**Visualizer.py**

**Main role:**

Visualise data from provided csv file containing x and y coordinates in 2D space (fourth and fifth column - float) bounded to specific neuron characterised by number (second column – integer). Script is lazily yielding data from csv file, lazily filtering duplicite points (when neuron stopped growing), harvesting all points of neuron and optionally normalising data for 0,0 graph root if needed. There are several possibilities to plot processed data.

Dependent on yielder.py.

**User interface:**

**For plot data from single file**

Required arguments (**flag / alternative flag,** [argument type], (options)):

>>> python visualizer.py **-f** name\_of\_file.csv **-m** single | burst | range | group **-n** number(s) of neuron

**-f / --filename**  - [string] (source\_file.csv) Data has to be presented in specified columns.

**-n / --neuron\_first** -[integer] (number(s) of neuron)

**-m / --mode** - [string] ( single | burst | range | group )

– single – plot one neuron in 0,0 graph root, **-n**  has to be equal exactly one integer -> **-n** 8 plots neuron 8\*.

– burst – plot several neurons with 0,0 graph root sequentially, **-n** has to contain exactly two integers (first lower, second higher) -> **-n** 4 9 plots sequence of graphs of neuron 4, 5, 6, 7 and 8.

– range – plot range of choosen non-normalized neurons into one graph -> **-n** 4 9 plots neurons 4, 5, 6, 7, 8 and 9 into single graph.

– group – plot random group of chosen non-normalized neurons into single graph -> **-n** 7 8 2 1 25 – plots choosen neurons.

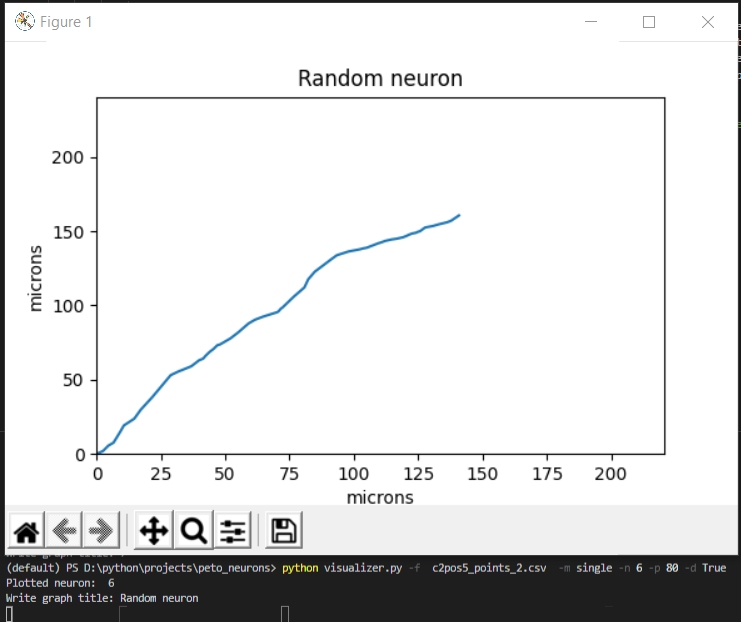
Optional arguments (**flag / alternative flag,** [argument type], (options)):

**-p / --padding** - [integer] padding around neuron, default = 20px.

**-d / --description** - [bool] Description of graph. If not specified in single and burst mode default = ‚Neuron + number of neuron‘. If needed: **-d** True. Modes range and group always requiring description by user input from command line (may be empty string) before graph plotting.

Example:

>>> python visualizer.py **-f** name\_of\_file.csv **-m** single **-n** 6 **-p** 80 **-d** True



**For plot data from two files at once**

Required arguments (**flag,** [argument type]):

**-f / --filename**  - [string] source file. Data has to be presented in specified columns.

**-f2 / --filename2**  - [string] second source file. Data has to be presented in specified columns.

**-n / --neuron\_first** -[integer] number(s) of neuron

**-n / --neuron\_other** -[integer] number(s) of neuron

**-m / --mode** - [string] ( range | group )

– range – plot range of choosen semi-normalized\* neurons -> **-n** 4 9 plots neurons 4, 5, 6, 7, 8 into first graph and **-n2** 2 3 plots 2 and 3 into secong graph. Both parameters has to be specified.

– group – plot random group of chosen semi-normalized\* neurons into single graph -> **-n** 7 8 2 1 25 – plots choosen neurons into first graph and **-n2**4 5 9 8 2 1 5. Both parameters has to be specified.

Optional arguments (**flag,** argument):

**-p / --padding** - [integer] padding around neuron, default = 20px.

**-d / --description** - [bool] Description of graph. If not specified default = ‚source\_file.csv‘. If needed: **-d** True. Description will be required by user input from command line (may be empty string) before graph plotting.

\* Script informs about found (Plotted neuron: [integer]) or not found (Not found: [integer]) neurons in file.

\*\* Whole group of neurons adjusted to 0,0 graph root