Simple user's manual for NeuroCharter.

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The program was programmed in python 2.7.2, The source code is available at NeuroCharter.py Due to some dependencies and required libraries, it is recommended to run it through PyCharm community edition, which is free and cross platform IDE.

Preparatory steps.

1. You should have a Python interpreter at your system, if not, the please download and install Anaconda for python 2 from the URL: https://www.continuum.io/downloads. This is highly recommended in order to make the next steps easier (for python experts, you can install the official Python 2.7.* interpreter from this URL: https://www.python.org/downloads/).

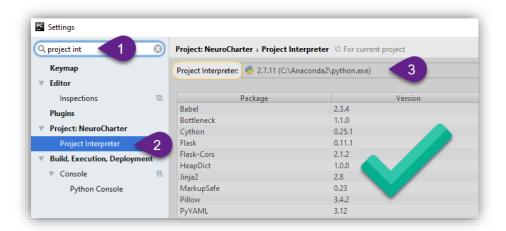




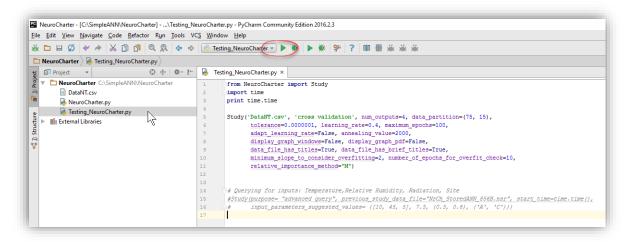
- 2. After installing Anaconda, go to the command prompt and update all modules as follows: conda update -all, then install the following libraries:
 - a. Install 'PrettyTable' library by the following command:
 conda install -c synthicity prettytable=0.7.2
 - b. Install 'ReportLab' library by the following command:conda install -c maggie-m reportlab=2.7
- 3. Depending on your operating system (Windows, iOS, or Linux), download the suitable version of PyCharm community edition from the URL: https://www.jetbrains.com/pycharm/download/ and install it.
- 4. You can perform the initial configuration of PyCharm as instructed here: https://www.jetbrains.com/help/pycharm/2016.1/quick-start-guide.html

In-Project steps.

5. Open a new project, then at the settings (File\Settings or Crtl+Alt+S), then configure the interpreter to point to python.exe at the Anaconda folder.

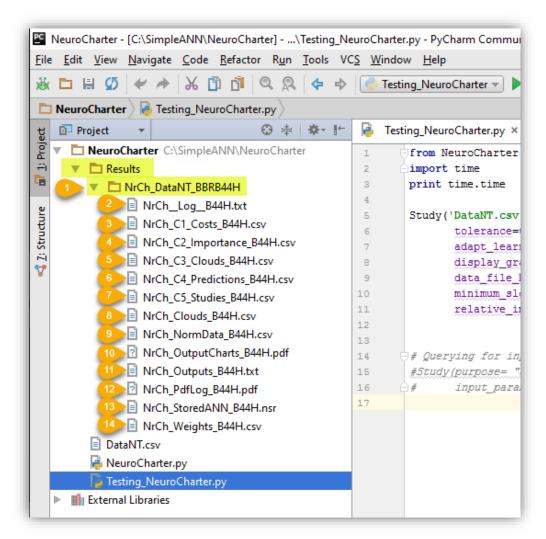


- 6. At the project folder put the following files (All are downloadable from the GIT page https://github.com/drnesr/NeuroCharter):
 - a. NeuroCharter.py
 - b. Testing_NeuroCharter.py
 - c. DataNT.csv
- 7. Open the Testing_NeuroCharter.py file by double-clicking it, the view will looks like the following:



8. Press the 'Play' button (marked at the screen shot above). The program will run for few seconds then the results will be placed in a subfolder under the 'Results' folder (Which will be created if

not exists), the subfolder's name (#1 below) contains 3 parts, the first is 'NrCh' as for NeuroCharter, then the source data filename, then an encrypted timestamp to ensure the uniqueness of folders names.



The folder contains a set of 13 files, which include:

- a. The complete log of the full run (files #2 and 12 in txt and pdf formats),
- b. A pdf file contains all the output charts of this run including a sketch of the neural networks, file #10.
- c. ... and the detailed data that was used in the charts in csv format (files #3-7),
- d. The normalized form of the data, file #9.
- e. Readable form of the outputs, file #11.
- f. A Neural Structured Repository file (*.nsr) that stores the network architecture and the data limits, in order to be used for querying data in the future, file #13.

- g. A csv file contains the weights of the network that can be imported for future training if required, file #14.
- 9. To perform query from an existing *.nsr file, please put the file at the root directory of the project as follows:

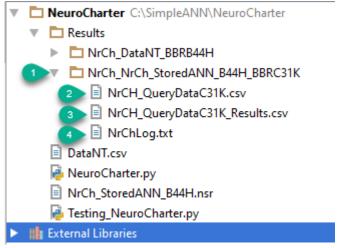
```
□ NeuroCharter C:\SimpleANN\Neu □ from NeuroCharter import Study
                                  import time
  Results
                                  print time.time
   ▶ ☐ NrCh_DataNT_BBRB44H
   DataNT.csv
                                  # Study('DataNT.csv', 'cross validation', num_outputs=4, data_partition=(75, 15),
   NeuroCharter.py
                                           tolerance=0.0000001, learning_rate=0.4, maximum_epochs=100,
   ■ NrCh_StoredANN_B44H.nsr
                                            adapt_learning_rate=False, annealing_value=2000,
   Testing_NeuroCharter.py
                                            display_graph_windows=False, display_graph_pdf=False,
                                            data_file_has_titles=True, data_file_has_brief_titles=True,
III External Libraries
                                           minimum_slope_to_consider_overfitting=2, number_of_epochs_for_overfit_check=10, relative_importance_method="\f"")
                                   # Querying for inputs: Temperature, Relative Humidity, Radiation, Site
                                  Study(purpose= "advanced query", previous_study_data_file="NrCh_StoredANN_B44H.nsr", start_time=time.time(),
                                       input parameters suggested values= ([10, 45, 5], 7.5, (0.5, 0.8), ('A', 'C')))
```

then write the command line as shown (and comment the original command by selecting all its lines and pressing Ctrl +?. Notice that the 'Advanced query mode allows entering the input data in three methods:

- a. A python range-form, by entering three values between square brackets, the 1st value is the start, the 2nd is the end (not included) and the 3rd is the step. For example, [1, 15, 3] will be translated as (1, 4, 7, 10, 13).
- b. A single value, either numeric or string, like 7.5 or 'B'.

A set of fixed values, that are placed between parenthesis, like (2, 6, 45).

The program creates a set of all possible permutations from the given values, then it executes the stored ANN to get the corresponding outputs, putting them in a new subfolder under 'Results'



folder, with the source *.nsr filename in its middle portion (#1 as seen bellow):

The data file is stored as #2, and the result prediction is as in #3, while the log file is #4.

The '_Results' files can easily imported to excel for analysis.