Key Variables	Description
A0s	Cell array. A0s{i} contains the A for sample data i.
File	Structure. Length of sample number. Containing two fields, 'options','Ysignal'. Options keeps the neuron.options. Ysignal keeps the background subtracted and de-noised data, which is essentially A*C after iteration.
Mode	String, either 'initiation' or 'massive', which means sampling and extracting all data respectively.
ACS	Structure. Length of sample number. Three fields. 'Ain','Cin','STD'. 'Ain' and 'Cin' is the BigA and BigC in Figure2(ReadMe). 'STD' is the standard deviation of each temporal traces(Cin).
ind_del	In the output of final result, neuron_batch. ind_del here is an index for neurons that have temporal traces not deconcolved successfully or are all zeros. From all files' ind_del, in output log file of each run, "First x neurons are successfully deconvolved in each files" is printed to inform you of this. The number of x is sum(~ind_del_final).
Afinal	The final A used to extract all file's C.
neuron_batch	Structure, length of data file number. Each row of neuron_batch stands for each data file, which has information/data in 4 fields, 'ind_del','signal','FileOrigin','neuron'. Ind_del, see above. signal is a matrix where each row is the neuron's background subtracted and denoised signal: median(jA(jA>0)*jC). FileOrigin is a structure, essentially a row of dir(Datadir). neuron is the result of CNMF-E using Afinal. This "neuron" does not contain full information as a normal CNMF-E due to the steps it skips. See section Summary of differences between CNMF-E (basic) and CNMF-E (BatchVer) in ReadMe for more information.