PhysioZoo Documentation

PhysioZoo Team

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TUTORIALS

ONE

INTRODUCTION

PhysioZoo is a collaborative platform dedicated to the study of the heart rate variability (HRV) from Humans and other mammals' electrophysiological recordings. The main components of the platform are:

- *Software*

    - An open-source algorithmic toolbox for matlab (`mhrv`), which implements all standard HRV analysis algorithms, a selection of peak detection algorithms and prefiltering routines. This can be used within your own data analysis code using the `mhrv` API.

    - An open-source graphical user interface (`PZ-UI`) that provides a user friendly interface for advanced HRV analysis of RR-intervals time series and data visualization tools. This enables easy access to HRV analysis without writing any code.

- *Databases*

    - A set of annotated databases (`PZ-DB`) of electrophysiological signals from different mammals (dog, rabbit and mouse). Available here.

    - Manually audited peak locations and signal quality annotations for each of the recordings.

- *Configuration*

    - A set of configuration files that adapt the HRV measures and `mhrv` algorithms to work with data from different mammals.

    - All HRV measures can be further adapted for the analysis of other mammals by creating simple human-readable mammal-specific configuration files.

Note: The `PZ-UI` user interface has two modules: a `Peak detection` (used to process electrophysiological signals and obtain the RR time series) module and a `HRV analysis` module (used to process the RR time series and compute HRV measures).

The **PhysioZoo** mission is to standardize and enable the reproducibility of HRV analysis in mammals' electrophysiological data. This is achieved through its open source code, freely available user interface and open access databases. It also aims to encourage the scientific community to contribute their electrophysiological databases and novel HRV algorithms/analysis tools for advancing the research in the field.

Feedback on how to improve the **PhysioZoo** platform is welcomed. Do not hesitate to drop us an email at:

physiozoolab@gmail.com

Source code, data or interface enhancement contributions are welcome. Look here on how to contribute to PhysioZoo.

Please include the standard citation to **PhysioZoo** when using the resources available on the platform:

Joachim A. Behar*, Aviv A. Rosenberg*, Ido Weiser-Bitoun, Ori Shemla, Alexandra Alexandrovich, Evgene Konyukhov, Yael Yaniv. 2018. 'PhysioZoo: a novel open access platform for heart rate variability analysis of mammalian electrocardiographic data.' Accepted for publication in Frontiers in Physiology.

*Equal contribution.

1.1 Installing PhysioZoo

The PhysioZoo user interface (`PZ-UI`) can be run from Matlab or be installed as a standalone application. If you do not need the graphic user interface then you can directly download the HRV source code (`mhrv` library). `PZ-UI` and `mhrv` were tested for Matlab 2016a and above running on Windows.

1.1.1 PhysioZoo `mhrv` matlab toolbox

The PhysioZoo platform includes the `mhrv` matlab toolbox which implements all the algorithmic functions required by PhysioZoo (and more). The toolbox is aimed at researchers or developers that wish to write their own code for ECG signal processing, HRV analysis or other applications by using the *mhrv* toolbox as a library.

See the toolbox's ../../mhrv/sections/getting_started page for installation and initial setup instructions. The API reference for the toolbox is available on this site.

The development version of the `mhrv` toolbox is available here.

1.1.2 PhysioZoo `PZ-UI` user interface

The PhysioZoo user interface (`PZ-UI`) is aimed mainly at researchers working with physiologic data who do not wish to write any code for data analysis. It provides many tools out of the box, all accessible from an interactive UI.

The UI can be run from Matlab or be installed as a standalone application. `PZ-UI` was tested for Matlab 2016a and above running on Windows.

Running `PZ-UI` from within Matlab

Versions supported: MATLAB 2016a and above.

1. Download or clone the source code from the repository.
2. From MATLAB launch PhysioZoo by running the script `PhysioZoo.m` from the root of the repo.

Note: The `PZ-UI` user interface has two modules: a `Peak detection` (used to process electrophysiological signals and obtain the RR time series) module and a `HRV analysis` module (used to process the RR time series and compute HRV measures).


Running `PZ-UI` as standalone software (.exe)

Operating system: Windows 10 (and above), 64 bits.

After downloading the software from the project's main page, run the `physiozoo.exe` file. This will start the installation process. You can then go through the following steps.

Note: Some of the screens might be slightly different depending on the version of Windows you are using and whether you already have the MATLAB runtime compiler installed. If Matlab runtime compiler is not installed then it will be done through this process but the installation might take some time.
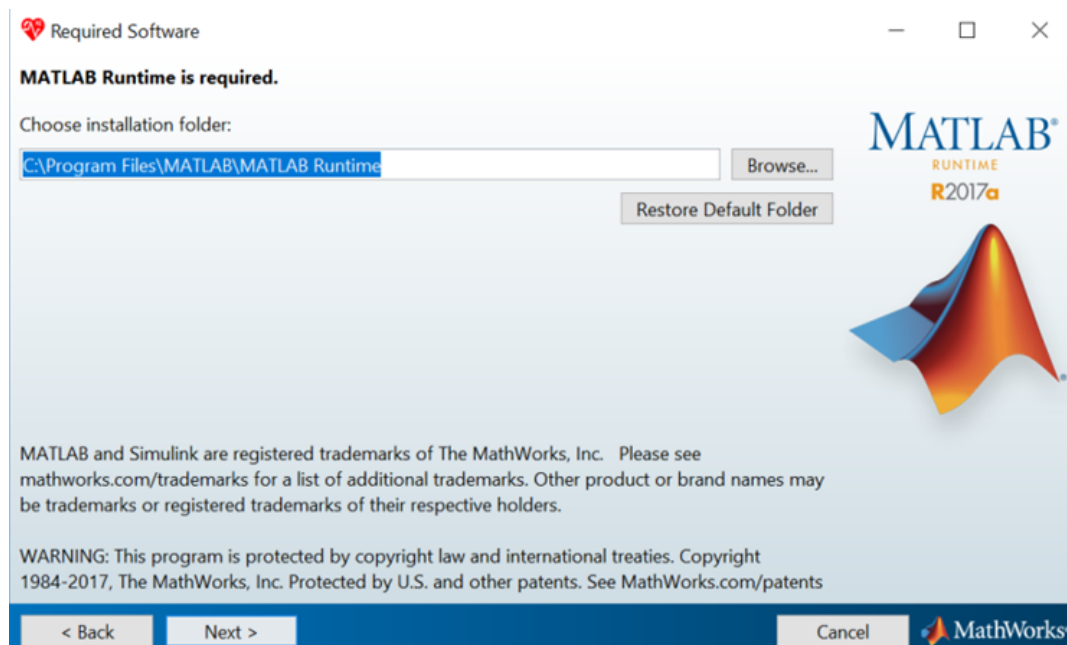
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1. If you get the following screen displayed then click "Run"
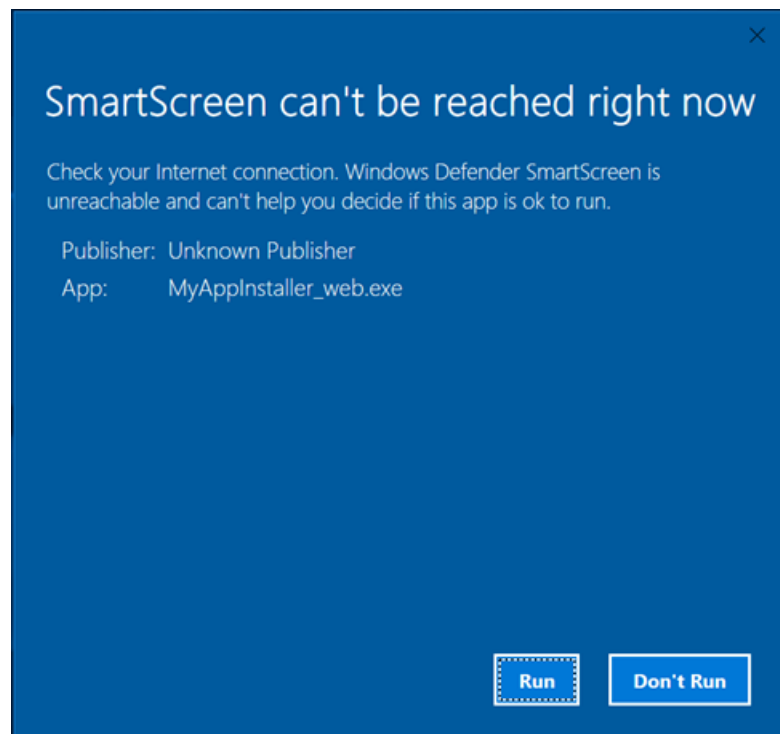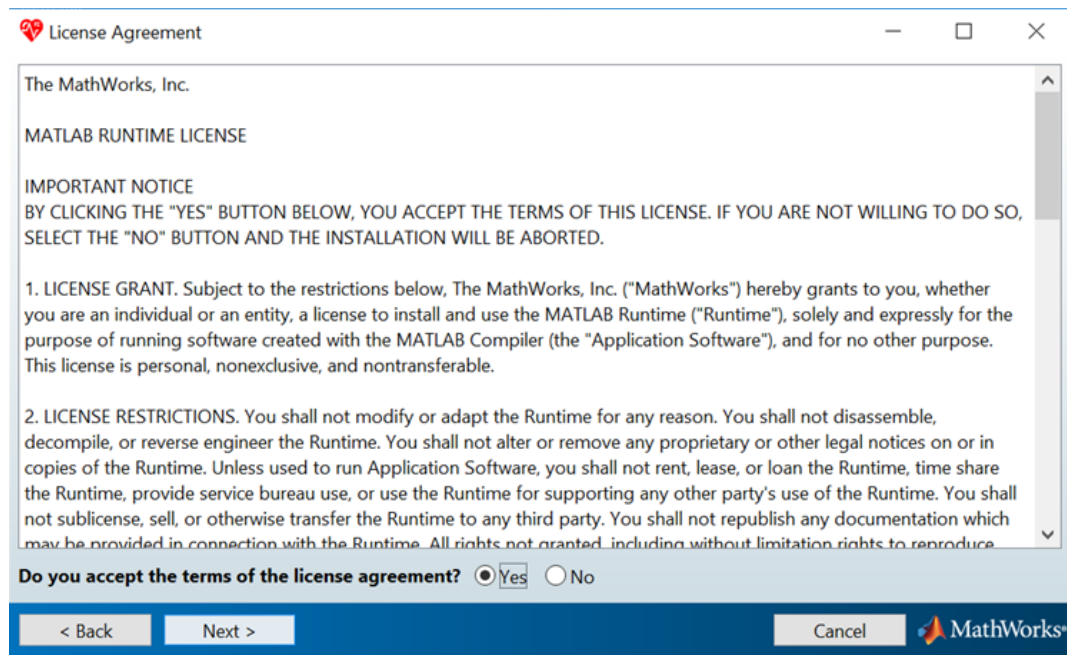

2. When the following screen is prompted then click "Next"
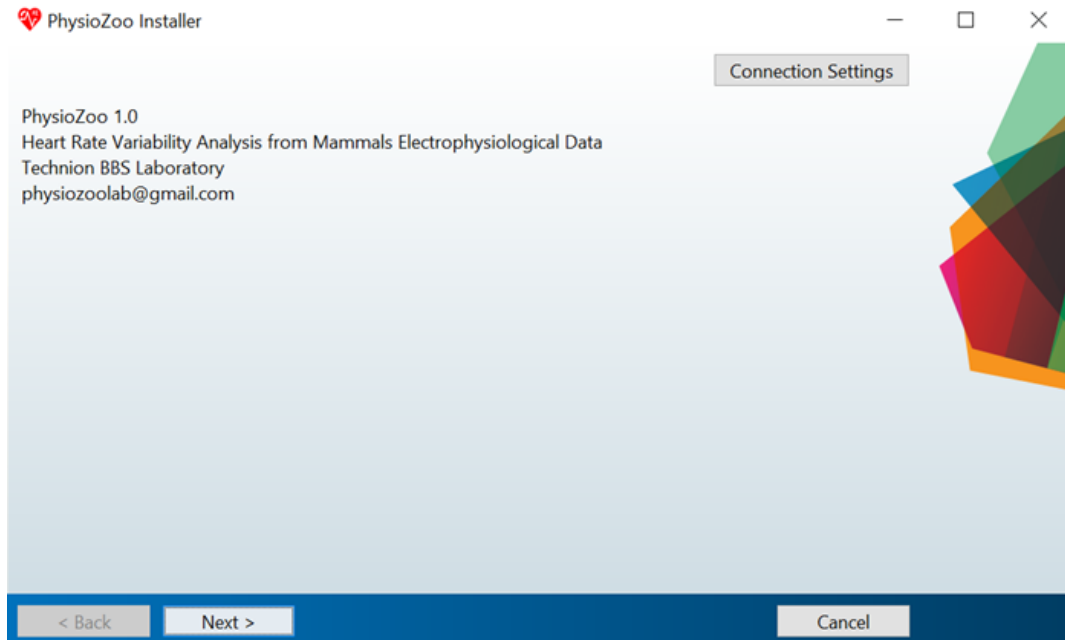
3. When the following screen is prompted then click "Next"

4. When the following screen is prompted check the "Yes" and then click "Next"

5. When the following screen is prompted then click "Install"
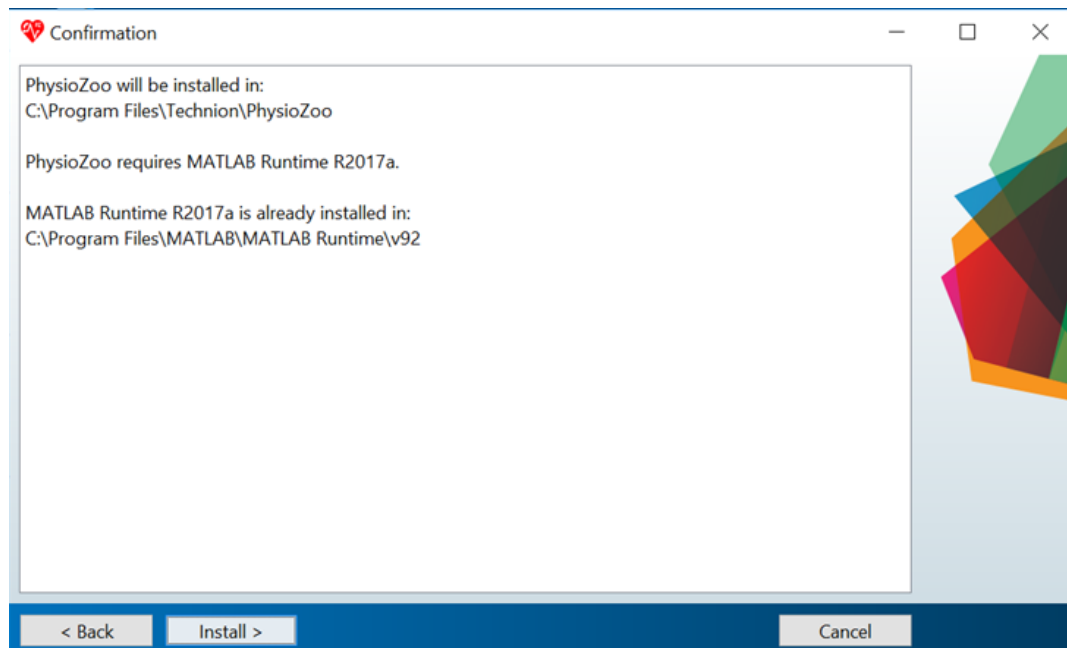
6. The installation will start. Wait until it is finished. Note that this might take quite some time.

7. When the installation is finished it will show the following screen.

You can now click on the **PhysioZoo** logo located on your desktop or in the list of programs.

1.2 Electrocardiographic recordings

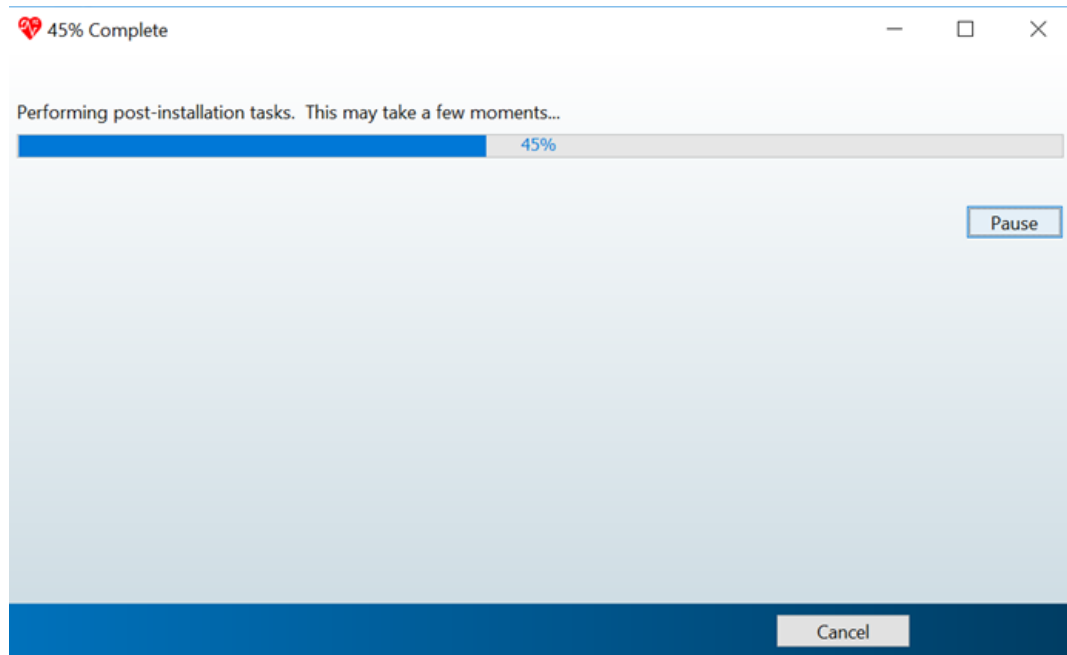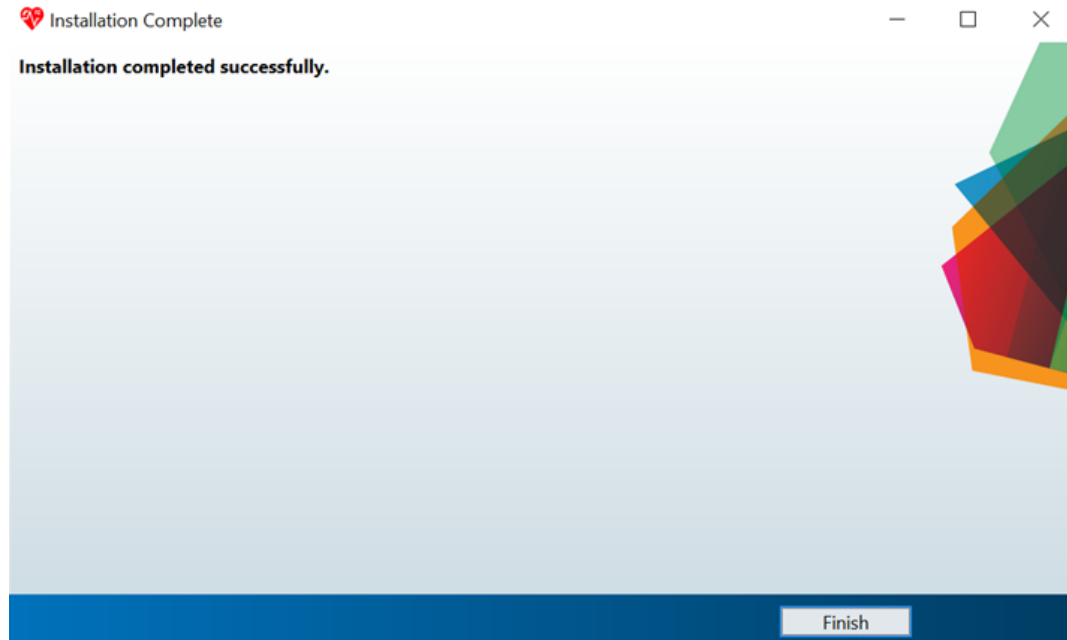Electrophysiological signals need to be digitized before they can be worked with. For that purpose both the range and domain need to be digitized. Important attention should be given to the sampling frequency and quantization level in order to ensure the integrity of the data and a meaningful HRV analysis.

1.2.1 Sampling frequency and quantization level

Sampling refers to the process of discretizing the time domain. The sampled time domain will be described by the sampling frequency (fs) corresponding to the number of samples per second. The resulting digital signal will have a discrete time domain.

Quantization refers to the process of constraining an input from a continuous signal to a discrete set of values. The resulting digital signal will have a discrete range.

The sampling frequency and the quantization that are used for recording data will affect the quality of the HRV analysis and thus it is important to inspect the raw data that are being recorded and eventually, when necessary, adjust the sampling frequency and quantization level of the recording device.

1.2.2 Examples of typical issues

The following example shows what happens when a mouse ECG recording is downsampled from 1000 Hz to 500 Hz and 250 Hz, thus simulating the type of signal you would record if your original sampling rate was below 1000 Hz. As you will observe, the exact peak location is significantly affected by the sampling frequency. It is degraded at 500 Hz and at 250 Hz it will be very poor. Thus for mouse data, 1000 Hz is really the minimal sampling frequency to use in order to ensure a meaningful HRV analysis. However, note that the adequate sampling frequency will be mammal specific.
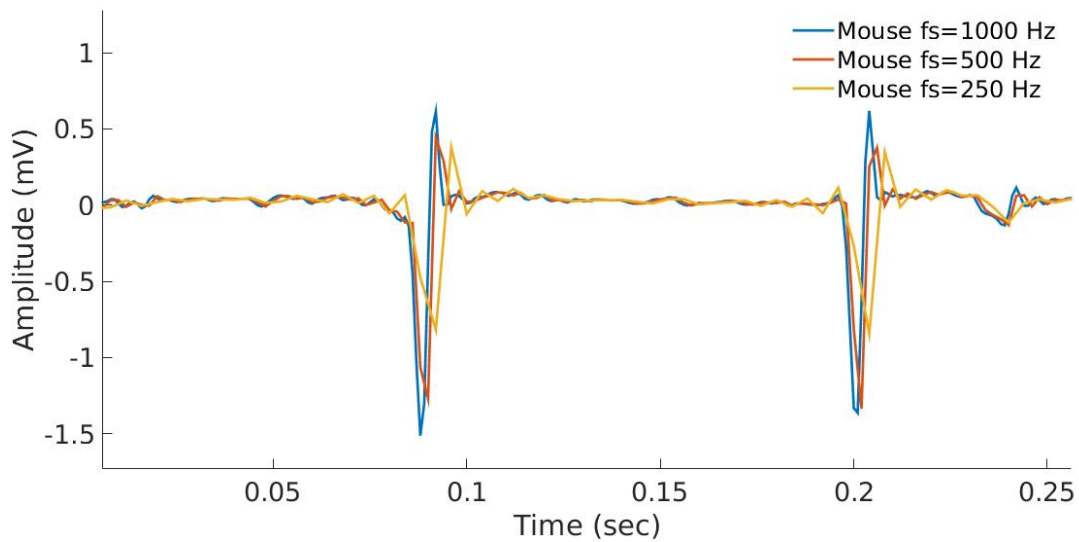
The following example shows a rabbit recording where the quantization level was poorly set. This can be observed by the low discretization levels / high amplitude `jumps' between consecutive samples. A poor quantization can affect the HRV analysis (as well as any morphological analysis).
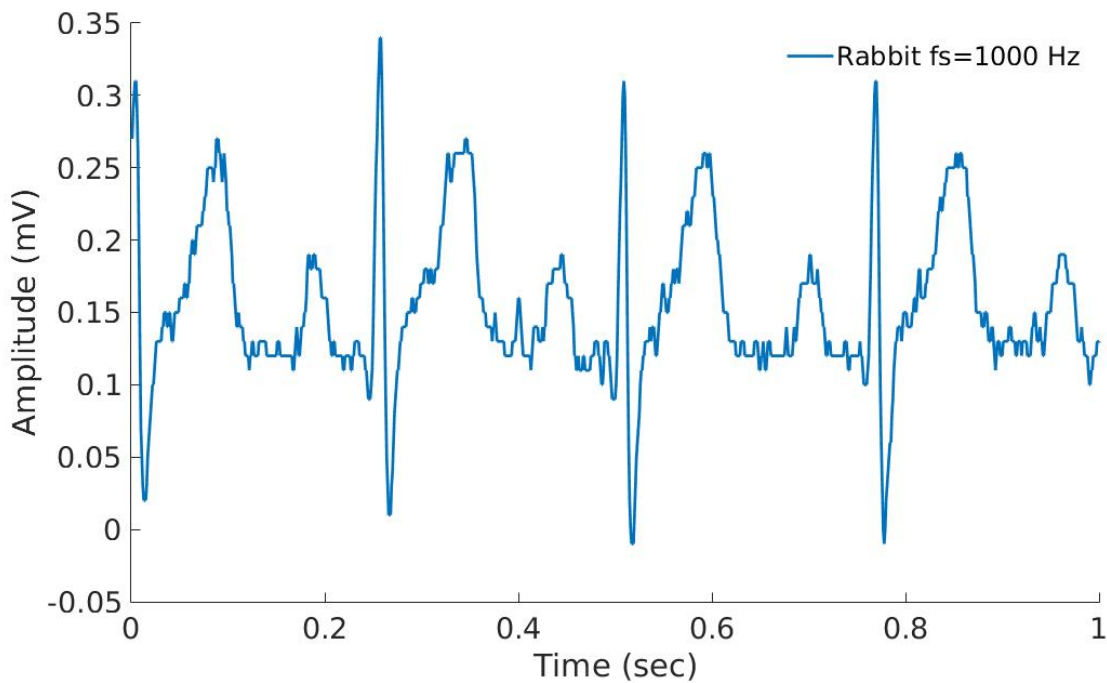
1.3 Peak detection

In this tutorial you will learn how to load an electrocardiogram (ECG) recording and perform R-peak detection. You will also learn how to manually correct misdetected peaks. Peak detection is performed in the `Peak detection` module.

1.3.1 Introduction

Accurate peak detection is critical for performing meaningfull HRV analysis. **PhysioZoo** provides a module to perform accurate peak detection from different mammalian species and the option to manually correct misdetected peaks to ensure the accuracy of the RR time series that will be analysed in the HRV analysis module.

1.3.2 Why mammal specific peak detection?

Numerous algorithms for finding R-peaks in human ECGs have been developped. However, these need to be adapted to the different dynamics accross mammalian species. **PhysioZoo** provides a set of peak detection algorithms (`rqrs`, `jqrs` and `wjqrs`) with parameters preset for human, dog, rabbit and mouse. Suitable parameters for other mammals can be specified by the user from the configuration panel.

Representative example of the R-peaks detected (A) using the original `gqrs` human peak detector and (B) using the `rqrs` **PhysioZoo** detector with parameters adapted for the different mammals. This figure illustrates the need for mammal-specific R-peak detectors to ensure a correct evaluation of the RR time series.
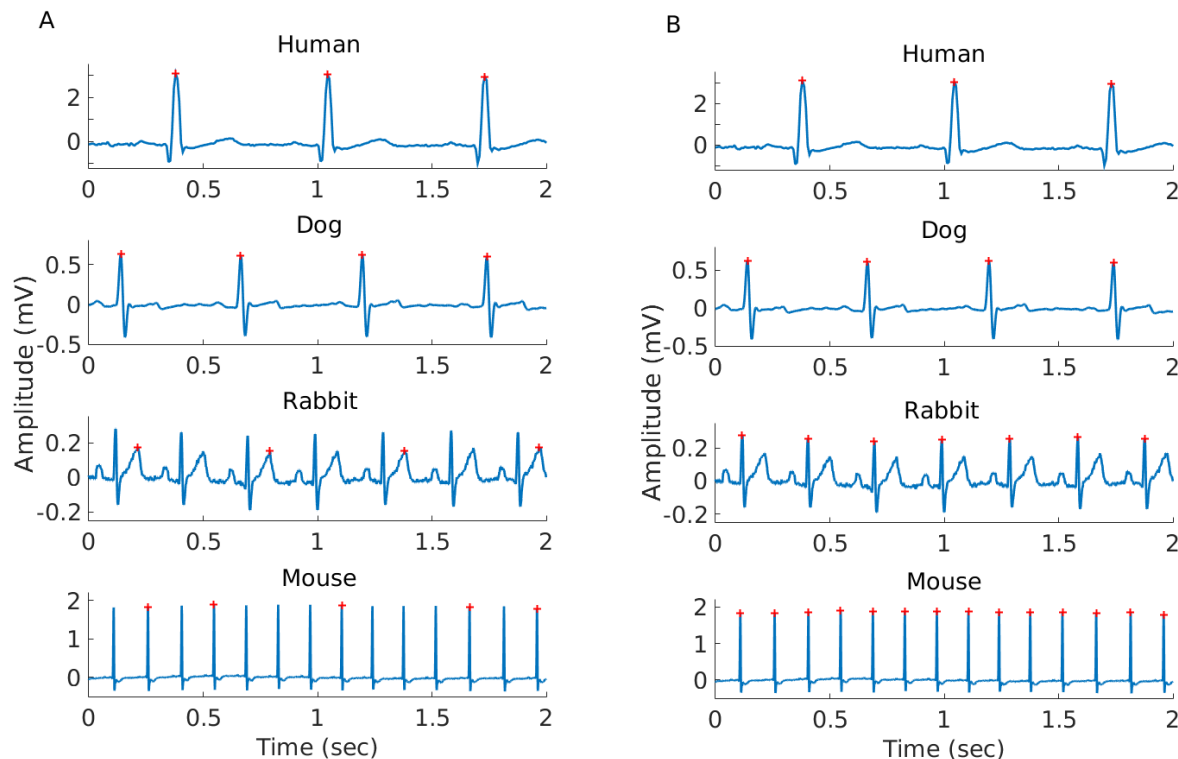
1.3.3 Performing peak detection in PhysioZoo

1. Open the PhysioZoo user interface `PZ-UI`.

2. Click "Peak Detection" on the Menu bar to open the peak detection interface.

3. Load an ECG recording (e.g. File -> Open File -> Rabbit_example.txt). The ECG will be displayed. The default R-peak detector (`rqrs`) will run automatically. You will see some red crosses appearing on the ECG signal at the locations that have been detected (panel A).

4. You can browse through the recording by stretching and moving the red window displayed in panel B. You can also move through the recording by using the arrows circled in red on the right hand side. Finally, you can also use the mouse scroll wheel and Ctrl scroll wheel.
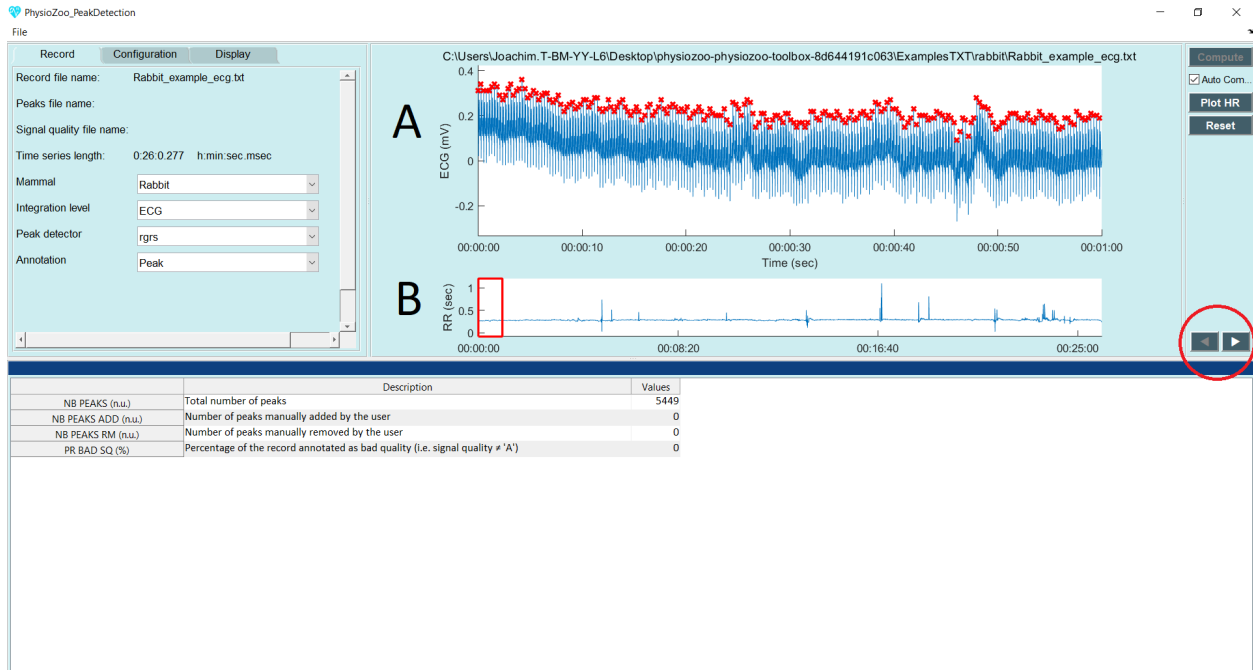
> **Warning:** The input ECG data imported in **PhysioZoo** MUST be in mV (i.e. physiological units). The R-peak detector might not run appropriately if the data are not correctly scaled.

1.3.4 Manual peak correction

Sometimes the R-peak detector might make mistakes and miss some R-peaks/detect some points which are not peaks. You can fix these mistakes manually using the **PhysioZoo** interface by using the following functionalities:

1. Select a part of the ECG which is noisy and where some peaks were misdetected.

2. Point your cursor on a misdetected peak or at the location where a peak is missing. When you click, **PhysioZoo** will automatically remove/add a peak at this location.

3. If a whole segment contains misdetection and you need to clear all the peaks within this section, draw a rectangle on the area where you want the peaks to be deleted (see dotted rectangle figure below). When you 'drop the rectangle', all the peaks contained within it will be deleted.

4. Save your R-peak time series: File -> Save Peaks.
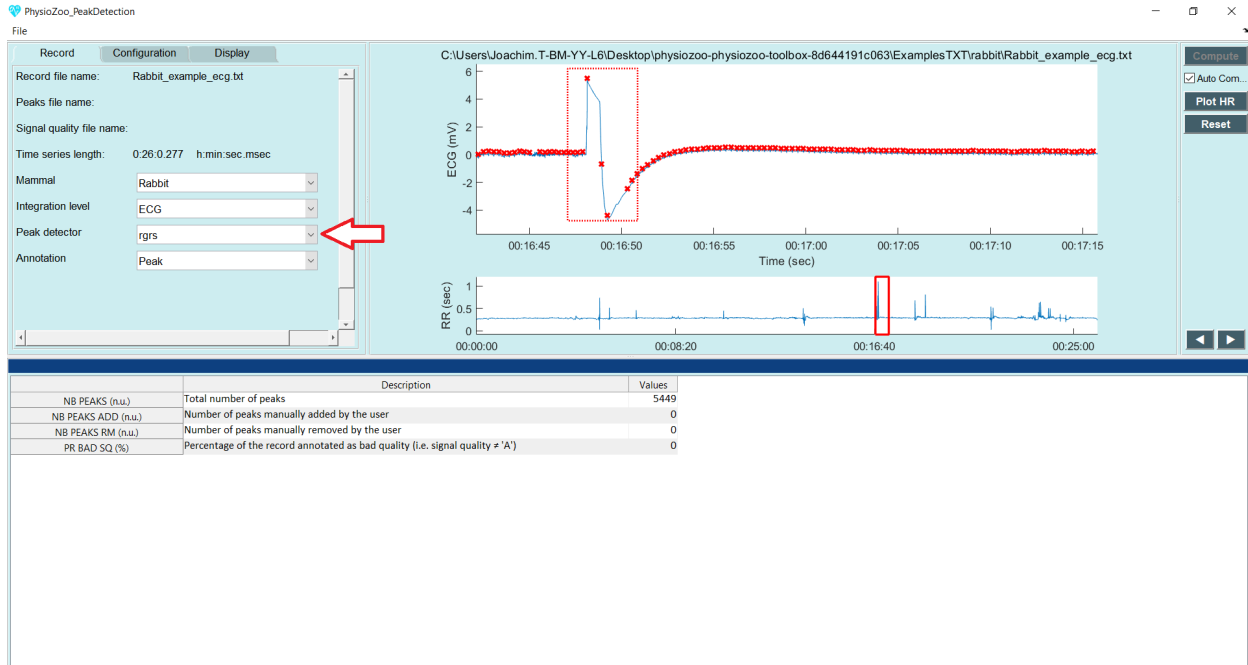
1.3.5 Configuration for other mammals

The **PhysioZoo** R-peak detectors are readily adapted for human, dog, rabbit and mouse ECG data. If you need to use them on another species then you will need to adapt their parameters accordingly. The parameters for the peak detectors can be found under the "Config Params" tab. You can save the configuration of the peak detectors in order to re-use it by going to File -> Save configuration file.

For `rqrs`:

- HR: Typical heart rate (beats/min)

- QS: Typical QRS duration (sec)

- QT: Typical QT interval duration (sec)

- QRSa: Typical QRS peak-to-peak amplitude (microVolt)

- QRSamin: Minimum QRS peak-to-peak amplitude (microVolt)

- RRmin: Minimum RR interval ("refractory period", sec)

- RRmax: Maximum RR interval (sec)

For `jqrs` and `wjqrs`:

- Lower cutoff frequency: the lower cutoff frequency of the bandpass filter used to prefilter the ECG (Hz)

- Upper cutoff frequency: the upper cutoff frequency of the bandpass filter used to prefilter the ECG (Hz)

- Threshold: the energy threshold (nu)

- Refractory period: the minimal time interval tolerated between two consecutive peaks (sec)

- Window size: this parameter is only used with `wjqrs`. This peak detector is applied on consecutive (non-overlapping) windows of size 'Window size' (sec).

Other:

- Peaks window: when manually correcting peaks, this parameter corresponds to the window size for which to look for a local maximum / minimum around the click location.

1.3.6 Frequently asked questions

What is a suitable sampling frequency for my data?

In order to locate the peaks accurately from the electrophysiological signal it is important to work with data sampled at a sufficiently high frequency. For example, for animal data with a high heart rate such as the mouse ECG, the QRS is only a few milliseconds long (~ 7 ms). Thus even at a relatively high sampling rate such as 1000 Hz the QRS will only be described by very few (~7) samples. See this tutorial for a visual example.

What's the difference between peak detectors?

Sometime a peak detector will fail to detect the R-peaks. This is due to the fact that these detectors were originally built for human ECG analysis and extended to work with mammalian data. In animal ECGs the position and type (e.g. subcutaneous) of the electrodes are not as standardized as for the uman. For that reason we included a set of three R-peak detectors so that it is possible to change to the one that is performing best for your specific dataset and electrodes configuration.

How best to deal with long recordings?

If you deal with long recordings (i.e. hours long) then use `rqrs` or `wjqrs`.

1.4 Preprocessing

In this tutorial you will learn how to preprocess your RR time series within the `HRV analysis` module. The resulting preprocessed time series is traditionally called the 'NN' time series.

1.4.1 Introduction

When loading an RR time series in the HRV module, one of the parameters you need to set is the preprocessing method.

We implemented in **PhysioZoo** three methods (and one combination of methods) for pre-filtering the RR-interval time series:

- Range,
- Moving average,
- Quotient,
- Combined (the combination of the Range and the Moving average filters).

1.4.2 Why is preprocessing important?

A preprocessing step is usually performed in HRV analysis to filter out suspected ectopic beats, missed beats and artifacts.

The example below shows an ECG segment with some transient noise. Note the miss-detected R-peaks. Leaving these miss-detected R-peaks could lead to the evaluation of incorrect HRV measures.
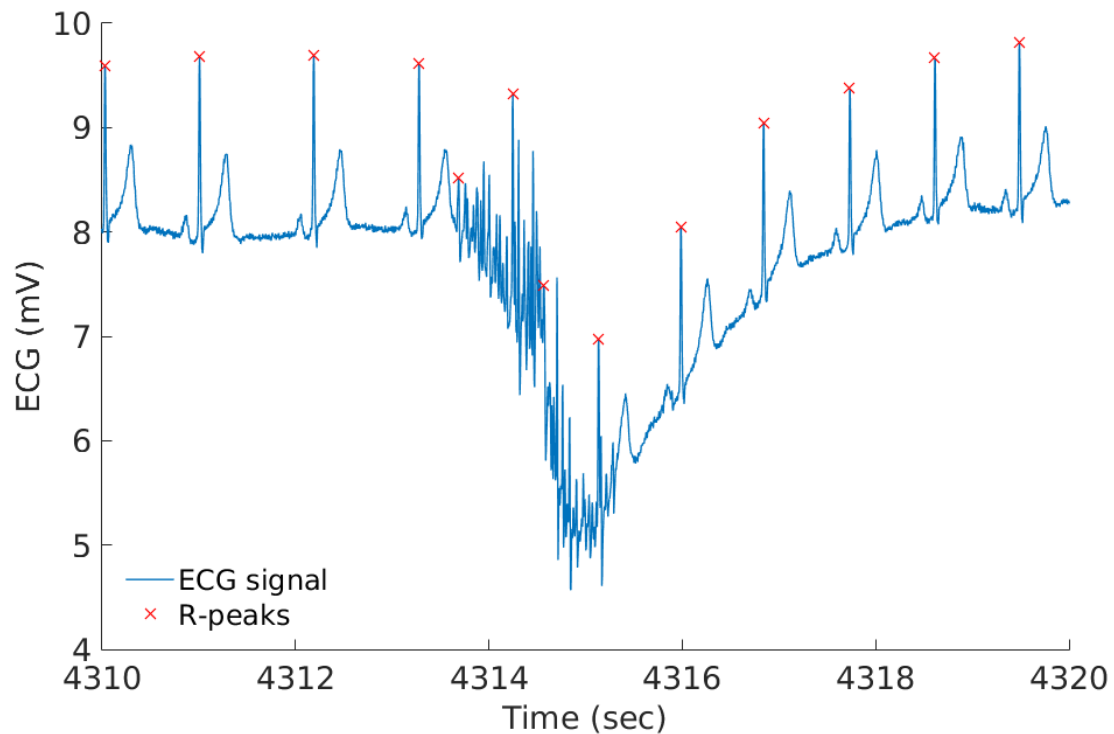
Below, the corresponding RR interval time series that is filtered. The filtering allows to remove the sudden increase and decrease in the RR time series that are caused by the miss-detected beats.
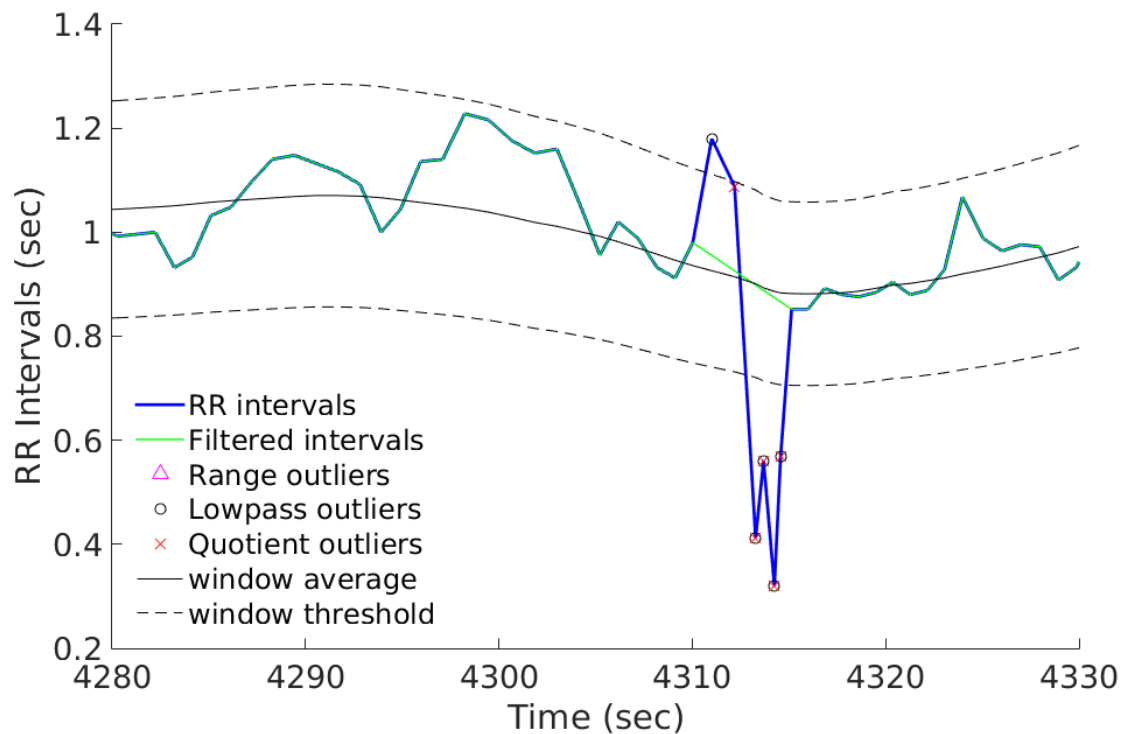
1.4.3 Preprocessing methods in PhysioZoo

You can select the preprocessing filter with the dropdown "Preprocessing" located under the Main tab. You can vary the level of preprocessing by using the dropdown "Preprocessing level" located under the Main tab. Three levels of preprocessing are available: "Weak", "Moderate" and "Strong". If you want to customize the preprocessing filters further then you can access each of the parameters of each filter by going to Options -> Filtering.

The image below shows an example of a rabbit RR time (blue time series) series which has been filtered over the selected window (green time series) using the Moving average filter.

1.4.4 Frequently asked questions

Why preprocessing the RR time series?

Preprocessing methods are useful to remove local miss-labelled beats caused by noise or sudden drop/increase in the RR time series due to ectopic beats.

What is the limitation of preprocessing routines?

In the presence of large segments of noise it will not help. Rather such large segments of bad quality data should be discarded from the analysis. You can annotate the quality of the electrophysiological time series in order to have this contexttual information when performing HRV analysis.

Is there instances when not to preprocess the RR time series?

If your aim is to use HRV measures for identifying certain arrythmic episodes for example then you might want to avoid preprocessing the RR time series or to use a weak preprocessing in order to only remove outliers beats. Indeed, in this use case you will want to capture the important irregularities (e.g. atrial fibrillation) in the RR intervals of the time series.

1.5 Heart Rate Variability analysis

In this tutorial you will learn how to compute the Heart Rate Variability (HRV) measures and export the computed values within the **PhysioZoo** `HRV analysis` module. You will learn how to analyse a single window of defined length and a series of consecutive windows.

1.5.1 Introduction

HRV analysis is particularly interesting because it provides a non-invasive way to monitor cardiac function and the autonomic system activity. In particular, in the context of animal studies, HRV tools can be used to study the effects of mutations and pharmacological treatments. **PhysioZoo** provides the framework and tools for performing HRV analysis from human and animal model data.

1.5.2 Why mammal specific HRV?

Because the heart rate range, dynamics and autonomic control can vary significantly between mammals, some HRV measures need to be adapted to the mammal whose data are being analysed. As an example, the following figure illustrates the important differences in the location of the characteristic power spectral peaks in analysing RR time series from different mammals using power spectral analysis. This highlights the need to re-define the spectral bands (VLF, LF and HF) for each mammal.
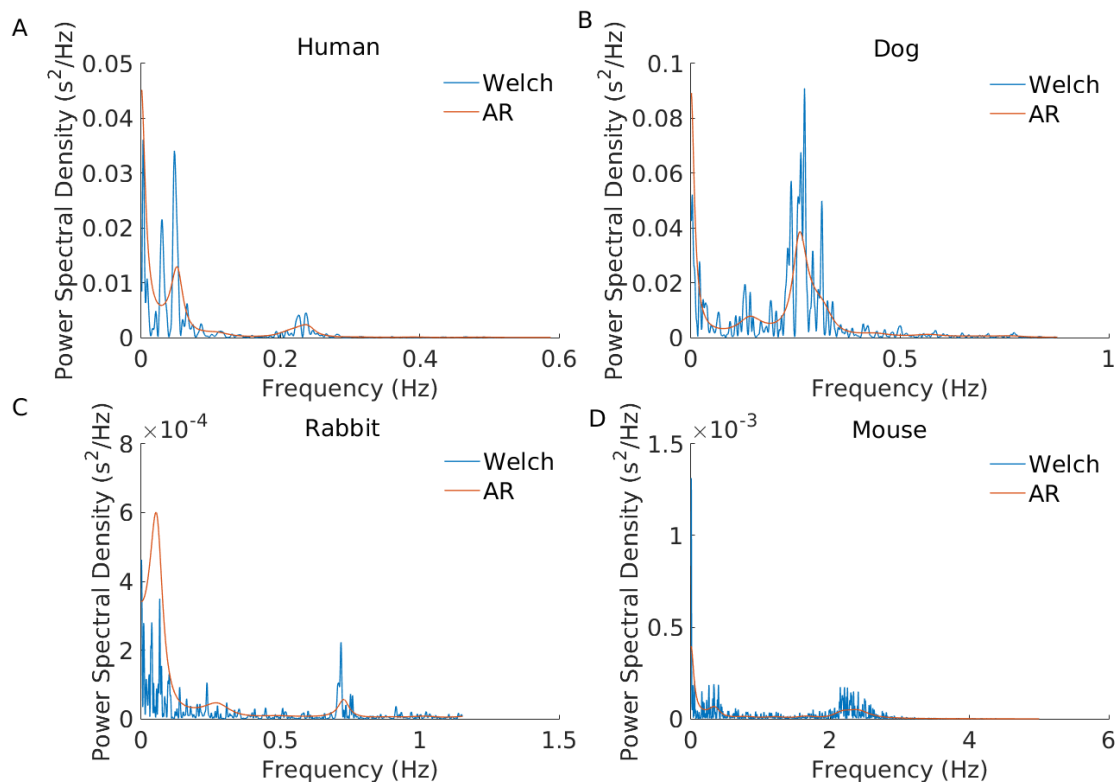
1.5.3 Performing HRV analysis

Start by loading some example data by clicking File -> Open data file -> mouse/Mouse_example_qrs.txt. The program will start the analysis automatically and display the following window:
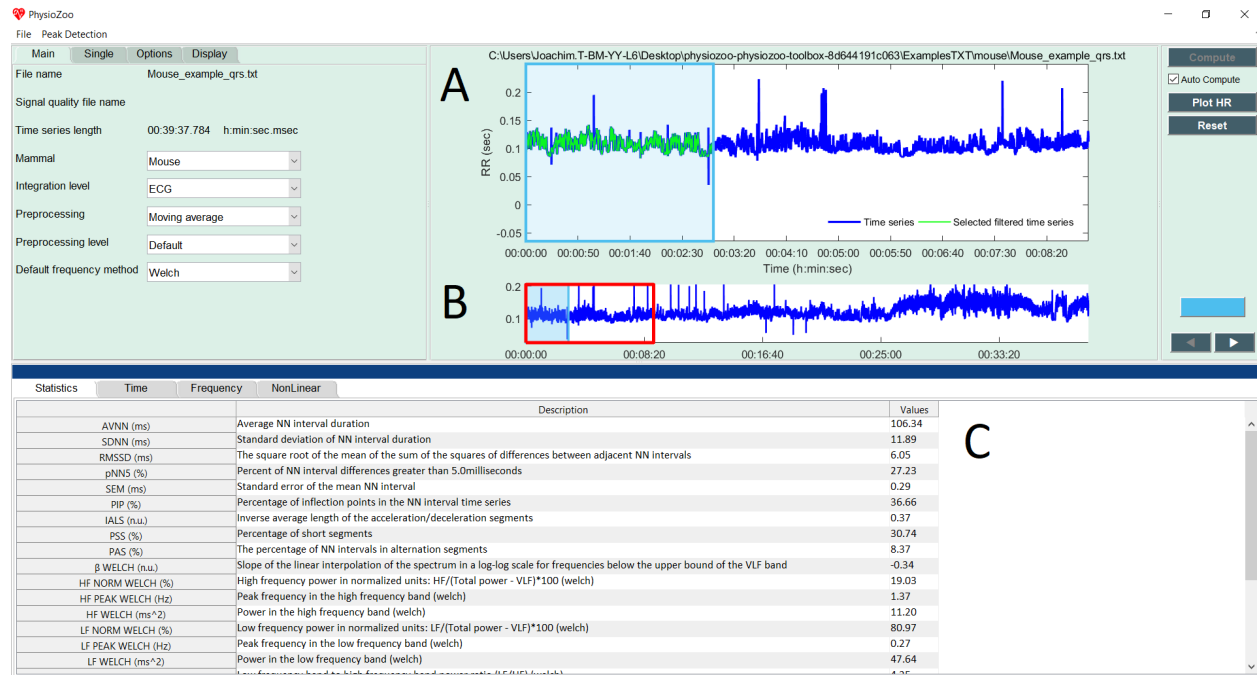
In the upper figure (A) the selected window (colored in blue) defines the time interval for which the HRV measures are computed. In the lower panel (B), the RR time series is plotted. Two windows are drawn on it: one window with a red frame and one with a blue frame (and alpha color from within.) The red window defines the part of the RR time series plotted in the larger upper figure (A). The blue frame defines the part of the RR time series for which the HRV measures will be computed. The window can be modified (extended/shrunk/moved) using the mouse. Pannel (C) shows all the HRV measures that have been computed.

Congrats! You have made your first HRV analysis with **PhysioZoo**!

Note: Every time you move the analysis window to another location the newly selected segment will be automatically analyzed. You can disable this by deselecting the checkbox "Auto Compute" located under the "Compute" button.

Note: The length of the selected window is important. Some HRV measures assume that the RR time series is stationary over the selected window. In our context stationary means that the statistical properties of the RR time series (such as mean and standard deviation) are about constant. Other measures such as the detrended fluctuation analysis ones do not assume stationarity and thus a long window may be used.

1.5.4 Exporting HRV measures

You can export the HRV measures and prefiltered NN intervals generated by **PhysioZoo**. Go to File -> Save HRV measures. The following window will display:
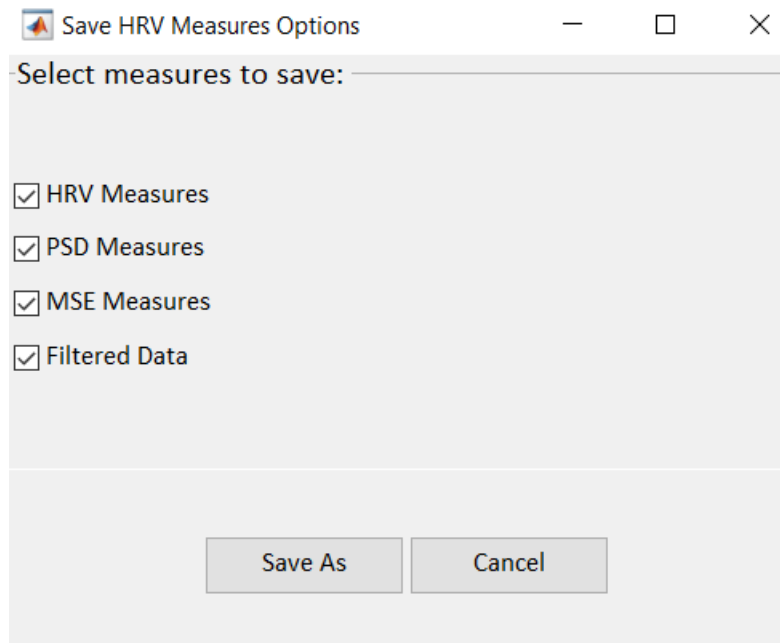
You can select the computation(s) you want to save with the checkboxes:

- **HRV Measures**: The HRV measures as displayed in the 'Statistics section' of the user interface.

- **Power Spectral Density**: the measure of signal's power content versus frequency. This corresponds to saving the power content for each frequency bin of the power spectral density displayed under the 'Frequency tab'.

- **Multi Scale Entropy**: the value of sample entropy for a range of scales as specified under Options->NonLinear and displayed under the 'NonLinear tab'.

- **Preprocessed RR intervals**: the RR interval time series after it was preprocessed by the filter you specified under Main-> Preprocessing. The resulting preprocessed time series is traditionally called the 'NN' time series.

Select the location where you want to save the HRV measures. Open the HRV Measures file and you will see the list of HRV measures together with their definitions and values for the window that was selected. For that purpose open the text file (Mouse_example_qrs_hrv.txt) you just saved.

```
📄 Mouse_example_qrs_hrv - Notepad
File  Edit  Format  View  Help
AVNN (ms)              :    Average NN interval duration                                                                      106.34
SDNN (ms)              :    Standard deviation of NN interval duration                                                         11.89
RMSSD (ms)             :    The square root of the mean of the sum of the squares of differences between adjacent NN intervals  6.05
pNN5 (%)               :    Percent of NN interval differences greater than 5.0milliseconds                                    27.23
SEM (ms)               :    Standard error of the mean NN interval                                                              0.29
PIP (%)                :    Percentage of inflection points in the NN interval time series                                    36.66
IALS (n.u.)            :    Inverse average length of the acceleration/deceleration segments                                   0.37
PSS (%)                :    Percentage of short segments                                                                       30.74
PAS (%)                :    The percentage of NN intervals in alternation segments                                              8.37
BETA_WELCH (n.u.)      :    Slope of the linear interpolation of the spectrum in a log-log scale for frequencies below the upper bound of the VLF band  -0.34
HF_NORM_WELCH (%)      :    High frequency power in normalized units: HF/(Total power - VLF)*100 (welch)                       19.03
HF_PEAK_WELCH (Hz)     :    Peak frequency in the high frequency band (welch)                                                   1.37
HF_POWER_WELCH (ms^2)  :    Power in the high frequency band (welch)                                                           11.20
LF_NORM_WELCH (%)      :    Low frequency power in normalized units: LF/(Total power - VLF)*100 (welch)                        80.97
LF_PEAK_WELCH (Hz)     :    Peak frequency in the low frequency band (welch)                                                    0.27
LF_POWER_WELCH (ms^2)  :    Power in the low frequency band (welch)                                                            47.64
LF_TO_HF_WELCH (n.u.)  :    Low frequency band to high frequency band power ratio (LF/HF) (welch)                               4.25
TOTAL_POWER_WELCH (ms^2): Total power (welch)                                                                                 117.94
VLF_NORM_WELCH (%)     :    Very low frequency power in normalized units: (welch)                                              45.54
VLF_POWER_WELCH (ms^2) :    Power in the very low frequency band (welch)                                                       53.71
BETA_AR (n.u.)         :    Slope of the linear interpolation of the spectrum in a log-log scale for frequencies below the upper bound of the VLF band  -0.85
HF_NORM_AR (%)         :    High frequency power in normalized units: HF/(Total power - VLF)*100 (ar)                           20.95
HF_PEAK_AR (Hz)        :    Peak frequency in the high frequency band (ar)                                                      1.45
HF_POWER_AR (ms^2)     :    Power in the high frequency band (ar)                                                               7.11
LF_NORM_AR (%)         :    Low frequency power in normalized units: LF/(Total power - VLF)*100 (ar)                           79.05
LF_PEAK_AR (Hz)        :    Peak frequency in the low frequency band (ar)                                                       0.36
LF_POWER_AR (ms^2)     :    Power in the low frequency band (ar)                                                               26.82
LF_TO_HF_AR (n.u.)     :    Low frequency band to high frequency band power ratio (LF/HF) (ar)                                  3.77
TOTAL_POWER_AR (ms^2)  :    Total power (ar)                                                                                   69.77
VLF_NORM_AR (%)        :    Very low frequency power in normalized units: (ar)                                                 47.74
VLF_POWER_AR (ms^2)    :    Power in the very low frequency band (ar)                                                          33.31
SD1 (ms)               :    NN interval standard deviation along the perpendicular to the line-of-identity                      4.28
SD2 (ms)               :    NN interval standard deviation along the line-of-identity                                          16.19
alpha1 (n.u.)          :    DFA low-scale slope                                                                                 1.32
alpha2 (n.u.)          :    DFA high-scale slope                                                                                0.96
SampEn (n.u.)          :    Sample entropy                                                                                      0.88
```
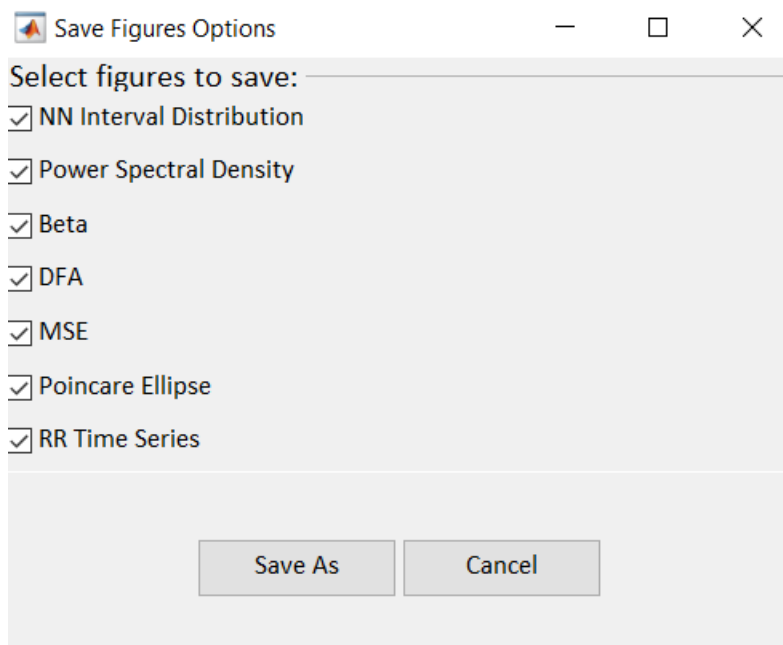
1.5.5 Exporting figures

Figures can be exported in high quality format and thus easily included in your research reports or papers. For exporting figures click File -> Export figures. You will be prompted with the following window on which you can choose what figures you want to export. After clicking 'Save As' you will be able to choose the format of the figure.

1.5.6 Consecutive windows analysis

You might want to track the evolution of the HRV measures over time: for example, if you are injecting some drug to the mammal and want to observe the resulting changes on the HRV measures over time. For that purpose **PhysioZoo** enables the analysis to be performed on consecutive segments.

Let's use a long RR time series: File -> Open data file -> Mouse_example_qrs

Click the "Single" Submenu in the left panel and click on the "Use full length" button. Then press the "Compute" button located on the top right of the interface. You will see the following screen, which contains all the HRV measures for each consecutive window over the whole recording.
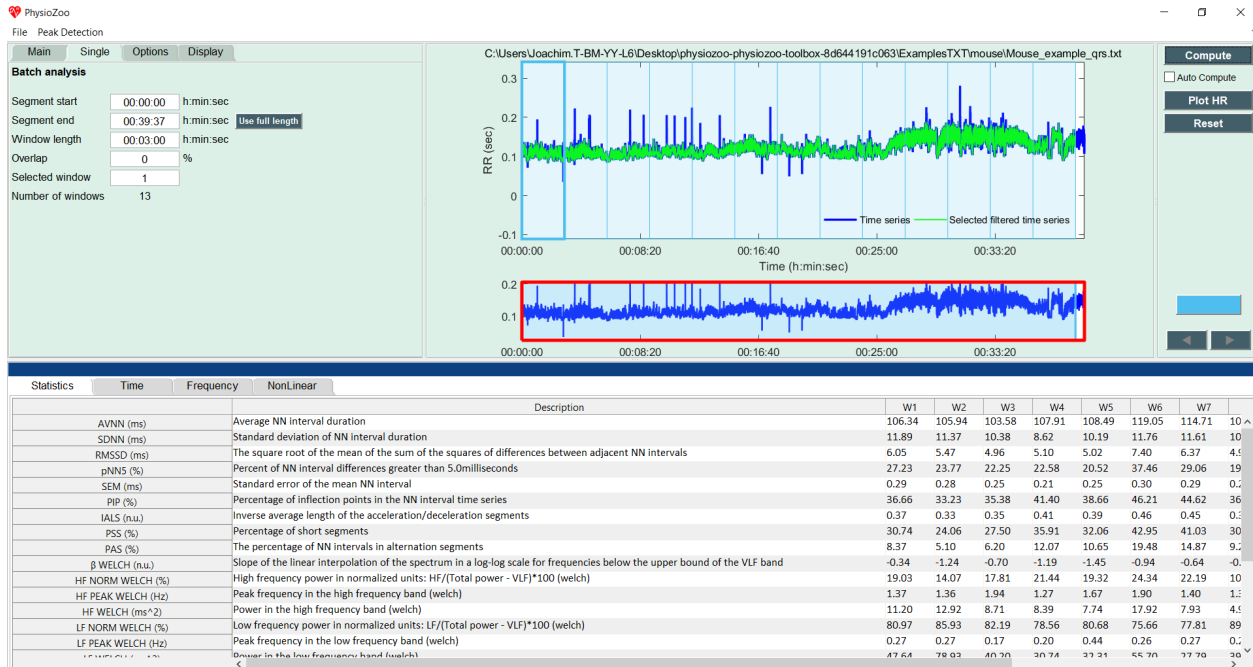
You can also enable the analysis window to be overlapping by using the "Overlap" entry in the Analysis menu. By default the value is 0% (i.e. no overlap between successive windows). Change it to 50% and re-run the analysis.
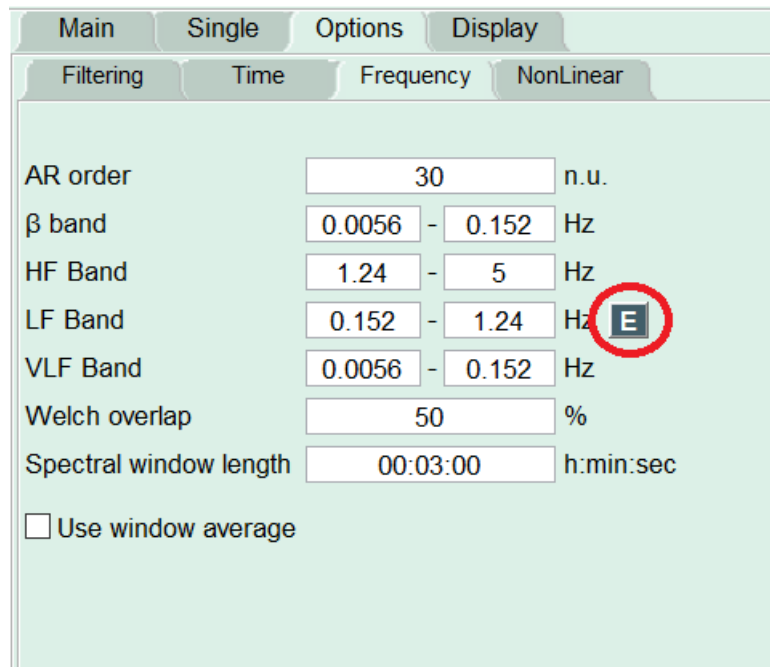
You can export all HRV measures from all consecutive windows (Main -> Save HRV measures as).

If you want to export figures, then select with the mouse the window you want to save the figures for.

Note: While using the successive segment analysis feature, it is possible to export the HRV measures and PSD from all the analyzed consecutive windows together. However, you can only export the figures from one single window at the time i.e. from the window that you select with the mouse (i.e. the 'selected window').

1.5.7 Adapting HRV measures to alternative mammals

If you want to adapt the HRV measures to other mammals you can create a new 'Configuration file' (see here) with parameters suitable to the specie you are studying. For some of the HRV measures (power frequency bands and pNNxx) you will find a button 'E' next to their parameters value under Options->Time/Frequency. You can use click on this button to adapt the HRV measure to the alternative mammalian model you are using.

1.5.8 Video Example

1.6 Signal quality annotations

In this tutorial you will learn how to perform signal quality annotations within the **PhysioZoo** `Peak detection` module and how to use these for your analysis in order to provide contextual information.

1.6.1 Introduction

PhysioZoo allows you to annotate and load signal quality annotations, which contain time intervals with quality annotations made on the original electrophysiological signal time series. The annotations highlight parts of the RR time series which are not to be trusted because the underlying ECG was of bad quality and the peak detector might have failed in estimating the heart rate within these intervals or just because you want to exclude these segments because they correspond to some transition period during drug injection and so you decide to label these time periods as 'bad quality'.

1.6.2 Annotating signal quality

To annotate the quality of an electrophysiological signal time series, follow these steps:

1. Select the rabbit ECG example: File-> Open data file-> Rabbit_example.txt

2. Under the record panel, select Annotation -> Signal quality. See the red rectangle on the figure below.

3. Look for a segment with some bad quality data and draw a rectangle around it with the mouse. The background of the area you have selected will become red.
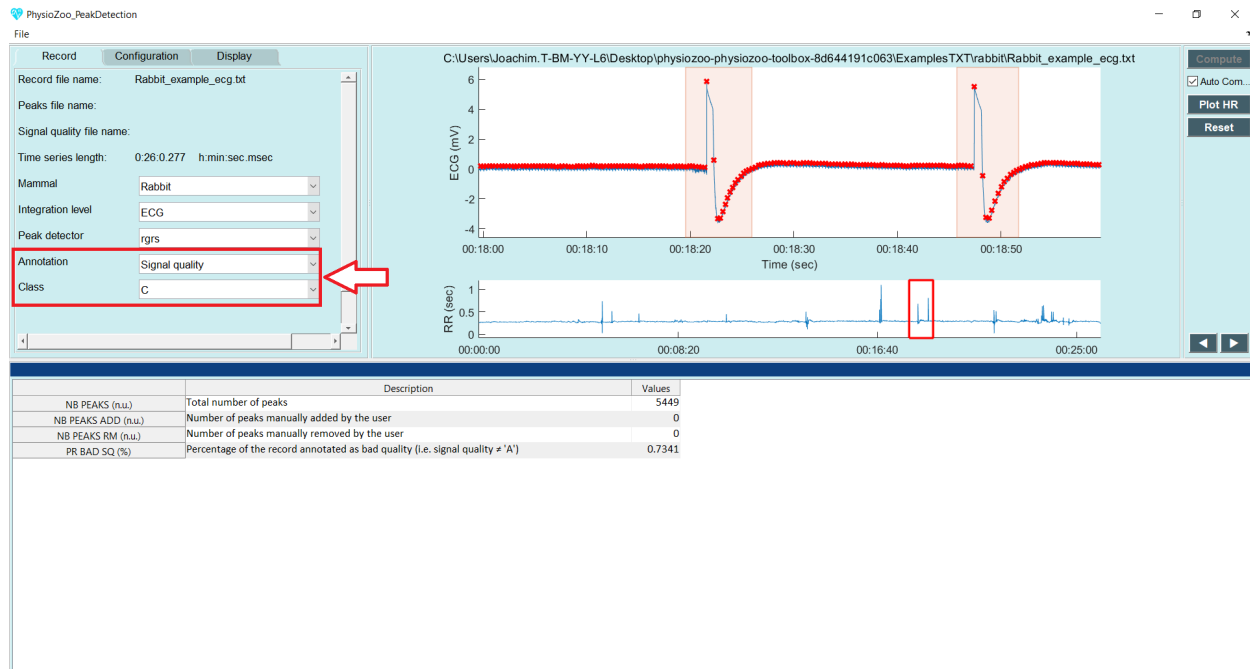

In **PhysioZoo** we define three levels of signal quality:

- "**A**": good quality signal where HRV and morphological analysis of the electrophysiological signal are possible. This means that the waveform is clean enough to detect the beats and to also study its morphology.

- "**B**": average quality signal where the beats can be detected and thus HRV analysis is possible but the signal quality is not good enough for morphological analysis.

- "**C**": bad quality signal. Neither HRV or morphological analysis is possible.

1.6.3 Loading signal quality

When using a recording for which you have performed signal quality annotations, you can load the signal quality annotations: Open -> Open signal quality file.

After the quality annotations are loaded, you will see a bar with green and red parts appearing on the top of the RR interval time series figure. The part in green corresponds to good quality data (i.e. data which analysis can be trusted) and the part in red corresponds to bad quality data (i.e. data which should not be trusted.) In addition, the RR time series is highlighted in red for the intervals which are indicated as bad quality.
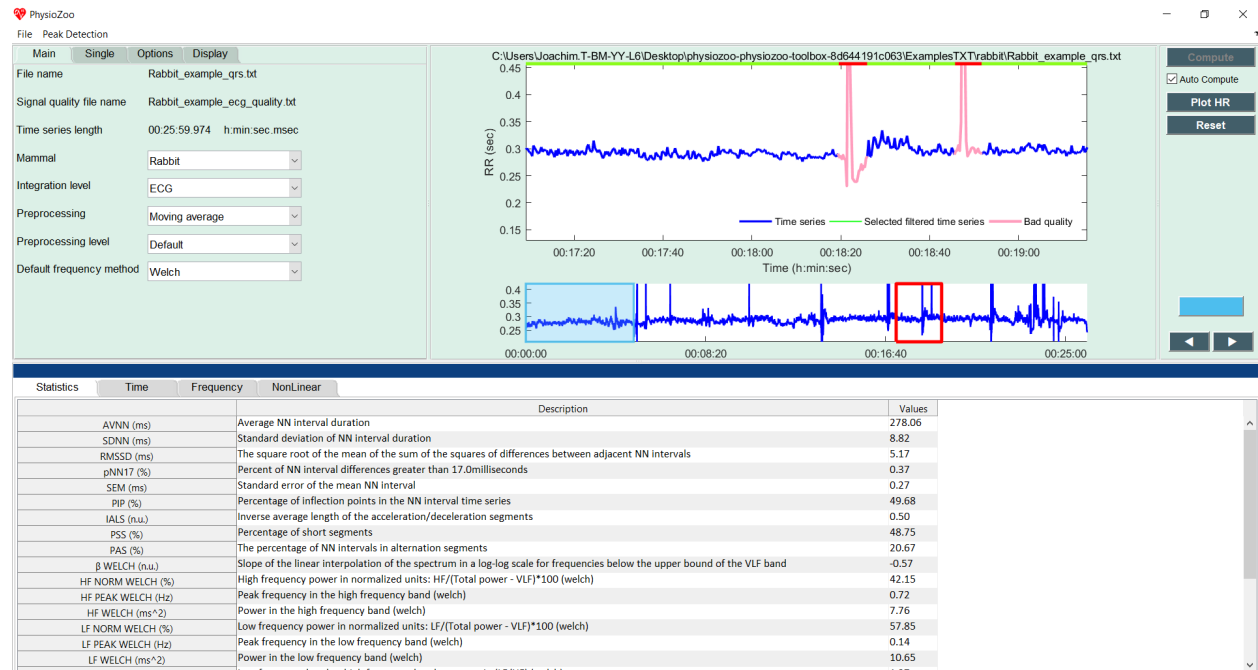
1.6.4 Frequently asked questions

When do we need to make signal quality annotations?

Small bad quality segments (few of beats) will be 'cleaned up' by the prefiltering step and so one should not worry too much about it. The signal quality annotations are more useful when a 'large' section of the recording is of bad quality in which case the prefiltering step will be useless or even misleading. Analysing such sections with large segments of bad quality data will provide meaningless results - the signal quality annotations are useful to prevent that.

1.7 Importing data

In this tutorial you will learn how to import data in **PhysioZoo**.

1.7.1 Introduction

Data loading in **PhysioZoo** is centralized and done through the `PZ Loader` tool. Three types of input formats are supported by **PhysioZoo** - see formats supported.

1.7.2 Concepts

- `PZ Loader`: three types of formats can be loaded in **PhysioZoo**. This is done through the `PZ Loader`. The `PZ Loader` will ensure that the data that enter the `PZ-UI` are properly formatted.

- Header: it is possible to include a header at the beginning of a record. This header will specify all the information that **PhysioZoo** needs to open a record. If all the information is specified in the header, then you will not need to go through populating the `PZ Loader` User Interface and the record will be directly opened in **PhysioZoo**.

See here for the formats supported and how to create **PhysioZoo** headers.

The figure below illustrates the pathway for loading a recording: the `PZ Loader` is used to load a recording from one of the supported formats. If no header is available, then the `PZ Loader` user interface is opened and the user is prompted to enter the necessary information. If the header is available, then the record is directly loaded in **PhysioZoo**.
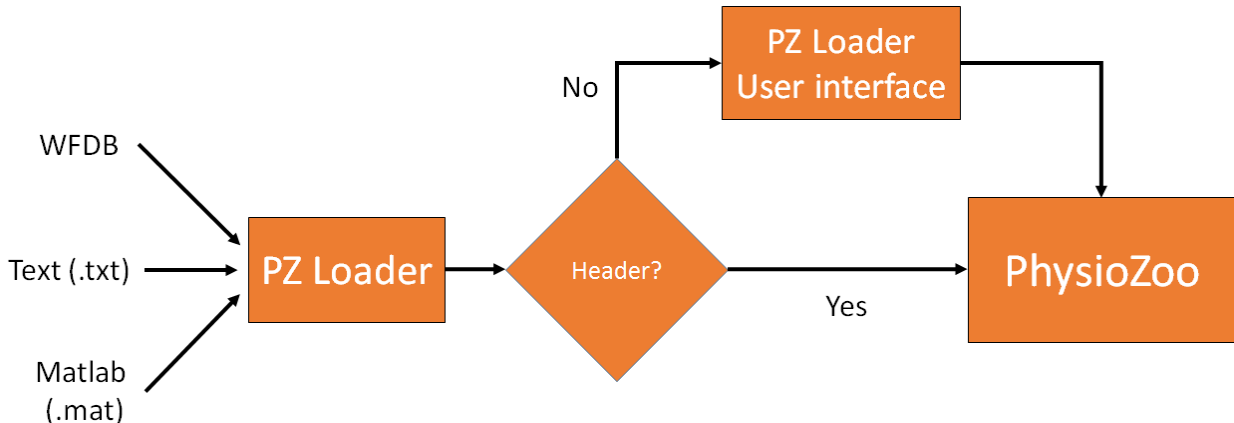
In this tutorial we will see how to make use of the `PZ Loader` user interface (UI) when no header is available.

1.7.3 PZ Loader User Interface

Open an example annotation file:

Download the following example file and load it in **PhysioZoo**.

In case some information is missing from the file (e.g. mammal type is not available in the header) then the `PZ Loader` will request the corresponding fields to be filled by the user. When all the fields have been filled then click OK and the data will be opened in **PhysioZoo**.

For the example provided, fill the fields as in the screenshot below and click OK:

1.8 Formats supported

In this tutorial you will learn about how to prepare your data for importing them in **PhysioZoo**. Data samples are available here.

1.8.1 Introduction

PhysioZoo supports three types of formats:

- WFDB,

- text (.txt),

- MATLAB (.mat).

The .txt and .mat files structures are specific to **PhysioZoo** whereas the WFDB follows the standard structure of WFDB powered by Physionet (physionet.org) with some additional fields in the WFDB header files. If you are experienced with WFDB then we recommend you use this format.

For any of the three formats a file consists of a "header" and the "data":

```
---
Mammal:            dog
Fs:                500
Integration_level: electrocardiogram

Channels:

    - type:   time
      name:   time
      unit:   second
      enable: yes

    - type:   electrography
      name:   data
      unit:   millivolt
      enable: yes

---
0.000000    0.060057
0.002000    0.064323
0.004000    0.068589
0.006000    0.073524
0.008000    0.077790
0.010000    0.080550
0.012000    0.083561
0.014000    0.085987
0.016000    0.088747
0.018000    0.090002
0.020000    0.090002
```

Note: When downloading **PhysioZoo** a set of examples (WFDB,.txt and .mat) are provided with the structure that is needed in **PhysioZoo**. You can use these as examples for formatting your own recordings.

1.8.2 General structure of the Header

For each of the files the following information can be specified in the header:

- Mammal: the name of the mammal (e.g. 'dog', 'mouse', 'rabbit', 'human'),

- Fs: the sampling frequency in Hertz,

- Integration_Level: 'electrocardiogram', 'electrogram' or 'action potential'.

As part of the header, information characterizing each channel available can be entered:

- type: 'peak', 'signal quality', 'time', 'interval', 'beating rate' and 'electrography'. See definitions of these in the next section,

- name: a name you want to give to the channel (of note this information is not used by the PZ Loader to load the data),

- unit: 'millisecond', 'second', 'index', 'bpm', 'millivolt', 'microvolt' and 'volt',

- enable: 'yes' or 'no'. If you specify 'no' then this channel will be ignored when the file is loaded by the PZ Loader. Only specify 'yes' for the channels you want to use.

In the case all or some of this information is missing from the Header then you will be prompted to enter it through the PZ Loader User Interface.

1.8.3 Channels Type

There are two categories of Channels: 'Annotations' and 'Time series'. Within these two categories the Channel can be one of the following type's (specified in the header):

Annotations

- 'peak': the location of the peaks (e.g. R-peak from an ECG time series). The peak locations can be specified in millisecond/second or index.

- 'signal quality': annotation on the signal quality. The signal quality annotations can be specified in millisecond/second or index.

Time series

- 'time': a time vector giving the position of each sample of another time series. An entry of type 'time' needs to be associated with another time series and must be in units of seconds or milliseconds.

- 'interval': the time interval between consecutive beats (e.g. RR time series). The interval length can be specified in second/millisecond or index.

- 'beating rate': the reciprocal of the interval in units of beats per minute (e.g. heart rate).

- 'electrography': the amplitude of an electrography time series (e.g. ECG). The electrography amplitude is given in microvolt, millivolt or volt. Thus only physiological units are allowed.

1.8.4 Headers in the different formats

Explanation of the structure of the different formats supported is provided below. Examples in all formats are also available in the 'Examples' folder provided with the **PhysioZoo** download.

Text format (.txt)

```
---
Mammal:              dog
Fs:                  500
Integration_level:   electrocardiogram

Channels:

    - type:    time
      name:    time
      unit:    second
      enable:  yes

    - type:    electrography
      name:    data
      unit:    millivolt
      enable:  yes

---

0.000000    0.060057
0.002000    0.064323
0.004000    0.068589
0.006000    0.073524
0.008000    0.077790
0.010000    0.080550
0.012000    0.083561
0.014000    0.085987
0.016000    0.088747
0.018000    0.090002
0.020000    0.090002
```
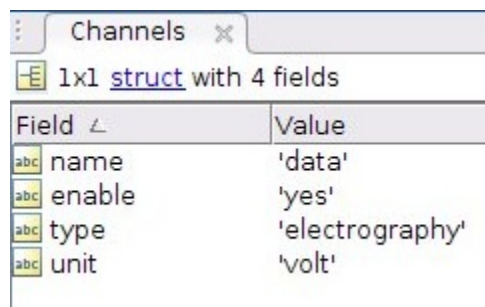
Header

Data

Matlab format (.mat)

A .mat file needs to contain the following fields:

Channels ✕

1x1 struct with 4 fields

Field ∠	Value
abc name	'data'
abc enable	'yes'
abc type	'electrography'
abc unit	'volt'

The Channels field is a Cell. Each element of the Channel Cell will contain the following fields : 'type', 'name', 'unit' and 'enable'.

WFDB (.hea)

WFDB files (annotation or data) will be accompanied by a header (.hea) file specifying the relevant information for reading an annotation or data file. Refer to the WFDB documentation for that. To the standard WFDB format of the header, you will need to add one comment line at the end of the header and starting '#' then followed by the mammal type and the integration level.

```
Dog_01 1 500 134258
Dog_01.dat 16 51300.0027(-1159)/mV 0 0 -1487 25886 0 Data
(electrography)
#Mammal:dog,Integration_level:electrocardiogram
```

1.8.5 Frequently asked questions

What if I am used to another format?

For now **PhysioZoo** only supports the WFDB, text and Matlab formats. Most commercial softwares enable you to export your data in text format which you can then import in **PhysioZoo** using the PZ Loader (see here).

Is there a way to import data without a formatted header?

Yes you can use the PZ Loader (see here) to import data which do not have a Header. You will use the PZ Loader User Interface to fill in the information needed and it will be opened in **PhysioZoo**.

1.9 Configuration files

In this tutorial you will learn how to create your custom configuration files for R-peak detection and for performing HRV analysis.

Note: In the next version of PhysioZoo the two configuration files will be merged in one unique configuration file.

1.9.1 Introduction

PhysioZoo enables you to work with HRV data from different mammals. Since the beating rate and its variability patterns vary across species then some parameters of the peak detectors and of the time, frequency and nonlinear HRV measures must be adjusted.

In the current version of the software these adaptations are readily available for the processing of Human, dog, rabbit and mouse electrocardiographic data. For processing data from other species or if you are using other data than ECG (e.g. electrogram, action potential) you will need to define your own configuration files. There are two types of configuration files in **PhysioZoo**: the peak detection configuration file and the HRV configuration file.
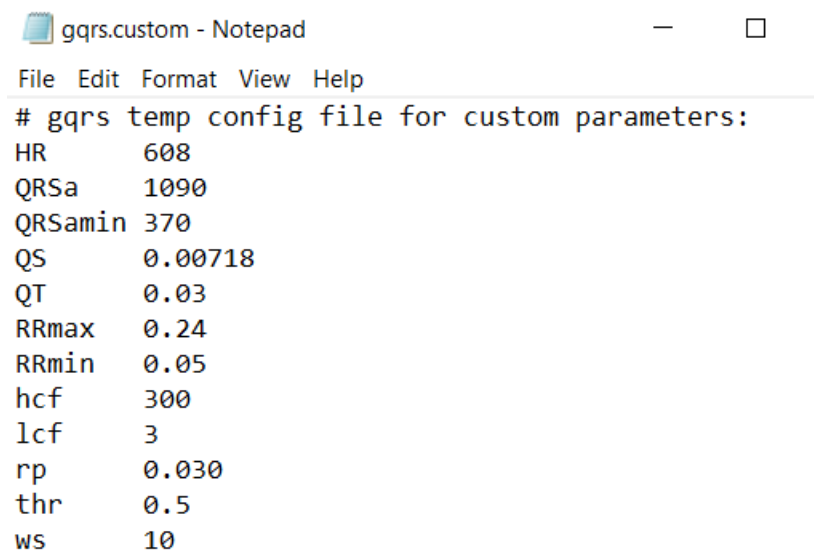
1.9.2 PhysioZoo software

Defining a peak detector configuration file

In the Peak detection module:

1. By choosing Mammal->Custom this will prompt you with a selection window. Select the configuration file of the closest mammal to the one you want to use. This will set the default HRV configuration parameters. Follow the following steps:

2. Modify the configuration of the peak detector you choose to use uder Configuration.

---

3. Save the peak detector configuration by clicking File -> Save configuration file.

4. To use this configuration file when you next use the **PhysioZoo** peak detection module: (1) File->Load custom config file or (2) Main->Mammal->Custom and choose your configuration file.

Defining an HRV configuration file

In the HRV module: under the "Main" tab you can change the Mammal type to one of the following options: Human, Dog, Rabbit, Mouse and Custom. In built in the software are configuration files for human, dog, rabbit and mouse electrocardiographic data. By choosing thee "Custom" option under `Mammal' you can define an HRV configuration file of your own. Follow the following steps:

1. By choosing Mammal->Custom this will prompt you with a selection window. Select the configuration file of the closest mammal to the one you want to use. This will set the default HRV configuration parameters.

2. Modify some of the HRV measures configuration by going to the "Options" menu (see screenshot below.) There you will find all the parameters of the HRV measures sorted with respect to their category: Time, Frequency and Nonlinear as well as the Preprocessing parameters. If, as an example, you want to change the cut-off frequency between the low frequency and high frequency bands ("LF Band" and "HF Band") in the frequency based methods then you can do so by changing the 0.341 Hz (see screen below) value to something else more suited to your data.

3. Go to File->Save config file and save the configuration file under the name of the mammal you are using.

4. To use this configuration file when you next use **PhysioZoo** HRV module: (1) File->Load custom config file or (2) Main->Mammal->Custom and choose your configuration file.

File   Help   Peak Detection

| Record | Analysis | Options | Display | Group |

Peaks file name   qrs_Rabbit_02_part_4.mat

Quality file name

Time series length   00:25:59.988   h:min:sec.msec

Mammal   Rabbit

Integration level   Human
                           Human (Task Force)
Preprocessing   Dog
                           Rabbit
Preprocessing level   Mouse
                           Custom
Default frequency method   Welch

☑ Auto Compute   **Compute**

File   Help   Peak Detection

| Record | Analysis | Options | Display | Group |

| Filtering | Time | Frequency | NonLinear |

AR order   20   n.u.

β band   0.0033 – 0.088   Hz

HF Band   0.341   – 1.155   Hz

LF Band   0.088   – 0.341   Hz   E

VLF Band   0.0033 – 0.088   Hz

Welch overlap   50   %

Spectral window length   00:05:00   h:min:sec

☐ Use window average

1.9.3 Frequently asked questions

Why configuration files?

The beating rate and its variability pattern vary across species thus some parameters of the peak detectors and of the time, frequency and nonlinear HRV measures must be adjusted.

1.10 Rhythm annotations

In this tutorial you will learn how to perform rhythms annotations from raw ECG recording within the **PhysioZoo** `Peak detection` module.

1.10.1 Introduction

PhysioZoo enables you to annotate and load rhythm annotations i.e. timestamped rhythm annotations marking the beginning and the end of a given rhythm. For example, rhythm annotations may have been produced by an original automated analysis machine (e.g. Holter ECG software) that you which to review and edit. The heart rhythms for wish annotations exist in **PhysioZoo** are:

Table 1: Available rhythms in **PhysioZoo**

Abbreviation	Condition
AFIB	Atrial fibrillation
AB	Atrial bigeminy
AFL	Atrial flutter
B	Ventricular bigeminy
BII	2° heart block
IVR	Idioventricular rhythm
NOD	Nodal (A-V junctional) rhythm
P	Paced rhythm
PREX	Pre-excitation (WPW)
SBR	Sinus bradycardia
SVTA	Supraventricular tachyarrhythmia
T	Ventricular trigeminy
VFL	Ventricular flutter
VT	Ventricular tachycardia
J	Junctional rhythm
PAT	Paroxysmal atrial tachycardia
AT	Atrial tachycardia
IVR	Idioventricular rhythm
AIVR	Accelerated idioventricular rhythm

1.10.2 Annotating rhythms

To annotate the quality of an electrophysiological signal time series, follow these steps:

1. Select the following ECG example: File-> Open data file-> physiozoo\ExamplesTXT\rhythms\ECG.txt.

2. Under the record panel, select Annotation -> Rhythms. See the red rectangle on the figure below. The different options will be displayed below in the same panel.

3. Draw a rectangle with your mouse on the desired window. The background behind the selected window will be displayed in color.

4. The rhythms can be exported under a .txt file: File -> Save Rhythms file (Ctrl+T).
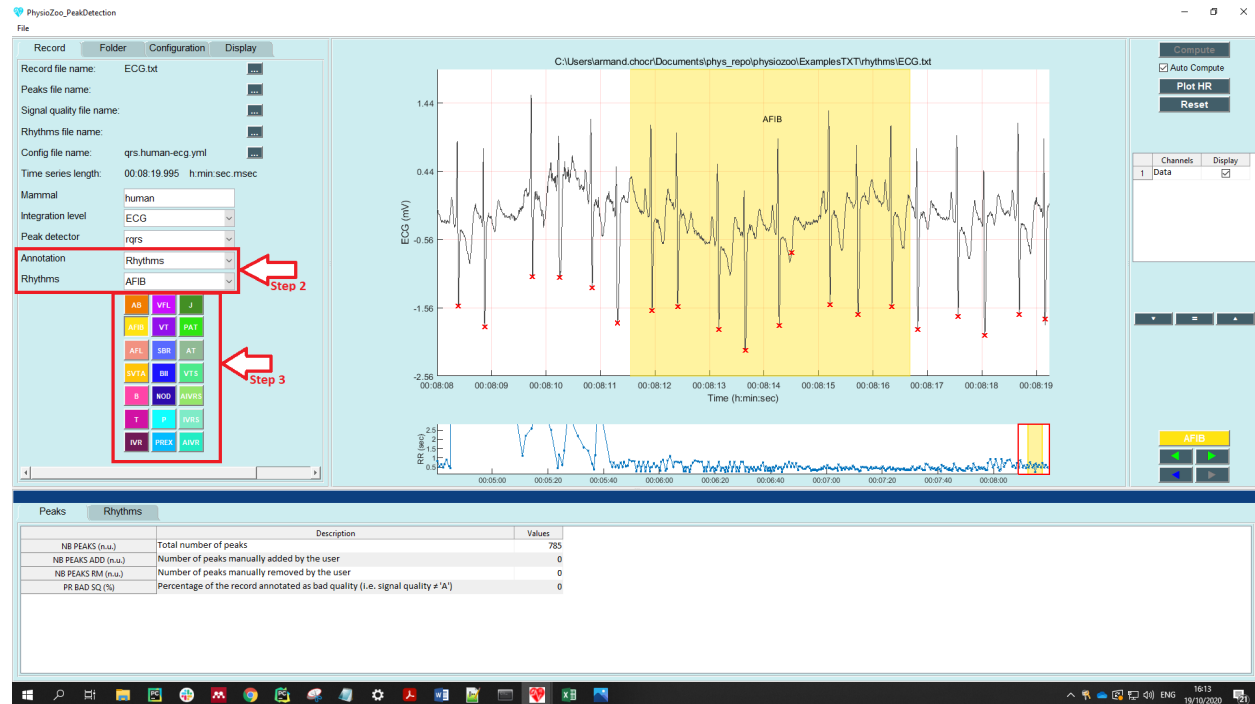
1.10.3 Loading rhythms

When using a recording for which you have performed rhythms annotations, you can load the rhythms annotations: Open -> Open rhythms file.

After the rhythms annotations are loaded, you will see a set of shaded areas with different colors appearing on the top of the RR interval time series figure as well as on the ECG raw data. These areas correspond to the rhythms annotations and each color is used to represent a different rhythm. These annotations may be further edited/saved.

On the bottom panel, you can find summary statistics for each rhythm: burden, minimal interval length, maximal interval length and 5 summary statistics.
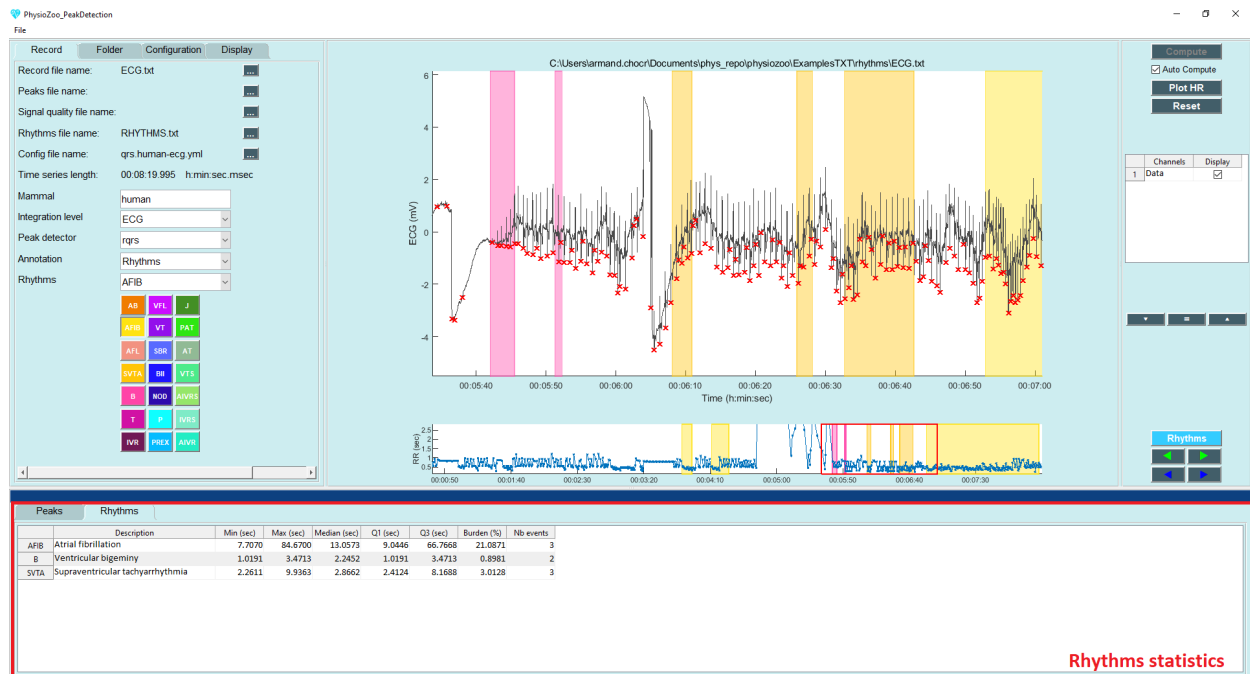
1.11 Multi-channel visualization

In this tutorial you will learn how to visualize several ECG channels within the **PhysioZoo** `Peak detection` module.

1.11.1 Introduction

PhysioZoo allows you to visualize several ECG channels in parallel. This can be use to facilitate the review of Holter recordings for example. This tutorial will show how to display several channels in parallel.

1.11.2 Displaying several channels

To display several channels of an ECG, follow these steps:

1. Select the multi-channel ECG example: File-> Open data file-> physiozoo\ExamplesTXT\multi-lead\multi-lead.txt.

2. On the right panel, select the desired leads to be displayed. By default, only channel 1 is selected.
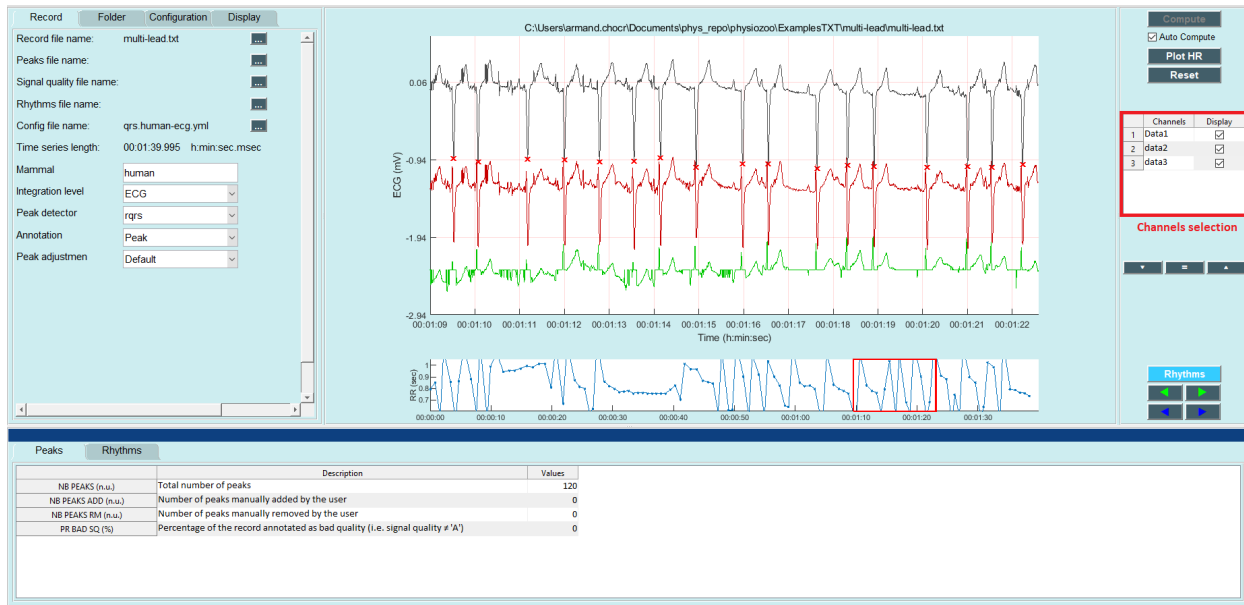
1.11.3 Frequently asked questions

What is the format of the files to be loaded to PhysioZoo to display several channels ?

If recordings are provided in .mat format then each column will represent a different channel.

An other option is to use a .txt file which will contain the following header:

> —
> Mammal: **Mammal type (human, rabbit...)**
> Fs: **Sampling frequency**
> Integration_level: electrocardiogram
>
> Channels:
>
> > - type: electrography
> >   name: **Channel name**
> >   unit: **Units (usually mV)**
> >   enable: yes
> >
> > - type: electrography
> >   name: **Channel name**
> >   unit: **Units (usually mV)**
> >   enable: yes
> >
> > - type: electrography
> >   name: **Lead name**
> >   unit: **Units (usually mV)**
> >   enable: yes

—

Following this header, the user shall place the samples in 3 distinct columns, separated by a space. The user is invited to open the 'multi-lead.txt' example to visualize the file structure.

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