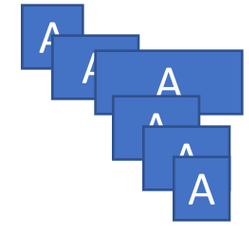
Sample folder

CaELM_row3275_b6938_20170405_205432.mat	Jun 22, 2017, 7:43 PM	196.2 MB
CaELM_row3276_b6938_20170405_205520.mat	Jun 22, 2017, 7:16 PM	186.6 MB
CaELM_row3277_b6938_20170405_210014.mat	Jun 22, 2017, 6:54 PM	164.3 MB
CaELM_row3278_b6938_20170405_210101.mat	Jun 22, 2017, 6:35 PM	159.7 MB
CaELM_row3279_b6938_20170405_210141.mat	Jun 22, 2017, 6:16 PM	189.5 MB
CaELM_row3280_b6938_20170405_210655.mat	Jun 22, 2017, 5:58 PM	189.7 MB
CaELM_row3281_b6938_20170405_210743.mat	Jun 22, 2017, 5:41 PM	192.7 MB
CaELM_row3282_b6938_20170405_213431.mat	Jun 22, 2017, 5:18 PM	169.1 MB
CaELM_row3283_b6938_20170405_213513.mat	Jun 22, 2017, 4:49 PM	164.5 MB
CaELM_row3284_b6938_20170405_213553.mat	Jun 22, 2017, 4:27 PM	166.3 MB



delete samples with empty A

A0s

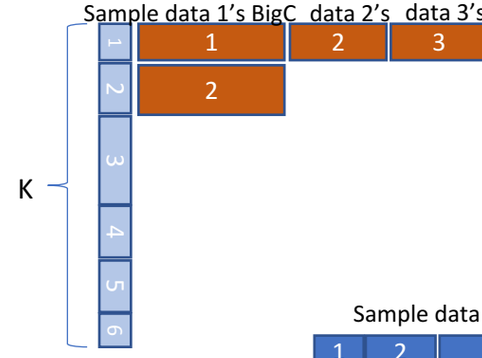
A0s' mask

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

② **For each sample data**
For each A0 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, re-estimate 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.

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. Output: ACS's updated A and STD field. (some neuron's A and STD deleted, while those merged have the same A and STD in each file's ACS)

ACS



Each sample file has a **BigC**

Each sample file has a **BigA**

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 weightedA=*ReducingA(…)* for detailed method.

Afinal

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_batch.neuron. See more in key variable table: **neuron_batch**.

data folder