

PhysioData Toolbox v0.5 Basic Walkthrough

This tutorial is a walkthrough of the basic features of the Toolbox, please also read the User Guide.

Important terminology:

- **PhysioData files:** toolbox-compatible Matlab files with the .physioData format. These files are the only files that the Toolbox can read, please see the User Guide for more information.
- **PhysioAnalyzers:** signal specific modules that the toolbox user can construct to analyze various types of physiological signals. If, for instance, a PhysioData file contains electrocardiogram (ECG) and skin conductance (SC) signals, the user can add ECG and SC modules to the file in order to perform ECG and SC specific analyses on the respective data.
- **Epochs:** sections of interest within a recording. Epochs, also called trails or segments, are generally defined relative to Markers, Labels, or Events, which are special timestamped moments within the recorded data. The toolbox is designed to automatically segment a signal into epochs using a collection of user-specified rules, and extract relevant metrics for each epoch.

The examples presented in this document use the PhysioData files provided with the toolbox. Also included in the toolbox package is a tool for converting different data file types to PhysioData, see the User Guide for more information.

1: Importing and Viewing Raw Data

This section shows how to import readymade PhysioData files and view their raw data. The example files should be located in the 'ExampleFiles' folder next to the 'Toolbox' folder containing PhysioDataToolbox.exe.

Import PhysioData Files:

1. Run the Toolbox by launching the PhysioDataToolbox.exe file. It may take a few minutes before the Toolbox loads. Exercise patience.
2. Once the Session Manager is visible, click on the 'Open' button and select the folder with the example files (the 'ECG_BP_EDA' folder inside the 'ExampleFiles' folder of the Toolbox package).

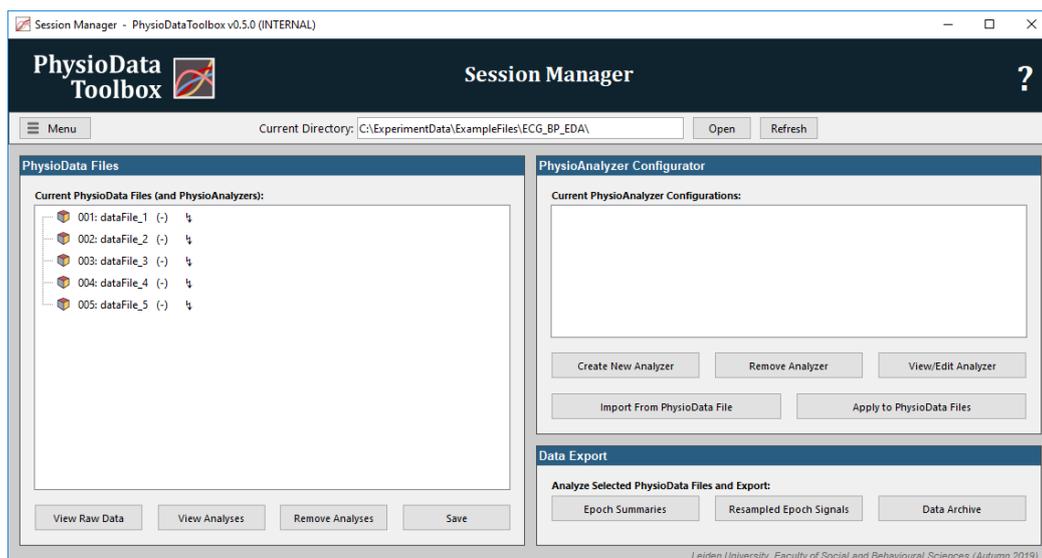


Figure 1: The Session Manager, with five empty PhysioData files.

3. The Session Manager should now list all PhysioData files inside the directory. Note that the files shown in Figure 1 do not contain any PhysioAnalyzers (the nodes within the PhysioData

file tree cannot be expanded). If any files already contain PhysioAnalyzers, remove them by clicking the ‘Remove Analyses’ button below the file tree, checking all ‘PhysioAnalyzer Tags’ checkboxes, and clicking the ‘Remove from all files’ button.

View Raw Data:

1. Select a file from the list, click the ‘View Raw Data’ button to open the Raw Data Viewer, and click on the ‘Raw Signals’ tab to see the data. Scroll up and down using the scrollbar to reveal more channels. Take note of what data are in which channel.
 - To zoom, select a section of the graph using the right mouse button. Double-clicking the graph resets the view. Additional zooming and panning options are available through (a combination of) the other mouse buttons, see the ‘Zooming’ chapter in the ‘Data Viewers’ section of the User Guide for more information.
 - Which file is currently being shown is specified in the bar above the tabs. To navigate to a different file, either select it using the dropdown menu, or use the buttons.
2. In the example files, channel 4 is a digital marker channel, which is automatically detected by the Toolbox. Click on the ‘Marker Signals’ tab to see the analysis of the marker channel.

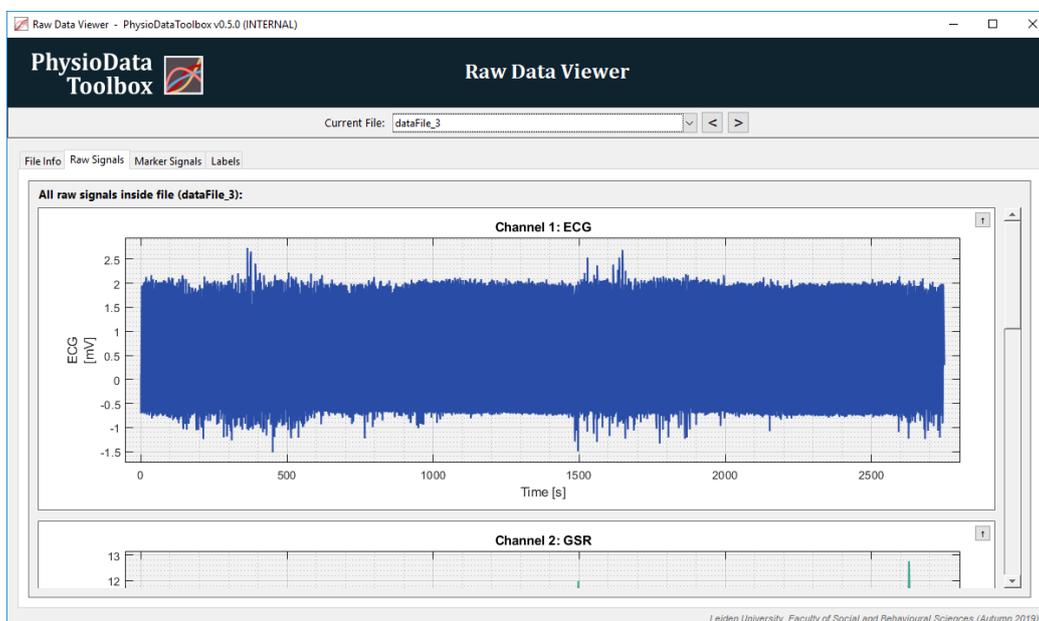


Figure 2: The ‘Raw Signals’ tab in the Raw Data Viewer. Scroll down using the scroll bar to reveal additional channels. You can collapse a channel using the upwards pointing arrow next to its graph.

3. Click on the ‘Labels’ tab to see the labels inside the current file.

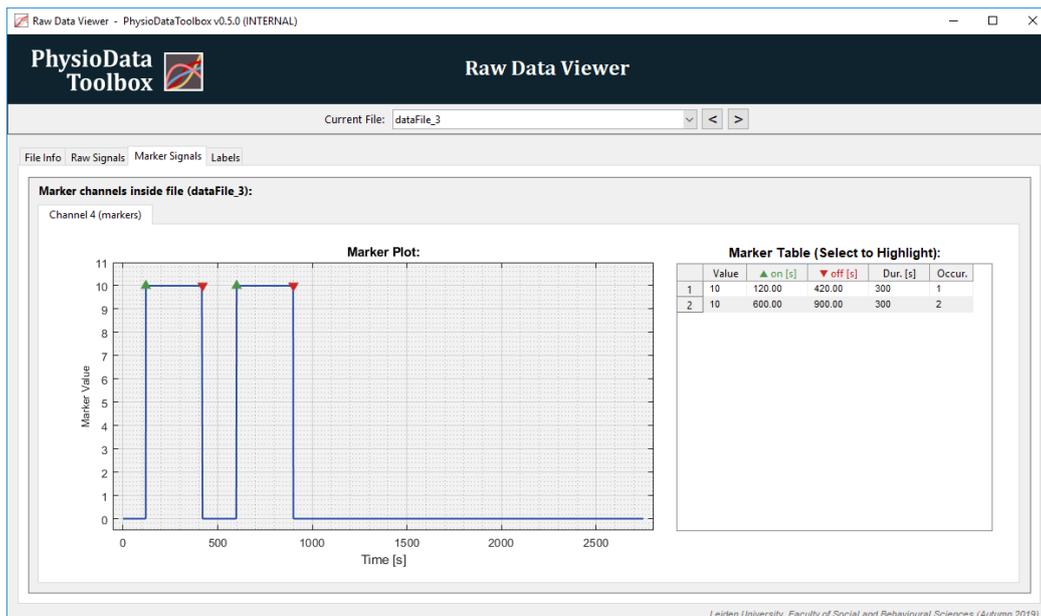


Figure 3: The Raw Data Viewer’s automatic marker analysis. All example files contain two markers with the value 10 and a duration of 300 seconds.

2: Defining and Propagating PhysioAnalyzer Settings

This section shows how to make ECG, SC (Skin Conductance), and HRV (Heart Rate Variability) modules, and how to define epochs. Additional information about defining epochs can be found in the ‘Epochs and Events’ section of the User Guide.

ECG PhysioAnalyzer Creation:

1. In the Session Manager, click on the ‘Create New Analyzer’ button and choose the ECG signal Analyzer.
2. Since ‘ECG’ is a fitting name for the module and the ECG signal is in channel 1 (click the ‘See Channels’ button to verify this), the settings can be left at their default values.
3. Click on the ‘Click to View/Edit Epochs’ button to open the Epochs Builder.

Defining Epochs:

1. The ‘Define Epochs’ tab of the Epochs Builder window shows the epoch definition table. By default, an epoch spanning the whole file is created.
2. Click on the second tab to see all data inside the file that can be referenced when defining epochs. In the example files, these are the markers in channel 4 and the labels.

Let’s say we want to create the following epochs:

- An epoch named ‘Epoch_1’ that spans the duration of the first marker in channel 4.
- An epoch named ‘Epoch_2’ that spans the duration of the second marker in channel 4.
- An epoch named ‘Epoch_3’ that starts at the ‘Start_Trial_3’ label, and ends 30 seconds after the ‘End_Trial_3’ label.
- Additionally, we want to cut up the ‘Epoch_3’ epoch into segments of 30 seconds.

3. Go back to the ‘Define Epochs’ tab and click add row 3 times.
4. Define the ‘Epoch_1’ epoch (the epoch definition of ‘Epoch_1’ is provided in Figure 4):
 - Defining the start of the epoch:
 - Since we want to reference the markers in channel 4, fill in <4> in the ‘StartChannel’ column (second row). Never include the < and > symbols.
 - We want to reference the marker with value 10, as such, fill in <10> in the StartValue column.
 - The start of the epoch must coincide with the ‘on’ event of the marker (the first green upward pointing arrow in Figure 3); as such, fill in <0> and <on> in the StartDelay and StartAt columns, respectively.
 - Since we want to reference the first marker of value 10 (of the two such markers in the example file), we need to specify the occurrence as <1>. Note that an occurrence always needs to be specified, even if only one such marker exists.
 - Defining the end of the epoch:
 - For the end of the epoch we are referencing the same marker as for the start of the epoch, except we are referencing the fall of the marker (its ‘off’ event) rather than its rise (its ‘on’ event). As such, fill in the same values except for ‘EndAt’, which should now be <off>.
 - Leave the EpochModify column empty, and fill in <Epoch_1> as the epoch name.

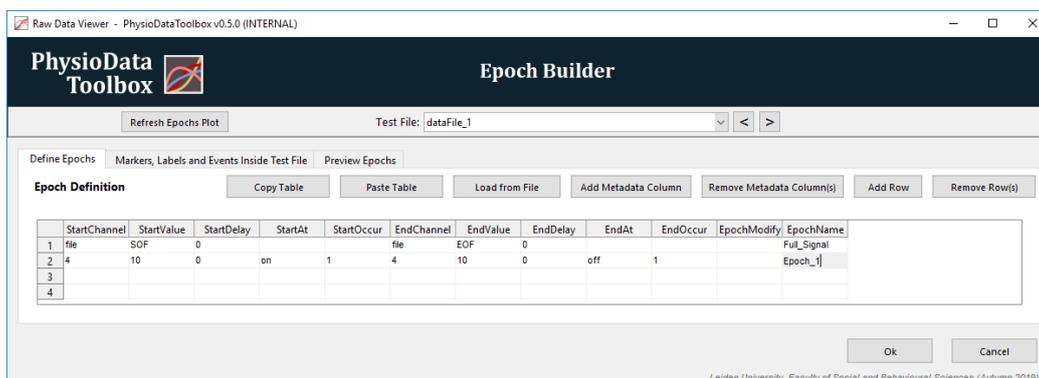


Figure 4: The epoch definition table with the Epoch_1 epoch added.

5. Define the ‘Epoch_2’ epoch in a similar manner to the ‘Epoch_1’ epoch. Do this below the row in which ‘Epoch_1’ was defined. The only differences are the start and end occurrences, which should now both be <2> since we are referencing the second marker of value 10. In addition, the name should now be <Epoch_2>.
6. Define ‘Epoch_3’:
 - To define the ‘Epoch_3’, we need to reference labels instead of markers, as such, the StartChannel and EndChannel cells should be set to <label> (without the < and >).
 - The StartValue and EndValue should be the values of the labels; i.e., <Start_Trial_3> and <End_Trial_3>, respectively. You can see the available labels in the second tab of the Epoch Builder window.
 - The StartDelay should be <0>, but since we want the epoch to end 30 seconds after the end-marker, the EndDelay should be set to <30>. Note that you can also use negative delays to start or end an epochs before a marker occurs.

- The start and end occurrences for this epoch should both be <1>, and since labels are discrete events without a start or stop, the StartAt and EndAt cells can be left empty.
- Fill in the correct EpochName.
- To slice the epoch into 30 second segments, fill in <timeSlice(30)> in the EpochModify column.

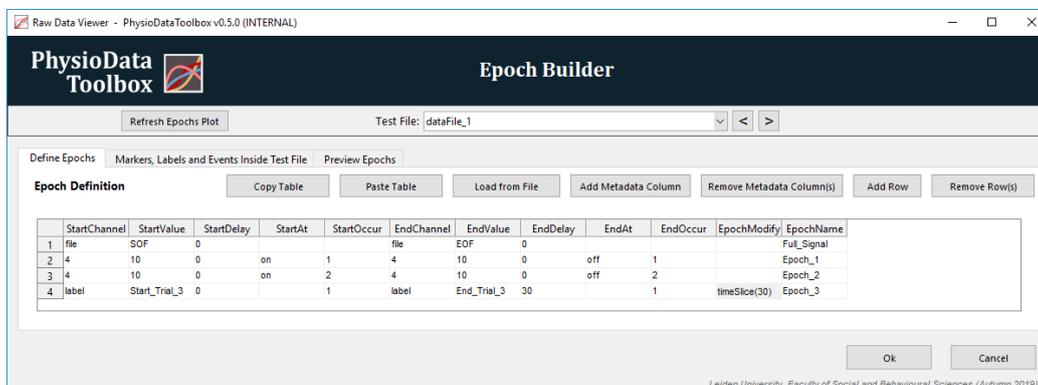


Figure 5: The completed epoch definition table.

7. Switch to the 'Preview Epochs' tab and click the 'Refresh Epochs Plot' button to see the epoch definition applied to the test file. Verify that the definition does what we want it to do. You can test the epoch definition on another file by switching the test file.

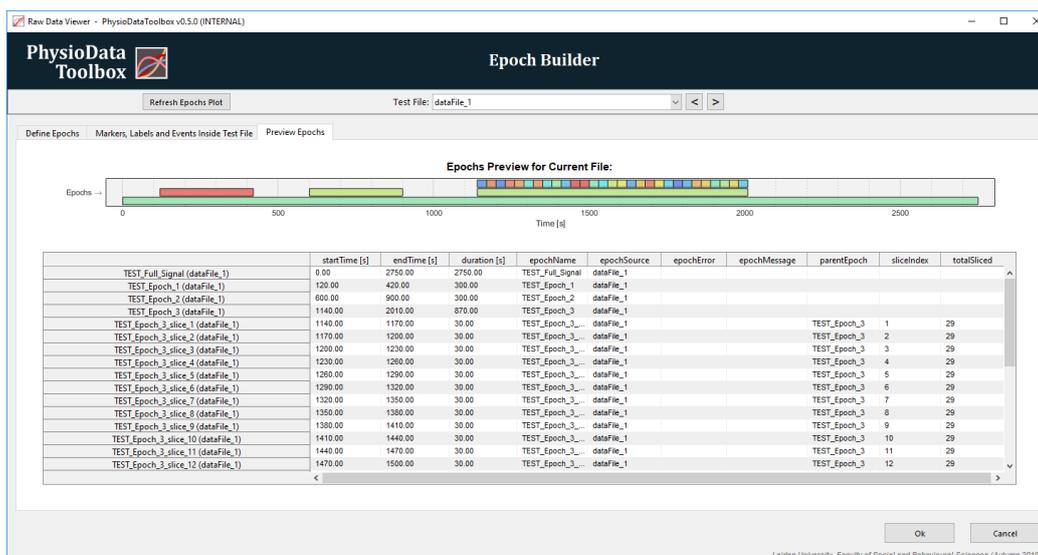


Figure 6: The epoch preview tab, showing the epoch definition applied to file 'dataFile_1'. The top graph shows the 'Full_Signal' epoch, which spans the whole duration of the file, as well as the three trials. In addition, the 30 second slices of 'Epoch_3' are shown.

8. Click 'Ok' to close the Epoch Builder window and return to the PhysioAnalyzer settings window. Click 'Ok' on that window as well to save the changes and return to the Session Manager.

Adding the SC PhysioAnalyzer and Referencing the ECG Epochs:

1. Click the 'Create New Analyzer' button again and select the Skin Conductance Analyzer.
2. Fill in <2> in the channel number field to make the module use the EDA signal in channel 2.

3. We will use the same epochs as we defined in the ECG module; therefore, select 'PhysioAnalyzer with tag' from the epoch drop down menu and fill in <ECG> in the field below. This will make this module dynamically use any epochs we defined in the ECG module.
4. Click 'Ok' to close the window and add these settings to the PhysioAnalyzer tree.

Adding the HRV Analyzer

1. Click the 'Create New Analyzer' button again and select the HRV Analyzer.
2. Fill in <ECG> in the 'Tag of the ECG Analyzer' field. In order for it to function, the HRV analyzer must be linked to an ECG module.
3. As with the previous analyzer, we will use the same epochs as we defined in the ECG module. Select 'PhysioAnalyzer with tag' from the epoch drop down menu and fill in <ECG> in the field below.
4. Users are advised to consult the most recent version of the User Guide for more information on the HRV settings, as it will not be described here. Click 'Ok' to close the window and add these settings to the PhysioAnalyzer tree.

Applying the Settings to the PhysioData files:

1. In the Session Manager's PhysioAnalyzer Configurator panel, click the 'Apply to PhysioData Files' and then 'Apply to all Files' buttons to propagate the settings of the listed PhysioAnalyzers to all the files. This will create one ECG, one SC, and one HRV module inside each file. Note that the modules inside the PhysioAnalyzer tree don't do anything until they are applied.
2. You should now see 'ECG, HRV and SC' after each file in the PhysioData file tree. The red color indicates that these modules have not yet been marked as 'accepted' by the user. You can expand each file to reveal the PhysioAnalyzers inside it, and each PhysioAnalyzer to reveal its current settings and state, see Figure 7.
3. Click 'Remove Analyzer' in the 'PhysioAnalyzer Configurator' panel three times to remove the settings you just made. Note that they are still in the files. To reimport the settings from a file, select the desired file in the list and click the 'Import from PhysioData File' button. This will copy the PhysioAnalyzer settings in that file back to the PhysioAnalyzer Configurator.

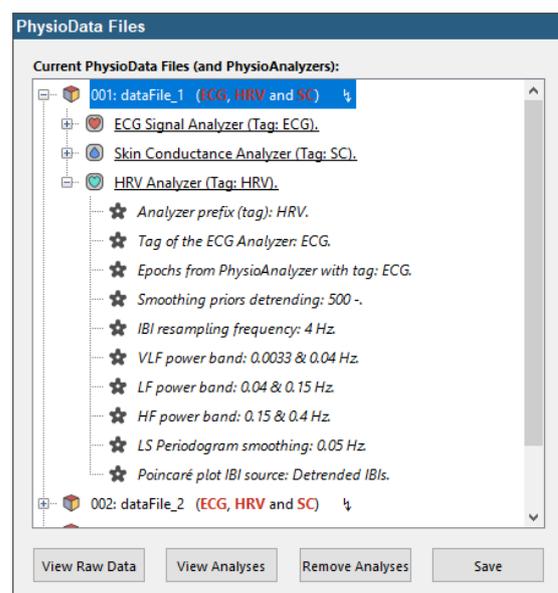


Figure 7: The 'PhysioData Files' panel showing file 001 with three PhysioAnalyzers.

3: Reviewing and Correcting PhysioAnalyzer Data

This section shows the basics of reviewing and correcting PhysioAnalyzer modules. Refer to the User Guide for additional information. The available interactions of each module is described in that module’s chapter.

Launching and Using the PhysioAnalyzer Viewer:

1. In the Session Manager, click the ‘View Analyses’ button in the PhysioData Files panel to open the PhysioAnalyzer Viewer window. This window visualizes each PhysioAnalyzer present inside the current file. One tab is created per analyzer.
2. The top graph shows the epochs that were generated from the epoch definition. Click on the epochs for info. Below that are the ECG, Interbeat Interval (IBI) and Instantaneous Heart Rate (IHR) plots. In the legend you can click on a line to hide it. Right-clicking the ECG graph reveals some extra option.
3. Inspect the plots inside the ECG and SC tabs using the zooming and panning commands described previously. Use the file bar to navigate through the files. Notice how all the PhysioAnalyzers appear artifact free, with the exception of those in dataFile_1, and the ECG module in dataFile_2.

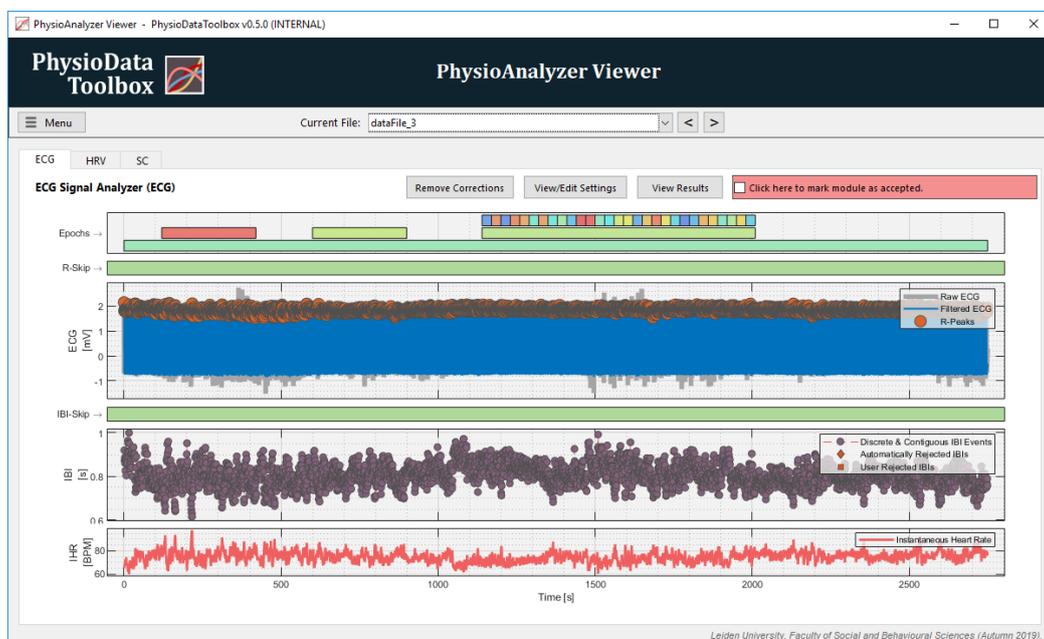


Figure 8: The PhysioAnalyzer Viewer window, showing the ECG PhysioAnalyzer inside dataFile_3. The top graph, labeled ‘epochs’, shows the segments generated from the epoch definition.

Correcting the ECG data:

The ECG module features the ability to mark and reject erroneous R-peaks and IBIs.

1. Navigate to the ECG tab in ‘dataFile_1’. Unlike in the correct files, the IBIs plotted here clearly show outliers around 700 s. Zoom in and notice how this is caused by missing R-waves in the ECG signal, resulting in several instances of doubly long IBIs. Since R-peaks cannot be manually added in this version of the toolbox, correction must involve removing the bad IBIs.
2. The IBI artifacts can be manually corrected by adding an ‘IBI skip zone’ around the outliers. Zoom in to the IBI artifact at 683 s, and, using the left mouse button, select an area covering the IBI. Subsequently, select ‘Disregard IBIs in selected section’ from the menu. The toolbox will now refrain from using any IBIs located inside this newly inserted ‘IBI skip zone’, which is visualized in the ‘IBI skip’ graph.

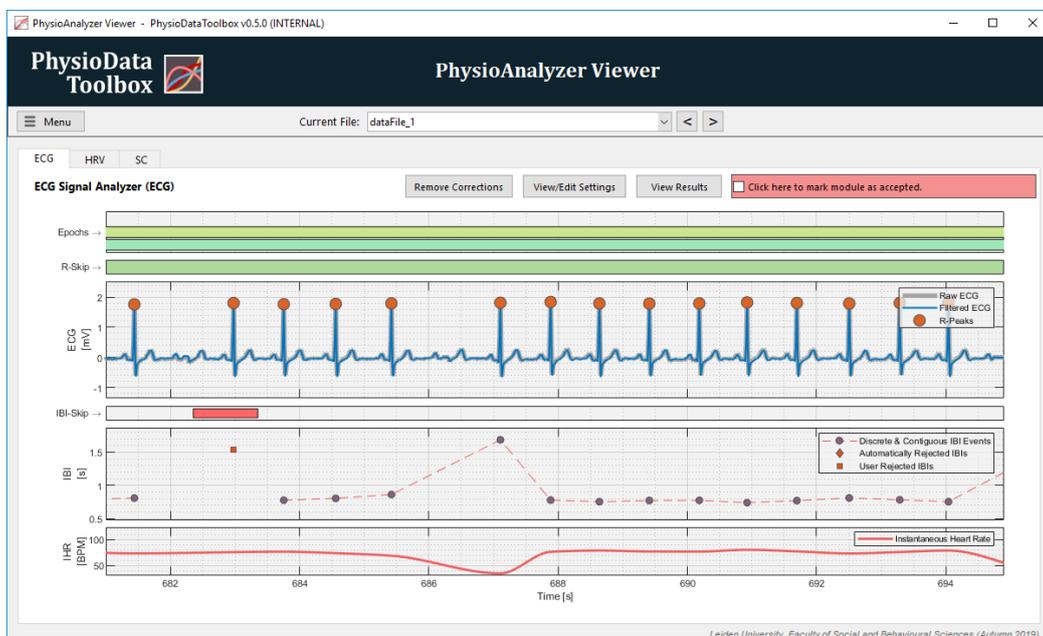
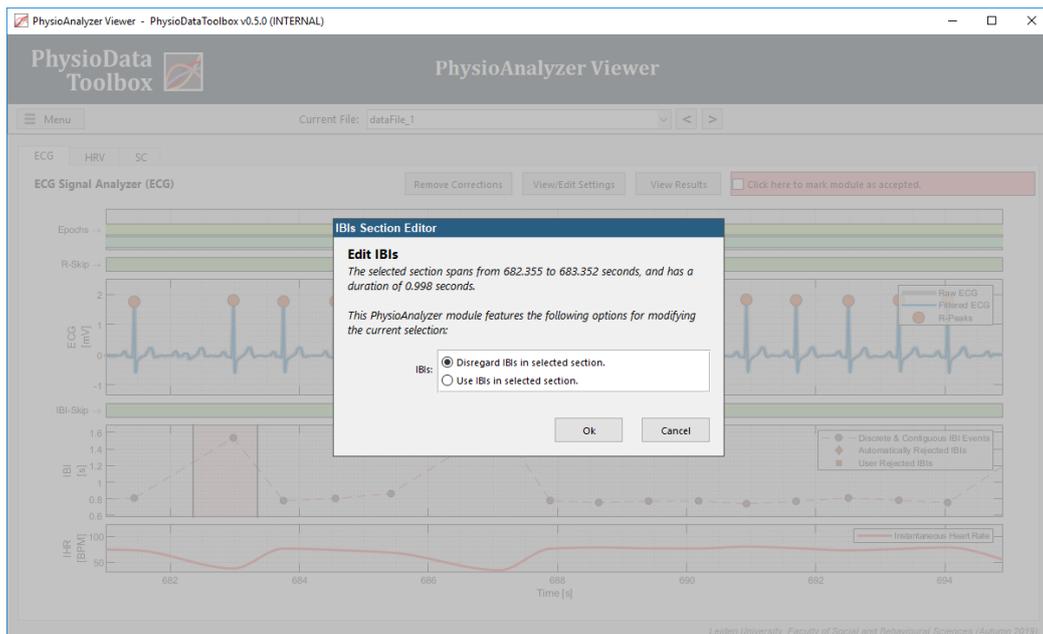


Figure 9: Manually correcting IBIs using ‘IBI skip zones’. Top: an IBI artifact is marked and the ‘disregard’ option is selected from the popup menu. Bottom: the IBI artifact inside the IBI-skip zone is removed.

3. Since manually removing individual IBIs can be time consuming, a better approach may be to adjust the ‘Maximum IBI value’ setting in this particular PhysioAnalyzer. Zoom the IBI plot completely out by double clicking it. Notice how the correct IBIs in this file are never located above 1.2 s. Click the ‘View/Edit Settings’ button in the ECG tab and set the ‘Maximum IBI value’ to 1.2. After clicking Ok, the ECG module will automatically remove all IBIs above the said threshold. In the IBI graph, these automatically rejected IBIs are displayed as diamonds, and are not used to generate the Instantaneous Heart Rate (IHR), which is calculated by interpolating all non-rejected IBIs.
4. Mark the module as ‘accepted’ by clicking the checkbox.
5. Now navigate to the ECG module in dataFile_2. Notice how in this file the ECG recording features an erroneous section between 80 and 110 s. This can be corrected in a similar manner as before, but instead using an R-skip zone. Select a zone spanning from 80 to 110 seconds and

select the ‘disregard’ option. You can remove a zone by making a part of it, and selecting the ‘Use R-peaks in selected section’ option from the popup menu. To re-include the usable ECG part in the middle of the noisy section, select the segment (92 to 101 seconds), and choose the ‘Use R-peaks’ option.

6. Mark the ECG module in dataFile_2 as accepted.

Correcting the SC data:

Data correction in the Skin Conductance graph consists of the user inserting ‘Raw-Skip’ zones inside which the raw data are not used. Instead, the data inside the zone are replaced by linear interpolation before applying the low-pass filter, and performing the subsequent processing and analysis actions.

1. Go to the SC module in dataFile_1. Notice how the skin conductance signal features several spikes, possibly caused by the electrodes coming loose (driving down the conductance) or the electrodes getting short circuited (driving up the conductance).
2. In the Skin Conductance graph, zoom in to the artifacts and select sections straddling a spike. Focus on covering the spike in the gray raw data signal. Use the ‘Disregards raw data in selected section and interpolate’ option to remove the spike. Do this for all spikes.

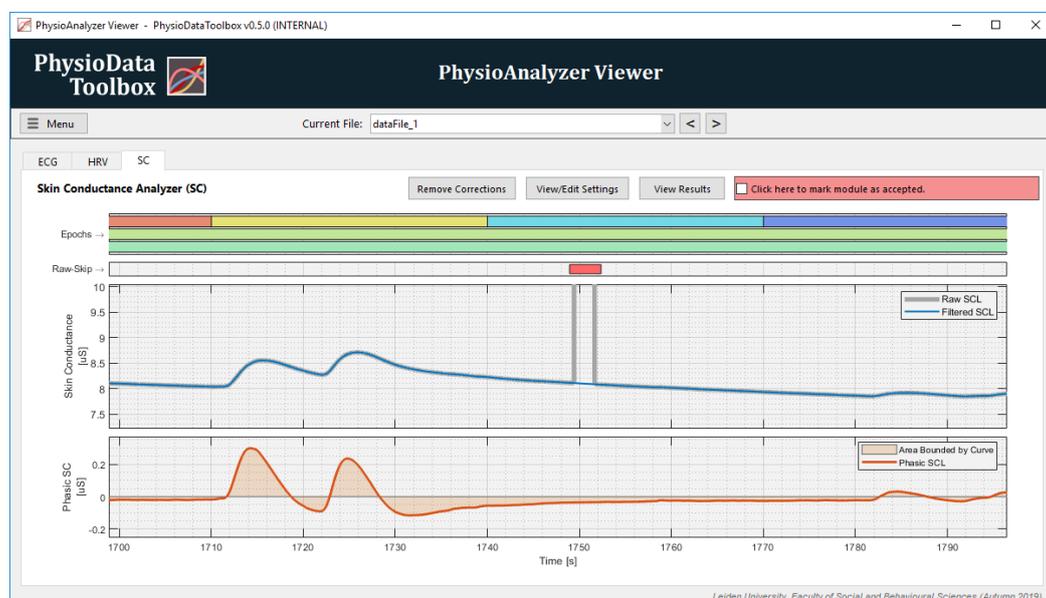


Figure 10: The Skin Conductance PhysioAnalyzer, showing an artifact (grey spike) that has been removed by inserting a ‘Raw-Skip’ zone.

3. Once all artifacts have been removed, mark the module as accepted. Note that with the exception of the artifacts in dataFile_1, the Skin Conductance signals in the example files are typical of well measured signals, both in terms of scale and shape.

Viewing the HRV data:

The HRV module itself does not allow users to correct artifacts, this must instead be done in the linked ECG module. Any changes made to the IBIs in the linked ECG module are automatically transmitted to the HRV module, and the graphs and results table are automatically updated. Note that it is important to remove artifacts in both the R-peak and IBI signals in the ECG module. When, for example, the analyzer incorrectly identified an extra R-peak, correcting the corresponding IBI alone will incorrectly mark the preceding and succeeding IBI as noncontiguous, which can have an effect on the HRV results.

1. Navigate to the HRV tab in 'dataFile_1'. Note that we previously corrected the IBI signal in the ECG module of this file and that this is also visible when looking at the IBI plot in the top. Zoom in and notice the missing IBIs around 700 s (see Figure 11).
2. Select the epoch that you wish to review the results of by using the dropdown menu at the left or by clicking the buttons next to it, or by clicking on one of the epoch rectangles in the epoch plot in the top of the window.
3. Inspect the plots using the zooming and panning commands described previously. In the right bottom part of the screen the Detrended IBIs, Successive Differences, Poincare Plot, and Lomb-Scargle Periodogram are displayed. These plots can be minimized by clicking the arrow button in the right upper corner of each of the plots.
4. When reviewed, mark the HRV module in dataFile_1 as accepted.

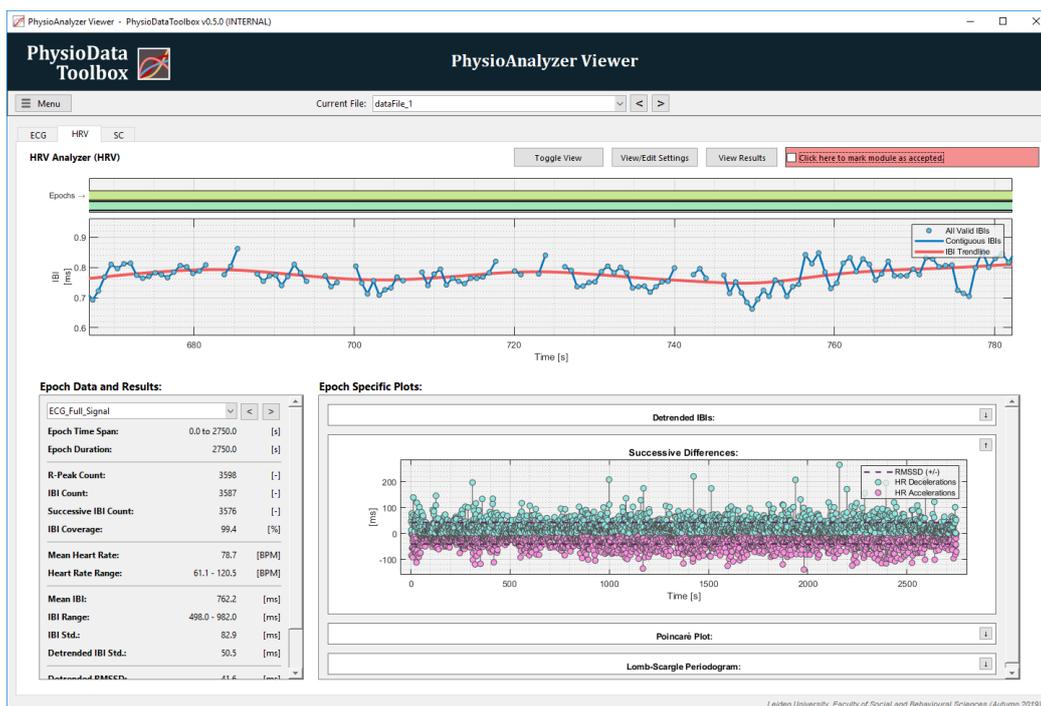


Figure 11: The HRV PhysioAnalyzer, showing the IBIs around 700 ms (top plot) and the Successive Differences for Epoch_1 (bottom right plot). Notice that the other plots are minimized.

Viewing Results:

1. Review the other modules in the other files, and mark them as accepted.
2. You can view each module's individual results by clicking the 'View Results' button. This will perform descriptive analysis on each epoch in the current PhysioAnalyzer, and show the results in Excel. Also in the 'metadata' tab are summaries of all current settings and states.
3. Close the PhysioAnalyzer Viewer when done and go back to the Session Manager.

4: Updating the Setting

It may be at times necessary to update one or more specific settings within multiple existing PhysioAnalyzers, without overwriting other customized settings—and without removing the corrections. This can be done using the PhysioAnalyzer Configurator in the Session Manager.

Say we want to update the epochs definitions in all files, but leave the other settings intact:

1. Select any file in the file tree, and click the 'Import from PhysioData file' button. Remove the 'Skin Conductance Analyzer' from the PhysioAnalyzer tree by selecting it (by clicking it) and clicking the 'Remove Analyzer' button.

2. Click the 'View/Edit Analyzer' button, then in the settings dialog, the 'Click to View/Edit Epochs' button.
3. In Epoch_3's row, change 'timeSlice(30)' to 'timeSlice(10)'. Also add 'timeSlice(10)' to the EpochModify cells of the 'Epoch_1' and 'Epoch_2' rows. All three epochs should now get sliced into section of 10 seconds.
4. Add a new row, and create an epoch called Epoch_3_REST that starts at the end of Epoch_3, and has a duration of 60 seconds. Use the 'Add Metadata Column' to create a new column called 'TYPE', and use it to mark 'Epoch_1', 'Epoch_2' and 'Epoch_3' as 'Trial'. Mark the last epoch as 'Rest'. See the figure below.

	StartChannel	StartValue	StartDelay	StartAt	StartOccur	EndChannel	EndValue	EndDelay	EndAt	EndOccur	EpochModify	EpochName	TYPE
1	file	SOF	0			file	EOF	0				Full_Signal	
2	4	10	0	on	1	4	10	0	off	1	timeSlice(10)	Epoch_1	Trial
3	4	10	0	on	2	4	10	0	off	2	timeSlice(10)	Epoch_2	Trial
4	label	Start_Trial_3	0		1	label	End_Trial_3	30		1	timeSlice(10)	Epoch_3	Trial
5	label	End_Trial_3	30		1	label	End_Trial_3	90		1		Epoch_3_REST	Rest

Figure 12: The new epoch definition.

5. Review the new epoch definition by going to the 'Preview Epochs' tab and clicking the 'Refresh Epochs Plot' button.
6. Click Ok in the Epoch builder and the Settings dialog to return to the Session Manager.
7. Expand the ECG module in the PhysioAnalyzer tree, and deselect all settings except the epochs (labeled 'Epochs from definition: 5 row(s) in table').

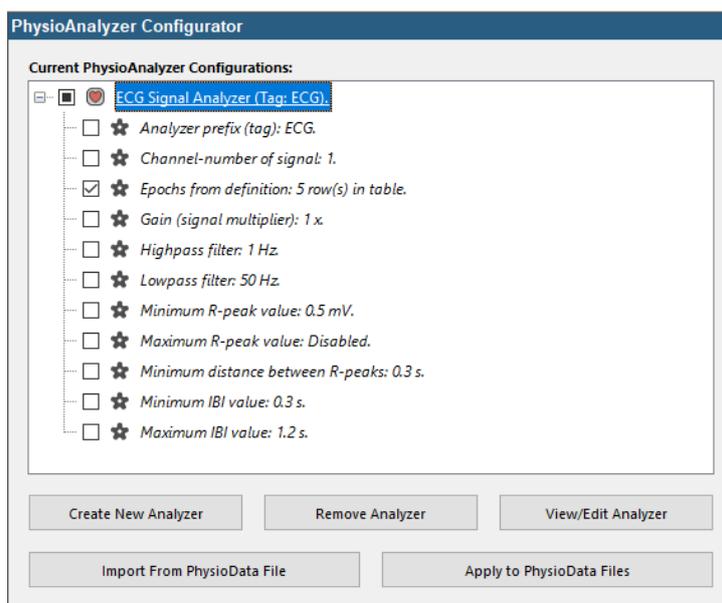


Figure 13: The ECG module with just the epoch settings checked.

8. Click the 'Apply to PhysioData Files'. This will open a summary of the settings that are to be pushed to the files, see Figure 14. In this window, click 'Apply to all files' to propagate the listed settings, in this case the epochs, to all the PhysioData files. This will leave the other settings intact.

Note that the 'Maximum IBI value' setting in dataFile_1 was previously customized to filter out the IBI artifacts and thus differs from the other files. As such, if that setting were not unchecked in the PhysioAnalyzer tree, its value would be pushed to all files overwriting any file-specific values.

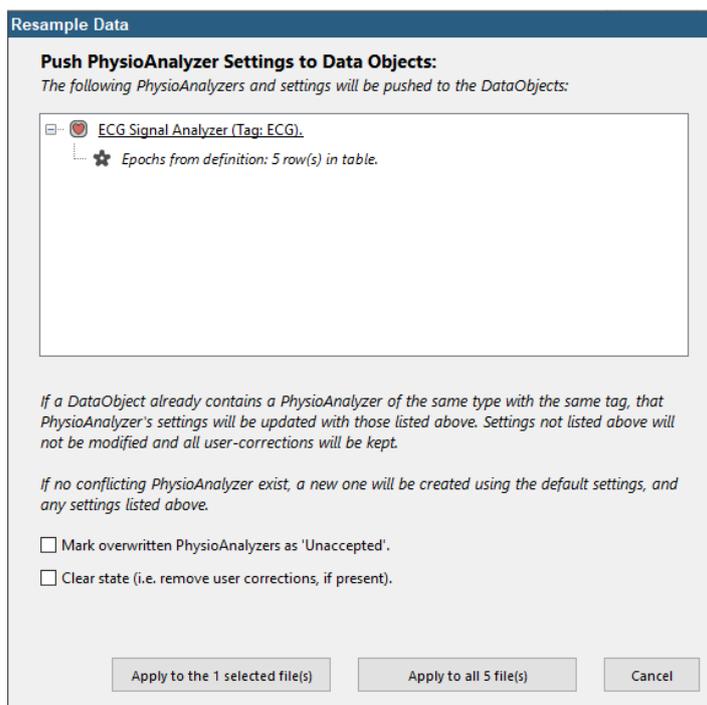


Figure 14: The ‘Batch PhysioAnalyzer Propagator’ window, which pops up when the ‘Apply to PhysioData Files’ button is clicked. It shows a summary of the PhysioAnalyzers that are about to be pushed to the files, including their settings.

9. Use the PhysioAnalyzer viewer to verify that the new epochs are present in all files, and that the customized ‘Maximum IBI value’ setting in dataFile_1 is still intact.

5: Exporting Analysis

The results of all the PhysioAnalyzers inside multiple PhysioData files can be exported to different file formats, by first selecting the desired PhysioData files in the file tree, then clicking the ‘Epoch Summaries’ button in the ‘Data Export’ panel. We will export the data to an Excel file.

1. Select all PhysioData files (tip: use ctrl + A).
2. Click the ‘Epoch Summaries’ button, then click ‘Analyze all files’, wait for the toolbox to collect the descriptive analyses and then click ‘As one Excel file, with one table per worksheet’. Finally, click the ‘Open Excel File’ button to view the file. The results are automatically saved to a new timestamped Excel file in the current data directory.



Figure 15: The ‘Data Export’ panel.

- For each unique PhysioAnalyzer tag, two new sheets are created: the <tag>_RESULTS and <tag>_INFO sheets. These sheets can be accessed using the tabs in the bottom left corner of the Excel window. The Results sheet contains all the results for all epochs in that PhysioAnalyzer, inside all selected files. The Info sheet contains information about the settings and state. Rows that belong to the same file are grouped together by color in the first column.
- Note that the data are automatically formatted as Excel tables, allowing you to easily filter and sort the data. As an example, the epochs representing the 10 second slices can be hidden by clicking the button in the 'sliceIdx' table header (cell J:5), and deselecting all values except '(blanks)'

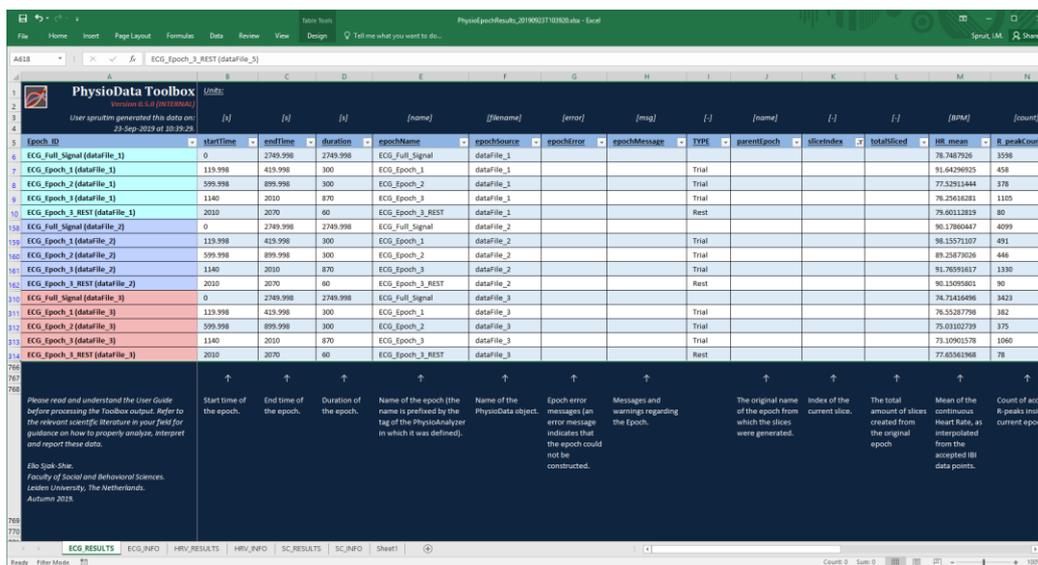


Figure 12: The Excel data export format. Certain rows have been hidden.

6: Saving the Session

At this point, the edits made to PhysioData files have not been saved yet. As such, if the Session Manager is closed without saving, all settings and corrections will be lost. To save the session, click the 'Save' button in the Session Manager. This causes the toolbox to store the PhysioAnalyzers, including their settings and state, inside their respective PhysioData files.

It is strongly advised to save often to prevent data loss in case the PhysioData Toolbox inadvertently closes.

Note, only PhysioAnalyzer that's have been applied to PhysioData files are saved inside their respective files file. Those PhysioAnalyzers are visualized in the file tree inside the PhysioData files panel in the Session Manager. PhysioAnalyzer in the PhysioAnalyzer configurator are not saved and will be lost when the Toolbox is closed.