



For each AO mask cell element, use it on background subtracted sample data to extract C (Each mask cell starts with fresh data). After extraction of one neuron, reestimate its A and peel the signal (A*C) off. The result is put in structure ACS. ACS(i) has file i's BigC, its STD, and BigA. See A2C2A() for details.

Each sample file has a BigC and a BigA



data folder