

Tutorial_0.0.9

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1 Tutorial - Pysiology 0.0.9

In this tutorial I will show how to analyze ECG, EMG and EDA signal easily with Pysiology.

First, we need to import the library. If installed correctly, the version should be printed.

```
In [1]: import matplotlib.pyplot as plt #used for visualization purposes in this tutorial.
import numpy as np
import pysiology
print(pysiology.__version__)
```

0.0.9.001

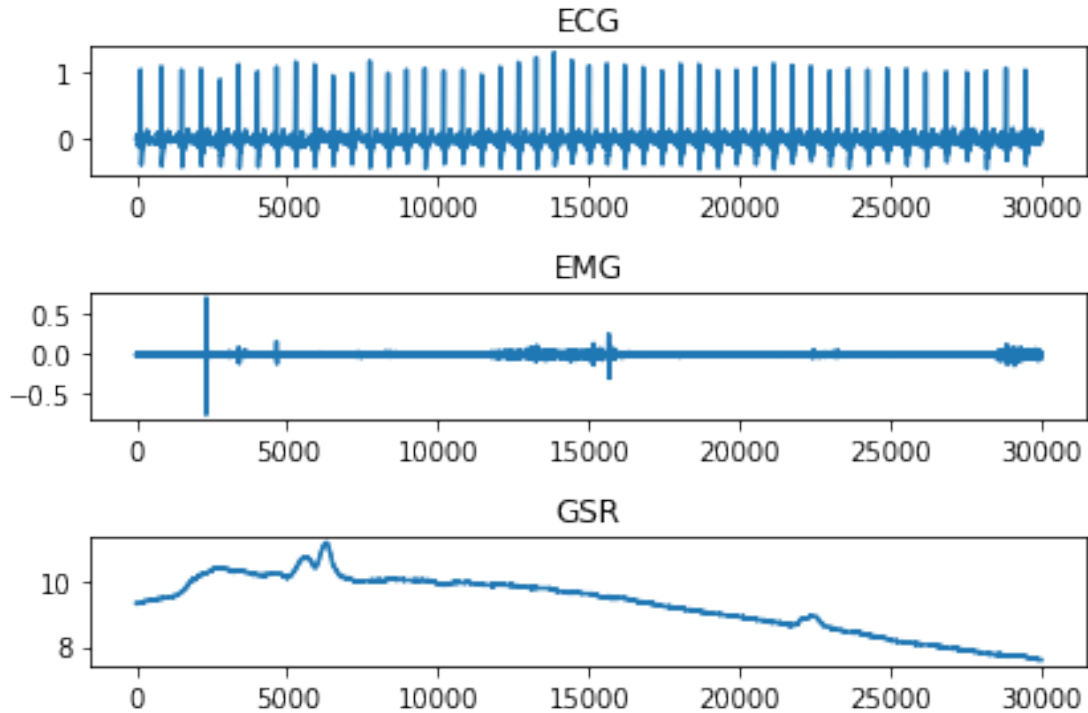
For this tutorial, I will use the sample data contained inside the package. We can load it through the `sampladata` method.

Sample data have been recorded using Bitalino Revolution Board at 1000 Hz.

```
In [2]: ECG = pysiology.sampladata.loadsampleECG() #load the sample ECG Signal
EMG = pysiology.sampladata.loadsampleEMG() #load the sample EMG Signal
GSR = pysiology.sampladata.loadsampleEDA() #load the sample GSR Signal

sr = 1000 #samplerate in Hz
```

```
In [3]: plt.figure("Sample data")
plt.subplot(3,1,1)
plt.plot(ECG[0:30000])
plt.title("ECG")
plt.subplot(3,1,2)
plt.plot(EMG[0:30000])
plt.title("EMG")
plt.subplot(3,1,3)
plt.plot(GSR[0:30000])
plt.title("GSR")
plt.tight_layout()
```



Let's say that we have two fake events, A and B, at 10 seconds (10'000 in samples) and 20s (20'000 in samples), and we want to compute the features from the onset of the event to 8 seconds later.

```
In [4]: #We can define the event in the way we prefer.
#In this example I will use a 2 x nEvent matrix, containing the name of the event and
events = [["A",10],
          ["B",20]]
eventLenght = 8 #lenght in seconds we want to use to compute feature estimation
results = {} #we will store the results in a dict for simplicity.
for event in events:
    startSample = sr * event[1] #samplerate of the signal multiplied by the onset of t
    endSample = startSample + (sr * eventLenght) #Final sample to use for estimation
    results[event[0]] = {} #initialize the results
    results[event[0]]["ECG"] = physiology.electrocardiography.analyzeECG(ECG[startSample:
    results[event[0]]["EMG"] = physiology.electromyography.analyzeEMG(EMG[startSample:

In [5]: # GSR features are listed by peaks
results["GSR"] = physiology.electrodermalactivity.analyzeGSR(GSR,sr,phasic_seconds=4) #
```

Results of features extraction are store inside the results dictionary.

We can try to print some of the results. For example, the BPM of the two events.

```
In [6]: #BPM from the ECG analysis
print("Example of ECG features:")
```

```

print("BPM - A",results["A"]["ECG"]["bpm"])
print("BPM - B",results["B"]["ECG"]["bpm"])

#peak frequency from the EMG analysis
print("Example of EMG features:")
print("Peak Frequency - A",results["A"]["EMG"]["FrequencyDomain"]["PeakFrequency"])
print("Peak Frequency - B",results["B"]["EMG"]["FrequencyDomain"]["PeakFrequency"])

print("Example of GSR Feature:")
print("Eda at Apex of the first peak",results["GSR"][0]["EDAatApex"]) #here we use 0 b

```

Example of ECG features:

BPM - A 97.5

BPM - B 90.0

Example of EMG features:

Peak Frequency - A 23.4375

Peak Frequency - B 27.34375

Example of GSR Feature:

Eda at Apex of the first peak 8.24983933156