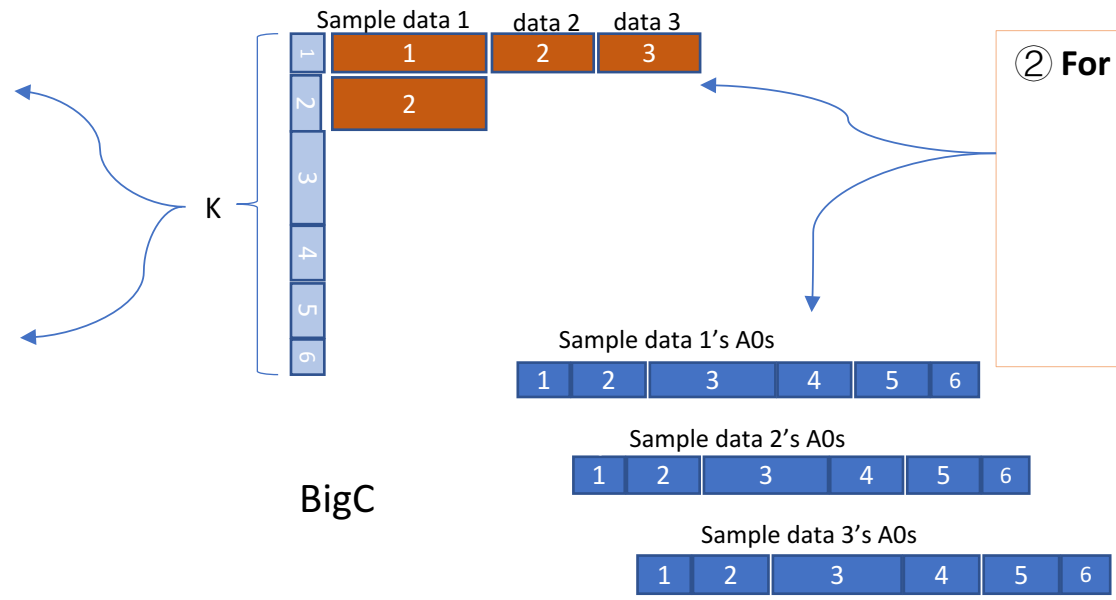


③ Similar neurons extracted in different files should have similar spatial footprint as well as similar temporal traces across files. User-specified correlation threshold is used in this step. Merge their A. See MergeAC() for detailed merging strategy.

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.



Each sample file has a BigA



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.

