Tutorial Pysiology

April 20, 2018

1 Tutorial - Pysyology 0.0.8

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 pysiology
        print(pysiology.__version__)
```

```
0.0.8
```

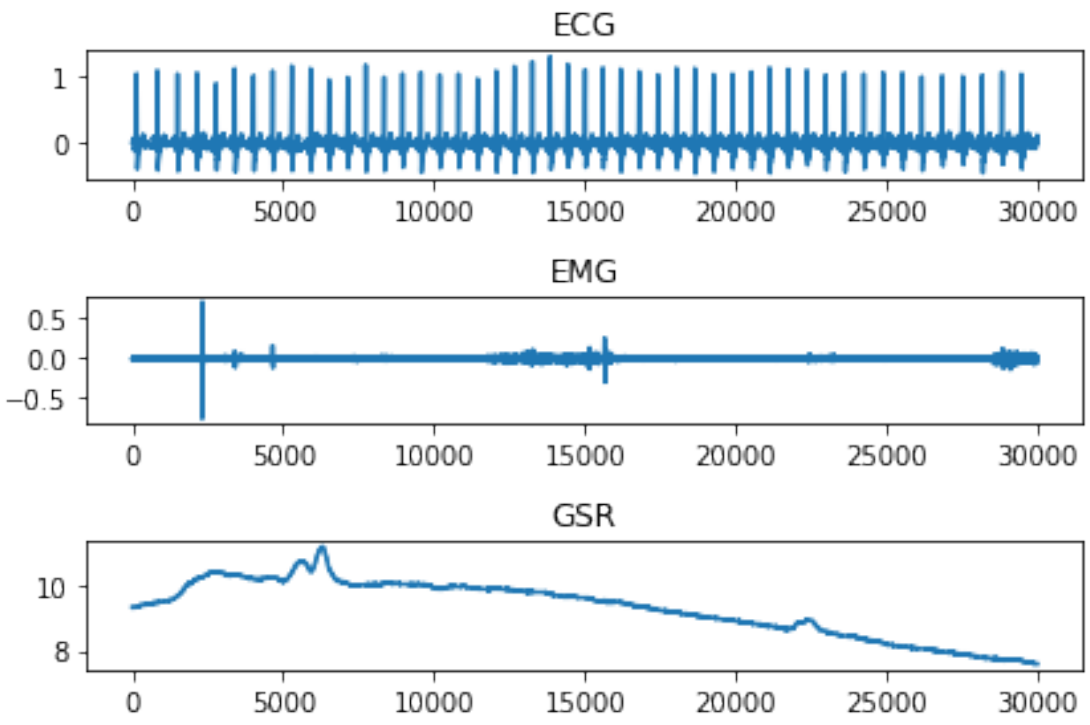
For this tutorial, I will use the sample data contained inside the package. We can load it through the sampledata method.

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

```
In [2]: ECG = pysiology.sampledata.loadsampleECG() #load the sample ECG Signal
        EMG = pysiology.sampledata.loadsampleEMG() #load the sample EMG Signal
        GSR = pysiology.sampledata.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"] = pysiology.heartrate.analyzeECG(ECG[startSample:endSample
            results[event[0]]["EMG"] = pysiology.electromiography.analyzeEMG(EMG[startSample:en
            results[event[0]]["GSR"] = pysiology.electrodermalactivity.analyzeGSR(GSR[startSam
```

Results of features extraction are not store inside the results dictionary.
We can try to print some of the results. For example, the BPM of the two events.

```
In [5]: #BPM from the ECG analysis
        print("Example of ECG feature:")
        print("BPM - A",results["A"]["ECG"]["bpm"])
        print("BPM - B",results["B"]["ECG"]["bpm"])
```

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

        print("Example of GSR Feature:")
        print("Decay Time - A",results["A"]["GSR"][0]["decayTime"]) #here we use 0 beacuse GSR
        print("Decay Time - B",results["B"]["GSR"][0]["decayTime"])
```

```
Example of ECG feature:
BPM - A 97.5
BPM - B 90.0
Example of EMG feature:
Peak Frequency - A 23.4375
Peak Frequency - B 27.34375
Example of GSR Feature:
Decay Time - A 1.9
Decay Time - B 2.2
```