pecg Documentation

Author

Jan 31, 2024

PECG API REFERENCE:

CHAPTER

ONE

PHYSIOZOO ECG DOCUMENTATION

Digital electrocardiography biomarkers to assess cardiac conduction.

Based on the paper S. Gendelman et al., "PhysioZoo ECG: Digital electrocardiography biomarkers to assess cardiac conduction," 2021 Computing in Cardiology (CinC), 2021, pp. 1-4, doi: 10.23919/CinC53138.2021.9662857.

https://youtu.be/2tfL3wckNcQ

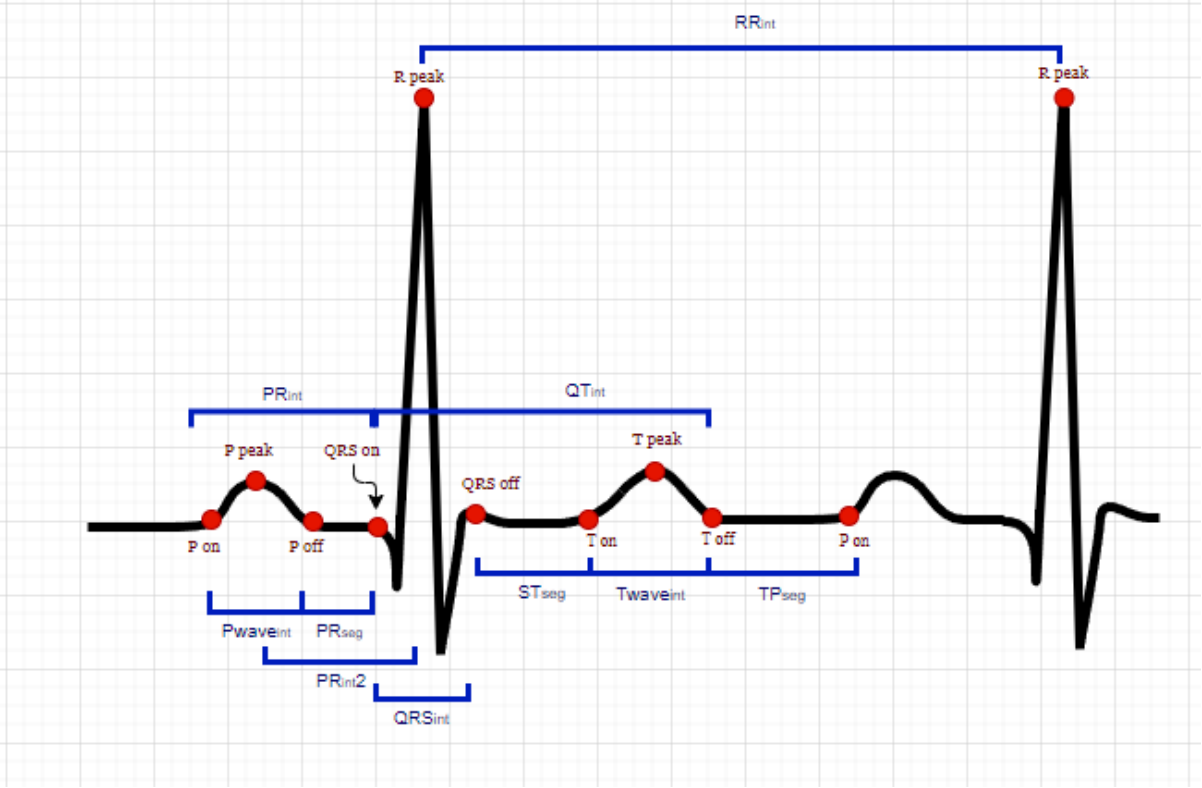
1.1 Introduction

The electrocardiogram (ECG) is a standard tool used in medical practice for identifying cardiac pathologies. Because the necessary expertise to interpret this tracing is not readily available in all medical institutions or at all in some large areas of developing countries, there is a need to create a data-driven approach that can automatically capture the information contained in this physiological time series. The primary objective of this package is to identify and implement clinically important digital ECG biomarkers for the purpose of creating a reference toolbox and software for ECG morphological analysis.

1.2 Description

Few steps are required to extract the morphological ECG biomarkers, those steps were implemented in the PECG toolbox:

1. ECG Signal Preprocessing - Before computing the ECG morphological biomarkers, prefiltering of the raw ECG time series is performed to remove the baseline wander and the high frequency noise. Specifically, the toolbox includes a zero phase second-order infinite impulse response bandpass filter with the passband of 0.67Hz - 100Hz. Also, the toolbox includes an optional Notch filter that can be set to 50 or 60Hz to remove the power-line interference.
2. ECG Fiducial Points Detection - The toolbox includes the epltd R-peaks algorithm, and the well-known wavedet algorithm for ECG fiducial points detection.
3. Engineering of ECG Biomarkers - Using the fiducial points ECG biomarkers are engineered for individual ECG cycles. When a biomarker cannot be engineered because some fiducial points could not be detected by wavedet, then the feature was marked as a NaN. For an ECG channel, a total of 14 features are extracted from intervals duration and 8 from waves characteristics to describe the ECG morphology.
4. Summary Statistics - For a specified time window the six summary statistics (mean, median, min, max, IQR and std) are computed for all ECG biomarkers.



1.3 Installation

Available on pip, with the command:

pip install pecg

1.4 Requirements

Python >= 3.6

numpy

mne

wfdb

All the python requirements except wfdb are installed when the toolbox is installed. To install wfbd run: pip install wfdb

1.5 System Requirements

To run the wavdet fiducial-points detector matlab runtime (MCR) 2021a is required.

If you wish to use the epltd peak detector additional wfdb toolbox is required.

If you don't want or can't install this - It's Ok! you can use another peak detector from the package.

1.6 Installation instructions:

1. Install the "pecg" package using pip by running the command line: "pip install pecg".
2. Install the "wfdb" package using pip by running the command line: "pip install wfdb".
3. Follow the guidelines provided in the link: https://www.mathworks.com/products/compiler/matlab-runtime.html, and choose the version of 2021a(9.10).

1.7 Documentation

https://pecg.readthedocs.io/en/latest/

An example code is available at https://github.com/aim-lab/pecg_tutorial/blob/main/FeatureEngineering.ipynb

1.7.1 pecg package

1.7.1.1 pecg.Example

pecg.Example.**load_example**(*ecg_type: str*) -> (<*class 'numpy.ndarray'*>, <*class 'int'*>)

The load_example function loads ECG signal from some of the PhysioNet open source datasets. There are three types of ECG examples: long single lead ECG, 12-lead and a Holter with two channels.

param ecg_type The type of the signal that you would like download: 'single-lead', '12-lead' and 'Holter'.

return

- signal: the ECG signal as a ndarray, with shape (L, N) when L is the number of channels or leads and N is the number of samples.
- fs: The sampling frequency of the signal [Hz].

```
import pecg
from pecg.Example import load_example
signal, fs = load_example(ecg_type='12-lead')
```

1.7.1.2 pecg.Preprocessing

class pecg.Preprocessing.**Preprocessing**(*signal: numpy.array*, *fs: int*)
Bases: object

The Preprocessing class provides some routines for pre-filtering the ECG signal as well as estimating the signal quality.

Parameters

- **signal** – the ECG signal as a ndarray, with shape (L, N) when L is the number of channels or leads and N i the number of samples.
- **fs** – The sampling frequency of the signal [Hz].

```
import pecg
from pecg.Example import load_example
from pecg import Preprocessing as Pre

signal, fs = load_example(ecg_type='single-lead')
pre = Pre.Preprocessing(signal, fs)
```

notch(*n_freq: int*)
The notch function applies a notch filter in order to remove the power line artefacts.

Parameters **n_freq** – The expected center frequency of the power line interference. Typically, 50Hz (e.g. Europe) or 60Hz (e.g. US)

Returns The filtered ECG signal, with shape (L, N) when L is the number of channels or leads and N is the number of samples.

```
filtered_ecg_rec = pre.notch(n_freq=60)
```

bpfilt()
The bpfilt function applies a bandpass filter between [0.67, 100] Hz, this function uses a zero-phase Butterworth filter with 75 coefficients.

Returns The filtered ECG signal, with shape (L, N) when L is the number of channels or leads and N is the number of samples.

```
filtered_ecg_rec = pre.bpfilt()
```

bsqi(*peaks: numpy.array = array([], dtype=float64)*, *test_peaks: numpy.array = array([], dtype=float64)*)
bSQI is an automated algorithm to detect poor-quality electrocardiograms. This function is based on the work of Li et al.[1] and Behar[2].

Parameters

- **peaks** – Optional input- Annotation of the reference peak detector (Indices of the peaks), as an ndarray of shape (L,N), when L is the number of channels or leads and N is the number of peaks. If peaks are not given, the peaks are calculated with jqrs detector.
- **test_peaks** – Optional input - Annotation of the anther reference peak detector (Indices of the peaks), as an ndarray of shape (L,N), when N is the number of peaks. If test peaks are not given, the test peaks are calculated with xqrs detector.

[1] Li, Qiao, Roger G. Mark, and Gari D. Clifford. "Robust heart rate estimation from multiple asynchronous noisy sources using signal quality indices and a Kalman filter." Physiological measurement 29.1 (2007): 15.

[2] Behar, J., Oster, J., Li, Q., & Clifford, G. D. (2013). ECG signal quality during arrhythmia and its application to false alarm reduction. IEEE transactions on biomedical engineering, 60(6), 1660-1666.

Returns The 'bsqi' score, a float between 0 and 1.

```
bsqi_score = pre.bsqi()
```

1.7.1.3 pecg.ecg

pecg.ecg package

pecg.ecg.FiducialPoints

class pecg.ecg.FiducialPoints.**FiducialPoints**(*signal: numpy.array*, *fs: int*)

Bases: object

The purpose of the FiducialPoints class is to calculate the fiducial points.

Parameters

- **signal** – the ECG signal as a ndarray, with shape (L, N) when L is the number of channels or leads and N is the number of samples.
- **fs** – The sampling frequency of the signal.[Hz]

```
import pecg
from pecg.Example import load_example
from pecg.ecg import FiducialPoints as Fp

signal, fs = load_example(ecg_type='Holter')
fp = Fp.FiducialPoints(signal, fs)
```

wavedet(*matlab_pat: str*, *peaks: numpy.array = array([], dtype=float64)*)

The wavedet function uses the matlab algorithm wavedet which was compiled for Windows OS for its usage in python. The algorithm is described in the the work of Martinez et al.[1]. The function is calculating the fiducial points of the ECG time series using the wavelet transform.

Parameters

- **matlab_pat** – path to matlab runtime 2021a directory
- **peaks** – Optional input- Annotation of the reference peak detector (Indices of the peaks), as an ndarray of shape (L,N), when L is the number of channels or leads and N is the number of peaks. If peaks are not provided they are calculated using the jqrs detector.

Returns fiducials: Nested dictionary of leads - For every lead there is a dictionary that includes indexes for each one of nine fiducials points.

```
matlab_pat = '/usr/local/MATLAB/R2021a'
fiducials = fp.wavedet(matlab_pat)
```

epltd()

This function calculates the indexes of the R-peaks with epltd peak detector algorithm. This algorithm were introduced by[2].

Returns indexes of the R-peaks in the ECG signal, as an ndarray of shape (L,N), when L is the number of channels or leads and N is the number of peaks.

[1] Martínez, Juan Pablo, Rute Almeida, Salvador Olmos, Ana Paula Rocha, and Pablo Laguna. "A wavelet-based ECG delineator: evaluation on standard databases." IEEE Transactions on biomedical engineering 51, no. 4 (2004): 570-581.

[2] Pan, Jiapu, and Willis J. Tompkins. "A real-time QRS detection algorithm." IEEE Trans. Biomed. Eng 32.3 (1985): 230-236.

```
peaks = fp.epltd()
```

xqrs()
This function wraps the XQRS function of the WFDB package.

Returns indexes of the R-peaks in the ECG signal, as an ndarray of shape (L,N), when L is the number of channels or leads and N is the number of peaks.

```
peaks = fp.xqrs()
```

jqrs(*thr: float = 0.8*, *rp: float = 0.25*)
The function is an Implementation of an energy based qrs detector[3]. The algorithm is an adaptation of the popular Pan & Tompkins algorithm[2]. The function assumes the input ecg is already pre-filtered i.e. bandpass filtered and that the power-line interference was removed. Of note, NaN should be represented by the value -32768 in the ecg (WFDB standard).

Parameters

- **thr** – threshold, default value is 0.8.
- **rp** – refractory period (sec), default value is 0.25.

Returns indexes of the R-peaks in the ECG signal, as an ndarray of shape (L,N), when L is the number of channels or leads and N is the number of peaks.

```
peaks = fp.jqrs()
```

pecg.ecg.Biomarkers

class pecg.ecg.Biomarkers.**Biomarkers**(*signal: numpy.array*, *fs: int*, *fiducials: dict*)
Bases: object

The purpose of the Biomarkers class is to calculate the biomarkers, we divided the morphological biomarkers into two main groups: intervals and waves.

Parameters

- **signal** – The ECG signal as a ndarray.
- **fs** – The sampling frequency of the signal [Hz].
- **fiducials** – Nested dictionary of leads - For every lead there is a dictionary that includes indexes for for each one of nine fiducials points. this nested dictionary can be calculated using the FiducialPoints module.

```
import pecg
from pecg.ecg import Biomarkers as Bm
from pecg.ecg import FiducialPoints as Fp
from pecg.Example import load_example

signal, fs = load_example(ecg_type='12-lead')
fp = Fp.FiducialPoints(signal, fs)
matlab_pat = '/usr/local/MATLAB/R2021a'
fiducials = fp.wavedet(matlab_pat)
bm = Bm.Biomarkers(signal, fs, fiducials)
```

(continues on next page)

[3] Behar, Joachim, Alistair Johnson, Gari D. Clifford, and Julien Oster. "A comparison of single channel fetal ECG extraction methods." Annals of biomedical engineering 42, no. 6 (2014): 1340-1353.

(continued from previous page)

```
ints, stat_i = bm.intervals()
waves, stat_w = bm.waves()
```

intervals()

Returns

- intervals_b: Dictionary that includes all the raw data, for the **Intervals and segments** biomarkers.
- intervals_statistics: Dictionary that includes the mean, median, min, max, iqr and std, for every **Intervals and segments** biomarker.

Table 1: **Intervals and segments**:

Biomarker	Description
P-waveint	Time interval between P-on and P-off.
PRint	Time interval between the P-on to the QRS-on.
PRseg	Time interval between the P-off to the QRS-on.
PRint2	Time interval between P-peak and R-peak as defined by Mao et al.
QRSint	Time interval between the QRS-on to the QRS-off.
QTint	Time interval between the QRS-on to the T-off.
QTcBint	Corrected QT interval (QTc) using Bazett's formula.
QTcFriint	QTc using the Fridericia formula.
QTcFraint	QTc using the Framingham formula.
QTcHint	QTc using the Hodges formula.
T-waveint	Time interval between T-on and T-off.
TPseg	Time interval between T-off and P-on.
RRint	Time interval between sequential R-peaks.
Rdep	Time interval betweem Q-on and R-peak.

waves()

Returns

- waves_b: Dictionary that includes all the raw data, for every **Wave characteristic** biomarker.
- wave_statistics: Dictionary that includes the mean, median, min, max, iqr and std, for every **Wave characteristic** biomarker.

Table 2: **Waves**:

Biomarker	Description
P-wave	Amplitude difference between P-peak and P-off.
T-wave	Amplitude difference between T-peak on and T-off.
R-wave:	R-peak amplitude.
P-waveArea	P-wave interval area defined as integral from the P-on to the P-off.
T-waveArea	T-wave interval area defined as integral from the T-on to the T-off.
QRSArea	QRS interval area defined as integral from the QRS-on to the QRS-off.
STseg	Amplitude difference between QRS-off and T-on.
J-point	Amplitude in 40ms after QRS-off as defined by Hollander et al.

Module contents

1.7.1.4 Module contents

CHAPTER

TWO

TUTORIALS

2.1 ECG morphological analysis

In this tutorial you will learn how to use **PhysioZoo ECG** to engineer morphological ECG biomarkers and export their values.

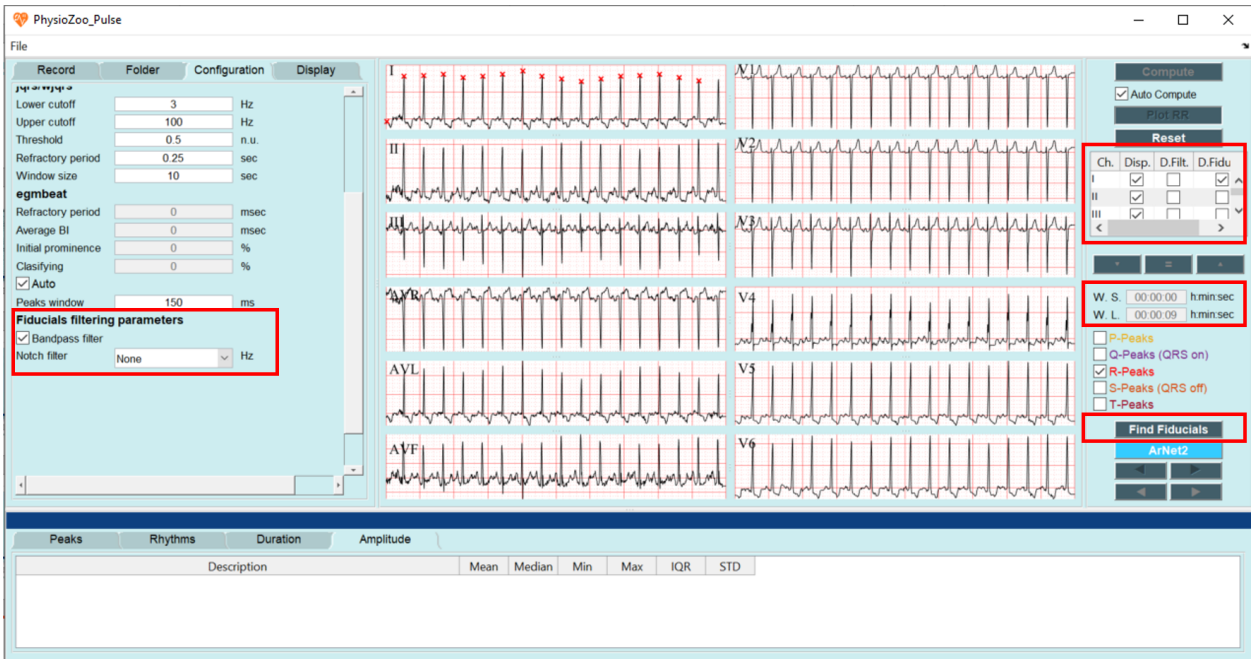
2.1.1 Introduction

An electrocardiogram (ECG) is a simple test that uses temporary electrodes on the chest and limbs to monitor, track, and document the heart's electrical activity. The ECG provides information about the function of the intracardiac conduction system, which is responsible for generating and propagating electrical impulses through the heart. The ECG records the sequence of depolarization and repolarization of the atria and ventricles, which are represented by different waves on the ECG.

Studying the morphological characteristics of the ECG may provide information on underlying physiological heart conditions. **PhysioZoo ECG** provides a framework and tools for extracting morphological biomarkers from the ECG signal.

2.1.2 Performing ECG morphological analysis

Start by entering the ECG interface by clicking on the 'Pulse' menu on the top left, then load some ECG example by clicking File -> Open data file -> Human_example_ecg_12_leads_short.txt. The program will automaticly present the ECG file you imported.



To perform the analysis, please follow the instructions:

1. Prefiltering the signal: On the left panel, select the "Configuration" tab. On the bottom of the tab, you will find a section labeled: **Fiducials filtering parameters** which refers to two filters applied to your signal before analysis:

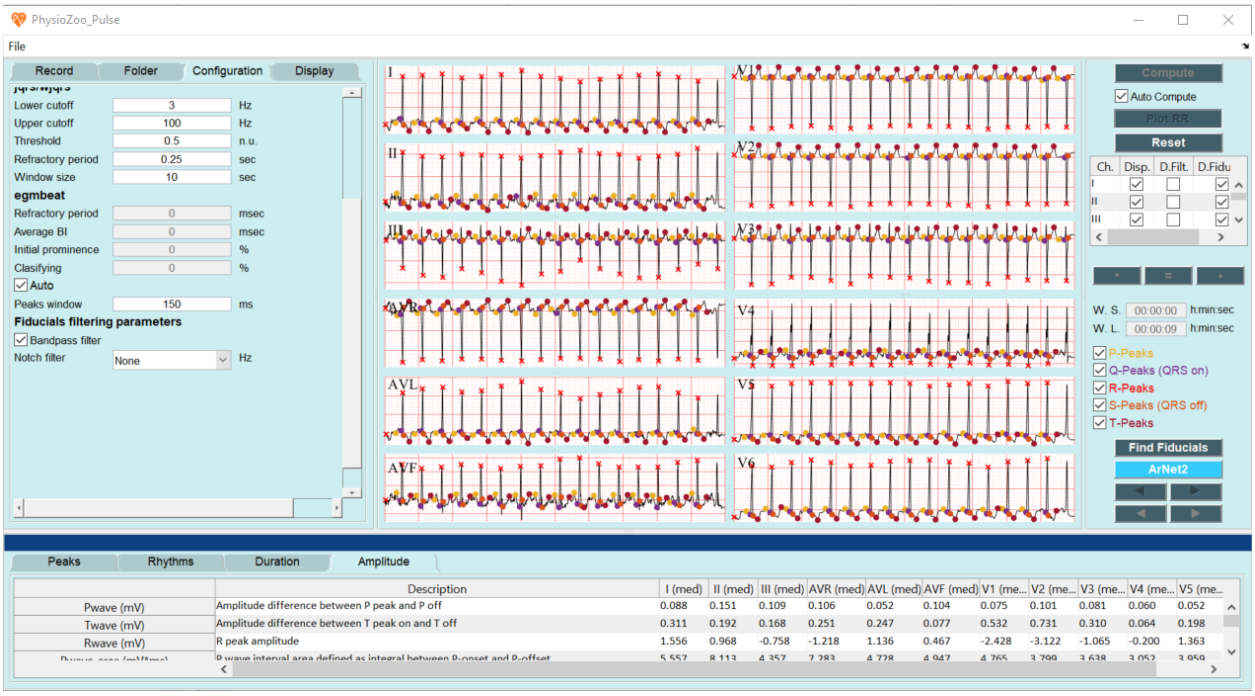
    - The bandpass filter in the range of [0.67,100] Hz. Its purpose is to remove the baseline wander and high frequency noise. Check the box labeled *Bandpass filter* if you want to use it
    - The notch filter. Its purpose is to remove the powerline interface. If you want to use it, choose the frequency of the powerline interface of the country where the ECG was recorded.

2. Definition of the window for anlysis: On the right panel, define the W.S. (start of the window) and the W.L. (length of the window) you want to analyze. You can analyze all of your signal or part of it. Note that if you analyze a long window,it may take some time.

3. Visualization of multiple leads: Choose the leads you want to visualize and the leads on which you want to plot the fiducial points (the fiducials points are calculated using the wavdet algorithm).

4. Click the **Find Fiducials** button. The fiducial poits will be detected and highlighted while the biomarkers will be automatically engineered and displayed on the lower pannels.

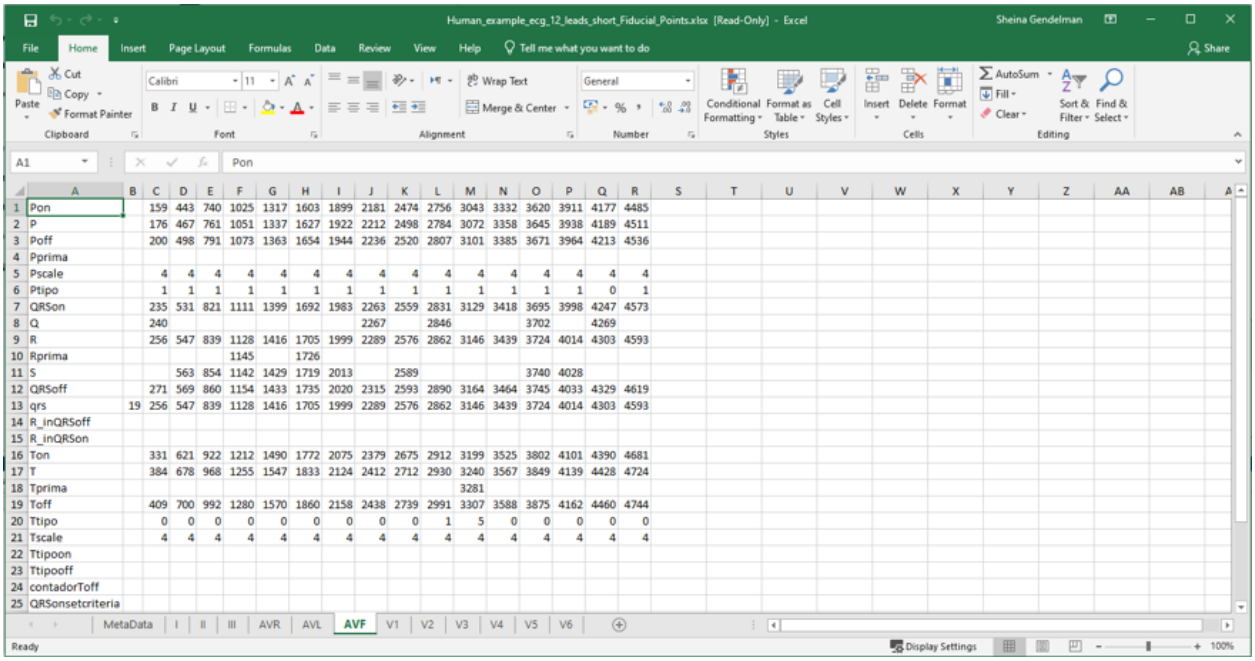
Congrats! You have made your first morphological analysis with **PhysioZoo ECG**! The biomarkers are divided into two different categories: Duration and Amplitudes, the statistical measurments of the biomarkers will be presented in a table, in the bottom panel.



Note: For multilead anlysis only the median of each biomarker will be presented in the table, while for single lead anlysis 6 statistical mesurment computed over the selected window (defined by W.S. W.L.) will be presented for each biomarker namely: mean, median, min, max. IQR and std.

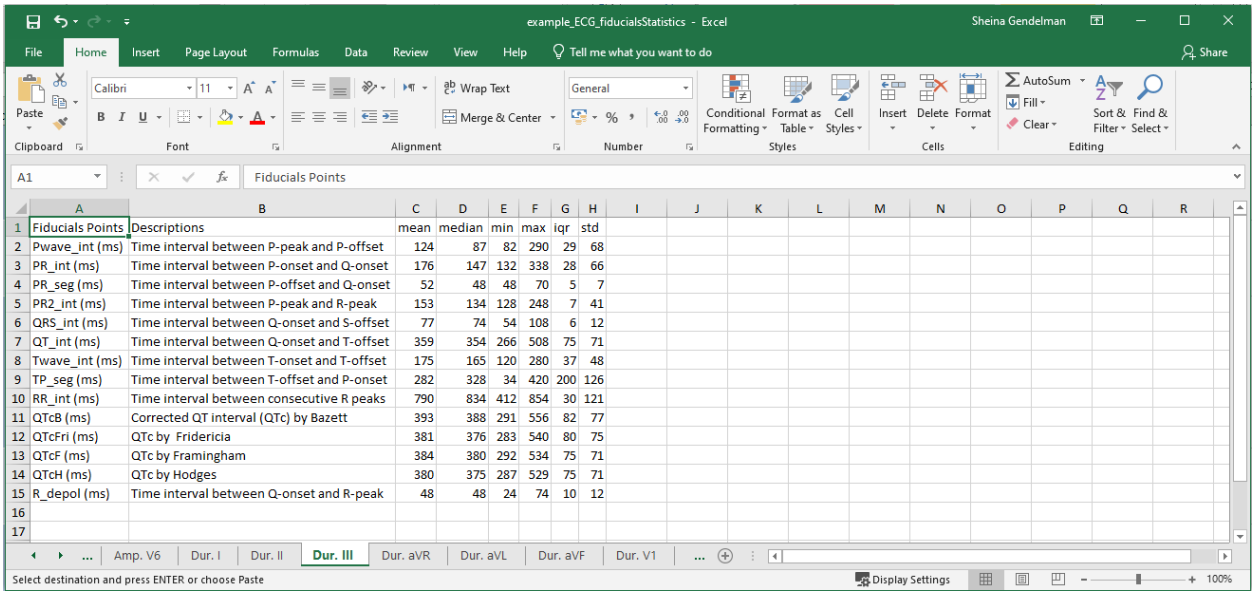
2.1.3 Exporting fiducial points

You can export the fiducial points. Go to File -> Save fiducial points. The excel file contains the computed fiducial points for each lead.



2.1.4 Exporting morphological biomarkers

You can export the morphological biomarkers. Go to File -> Save fiducial biomarkers. The excel file contains the engineered ECG biomarkers for each lead.



	A	B	C	D	E	F	G	H
1	Fiducials Points	Descriptions	mean	median	min	max	iqr	std
2	Pwave_int (ms)	Time interval between P-peak and P-offset	124	87	82	290	29	68
3	PR_int (ms)	Time interval between P-onset and Q-onset	176	147	132	338	28	66
4	PR_seg (ms)	Time interval between P-offset and Q-onset	52	48	48	70	5	7
5	PR2_int (ms)	Time interval between P-peak and R-peak	153	134	128	248	7	41
6	QRS_int (ms)	Time interval between Q-onset and S-offset	77	74	54	108	6	12
7	QT_int (ms)	Time interval between Q-onset and T-offset	359	354	266	508	75	71
8	Twave_int (ms)	Time interval between T-onset and T-offset	175	165	120	280	37	48
9	TP_seg (ms)	Time interval between T-offset and P-onset	282	328	34	420	200	126
10	RR_int (ms)	Time interval between consecutive R peaks	790	834	412	854	30	121
11	QTcB (ms)	Corrected QT interval (QTc) by Bazett	393	388	291	556	82	77
12	QTcFri (ms)	QTc by Fridericia	381	376	283	540	80	75
13	QTcF (ms)	QTc by Framingham	384	380	292	534	75	71
14	QTcH (ms)	QTc by Hodges	380	375	287	529	75	71
15	R_depol (ms)	Time interval between Q-onset and R-peak	48	48	24	74	10	12
16								
17								

CHAPTER

THREE

INDICES AND TABLES

- genindex
- modindex
- search

PYTHON MODULE INDEX

p

INDEX