**SOLUTION: Converting the file “02\_single\_cell\_syn.ijypnb” file to run in python**

* Your working directory should have two folders: ‘Sources’ (with lots of files from bmtk) and ‘Output’ (empty) from bmtk. Then you create two files build\_network.py and build\_env\_bionet.py as in the previous tutorial. These are also provided in the folder (generated from the notebook files)
* When you run the file “build\_network.py”….
* this will build the network. It will create a folder ‘network’ and then save the files ‘mcortex\_nodes\_types’ and ‘mcortex\_nodes.h5’ files. Do check this and confirm they are there, after this step.
* Then create and run build\_env\_bionet.py
* this creates standard SONATA configuration files for BioNet, using the built network files in ./network and having a simulation run-time of 2 seconds. The membrane\_report-vars and membrane\_report-sections sets it so that we are recording membrane potential (v) and calcium concentration (cai) at the soma. It also creates the directory “biophys\_components” with five sub-directories, and only populates the ‘Mechanisms’ (with mod files; also add the compiled folder x86\_64 in Ubuntu) and ‘Synaptic models’ (with ampa, gaba, …files) directories. The others have to be populated by the user separately – see Notebook file. The command also creates two .json files and the file run\_bionet.py
* #1/2 of what YOU HAVE TO DO: copy files using the following commands:

$ cp sources/bionet\_files/components/biophysical/electrophysiology/472363762\_fit.json biophys\_components/biophysical\_neuron\_templates/

$ cp sources/bionet\_files/components/biophysical/morphology/Scnn1a\_473845048\_m.swc biophys\_components/morphologies/

* #2/2 of what YOU HAVE TO DO: You don’t have to change the ‘circuit\_config.json’ file, but have to populate the empty ‘inputs’ section in the ‘simulation\_config.json’ file…..as indicated in the notebook file. Its contents should be the following:

"inputs": {

"lgn\_spikes": {

"input\_type": "spikes",

"module": "csv",

"input\_file": "${BASE\_DIR}/thalamus\_spikes.csv",

"node\_set": "mthalamus"

}

},

* If you are running Windows, there is one more step: make sure you compile the .mod files in biophysics\_components\mechanisms\modfiles and then copy the nrmmech.dll file into the previous directory also, i.e., biophysics\_components\mechanisms. Nothing needs to be done if you are running linux.
* Then ‘python run\_bionet.py simulation\_config.json’ should provide an output file.
* Create the following file ‘plot.py’ with the text below, and use that to plot the results.

from bmtk.analyzer.spike\_trains import to\_dataframe

to\_dataframe(config\_file='simulation\_config.json')

from bmtk.analyzer.cell\_vars import plot\_report

plot\_report(config\_file='simulation\_config.json')