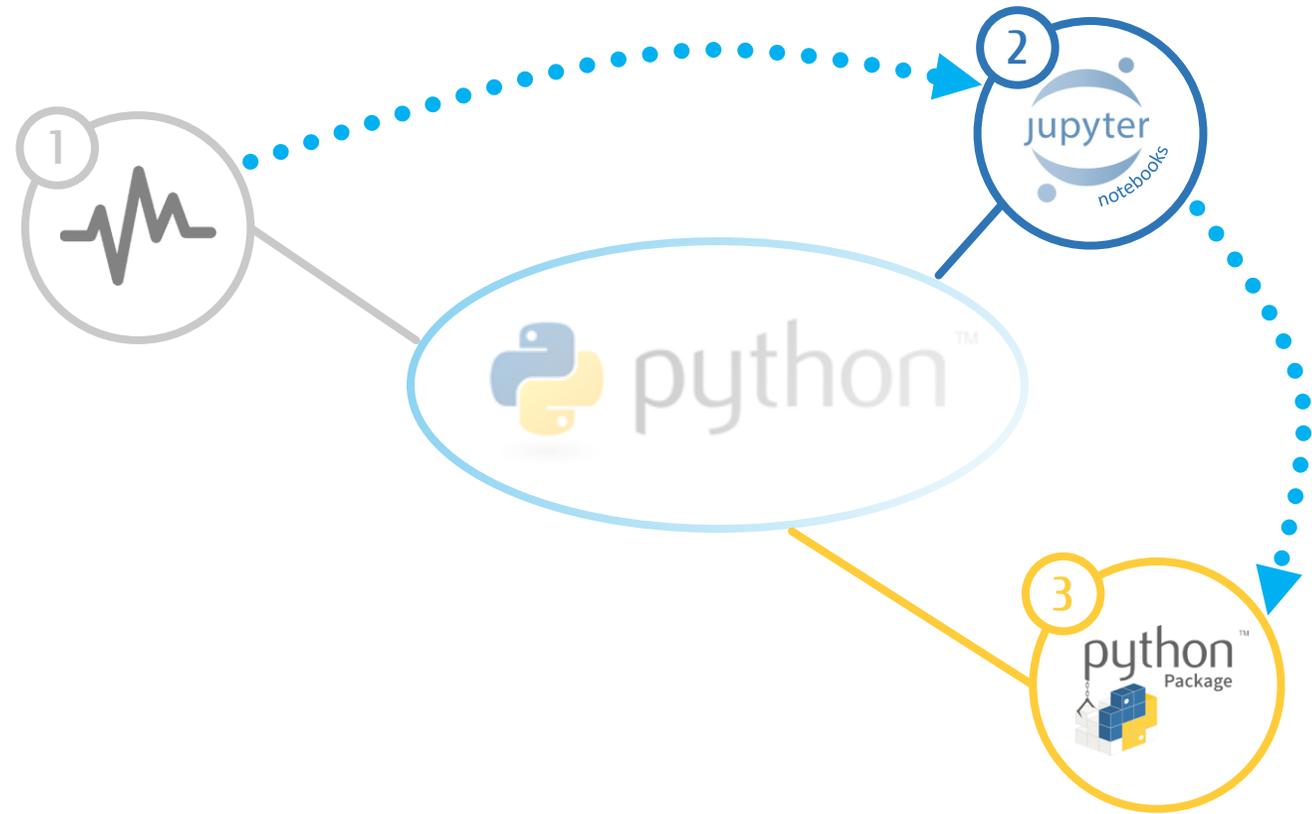


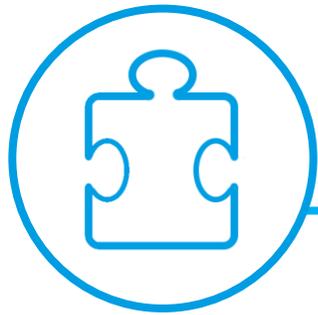
biosignals
notebooks

Description

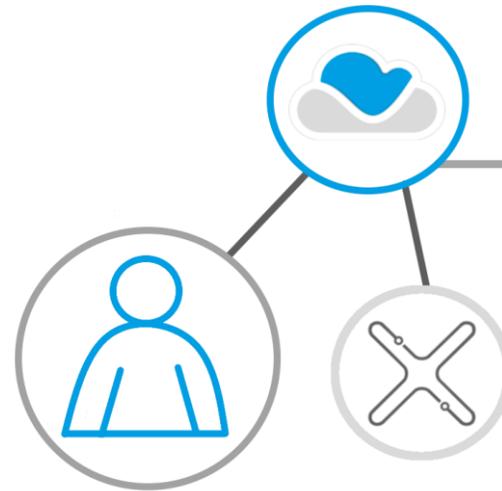
Through Python language, some signal processing tasks ① are illustrated following a step by step methodology supported by Jupyter Notebook ② environment. This interactive experience can be complemented and developed with the biosignalsnotebooks ③ Python package, which synthesises the described processing functionalities in different modules and their functions.



✕ Purposes



Extension of OpenSignals

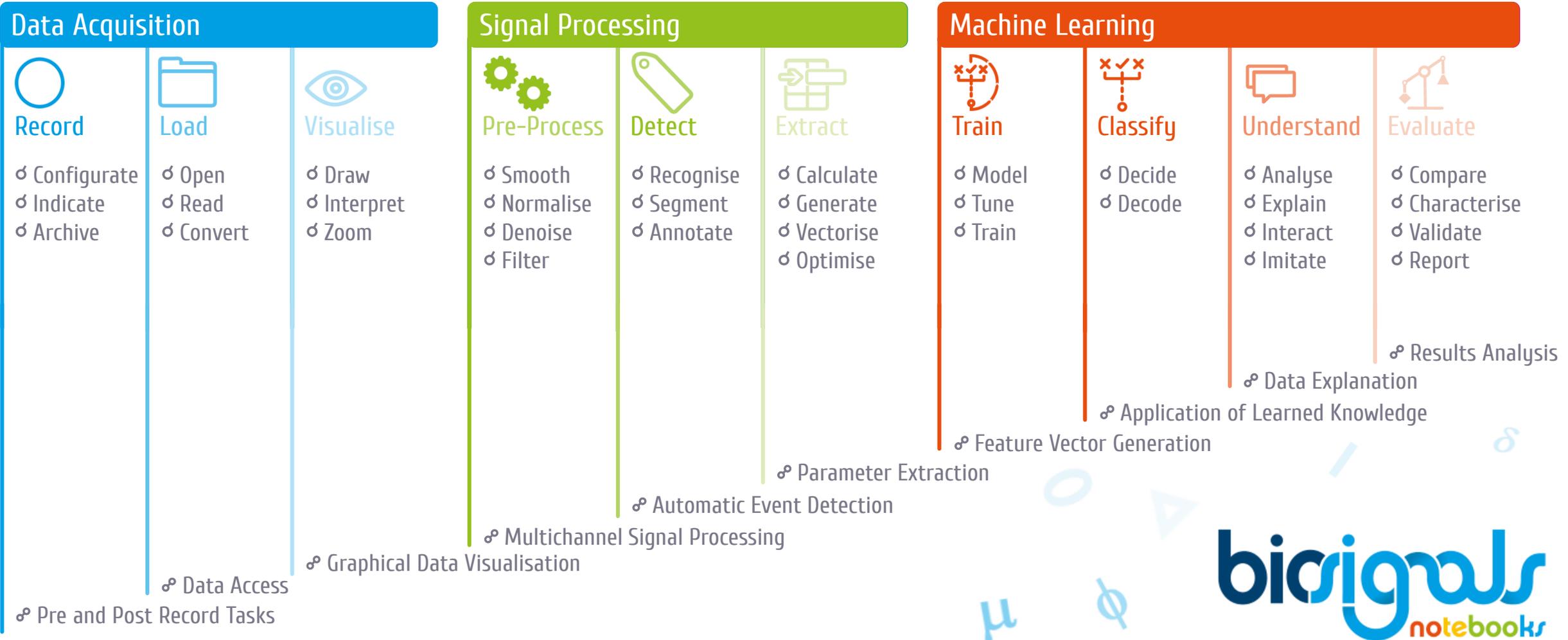


Open Contribution
to the User



Facilitates Learning

✕ Notebook Categories



Notebook Example





Notebook Title

Difficulty Level: ★★★★★ Tags tag_list

Presentation of a small description of the notebook content

1 - Step 1 description

```
In [2]: # Python code
```

...



Load the acquired data from .h5 file

Difficulty Level: ★★★★★ Tags load|h5

For storing large amounts of data a .h5 (hierarchical data format) file defines an interesting approach. This is one of the predefined outputted files formats of [OpenSignals](#) .

It will be explained how to load/transpose the data inside .h5 file to a [Python](#) list, that can easily be manipulated in the processing operations.

1 - Importation of the needed packages

```
In [1]: # Package used for Loading data from the input h5 file
import h5py
```

2 - Creation of a h5py object from the file named "biosignalsplus_Electrocardiogram_(ECG)_Sample.h5"

```
In [2]: file_folder = "signals"
file_name = "biosignalsplus_Electrocardiogram_(ECG)_Sample.h5"
file_path = file_folder + "/" + file_name
h5_object = h5py.File(file_path)
```

...

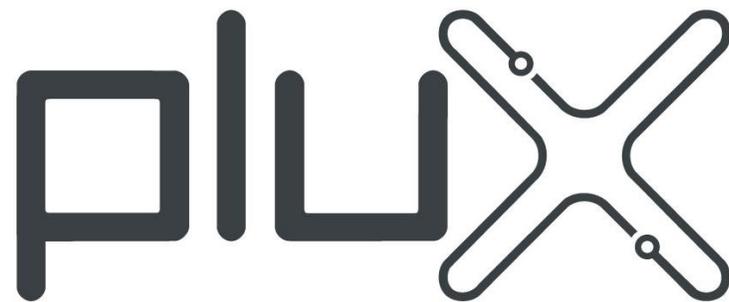
✕ Link to biosignalsnotebooks



Image Source: 



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