File information for pyramidal neuron simulation

LSS 8 November 2018.

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If the -fileprefix flag is provided, the string following this will be prepended to all the file names. Note that if a null filename is supplied, no file will be read.

***Network configuration***: -n flag, followed by filename

Calls readNetworkFromFile

@param filename: name of file from which network configuration is to be read

@return string of length number of neurons with each character being the type of the neuron (P or I currently).

Each line has from <n> <P|I>

and there has to be an entry for each n, from 1 up to number of neurons.

Note that neurons in the simulation are numbered from 0 to n-1

***Weights:***

*Driving weights*: -wd flag, followed by filename. Filename can be null, bu oprogram wikll complain and terminate.

Calls readInputsToArrayFromFile.

Expects 3 values per line, read as doubles. Neuron number, synapse number, weight. Allows spaces or single commas as separators.

*Contextual weights*: -wc flag, followed by filename. Filename can eb null, but program will complaine and then terminate.

Calls readInputsToArrayFromFile

Expects 3 values per line, read as doubles. Neuron number, synapse number, weight.

Allows spaces or single commas as separators

*Internal weights and delays*: -wi flag, followed by filename. Filename can be null, in which case program will have no internal weights.

Calls readInputsToArrayFromFile

Expects 5 value per line, read as doubles, presynaptic neuron, postsynaptic neuron, postsynaptic compartment, weight, delay. Allows spaces or single commas as separators. Note that there must not be any blank lines (including at the end of the file).

***Inputs:***

*Driving inputs*: -d flag, followed by filename. Filename can be null.

Calls readInputsToArrayFromFile.

Expects 3 values per line, read as doubles: neuron number, synapse number, time. Note that the system expects this to be a P neuron, and the input will go to the basal compartment.

*Contextual inputs*: -c flag, followed by filename. Filename can be null.

Calls readInputsToArrayFromFile.

Expects 3 values per line, read as doubles: neuron number, synapse number, time. Note that the system expects this to be a P neuron, and the input will go to the apical tuft compartment.

***Output:***

Single output, -sout flag, followed by filename. Discarded if no –sout flag. Also discarded if -sout flag is followed by a null string.

2 values per line, neuron number, time, comma separated.