FireLearn GUI v0.5.0-alpha: Walkthrough tutorial

This document is aimed at the users of FireLearn GUI.

This README file will use the firelearnGUI_demo data that is available on the github in the `demo` folder as a .zip file.

Processing

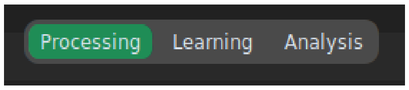
> Please note that the different processes are following a specific sequence, and can not be modified at the moment. Consider the order to be the order of presentation of the functionalities in this document. As such, it can be considered to be
>
> sorting > file beheading > column-based selection > down sampling > filtering > fast fourier transform > interpolation > averaging electrode signal > dataset making > post-processing
>
> Depending on which feature is enabled or disabled.

Example: directory structure

For this document we will proceed considering this recommended directory structure :

```
DATA (most parent common directory)
|
└───condA
|   └───sample1
|   |   file.txt
|   |   rec1_Analog.csv
|   |   rec2_Analog.csv
|   |   rec3_Analog.csv
|   |   some_useless_file_Analog1.txt
|   └───sample2
|       └───[...]
└───condB
|   └───[...]
└───condC
    └───[...]
```

Processing steps

In the processing tab 

, you will find three image buttons, representing respectively `File selection` , `Signal processing` , and `File name post-processing` as below:

Clicking those will change the middle panel accordingly, allowing you to specify the different processing steps you wish to apply to your files and data. These buttons will change colors depending on the step value verification, as green for no errors detected, red for errors detected, blue for current selected panel (will also grow bigger), and gray for unvisited panel.

For the demonstration purpose, all the functions available will be enabled.

Sorting multiple files

This functionality aims at looking for and using multiple files under a common parent directory, no matter how distant it is.

Selecting parent directory

Click the `Open` button of `Path to parent directory` entry to select the parent directory. The selected directory must be a parent of all the files you want to process. For a multiple files processing, you *must* switch on the `Sorting multiple files` switch.

For instance, using this directory structure, all the files that are children to the most parent directory (here `/DATA`) are subject to be comprised in the processing.

To specify which files to include or exclude of the processing, refer to the include/exclude option.

Include and exclude files for the processing

With this functionality, you can specify which file to include or exclude from the selection. Both the inclusion and exclusion works by looking at the content of the absolute paths of the files (e.g. `H:\Electrical activity\DATA\condA\sample1\rec1_Analog.csv`).

As such, the inclusion uses the AND logic operator : **The file is included if ALL the `to include` specifications are present in the absolute path**. On the other hand, the exclusion uses the OR logic operation : **The file is excluded if ANY of the 'to exclude' specifications are present in the absolute path**. Combining both gates, a file will be included for the processing if its absolute path **contains all the `to include` specifications and none of the `to exclude` specifications**.

Those `to include` and `to exclude` specifications are case-sensitive, so `Analog.csv` is different from `analog.csv`.

To add a specification, type it in the corresponding entry, then either click on the `+` button, or press the `Return` key. To remove a specification, type it in the corresponding entry, then either click on the `-` button or press `Ctrl-BackSpace` combination.

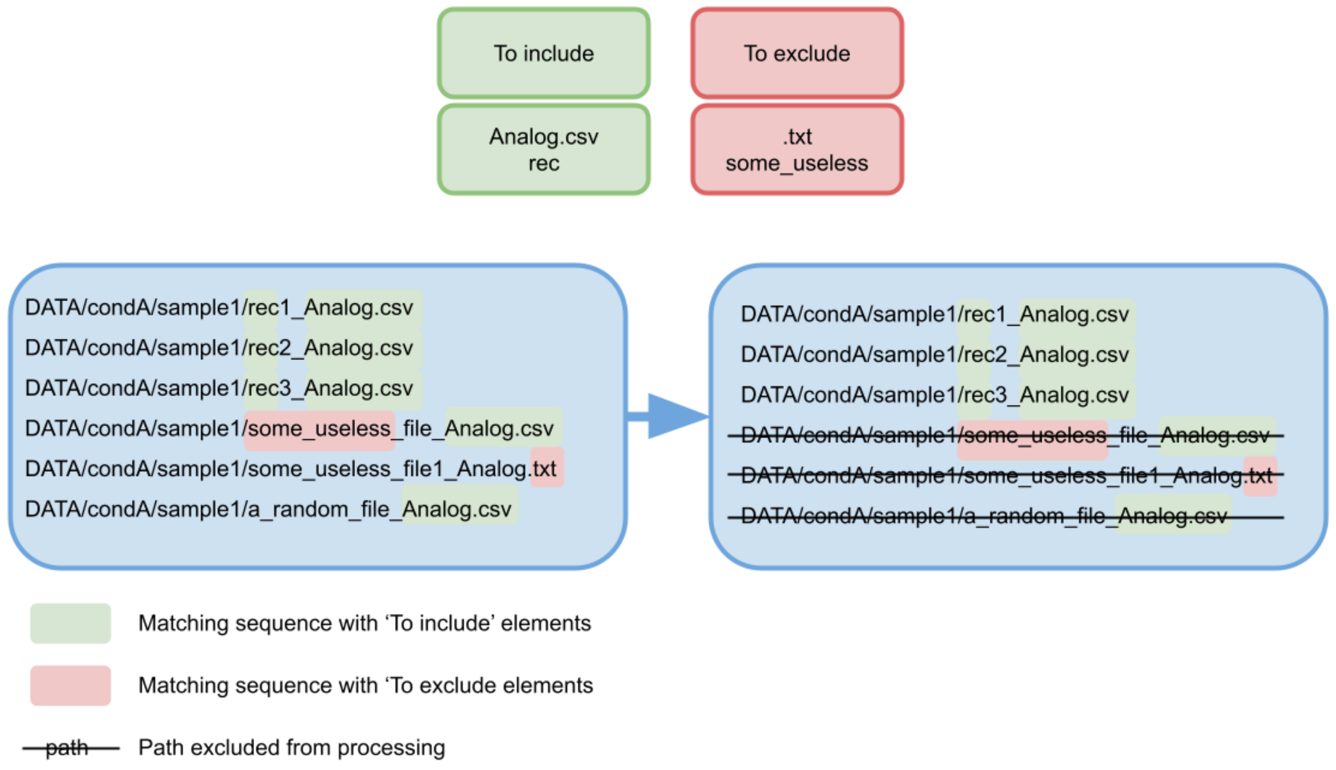
In this example, all the files containing `Analog.csv` and who does not contain `T30` in their absolute paths will be included for further processing.

> In the entries `to include`, `to exclude`, and `target key` you can use the key combination `Enter` as a substitute to the '+' button, and `Ctrl+Backspace` for the '-' button.

Indicating targets for learning

It is possible to make an entry correspond with a label, based on its path. To do so, indicate in the `Target key` entry a sequence of characters to find in the path of the file. Then indicate in the `Target value` entry the corresponding label. When creating the resulting files for the analysis, a `key` (label) will then be attributed to an entry.

E.g. : As per the following figure, only the files that contains "Analog.csv" **AND** "T0" **AND DO NOT CONTAIN** "TTX" in their absolute paths will be used for further processing.


To include
Analog.csv
rec
To exclude
.txt
some_useless
DATA/condA/sample1/rec1_Analog.csv
DATA/condA/sample1/rec2_Analog.csv
DATA/condA/sample1/rec3_Analog.csv
DATA/condA/sample1/some_useless_file_Analog.csv
DATA/condA/sample1/some_useless_file1_Analog.txt
DATA/condA/sample1/a_random_file_Analog.csv
DATA/condA/sample1/rec1_Analog.csv
DATA/condA/sample1/rec2_Analog.csv
DATA/condA/sample1/rec3_Analog.csv
~~DATA/condA/sample1/some_useless_file_Analog.csv~~
~~DATA/condA/sample1/some_useless_file1_Analog.txt~~
~~DATA/condA/sample1/a_random_file_Analog.csv~~
Matching sequence with 'To include' elements
Matching sequence with 'To exclude elements
~~path~~
Path excluded from processing

In our demonstration, we want to have our three conditions condA, condB, and condC. However, we want to rename them for the final dataset. Thus, we indicate the couples `condA => targetA`, `condB => targetB`, and `condC => targetC`, as `Target key` and `Target value` respectively.

Be it for including or excluding, the sequence will be searched in the absolute path and not only on the file name.

The said sequences does not search for "separated sequences" and does not recognise if the sequence is a word in itself. It will only look at the sequence character-wise. As such when choosing the sequences you want to include or exclude, be aware of what can be in your absolute paths.

> E.g.: Your project is in a folder named 'HIV PROJECT', and further away in the children folders you name the different recording conditions such as 'NI' (not infected), 'HIV' (infected by HIV) BUT to select the files you specify in To exclude 'HIV', **all of your files will be excluded since 'HIV' as a sequence is also present in the project folder 'HIV PROJECT' and not only as a 'condition'**.
>
> To remediate to such issue, it is possible to look for the sequence '/HIV/' (use your operating system path separator) instead to ensure that we only look at the folder named 'HIV' and not 'HIV PROJECT'.

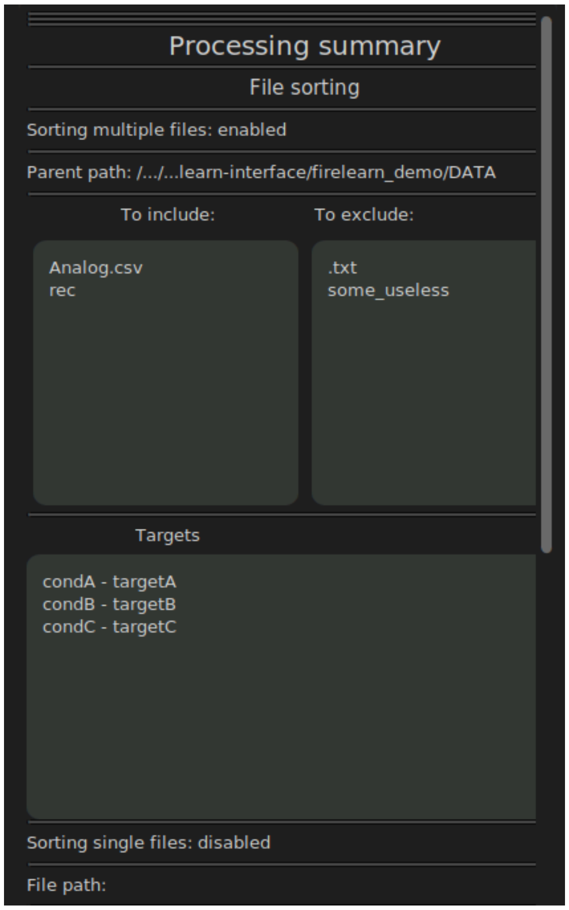
> 💡
>
> If you do not wish for your key to be different from your file label, you can leave the `Target value` entry empty - the value will take the same value as the key.

Single file analysis

In order to process a single file, switch on the corresponding switch and select the wanted file using the `Open` button.

On this demo, we will not use the 'Single file processing' option. Note that it is not compatible with the sorting multiple files option.

At this point, our summary of the 'File sorting' panel section should look like this:



Processing summary

File sorting

Sorting multiple files: enabled

Parent path: /.../...learn-interface/firelearn_demo/DATA

To include:	To exclude:
Analog.csv rec	.txt some_useless

Targets

condA - targetA
condB - targetB
condC - targetC

Sorting single files: disabled

File path:

File beheading

This functionality simply behead the file a specified number of rows. In the case of normed files from MEA recordings (as is our example), there is a header of 6 rows containing metadata before the actual recording data. Be aware that there must not be anything apart from the data and a row of headers for further processing.

Column-based selection

Allow to select the columns (electrodes, in case of MEA recordings) with a `mode` `metric` combination. Any column that contains the exception value (case-sensitive) in its header will be ignored.

In our demo we choose to keep the 35 columns with the biggest (max) standard deviation (std).

Down sampling

This functionality will divide row-wisely every file in `n` selected pieces of equal lengths. e.g. In our walkthrough example, we use 1 minute long recordings. Specifying a down sampling at `30` implies that the recordings will be divided in 30 pieces of 2 seconds.

In our demo, we choose to use 20, as it will produce sub-samples of 3 seconds.

> If the make resulting files as dataset function is not used, be aware that each file selected during the selection process will generate an equal number of different files based on the down sampling.

Filtering

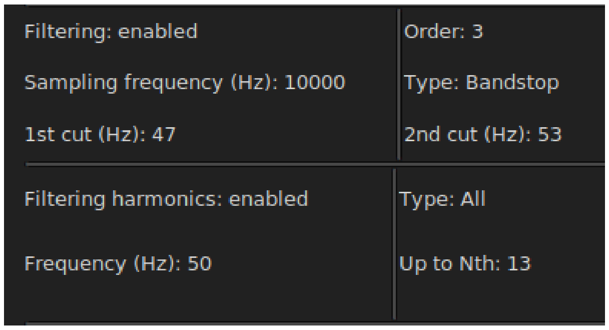
Allow the user to apply a Butterworth filter to the data.

For the use of `Lowpass` and `Highpass` filters, the first frequency `1st cut frequency (Hz)` corresponds to the cut frequency, and the second frequency `2nd cut frequency (Hz)` must be left emptied. For the use of `Bandstop` and `Bandpass` filters, the second frequency `2nd cut frequency (Hz)` corresponds to the high-cut frequency and must be specified.

In order to filter harmonics, the user can choose to filter only the `Even` harmonics (2nd, 4th, 6th...), or the `Odd` harmonics (1st, 3rd, 5th...) or `All` (1st, 2nd, 3rd, 4th...) up till the `nth` harmonic.

E.g. with an harmonic frequency of 100 Hz, filtering the odd harmonics up to the 10th will filter the following frequencies : *100 Hz(1st), 300 Hz(3rd), 500 Hz(5th), 700 Hz(7th), 900 Hz(9th)*

For the demonstration, we use the following parameters (screenshot from the summary panel):



Filtering: enabled	Order: 3
Sampling frequency (Hz): 10000	Type: Bandstop
1st cut (Hz): 47	2nd cut (Hz): 53
Filtering harmonics: enabled	Type: All
Frequency (Hz): 50	Up to Nth: 13

Fast Fourier Transform

Applies a Fast Fourier Transform to the data (post-filtering, if the filtering is enabled). The sampling rate must be specified.

In the demonstration case, we have a sampling rate of 10000 Hz

Interpolation

Use a linear interpolation on the signal down to `n` final values. `n` must be inferior to the number of data point.

For the demonstration we choose to down-interpolate the 10000 values into 1000 values.

Averaging columns

Average all columns (except the exception column, usually the time) into one column.

We enable this feature in the demonstration.

Exception column

Allow the user to specify a character chain that will exclude certain columns from the processing. If the entered value is **found** in a column name in the file, this column will then not be processed if possible (e.g. when averaging columns, or selecting columns)

In our demonstration, we choose to except our column `Time` .

> ⚠
>
> Note that this feature looks for the value in the column name, and does not require the column name to be exactly the same as the Exception value.
>
> e.g. 'Time' is found in 'TimeStamp [µs]' so this column will be excluded from processing. However, 'time' is not found in the column name (case-sensitive function).

Resulting datasets

> ⚠
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> This feature overwrites the saving of the intermediate files (e.g. those created from the down sampling functionality) and save only a final file 'DATASET' csv file.

> ⚠
>
> This feature is only available if the average electrode signal is enabled.

Enabling this feature will merge all the processed files issued from the signal averaging such as each merged signal results in one row in the dataset.

We enable this feature for the demonstration.

Post-processing

The `Add random key` option allows to add a random key as combination of 6 alphanumerical characters to the resulting filenames.

The `Add timestamp to file names` adds a timestamp of format `year-month-day-hour-minute` (at the time the file is being processed).

The `Add keyword` adds a specified keyword to the resulting filenames.

> ⚠
>
> These customisations do not replace the file name, which will depend on the processes it will undergo. They only are added at the end of the standard file name.

The `Specify file name` allows the user to specify the file name(s). A tag '_FL_processed' is added at the end.

The `Save processed files under` allow to specify the directory where the resulting files will be saved.

For the demonstration, you are free to specify what you wish. In our case, all specifications are disable except for the `Specify file name` set to `demo_dataset`. The dataset is daved under the `DATASETS` forlder of the demonstration.

Note that the extension is not required when specifying a file name.

Then, you can click the `Process` button to start the processing (this operation may be a bit time-consuming depending on the scale of the processing).

Miscellaneous

Check all steps

On the left side of the processing tab, you have a `check all steps` button. It allows you to check if there are any errors of teh different fields you filled. If so, a popup will show with some error context. The processing steps where errors have been spotted will be red colored.

> ⚠
>
> The software will only check for simple errors such as if you wrote letters where numbers where expected. Additionally it will check for errors in the options that have been checked, for example if incompatible options have been both enabled.

Open config / Load config

> ⚠
>
> This functionality is in experimental phase so bugs may occur

On the menu bar, in `File` > `Save config`, it will store the software variable state into a `.pcfg` file. This file can then be opened with the the `Load config` option to restore the software variable state, to avoid having to fill everything again between different runs of the software if the same (or close) processing is needed.

Summary (and export)

On the right side of the processing tab, there is a 'Summary' panel that will update based on the processing steps selected and their values. This summary can be exported using the `Export summary` button on le left side. It will produce a `.txt` file that sums up all the processing steps used when exporting.

Learning

At this moment, FireLearn offers only the possibility to use Random forest classifier. With time, many more algorithms will be added.

Random Forest classifier

We use random forest classifier of the `scikit learn` library, as of version 1.3.1. On the left panel, there are the parameters than can be used with the RFC. To know how to modify them or what they are, please refer to the scikit-learn documentation .

Splitting

On the middle panel, you can either split your dataset or train/test an RFC instance on your data. Either way, you need to load your dataset in the 'load dataset' section. It is recommended to keep a train/test ratio of 0.7 (70% of the data in the train set), as good practice, except for large datasets. The `Split` function will create two .csv files have the same name as the original dataset with `Xy_train` or `Xy_test` . Those sub datasets are the ones to be used on the train and test sections, respectively. The split is done row-wisely. Before splitting, the dataset is randomly shuffled, and the splitting is done by respecting the ratio of elements in a column named `label` in the dataset that correspond to the labels of each row, usually obtained by the processing functions of the software.

In future versions, it will be possible to select the label column before splitting.

For the demonstration, we split our previously computed dataset with a 0.7 ratio.

Training and testing

After loading the train and test datasets, it is needed to select the target/label column. In the next field, add the targets you wish to train your RFC instance on.

Tre `Train/test iteration` option allows to train the model multiple times, and return average metrics in the right panel 'METRICS', and save le last trained.

> ⚠
>
> In future versions, it will actually keep only the best performing model out of the n iterations, instead of averaging results and returning the last trained.

In our demonstration case, our label column is `label` , and we want to train our model on targets `targetA` and `targetB` .

You can specify the model hyperparameters on the left panel. They are at the documentation state by default. To know what are the allowed values, please refer to the scikit-learn documentation.

As quick start, you can change the `n_estimator params` that represents the number of trees in the forest and the `criterion` which is the function to measure the quality of a split. For our demo, we set them as `150` and `entropy` respectively.

K-Fold Cross Validation

You can choose to enable or disabled K-Fold cross validation using the Checkbox, and specifying a number of folds in the entry. It is recommended to keep it enabled to detect potential overfitting that may happen.

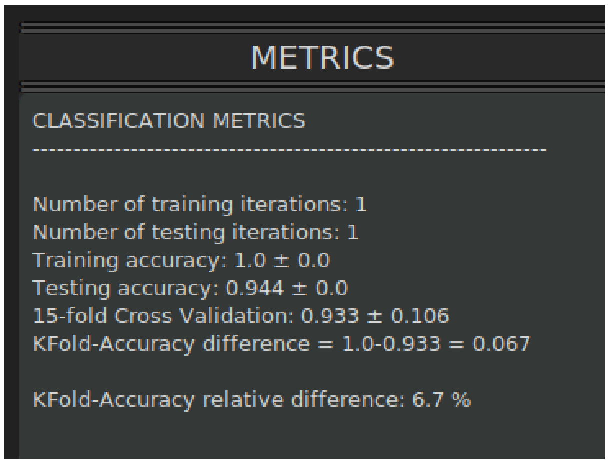
Usually, it is preferred to keep it between 5 and 15, depending on the size of you dataset, 5 being better for small datasets and 15 for big datasets. You are however free to go above 15 if you consider you dataset to be big enough.

The risk of overfitting can be subjectively considered depending on the K-Fold CV scores, such as below.

> Note: Those are only subjective indicators, and may or may not be appropriate considering your problematic

Range (%)	Overfitting risk
0-2	Minor
2-5	Moderate
5-10	Significant
10-100	Very high

In the demonstration case, we have the following metrics after fitting:



```
METRICS

CLASSIFICATION METRICS
--------------------------------------------------------------

Number of training iterations: 1
Number of testing iterations: 1
Training accuracy: 1.0 ± 0.0
Testing accuracy: 0.944 ± 0.0
15-fold Cross Validation: 0.933 ± 0.106
KFold-Accuracy difference = 1.0-0.933 = 0.067

KFold-Accuracy relative difference: 6.7 %
```

> Note: Those metrics may change slightly between users, and between each run, as some steps in the learning and in the processing involve random steps (shuffling, etc.).

Saving

at last, you can choose to save your trained RFC instance in order to use it later, such as when computing confusion matrices.

For the demonstration purpose we save it as `MODELS/demo_classifier.rfc`

Analysis

> Note that on most analysis tabs, in the figure section, you have a toolbar directly issued from matplotlib. It will allow you to resize the figure, zoom in/out, save the figure, and other.

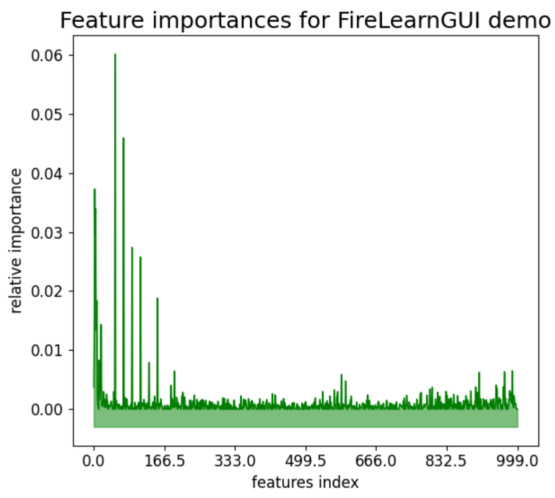
> Note that on most analysis tabs, only the `SPECIFIC PARAMETERS` panel will change significantly, as the other sections are for the plot customization and not related to the data itself.

Features importance

> This feature has only been tested in the case of an RFC instance created using this software. It should be able to process any RFC instance created using scikit-learn if the versions are compatible, but it has not been tested, so use at your own risk.

This functionality allows the user to plot the relative feature importances of a loaded Random Forest classifier, in the corresponding section in the middle panel `SPECIFIC PARAMETERS` . All the other options on the other panels are to customize the plot such as the title, labels, axes, and so on.

In the demonstration case, after loading the previously fitted model, tweaking some plot parameters, and drawing the figure, we should have something similar :



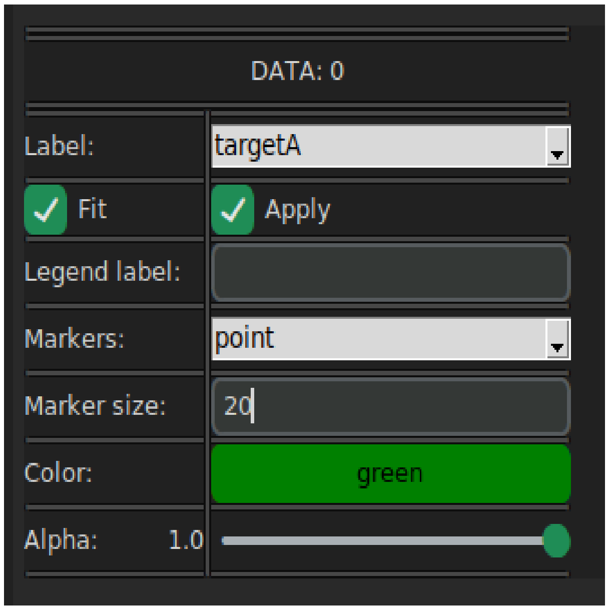
Principal Component Analysis

To use the principal component analysis, you first need to load your dataset using the `load dataset` button.

If your dataset contains a column with 'label' or 'target' in its name, it will automatically be selected as the label column. Else, you need to select it manually using the combobox.

By default, no data is analyzed. To do so, use the `Add data +` (or `Add data -` to remove) to add data that will be analyzed.

The following section should appear in the middle panel:


DATA: 0

Label: targetA

Fit ✓ Apply ✓

Legend label:

Markers: point

Marker size: 20

Color: green

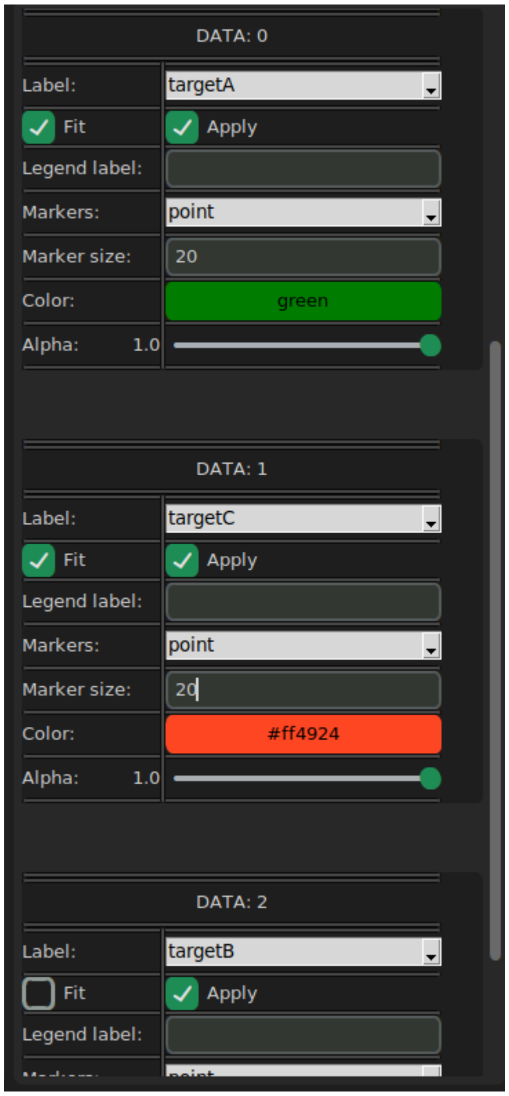
Alpha: 1.0

The `label` combobox will allow you to select which label you want to analyze with PCA. The proposed values are based on the unique values in the `labels column` specified beforehand. Make sure your `labels column` is correct.

You can choose whether to fit, apply, or fit and apply the PCA transformation on the said label. After this is customization for this label.

> ⚠
>
> Beware, as scrolling the middle mouse button above a combobox will change its value. The scrolling of the panels with the middle mouse button are yet to be implemented.

For the demonstration we chose to fit our PCA on ours targets `targetA` and `targetC` , and apply on our three targets, as in the following screenshot:


DATA: 0

Label:	targetA
✓ Fit	✓ Apply
Legend label:	
Markers:	point
Marker size:	20
Color:	green
Alpha: 1.0	

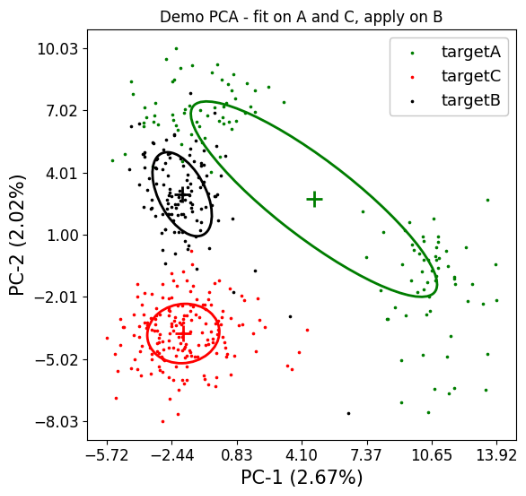
DATA: 1

Label:	targetC
✓ Fit	✓ Apply
Legend label:	
Markers:	point
Marker size:	20
Color:	#ff4924
Alpha: 1.0	

DATA: 2

Label:	targetB
☐ Fit	✓ Apply
Legend label:	

Computing the PCA and drawing it (after tweaking some graphical parameters) would show results similar as the following:



Confusion matrix

The confusion matrix is a plot showing the prediction performance of a machine learning model on provided data.

To use it, you will need to have a trained machine learning instance (at the moment, only RFC support is provided), and a test dataset.

> You **MUST** have a test dataset, independent of a training dataset that have been used to train your machine learning instance. Your machine learning instance must not have already seen any of the data present in your testing dataset, as this issue is known as 'data leakage', and will cause serious issues and may invalidate any results obtained. To make sure that you produce no data leakage, you can use the splitting feature of the `Learning` section of this software, and use the `_Xy_train.csv` file to train your model and the `_Xy_test.csv` file for your testing and analysis.

Once the testing dataset and the classifier have been loaded, if your dataset contains a column with 'label' or 'target' in its name, it will automatically be selected as the label column. Else, you need to select it manually using the combobox.

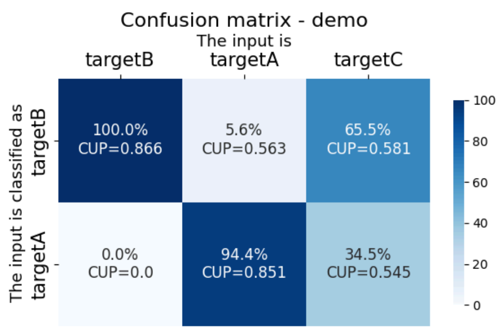
> When selecting a label column, its unique values will be shown as testing labels in the corresponding section in the `SPECIFIC PARAMETERS` panel. If you miss click and no do select your label column, or if there is too many unique values to unpack, a warning window will pop up. It is advised to not proceed, as too many values to unpack may crash the software.

The training section shows you what labels the machine learning instance has been trained to classify. The testing section allows you to select on which one of the labels contained in your dataset you want your machine learning instance to predict.

You can then choose to have to results presented on percentage or numeric mode, and whether you decide to annotate only the CUPs (Confidence Upon Prediction) onto your confusion matrix or having also the percentage/numerical value.

> Note that `compute confusion` will do the whole computation and display the figure according to the specified parameters in the other panels, so the process may be long. If you only want to change the plot appearance (axes, titles...), please use the `update figure` button.

In our demonstration, we loaded the `demo_dataset_Xy_test.csv` dataset, and enabled the classification on all three of our targets A, B and C. After computing, we obtained a result similar as following:

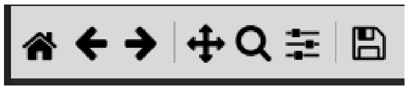


As of now, you can not choose the position of the columns and rows, and they will appear on a basis of "first-encountered in the dataset, first-drawn" which can be highly inconvenient for readability purpose. Note that this issue is in our priority list to fix for future versions.

Miscellaneous

Plot customization toolbar

For every plot, after drawing, you will have access to the following toolbar under the plot canvas:



This will allow you to navigate in your plot with the following functionalities respectively:

- "Home" : Reset to original view
- "Left arrow" : Back to previous view
- "Right arrow" : Forward to next view
- "Cross arrow" : Move and slide in the plot. The left button pans, the right button zooms. Holding CTRL keep the aspect.
- "Lens" : Zoom in with left click, zoom out with right click.
- "Configure": configure plot aspect (spaces on the sides of the figure etc.)
- "Save" : save the figure as it is now (keep the changes done with the previous tools).

Issues and suggestions

Note that multiple features are already planned, such as simple data plot, spike detection, more machine learning models, more customization on some analysis types... for future versions.

However, if you have any suggestion, you are free and welcomed to use the issues section of the GitHub repository, and to use the in-place tags system to specify your post, such as below.

Tag	Description
Bugs	Something isn't working
Documentation	Improvements or additions to documentation
Duplicate	This issue or pull request already exists
Enhancement	New feature or request
Good first issue	Good for newcomers
Help wanted	Extra attention is needed
Invalid	This doesn't seem right
Question	Further information is requested
Wontfix	This will not be worked on