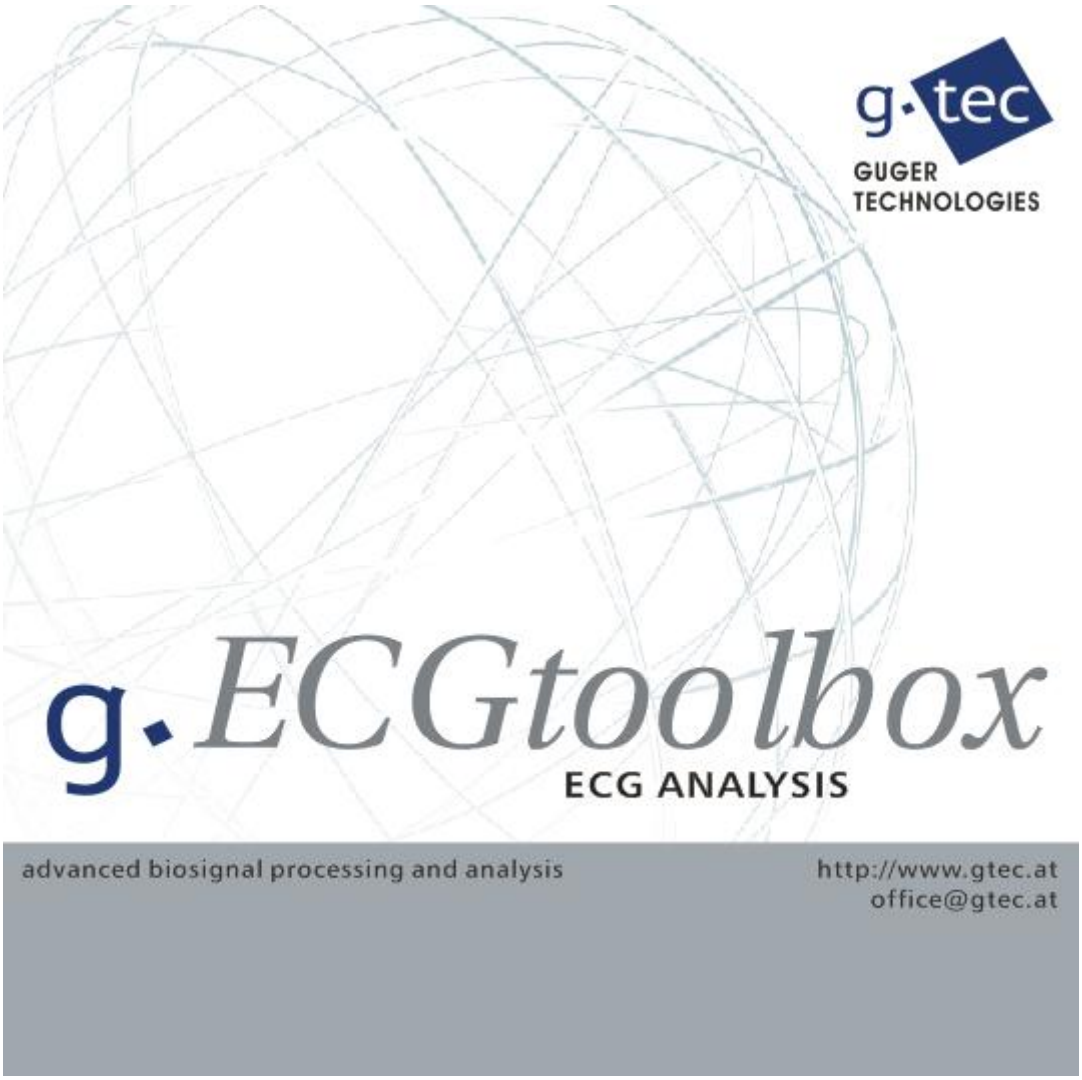


VERSION 5.16.02

USER MANUAL

CONTENT:

To the Reader

Welcome to g.tec's world of medical and electrical engineering!
Discover the only professional biomedical signal processing platform under MATLAB and Simulink. Your ingenuity finds the appropriate tools in the g.tec elements and systems. Choose and combine flexibly the elements for biosignal amplification, signal processing and stimulation to perform even real-time feedback.

Our team is prepared to find the better solution for your needs.

Take advantage of our experience!

Dr. Christoph Guger Dr. Guenter Edlinger

Researcher and Developer

Reduce development time for sophisticated real-time applications from month to hours.
Integrate g.tec's open platform seamlessly into your processing system.
g.tec's rapid prototyping environment encourages your creativity.

Scientist

Open new research fields with amazing feedback experiments.
Process your EEG/ECG/EMG/EOG data with g.tec's biosignal analyzing tools.
Concentrate on your core problems when relying on g.tec's new software features like ICA, AAR or online Hjorth's source derivation.

Study design and data analysis

You are planning an experimental study in the field of brain or life sciences? We can offer consultation in experimental planning, hardware and software selection and can even do the measurements for you. If you have already collected EEG/ECG/EMG/EOG, g.tec can analyze the data starting from artifact control, do feature extraction and prepare the results ready for publication.

Preface

This section includes the following topics:

Required Products

g®.ECGtoolbox uses:

g®.BSanalyze – the advanced biosignal analysis software package from g.tec

MATLAB – as basic matrix operation platform

Signal Processing Toolbox - to give access to standard signal analysis tools

Using This Guide

Chapter "Running g.BSanalyze" shows how to start the Data Editor.

Chapter "Detecting QRS Complexes" shows how to work with the Complex Detector and how to manually edit the ECG data.

Chapter "Calculating a Heart Rate Feature Channel" explains the generation of a heart rate channel that is also visible in the Data Editor.

Chapters "Heart Rate Variability Time Domain Measures", "Heart Rate Variability Frequency Domain Measures" and "Heart Rate Variability Maps" explain in detail how to calculate the most important parameters in heart rate variability analysis based on the example of a tilt-table experiment.

Chapter "Help" explains the usage of the on-line help, the printable documentation and the function help.

Chapter "Batch-Mode" shows how to use the g.BSanalyze commands from the MATLAB command line.

Conventions

Item	Format	Example
MATLAB code	Courier	to start simulink, type `simulink`
String variables	*Courier italics*	`set(P_C,'PropertyName',...)`
Menu items	**Boldface**	Select **Save** from the **File** menu.

Hardware and Software Requirements

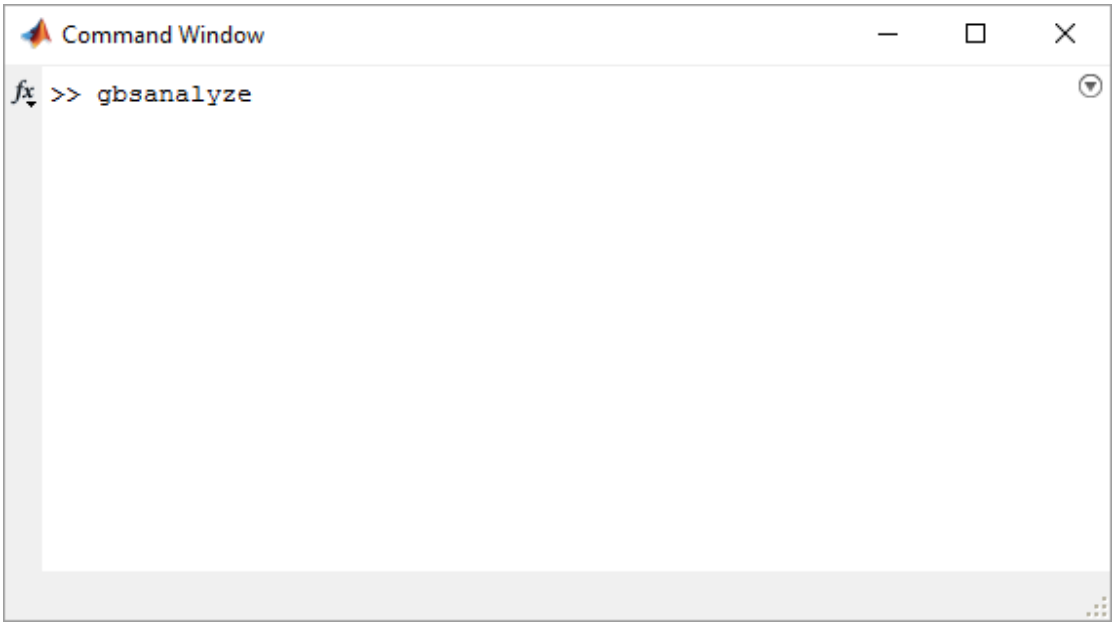
For Hardware and Software Requirements see the g.BSanalyze manual.

Running g.BSanalyze

After starting MATLAB and setting the correct path, type:

```
gbsanalyze
```

in the MATLAB command line



g.BSanalyze starts with a blank data window.

Detecting QRS Complexes

The first step in ECG analysis is to find the QRS complexes in the time series. The algorithm finds a number set that corresponds to the temporal position of successive QRS complexes in the ECG. Time differences between adjacent QRS complexes can be shown as Tachogram (successive RR interval values are plotted against the 'beat number').

The implemented QRS detector bandpass filters and squares the ECG signal. Then a threshold detector identifies the QRS complexes.

Complex Detector Window

The **Complex Detector** window has the following control elements:

Use complex markers – use already assigned markers to generate a heart rate feature channel

Use input channel – specify an ECG channel to detect QRS complexes

Advanced settings:

Bandpass filter:

Lower cutoff frequency – defined in Hz
Upper cutoff frequency – defined in Hz

Threshold – the level when a QRS peak is detected in mV

Accepted heart rate change:

Min – a QRS complex is only accepted if the actual RR interval is not smaller than e.g. 60 % of the previous interval
Max – the complex is rejected if the RR interval is longer than e.g. 140 % of the previous interval
Highest accepted heart rate – the QRS detector does not accept heart rates above this level

Generate marker names:

Detected events – assign QRS markers to the detected events

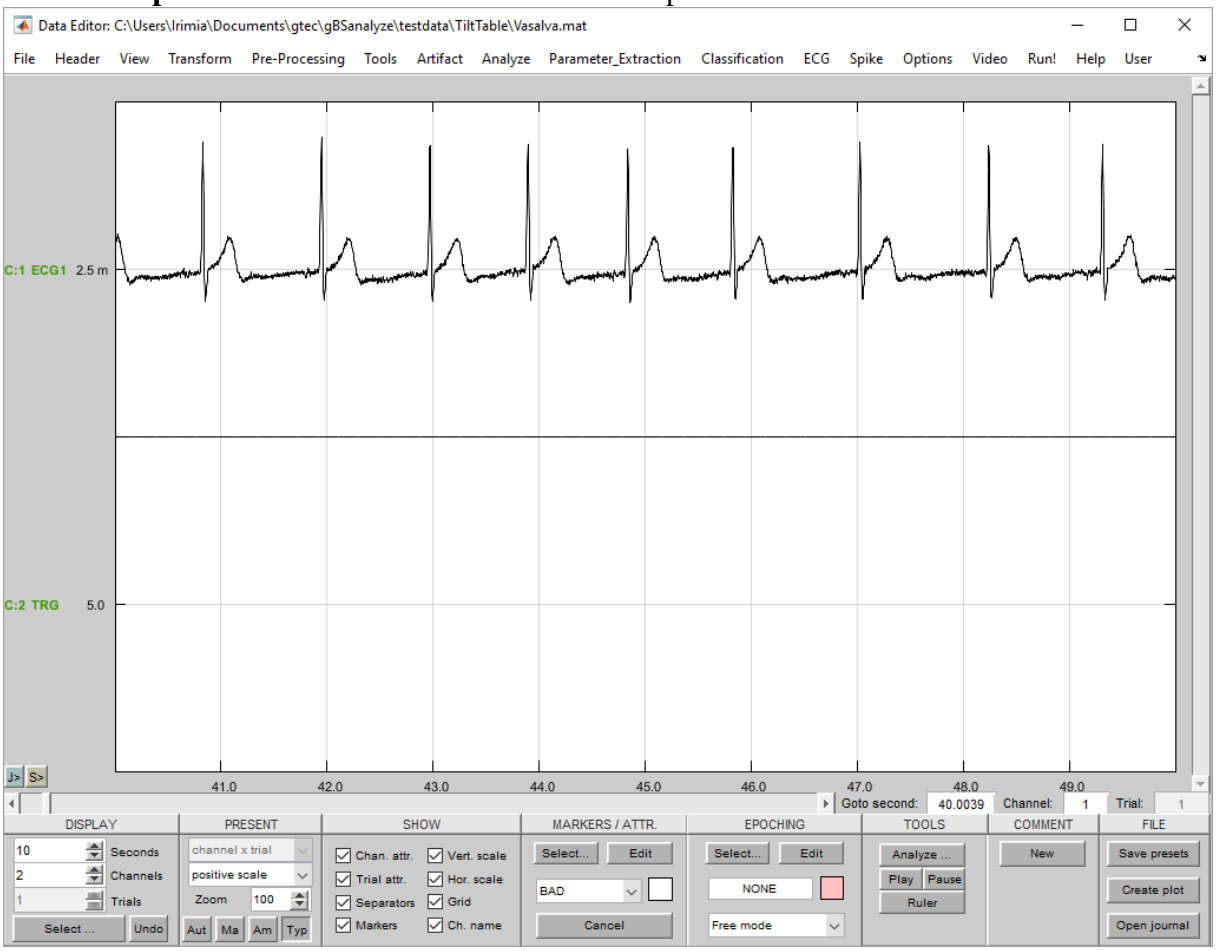
Generate feature channel – adds a new heart rate channel to the raw-data. The scaling can be in `ms`, `samples` or `beats per minute`.

Example

1. Click on **Load Data** under the **File** menu of g.BSanalyze and select the file `Vasalva.mat` from

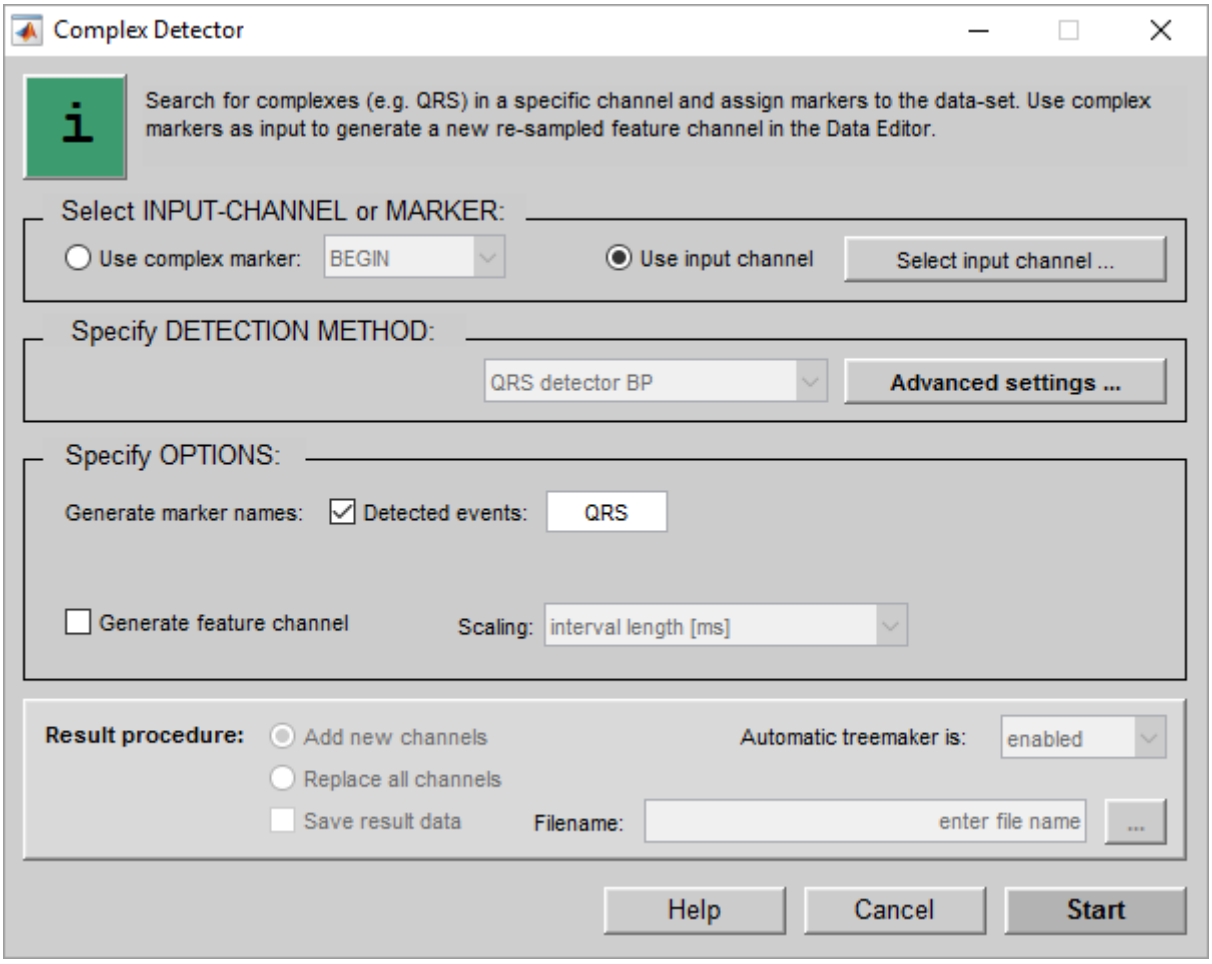
   `Documents\gtec\gBSanalyze\testdata\TiltTable`

2. Press **Open** to load the data file of a tilt table experiment.



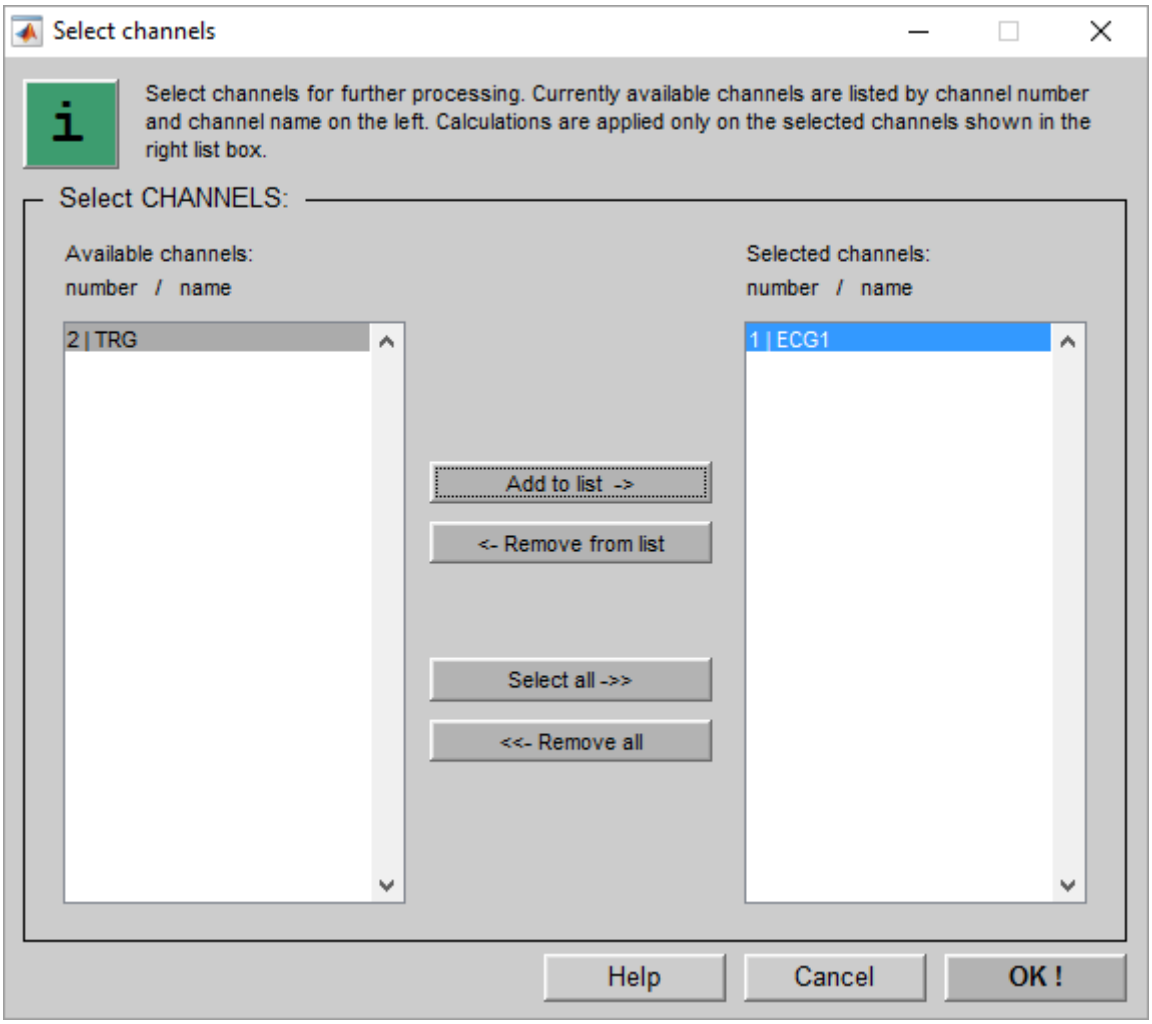
Channel 1 shows the recorded ECG derivation, channel 2 the trigger signal which indicates the time point when the subject was standing up. The subject was lying on a table from second 1 to 633 and was standing from second 633 until 1490.

3. Select the **Complex Detector** from the **ECG** menu to open the following window:

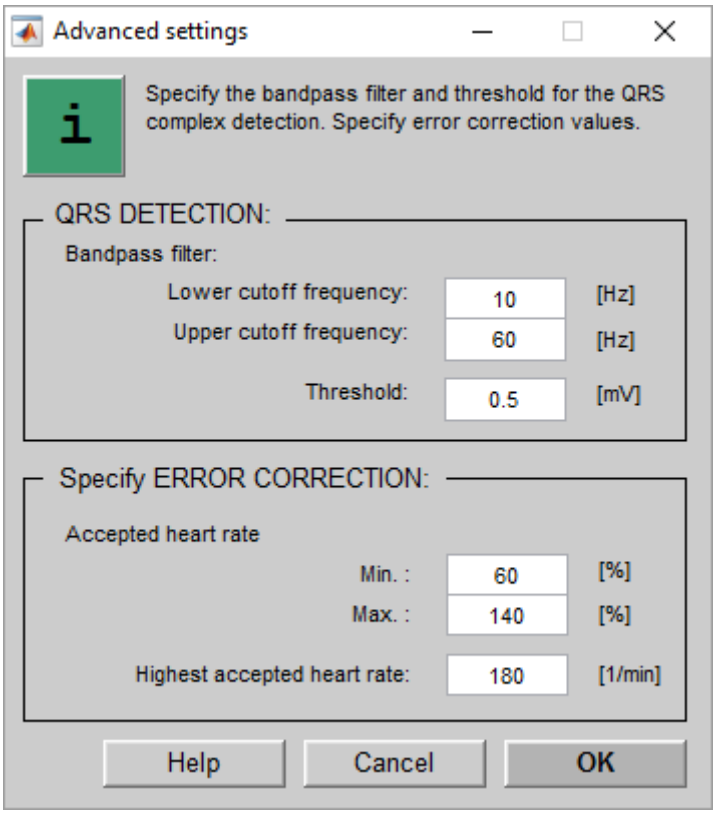


4. Select the radio button **Use input channel** to search for QRS complexes and press **Select input channel…**

5. Add the ECG channel to the **Selected channels** list box by pressing the **Add to List ->** button and confirm the selection with the **OK !** button.



6. Press the **Advanced settings…** button to open the following window:



   The QRS detector uses bandpass filter to remove artefacts. Enter a **Lower cutoff frequency** of `10` Hz and an **Upper cutoff frequency** of `60` Hz. Set the **Threshold** to `0.5` mV.

   The **Accepted heart rate change Min** should be set to `60` % and the **Max** to `140` %. The algorithm allows therefore only RR intervals which increase or decrease by 40 % compared to the previous interval.

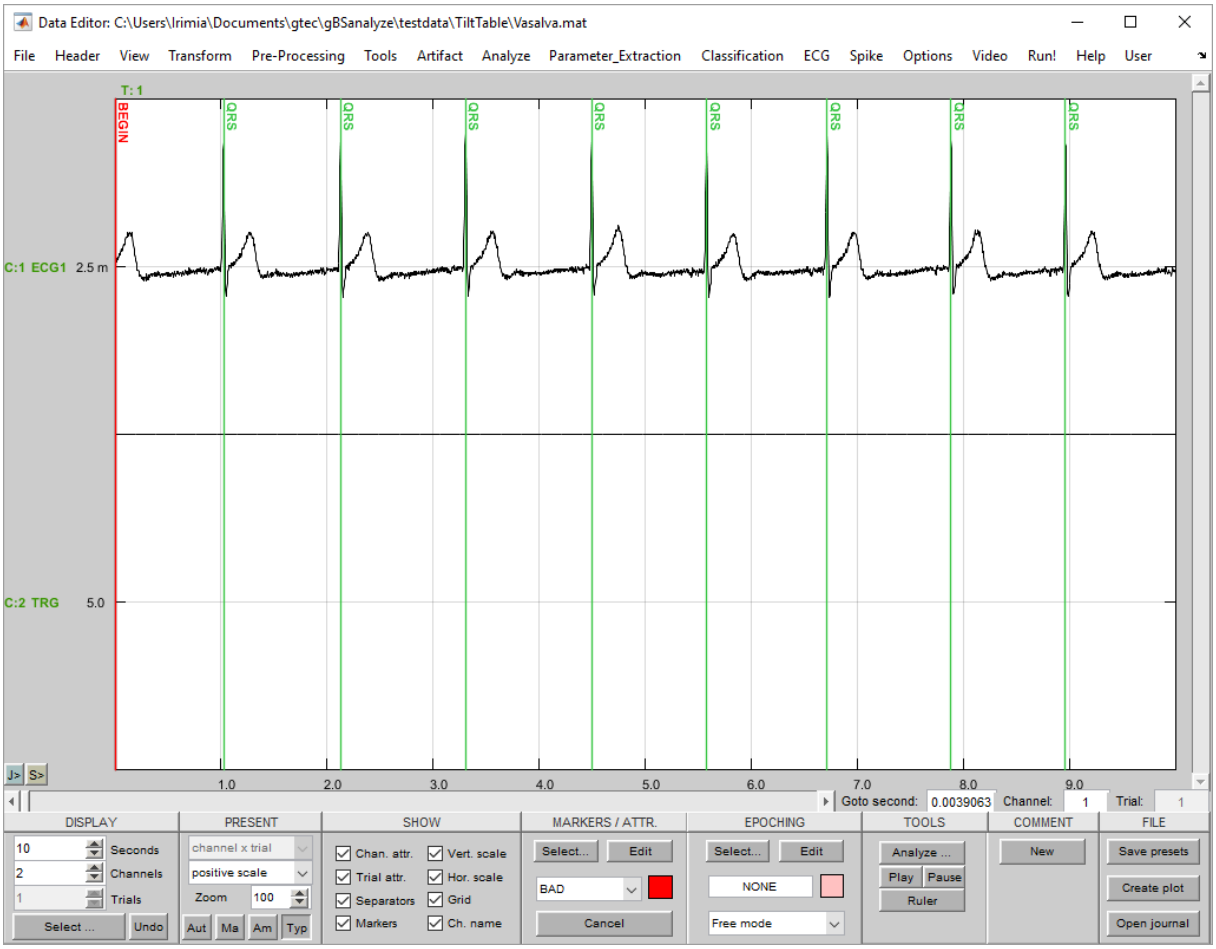
   Set the **Highest accepted heart rate** to `180` beats per minute.

7. Confirm the settings with the **OK** button.

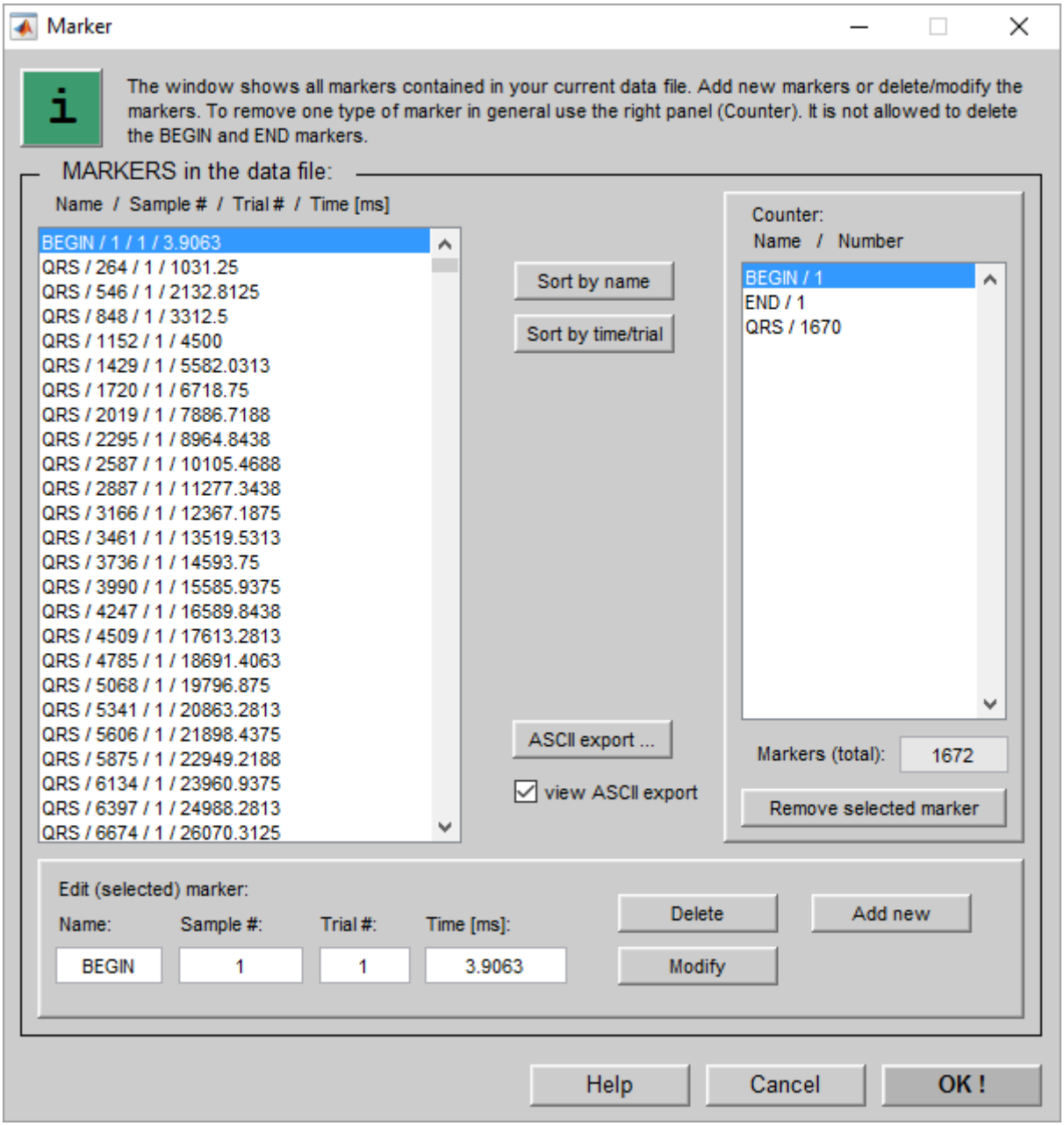
8. To assign `QRS` markers to the detected QRS complexes check the **Detected events** box.

9. Press the **Start** button to search for the QRS complexes.

   The `QRS` markers are assigned to the data in the Data Editor. Use the slider to investigate the detection accuracy.


Data Editor: C:\Users\Irimia\Documents\gtec\gBSanalyze\testdata\TiltTable\Vasalva.mat
File Header View Transform Pre-Processing Tools Artifact Analyze Parameter_Extraction Classification ECG Spike Options Video Run! Help User
T: 1
BEGIN
QRS
C:1 ECG1 2.5 m
C:2 TRG 5.0
1.0 2.0 3.0 4.0 5.0 6.0 7.0 8.0 9.0
Goto second: 0.0039063 Channel: 1 Trial: 1
DISPLAY PRESENT SHOW MARKERS / ATTR. EPOCHING TOOLS COMMENT FILE
Seconds Channels Trials
channel x trial
positive scale
Zoom 100
Chan. attr. Vert. scale
Trial attr. Hor. scale
Separators Grid
Markers Ch. name
Select... Edit
BAD
Cancel
NONE
Free mode
Analyze ...
Play Pause
Ruler
New
Save presets
Create plot
Open journal
Select ... Undo
Aut Ma Am Typ

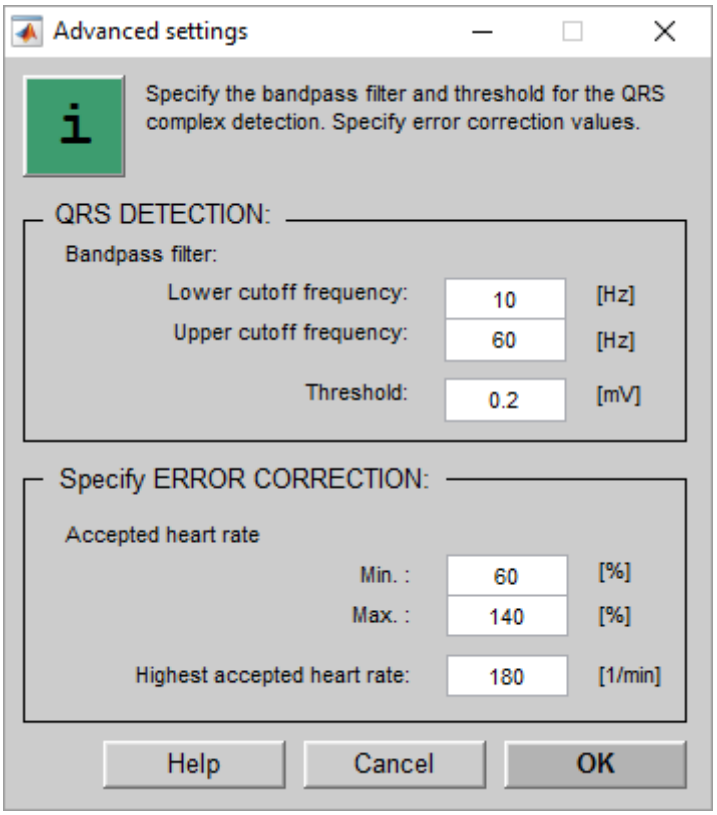
10. Click on **Marker** under the **Header** menu to see the amount of assigned `QRS` markers.



The algorithm with the specific settings detected `1670` QRS complexes. Mark the `QRS/1670` line in the **Counter** list box and press the **Remove selected marker** button.

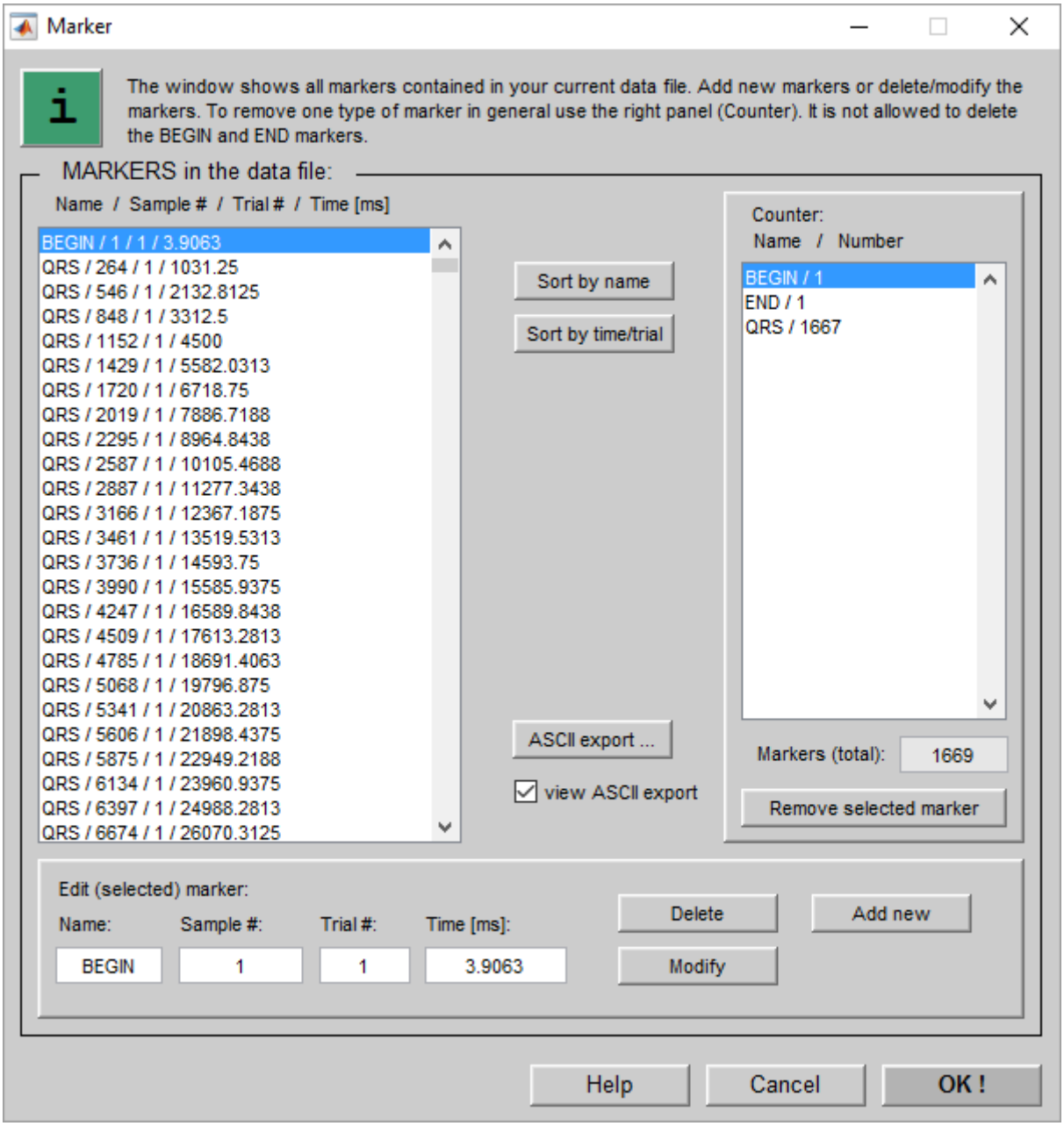
11. Close the window with the **OK** button. All makers are deleted in the Data Editor.

12. Open the **Complex Detector** again and set under **Advanced settings…** the **Threshold** to `0.2` mV.



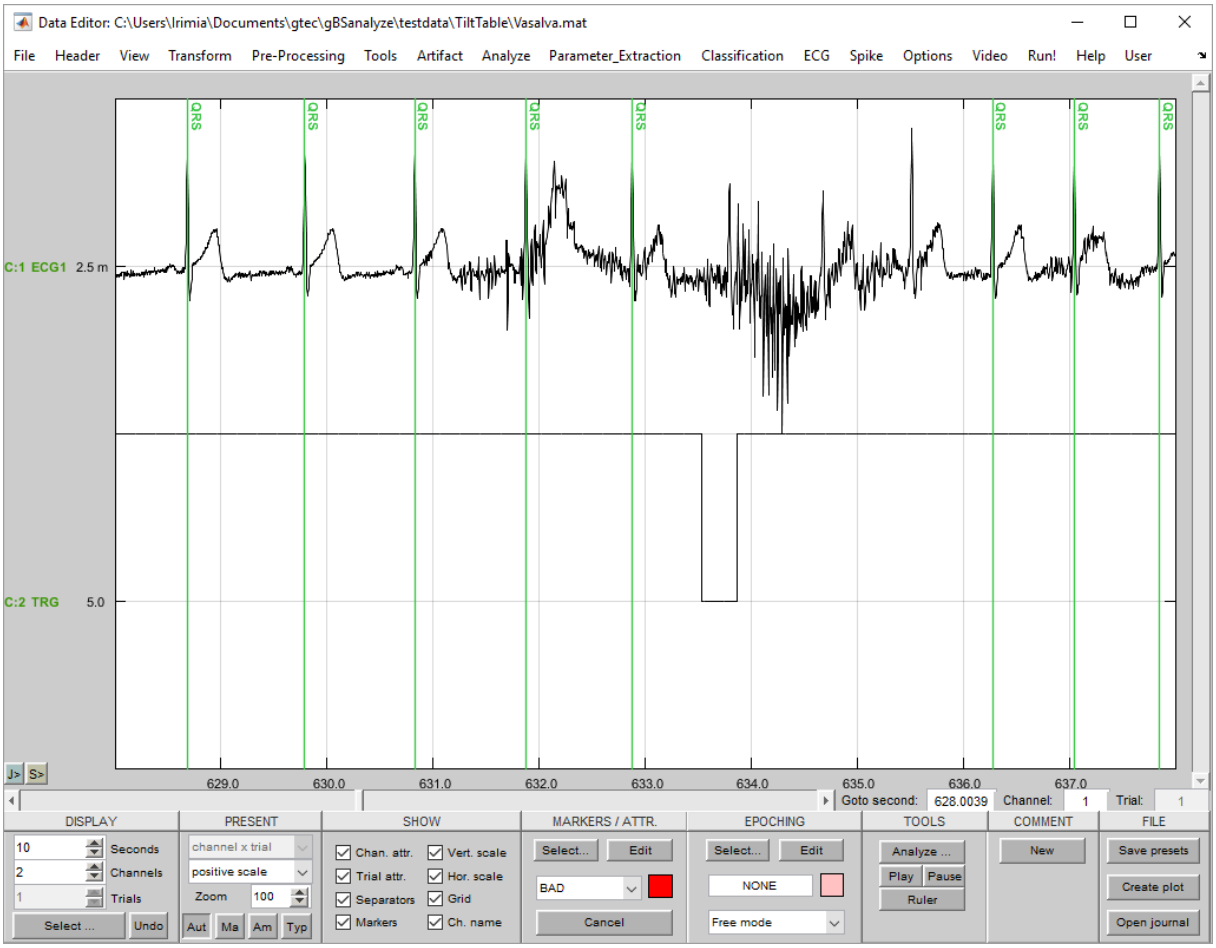
13. Confirm the settings with the **OK** button and search again for the QRS complexes.

Open the **Marker** window from the **Header** menu:



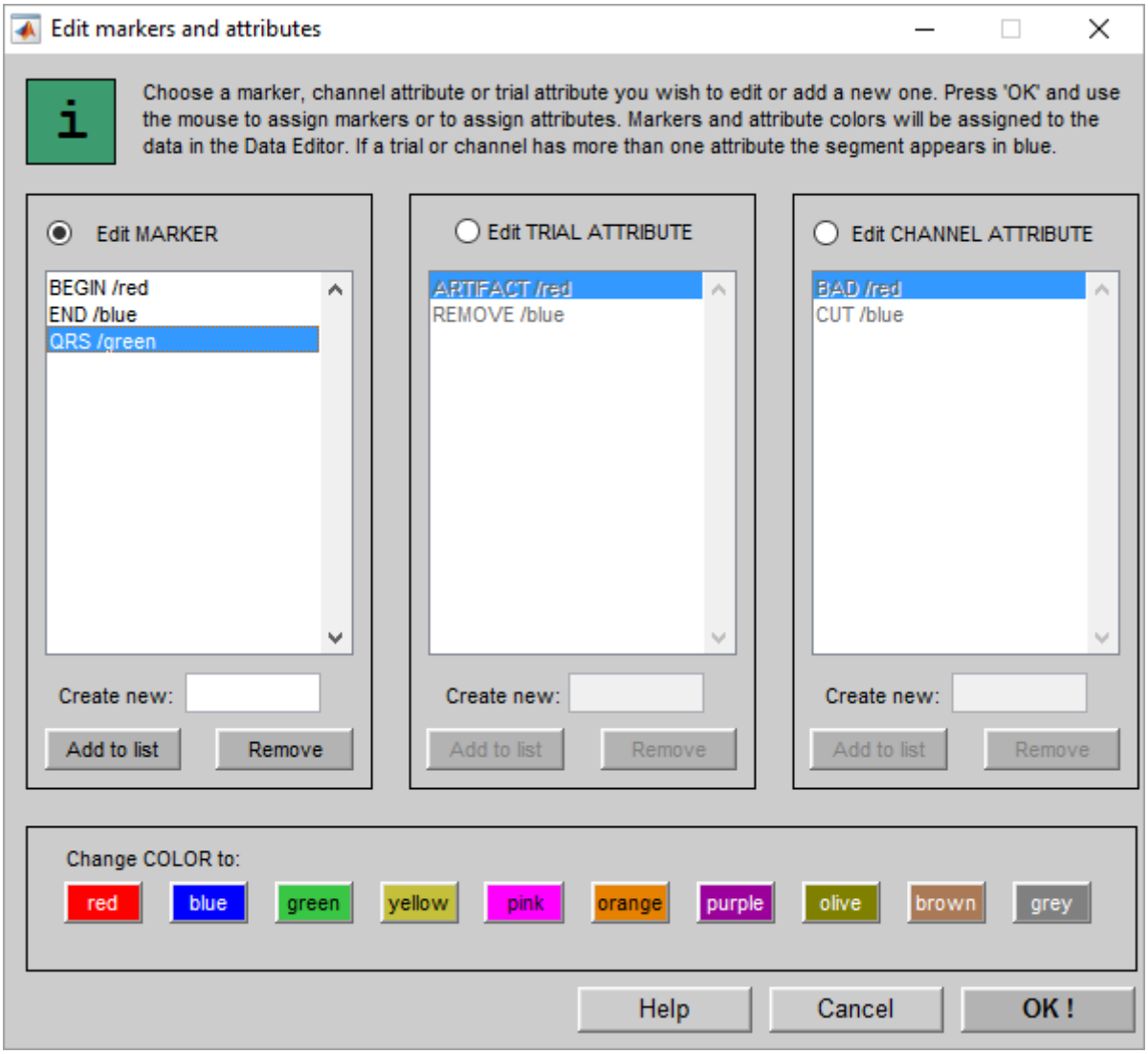
With the modified settings the method has now detected 1667 QRS complexes. Therefore, the threshold was too low to find all QRS complexes correctly.

14. Scroll in the Data Editor to second 628



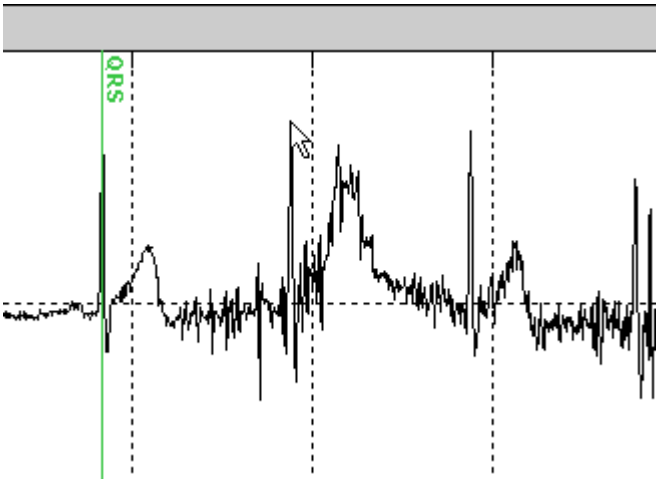
The algorithm missed 3 QRS complexes because of the movement artefacts in the ECG data caused at the time when the subject stood up.

15. Click on the **Select…** button in the **MARKERS / ATTR.** field of the Data Editor and select the `QRS` marker.



16. Confirm the selection with the **OK** button.

17. Assign the correct `QRS` markers manually by clicking next to the R-peak of each QRS complex.



18. Select **Save as…** under the **File** menu and store the edited data-set under `DataCorrected.mat` in

    `Documents\gtec\gBSanalyze\testdata\TiltTable`

The following code show how to perform the example demonstrated above from the MATLAB command line.

```
%Load Data
P_C=data;
File=['C:\Users\' getenv('USERNAME')
'\Documents\gtec\gBSanalyze\testdata\TiltTable\Vasalva.mat'];
P_C=load(P_C,File);

% Complex Detector
SelectInput = ['channel'];
ChannelExclude = [2];
Method = ['QRS detector BP'];
Parameters.BP = [10  60];
Parameters.Threshold = [0.5];
Parameters.IntervalMin = [60];
Parameters.IntervalMax = [140];
Parameters.MaxBPM = [180];
MarkerName.Accepted = ['QRS'];
Feature.Generate = [0];
Feature.Scaling = ['ms'];
Feature.Replace = ['add channel'];
Feature.FileName = [''];
ProgressBarFlag = 0;
[P_C] = gBScomplexdetector(P_C,...
    SelectInput, ChannelExclude, Method, Parameters, MarkerName,...
    Feature, ProgressBarFlag);ProgressBarFlag = 0;

% Complex Detector
SelectInput = ['channel'];
ChannelExclude = [2];
Method = ['QRS detector BP'];
Parameters.BP = [10  60];
Parameters.Threshold = [0.2];
Parameters.IntervalMin = [60];
Parameters.IntervalMax = [140];
Parameters.MaxBPM = [180];
MarkerName.Accepted = ['QRS'];
Feature.Generate = [0];
Feature.Scaling = ['ms'];
Feature.Replace = ['add channel'];
Feature.FileName = [''];
ProgressBarFlag = 0;
[P_C] = gBScomplexdetector(P_C,...
    SelectInput, ChannelExclude, Method, Parameters, MarkerName,...
    Feature, ProgressBarFlag);ProgressBarFlag = 0;
```

Calculating a Heart Rate Feature Channel

The Complex Detector window allows to add a heart rate feature channel to the raw-data in the Data Editor. Follow these steps:

1. Click on **Load Data** from the **File** menu and select the file `DataCorrected.mat` from

   `Documents\gtec\gBSanalyze\testdata\TiltTable`

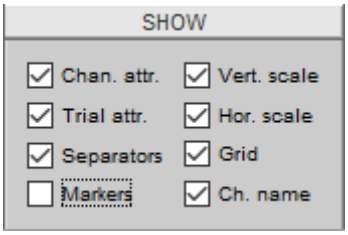
   The Data Editor shows the ECG channel with the already assign QRS markers.

2. Open the **Complex Detector** window from the **ECG** menu and select `QRS` under **Use complex marker** to use the markers as input for the feature channel generation. If the QRS complexes are not already detected select **Use input channel** for the calculation.

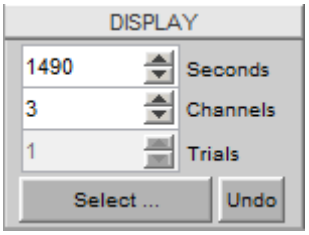
3. Activate the **Generate feature channel** checkbox and select as **Scaling** `beats per minute (1/min)`.

4. Check the **Add new channels** radio button and press **Start**.

5. The Data Editor shows now a third channel which is the heart rate in beats per minute. Deactivate the **Markers** in the **SHOW** field of the Data Editor.

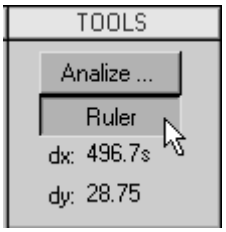


6. Set the **Seconds** in the **DISPLAY** field to `1490` to show the total recording.

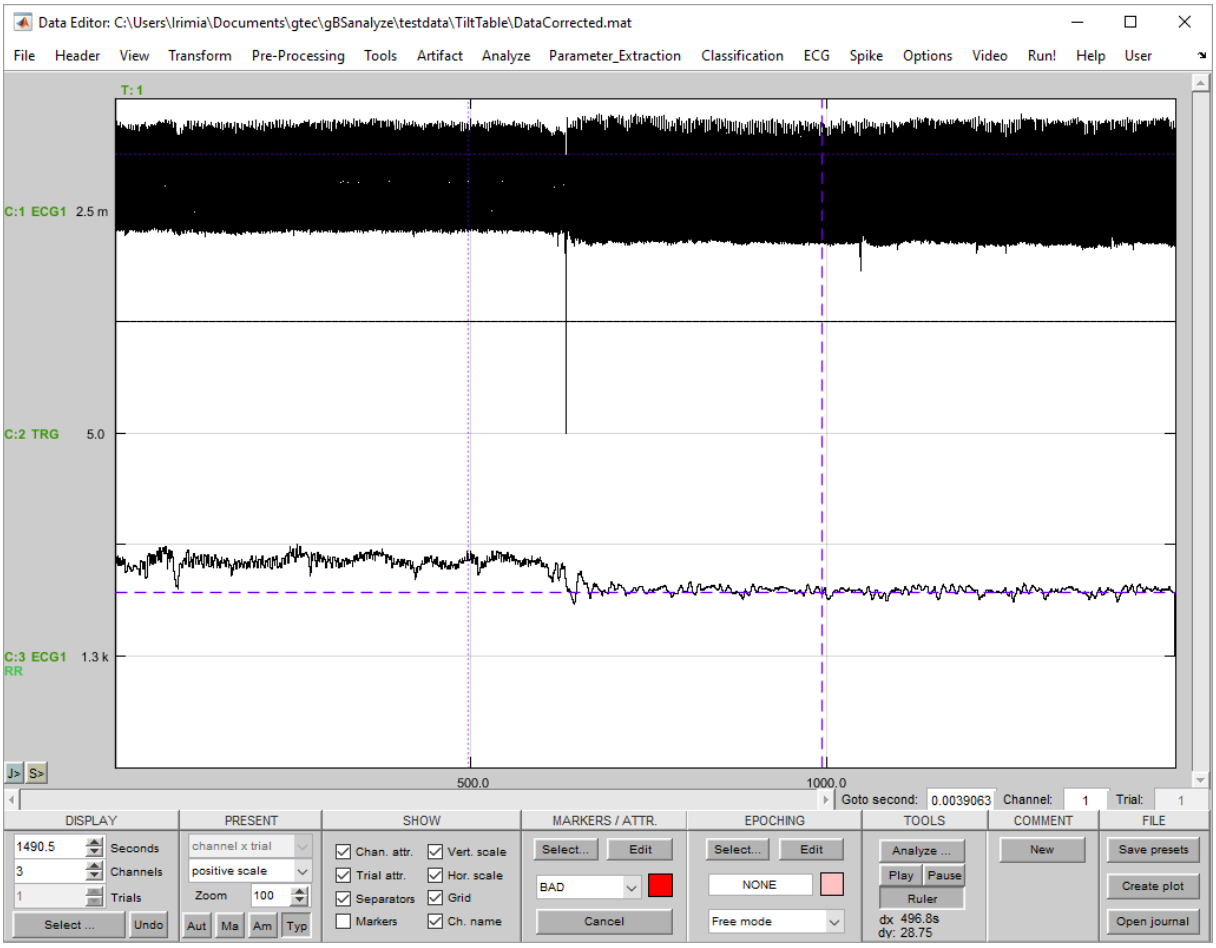


Channel 3 displays the increase in heart rate when the subject changes position from lying on the table to standing..

7. To quantify the increase in heart rate click the **Ruler** button in the **TOOLS** field and drag the horizontal ruler lines to a segment where the subject is lying on the table and to a segment where the subject is already standing.



8. The ruler measures an increase in heart rate of around 28 beats per minute.



The following code show how to perform the example demonstrated above from the MATLAB command line.

```
%Load Data
P_C=data;
File=['C:\Users\' getenv('USERNAME')
'\Documents\gtec\gBSanalyze\testdata\TiltTable\DataCorrected.mat'];
P_C=load(P_C,File);

% Complex Detector
SelectInput = 'QRS';
ChannelExclude = [];
Method = 'QRS detector';
Parameters.Wavelet = 'MEXICAN';
Parameters.CenterFreq = 30;
Parameters.MAWindow = 200;
Parameters.DecisionLevel = 2.5;
Parameters.IntervalMin = 60;
Parameters.IntervalMax = 140;
Parameters.MinBPM = 30;
MarkerName.Accepted = '';
MarkerName.Rejected = '';
Feature.Generate = 1;
Feature.Scaling = 'BPM';
Feature.Replace = 'add channel';
Feature.FileName = '';
ProgressBarFlag = 0;
[P_C] = gBScomplexdetector(P_C,...
    SelectInput, ChannelExclude, Method, Parameters, MarkerName,...
    Feature, ProgressBarFlag);
```

Heart Rate Variability Time Domain Measures

Time domain methods determine either the heart rate at any point in time or determine the intervals between successive complexes. In a continuous ECG recording the normal-to-normal (NN or RR) intervals can be determined (interval from one QRS complex to the next). This measures can be used to investigate variations of the heart rate secondary to tilt, Valsalva manoeuvre or to describe the difference between night and day,…

Time Domain Measures

The simplest parameters are the time domain measures:
MeanRR…mean RR interval in [ms]
MeanHR…mean heart rate in [1/min]
MaxRR…longest RR interval in [ms]
MinRR…shortest RR interval in [ms]
MinMaxRRDiff…difference between the longest and the shortest RR interval in [ms]

Statistical methods derived from RR intervals:
SDNN…standard deviation of RR interval [ms]
Note that the segments used to derive the SDNN measures should be standardized to 5 minutes or to 24 hours to make comparisons possible.
SDHR…standard deviation of heart rate (HR) in [1/min]

Segmented Measures

Statistical measures calculated from segments of the total recording:
SDANN…standard deviation of the averages of RR intervals in all segments of the recording in [ms]
SDNNindex…mean of the standard deviation of all RR intervals in all segments of the recording in [ms]
The segment length is normally set to 5 minutes. The SDANN measures the changes in heart rate due to cycles longer than 5 minutes. The SDNNindex measures the variability due to cycles shorter than 5 minutes. Note that the segment length must be specified to be able to interpret the result properly.

RR Difference Measures

Statistical methods derived from differences between RR intervals:
RMSSD…the square root of the mean of the square of differences between adjacent RR intervals in [ms]
SDSD…standard deviation of differences between adjacent RR intervals in [ms]
NN50…number of RR intervals differing by more than 50 ms
pNN50…NN50 divided by the total number of RR intervals in [%]

Geometric Measures

HRVindex…total number of RR intervals divided by the number of RR intervals which correspond to the highest bin in the histogram. Note that the bin width of the histogram must be specified to interpret the measure (e.g. 1/128).

HRV Time Domain Window

The **HRV Time Domain** window has the following control elements:

Use complex marker – define the marker that is already assigned to the QRS complexes (manually or with the **Complex Detector**)

Specify DATA INTERVAL:

> **Start interval at** – define the start time point for the calculation
> **End at –** define the end point of the interval used for the calculation

Tachogram unit – the unit of the calculated tachogram can be in `ms`, `samples` or `beats per minute`

Resample tachogram – normally the QRS complexes are not uniformly sampled. Check the box to resample the RR intervals by 4 Hz.

Interval length (segmented measures) – define the segment length for the SDANN and SDNNindex calculation

Histogram unit – the histogram can be shown in `ms` or `beats per minute`. If beats per minute is selected than the histogram bins are of width 1 beat per minute. If ms is selected than the **Bin resolution** must be specified.

Bin resolution – defines the width of the histogram bars. The **Bin resolution** effects also the HRVindex calculation.

Correct RR-intervals:

> **Min** – a QRS complex is only accepted if the actual RR interval is not smaller than e.g. 60 % of the average interval
> **Max** – the complex is rejected if the RR interval is longer than e.g. 140 % of the average interval

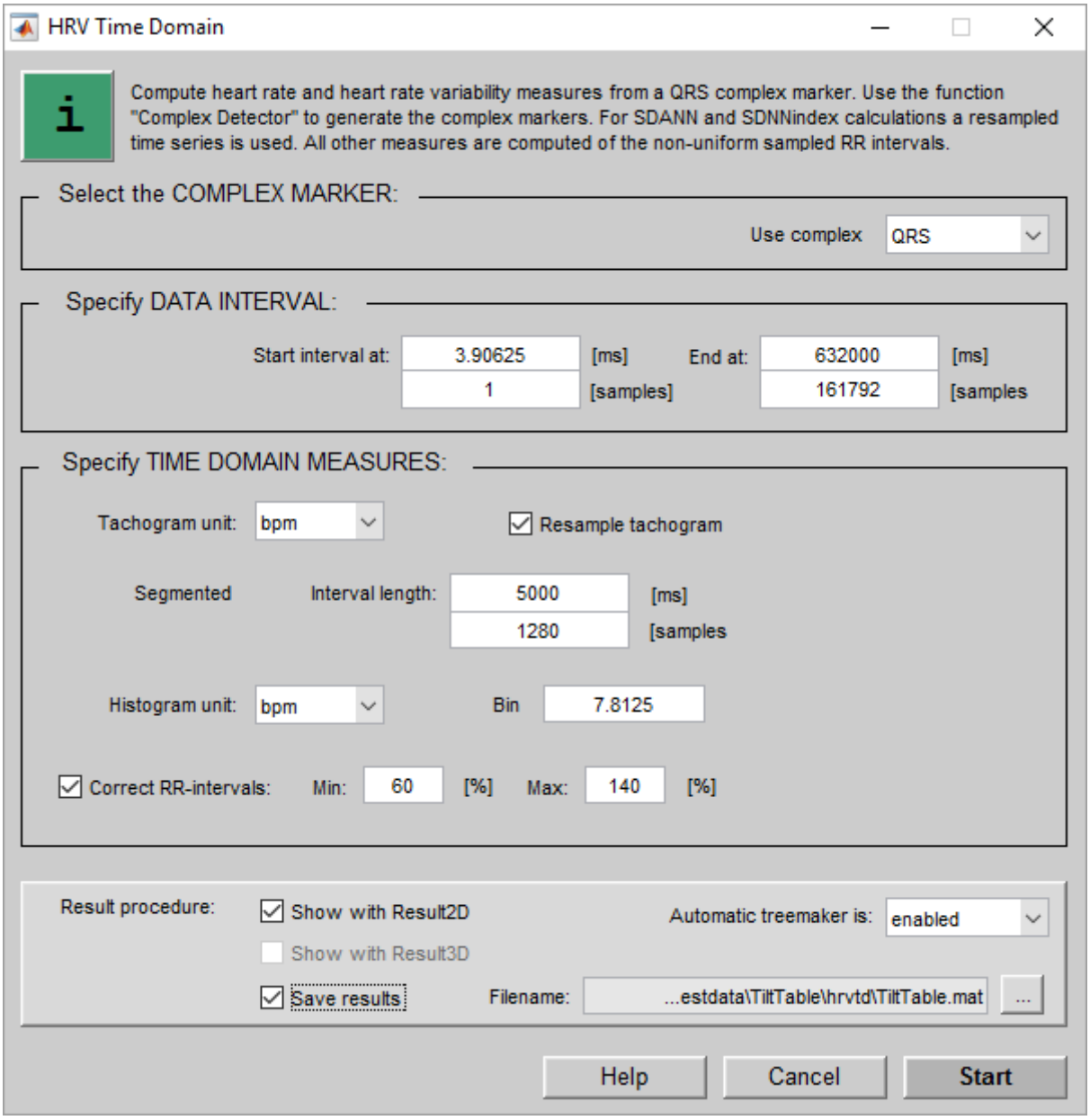
Example

1. Click on **Load Data** from the **File** menu and select the file `DataCorrected.mat` from

   `Documents\gtec\gBSanalyze\testdata\TiltTable`

   The Data Editor shows the ECG channel with already assign QRS markers.

2. Open the **HRV Time Domain** window from the **ECG** menu and select under **Use**



complex marker `QRS`.

3. Specify the **DATA INTERVAL** for the lying period from the beginning until second 632.

4. Set the **Tachogram unit** to `bpm` and check **Resample tachogram**.

5. Enter under **Interval length** `5000` ms. This interval is used for the segmented measures calculation.

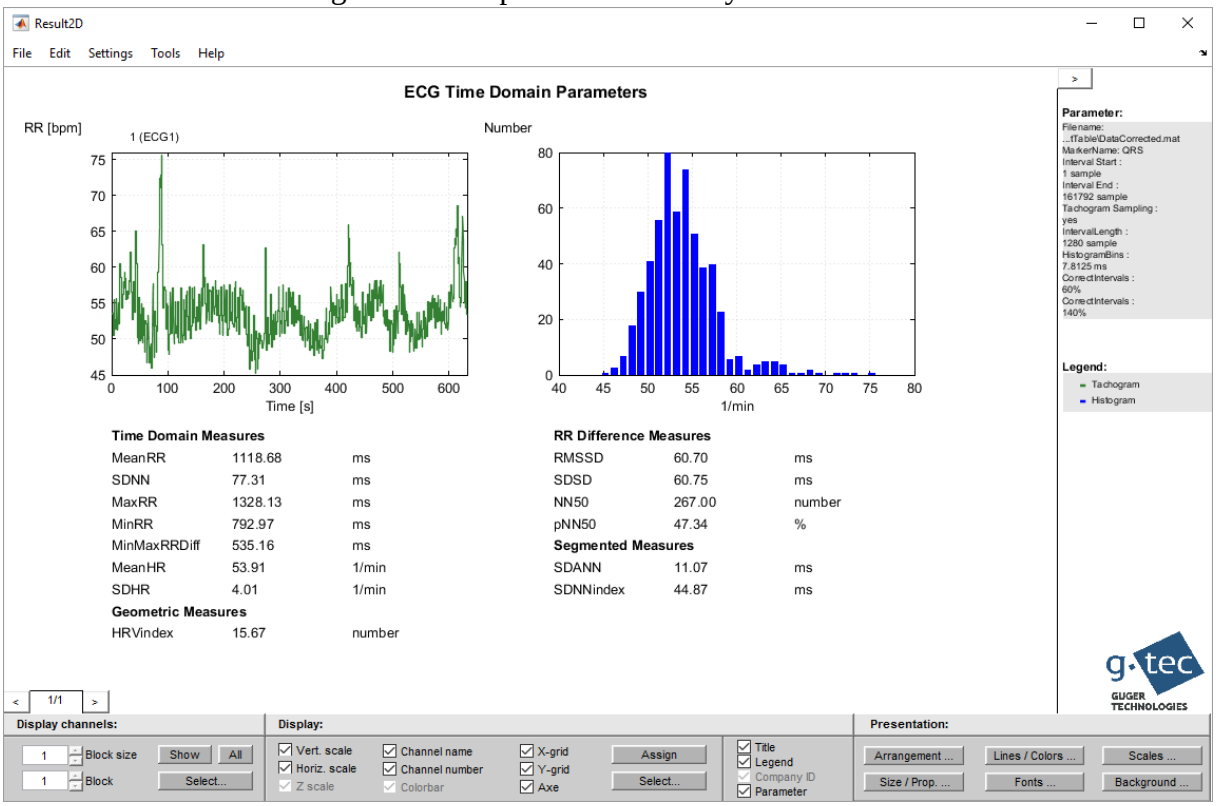
6. Set the **Histogram unit** to `bpm`. In this mode the **Bin resolution** is automatically set to 1 for the histogram presentation. For the HRVindex calculation enter a **Bin resolution** of `7.8125` ms.

7. Check the **Correct RR-intervals** box to eliminate intervals which are below `60` % or above `140` % of the average interval.

8. Check **Show with Result2D** to open the graphical output of the calculation with g.Result2D.

9. Check **Save results** to save the calculation result to harddisk. The **Automatic treemaker** creates a subdirectory `hrvtd`. Enter `TiltTable.mat` as filename.

10. **Start** the calculation. g.Result2D opens automatically with the calculation result:

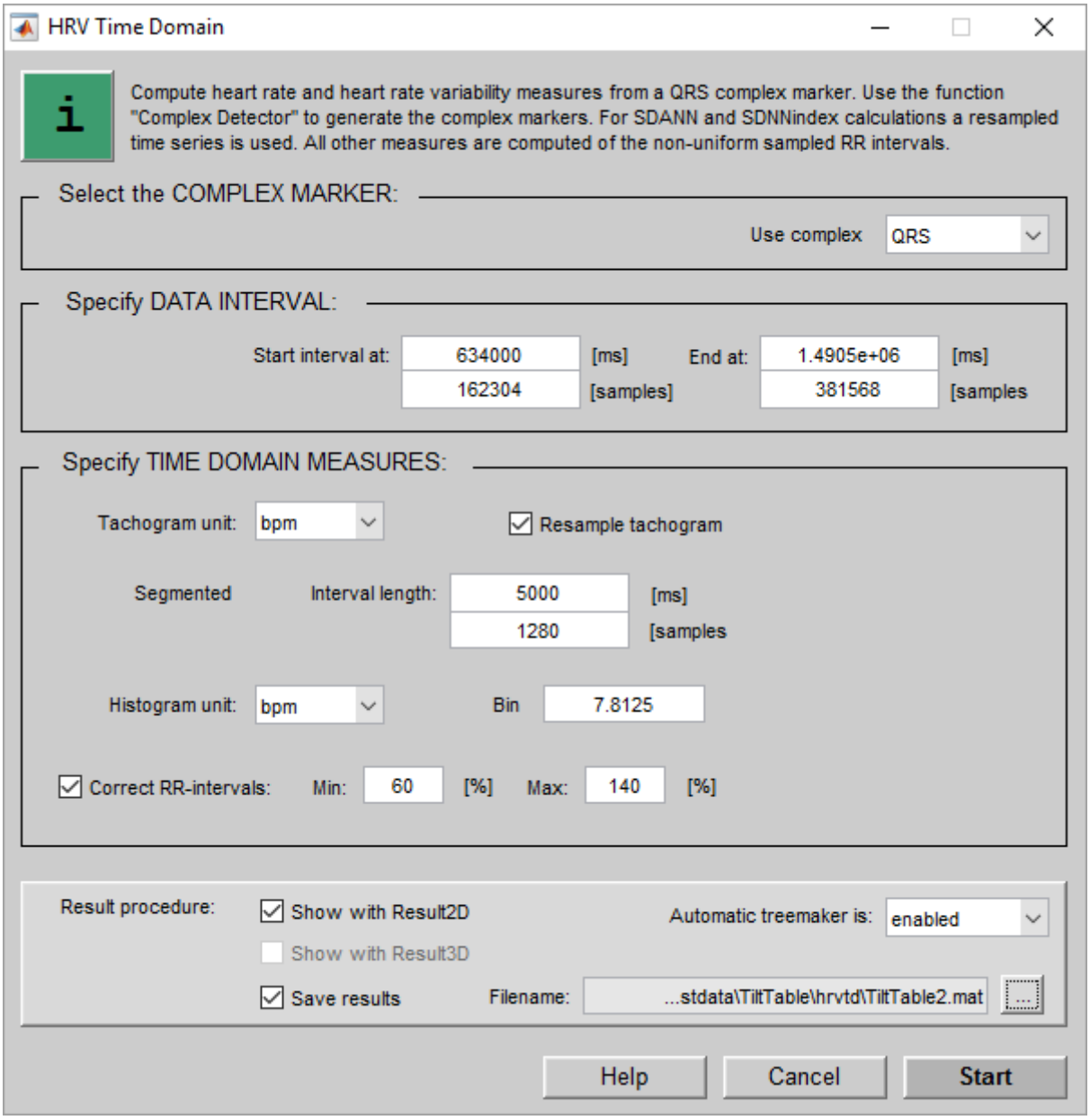


The green line in the top-left plot represents the tachogram in beats per minute and seconds. The blue bars in the top-right plot represent the histogram where the beats per minute are counted with a bin size of 1.

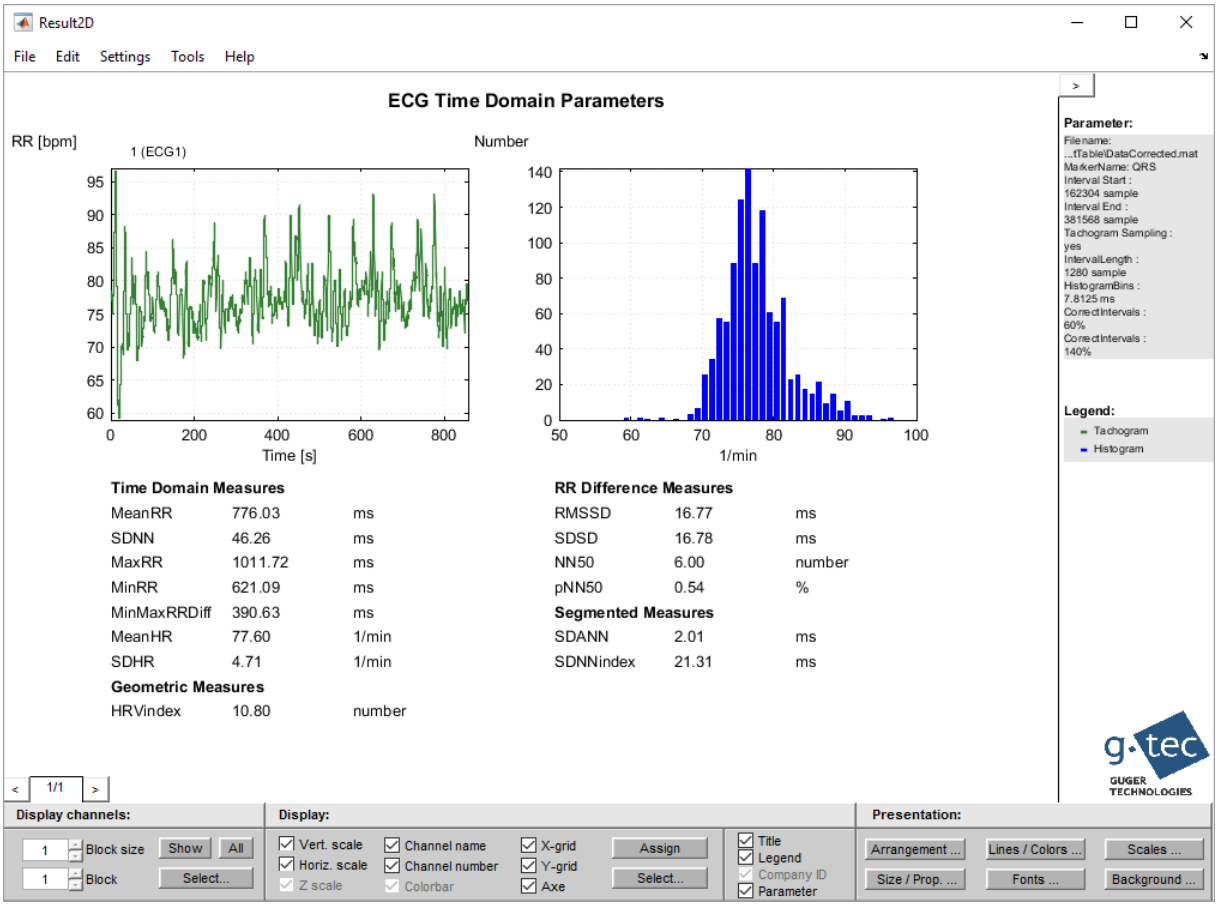
The bottom-half shows the **Time Domain Measures**, **Geometric Measures**, **RR Difference Measures** and **Segmented Measures**.

11. Perform the same calculation for the second part of the data (standing period). Enter under **Start interval at** `634` seconds and under **End at** `1490` seconds.

12. Change the filename to `TiltTable2.mat` and **Start** the calculation.



13. g.Result2D shows the analysis of the standing period:



The following code show how to perform the example demonstrated above from the MATLAB command line.

```
%Load Data
P_C=data;
File=['C:\Users\' getenv('USERNAME')
'\Documents\gtec\gBSanalyze\testdata\TiltTable\DataCorrected.mat'];
P_C=load(P_C,File);

%HRV time domain
MarkerName='QRS';
Interval=[1  161792];
Tachogram.Unit='bpm';
Tachogram.Sampling=['yes'];
IntervalLength=1280;
Histogram.Unit='bpm';
Histogram.Bins=7812.5;
CorrectIntervals=[60  140];
FileName=['C:\Users\' getenv('USERNAME')
'\Documents\gtec\gBSanalyze\testdata\TiltTable\TiltTable.mat'];
ProgressBarFlag=0;
H_O=gBShrvtimedomain(P_C,MarkerName,Interval,Tachogram,...
IntervalLength,Histogram,CorrectIntervals,FileName,...
ProgressBarFlag);

%HRV time domain
MarkerName='QRS';
Interval=[162304  381440];
Tachogram.Unit='bpm';
Tachogram.Sampling=['yes'];
IntervalLength=1280;
Histogram.Unit='bpm';
Histogram.Bins=7812.5;
CorrectIntervals=[60  140];
FileName=['C:\Users\' getenv('USERNAME')
'\Documents\gtec\gBSanalyze\testdata\TiltTable\TiltTable2.mat'];
ProgressBarFlag=0;
H_O=gBShrvtimedomain(P_C,MarkerName,Interval,Tachogram,...
IntervalLength,Histogram,CorrectIntervals,FileName,...
ProgressBarFlag);
```

Heart Rate Variability Frequency Domain Measures

Power spectral density (PSD) is a measure of how power in a signal changes as a function of frequency. The spectral analysis detects periodic oscillations (amplitude and frequency) and has been employed in a great variety of signal processing applications. The heart rate variability (HRV) has oscillations at different frequencies that are originated by different physiological systems. The parasympathetic and sympathetic systems transmit the oscillations to the heart. High frequency oscillations are vagally mediated and low frequency oscillations are due both parasympathetic and sympathetic systems. The sinorespiratory arrhythmia is vagal mediated and has a frequency synchronous to the respiratory cycle (between 0.2 and 0.35 Hz). The oscillation due to baroreflex (around 0.1 Hz) is related to the vasomotor system and is synchronous to the Mayer waves at the pressure signal. Very low frequency components are associated with slow regulation mechanisms such as humoral and thermoregulation factors.
To analyze the oscillations a PSD analysis is performed with parametric (autoregressive model, AR) or non-parametric (FFT, Fast Fourier Transformation) methods. Because of the high degree of randomness of the RR signal, the autoregressive model is preferable. Then the power spectrum is divided into bands to quantify the energy in each one.

Absolute Measures

4 main spectral components are extracted from a calculated spectrum:
ULF…ultra low frequency components in [ms^2]
VLF…very low frequency components in [ms^2]
LF…low frequency components in [ms^2]
HF…high frequency components in [ms^2]
The distribution of the LF and HF frequencies are not fixed and vary with the autonomic modulations of the heart rate. The energy in HF is vagal mediated, the energy in LF and VLF are due to both sympathetic and parasympathetic systems.

Relative Measures

ULF, VLF, LF AND HF ARE NORMALLY MEASURED IN ABSOLUTE POWER VALUES. THE FOLLOWING MEASURES ARE NORMALIZED BY THE TP (TOTAL POWER) MINUS THE VLF COMPONENT AND ARE REPRESENTED IN NORMALIZED UNITS [N.U.]

***LFNORM**…LF/(TP-VLF)*100 IN [N.U.]*

HFnorm…HF/(TP-VLF)*100 in [n.u.]
LF/HF…ratio of LF and HF
The normalization minimizes the effect of changes in TP on LF and HF.

For short-term recording (e.g. 2 to 5 min) normally VLF, LF and HF are specified. Note that VLF is difficult to interpret for such short segments. For long-term recordings (24 h) also the VLF and ULF components can be considered.

HRV Frequency Domain Window

The **HRV Frequency Domain** window has the following control elements:

Use complex marker – define the marker that is already assigned to the QRS complexes (manually or with the **Complex Detector**)

Specify DATA INTERVAL:

> **Start interval at** – define the start time point for the calculation
> **End at –** define the end point of the interval used for the calculation

Tachogram sampling frequency – the RR intervals are resampled with the defined sampling rate before the spectral analysis is performed.

Correct RR-intervals:

> **Min** – a QRS complex is only accepted if the actual RR interval is not smaller than e.g. 60 % of the average interval
> **Max** – the complex is rejected if the RR interval is longer than e.g. 140 % of the average interval

ULF – calculate the power in the ultra low frequency band (e.g. ≤0.003 Hz)
VLF - very low frequency band (0.003 – 0.04 Hz)
LF – low frequency band (0.04 – 0.15 Hz)
HF – high frequency band (0.15 – 0.4 Hz)

Method – the spectral analysis method can be `FFT` (non-parametric) or `Burg`, `Yule Waker` or `Music` (parametric methods).
NFFT – specify the FFT points used for the spectral analysis for the non-parametric and parametric methods
Overlap – specify the FFT segment overlap for the FFT analysis
Order – specify the autoregressive model order for the parametric methods
Windowing function – select a `hanning`, `hamming` or `boxcar` window for the FFT analysis

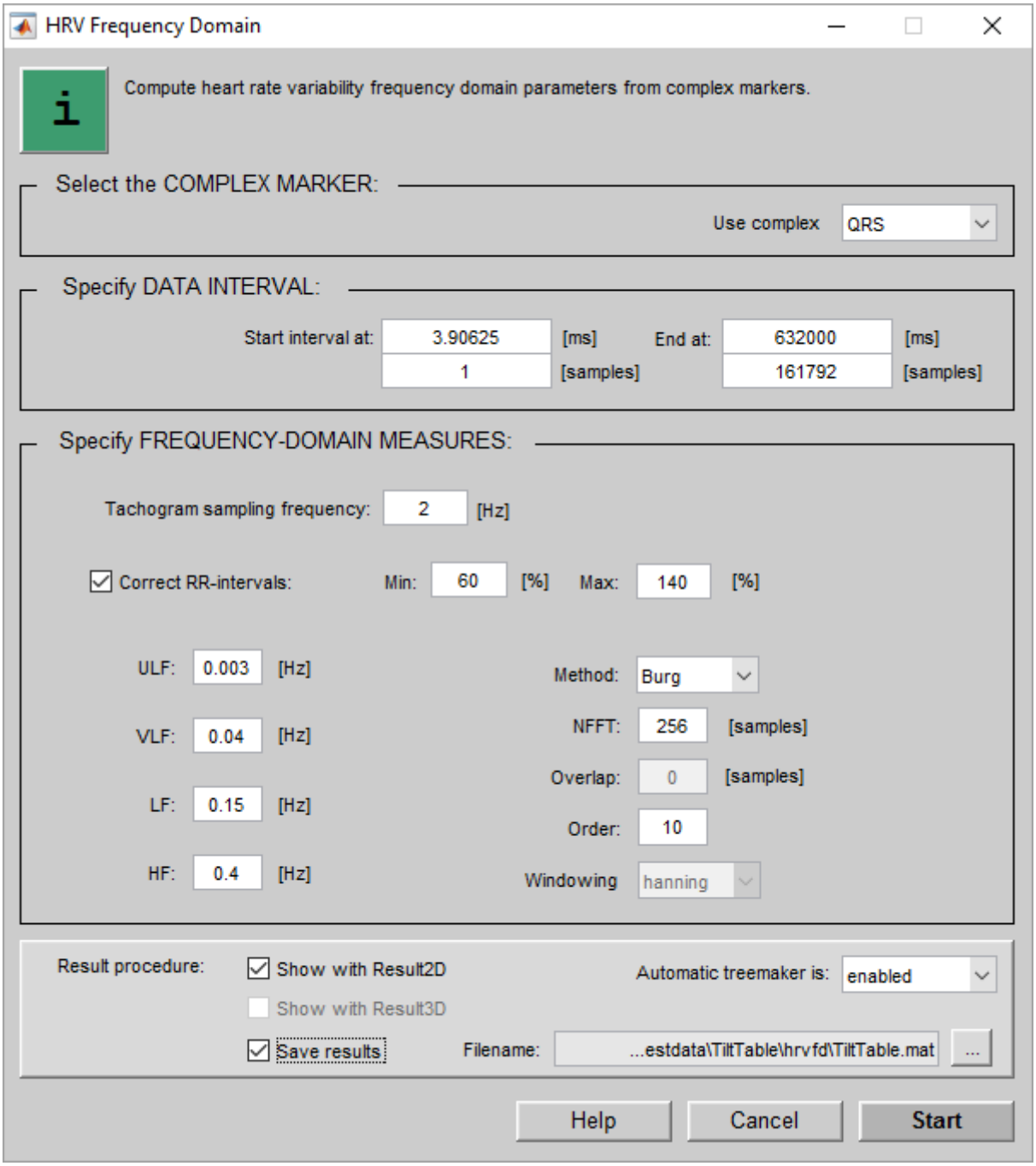
Example

1. Click on **Load Data** from the **File** menu and select the file `DataCorrected.mat` from

   `Documents\gtec\gBSanalyze\testdata\TiltTable`

   The Data Editor shows the ECG channel with already assign QRS markers.

2. Open the **HRV Frequency Domain** window from the ECG menu and select under **Use complex marker** `QRS`.



3. Specify the **DATA INTERVAL** for the lying period from the beginning until second 632.

4. Enter as **Tachogram sampling frequency** `2` Hz.

5. Check the **Correct RR-intervals** box to eliminate intervals which are below `60` % or above `140` % of the average interval.

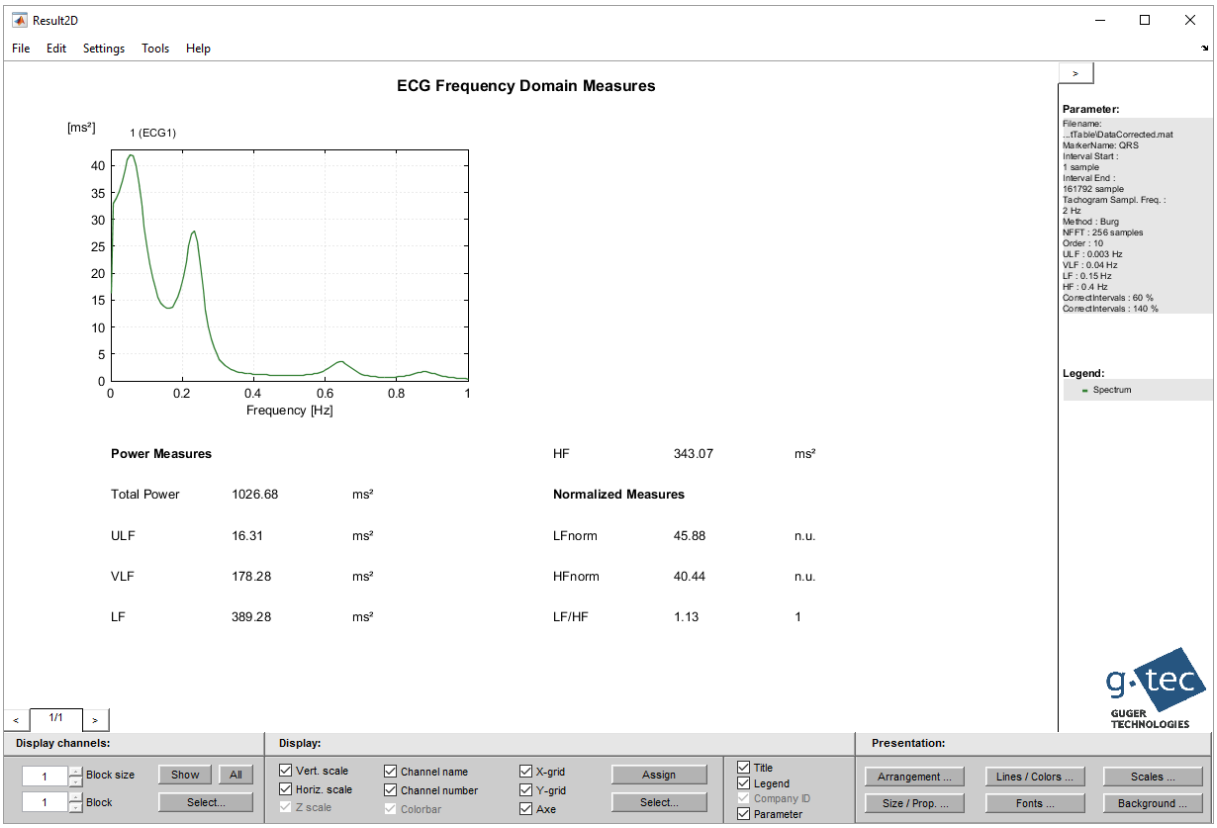
6. Enter under **ULF** `0.003` Hz, under **VLF** `0.04` Hz, under **LF** `0.15` Hz and under **HF** `0.4` Hz.

7. Select the parametric **Method** `Burg` with an **NFFT** length of `256` samples and an **Order** of `10`.

8. Check **Show with Result2D** to open the graphical output of the calculation with g.Result2D

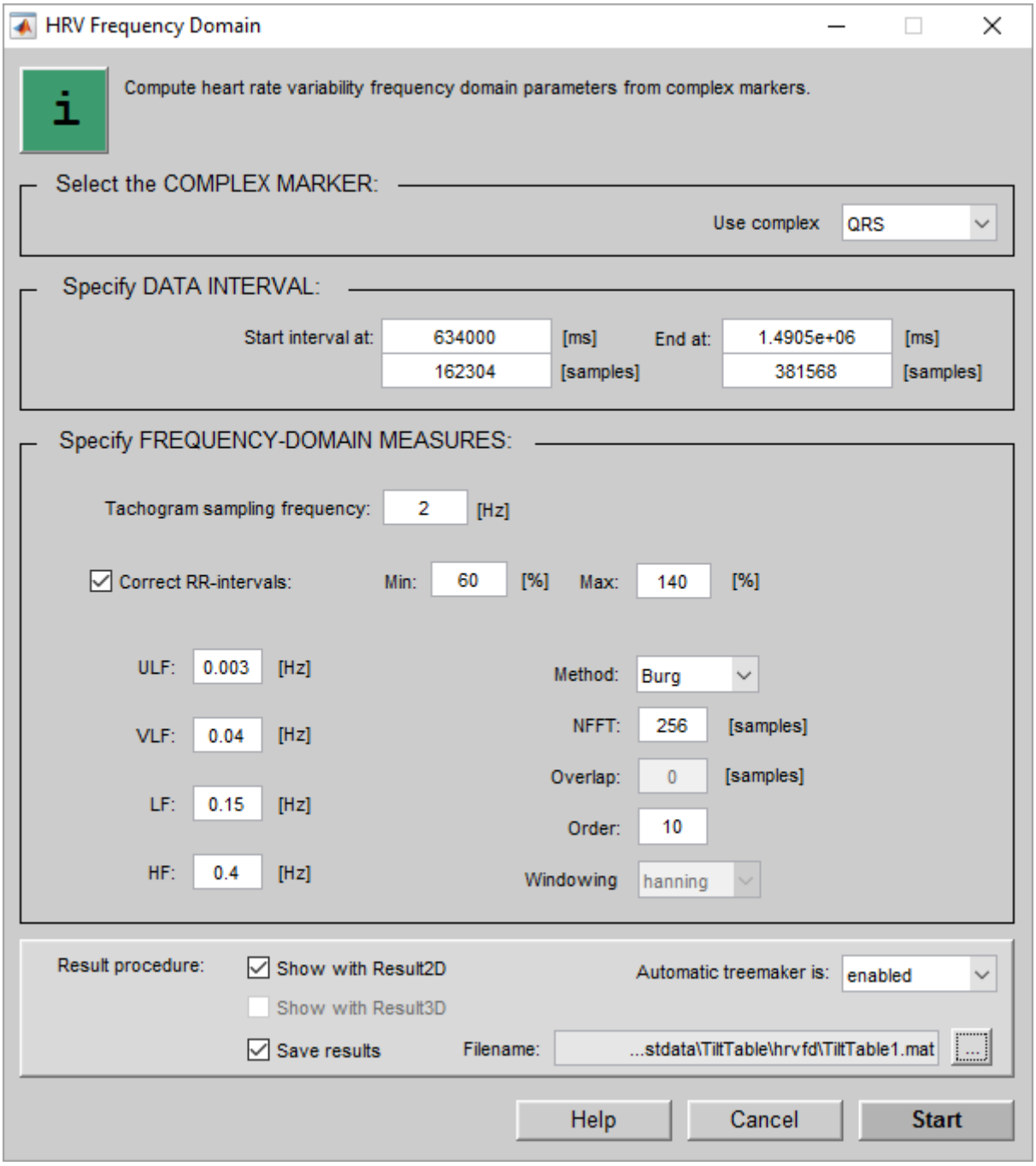
9. Check **Save results** to save the calculation result to harddisk. The **Automatic treemaker** creates a subdirectory `hrvfd`. Enter `TiltTable.mat` as filename.

10. **Start** the calculation. g.Result2D opens automatically with the calculation result:

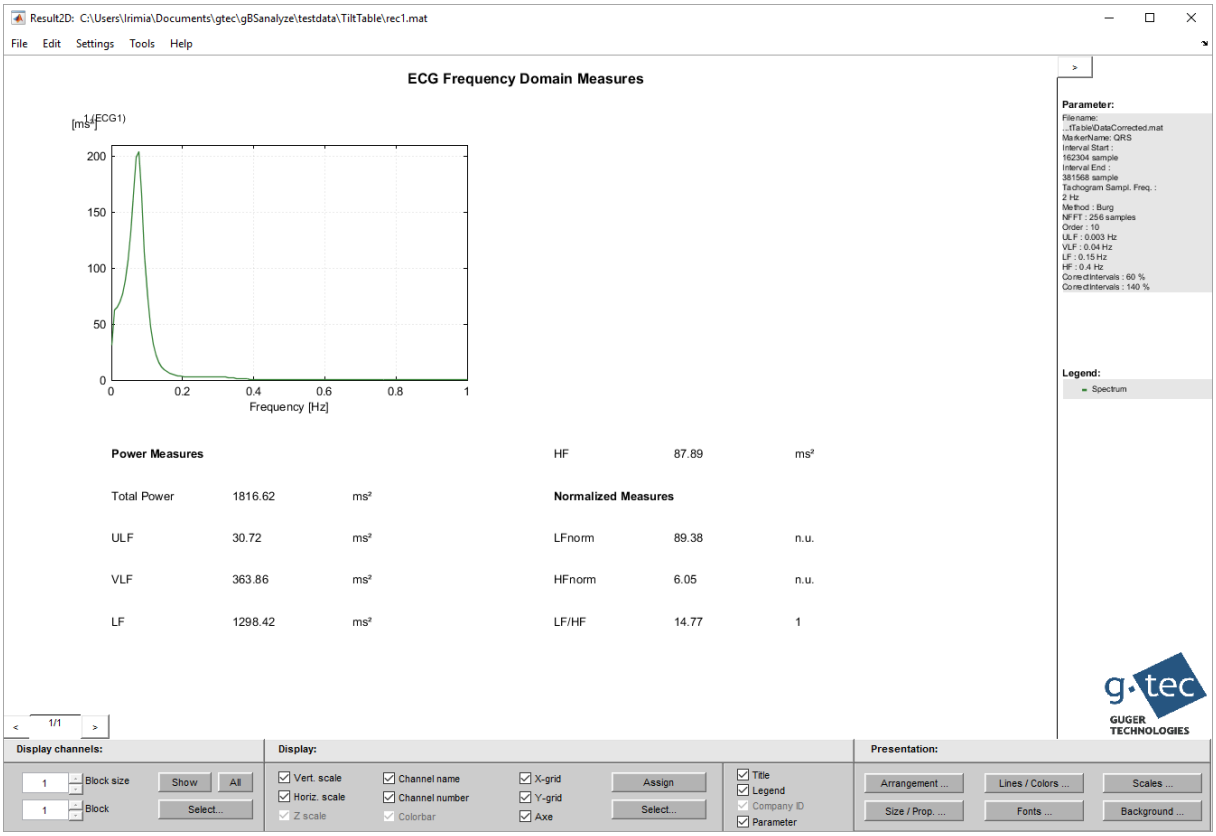


11. Perform the same calculation for the second part of the data (standing period). Enter under **Start interval at** `634` seconds and under **End at** `1490` seconds.

12. Change the filename to `TiltTable1.mat` and **Start** the calculation.



13. g.Result2D opens with the result:



The following code show how to perform the example demonstrated above from the MATLAB command line.

```
%Load Data
P_C=data;
File=['C:\Users\' getenv('USERNAME')
'\Documents\gtec\gBSanalyze\testdata\TiltTable\DataCorrected.mat'];
P_C=load(P_C,File);

%HRV frequency domain
MarkerName='QRS';
Interval=[1  161792];
TachogramSampling=[2];
CorrectIntervals=[60  140];
F=[0.003        0.04        0.15         0.4];
Method='Burg';
NFFT=[256];
Overlap=[0];
Order=[10];
Window=['hanning'];
FileName=['C:\Users\' getenv('USERNAME')
'\Documents\gtec\gBSanalyze\testdata\TiltTable\TiltTable.mat'];
ProgressBarFlag=0;
[H_O]=gBShrvfrequencydomain(P_C,MarkerName,Interval,...
CorrectIntervals,TachogramSampling,Method,NFFT,Overlap,Window,...
Order,F,FileName,ProgressBarFlag);

%HRV frequency domain
MarkerName='QRS';
Interval=[162304  381440];
TachogramSampling=[2];
CorrectIntervals=[60  140];
F=[0.003        0.04        0.15         0.4];
Method='Burg';
NFFT=[256];
Overlap=[0];
Order=[10];
Window=['hanning'];
FileName=['C:\Users\' getenv('USERNAME')
'\Documents\gtec\gBSanalyze\testdata\TiltTable\TiltTable1.mat'];
ProgressBarFlag=0;
[H_O]=gBShrvfrequencydomain(P_C,MarkerName,Interval,...
CorrectIntervals,TachogramSampling,Method,NFFT,Overlap,Window,...
Order,F,FileName,ProgressBarFlag);
```

Heart Rate Variability Maps

To simplify the data analysis and interpretation of the ECG data **HRV Maps** allow to estimate the temporal evolution of PSD. Therefore the PSD is computed within a certain segment. Then the segment is shifted by a specific stepsize and the PSD is calculated again. This is done until the end of the data-set is reached. The resulting plot shows the power distribution over the whole recording time. High power values are displayed color coded red, low power values are displayed color coded blue.

HRV Map Window

The **HRV Frequency Domain** window has the following control elements:

Use complex marker – define the marker that is already assigned to the QRS complexes (manually or with the **Complex Detector**)

Specify DATA INTERVAL:

Start interval at – define the start time point for the calculation
End at – define the end point of the interval used for the calculation

Specify PSD INTERVAL:

Interval length – defines the spectral analysis segments that contribute to one time point in the HRV map
Stepsize – defines the stepsize for shifting the spectral analysis window over the data set

Tachogram sampling frequency – the RR intervals are resampled with the defined sampling rate before the spectral analysis is performed.

Correct RR-intervals:

Min – a QRS complex is only accepted if the actual RR interval is not smaller than e.g. 60 % of the average interval
Max – the complex is rejected if the RR interval is longer than e.g. 140 % of the average interval

ULF – calculate the power in the ultra low frequency band (e.g. ≤0.003 Hz)
VLF - very low frequency band (0.003 – 0.04 Hz)
LF – low frequency band (0.04 – 0.15 Hz)
HF – high frequency band (0.15 – 0.4 Hz)

Method – the spectral analysis method can be `FFT` (non-parametric) or `Burg`, `Yule Waker` or `Music` (parametric methods).
NFFT – specify the FFT points used for the spectral analysis for the non-parametric and parametric methods
Overlap – specify the FFT segment overlap for the FFT analysis
Order – specify the autoregressive model order for the parametric methods

Windowing function – select a `hanning`, `hamming` or `boxcar` window for the FFT analysis

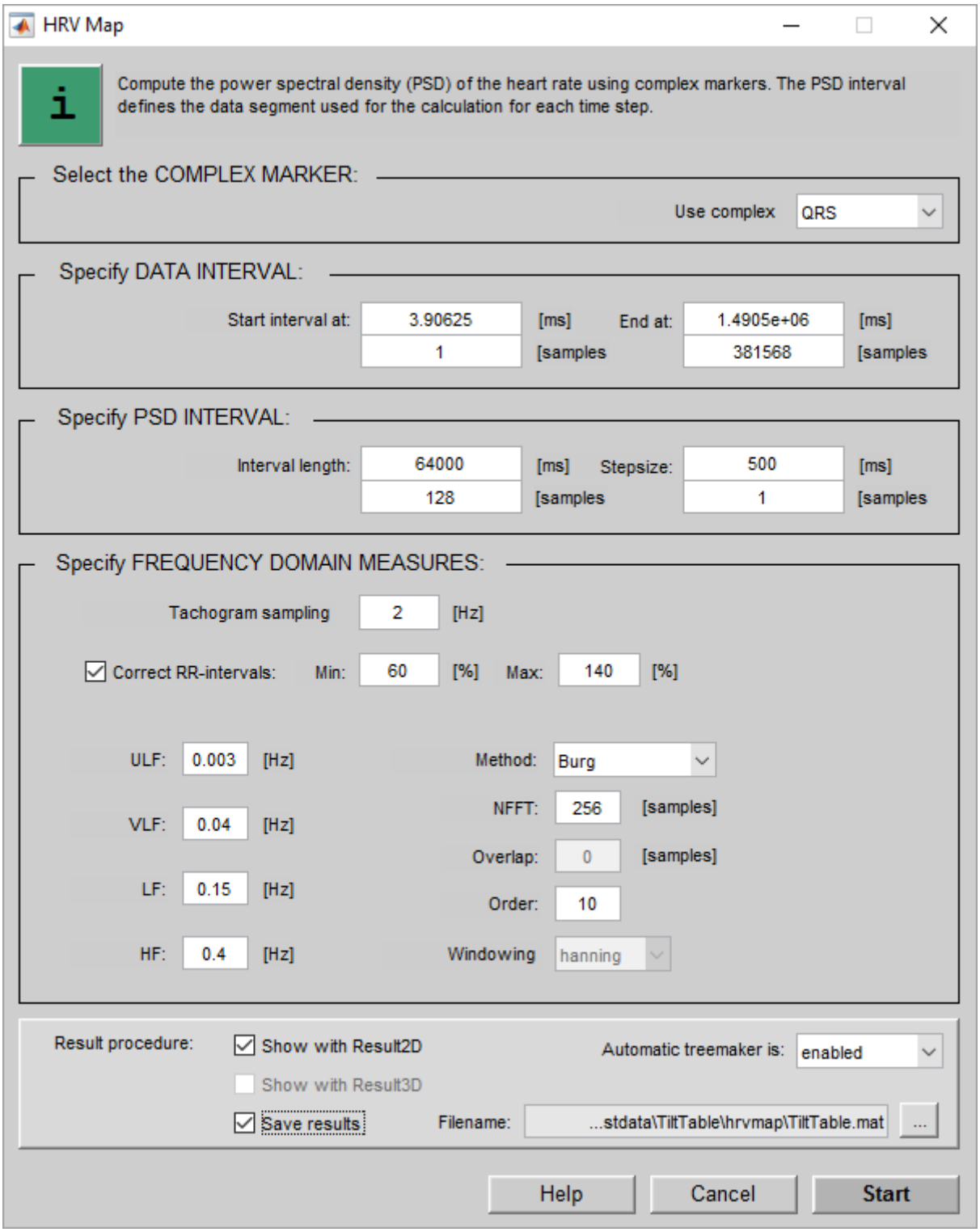
Example

1. Click on **Load Data** from the **File** menu and select the file `DataCorrected.mat` from

   `Documents\gtec\gBSanalyze\testdata\TiltTable`

   The Data Editor shows an ECG channel with already assign QRS markers.

2. Open the **HRV Map** window from the **ECG** menu and select under **Use complex marker** `QRS`.



3. Select the total data-set under **Specify DATA INTERVAL** for the analysis.

4. Enter an **Interval length** of `128` samples as data segment length for the spectral analysis. Set the **Stepsize** of the data segment to `1` sample. These settings shift the 128 sample

window by 1 sample until the end of the data-set.

5. Check the **Correct RR-intervals** box to eliminate intervals which are below `60` % or above `140` % of the average interval.

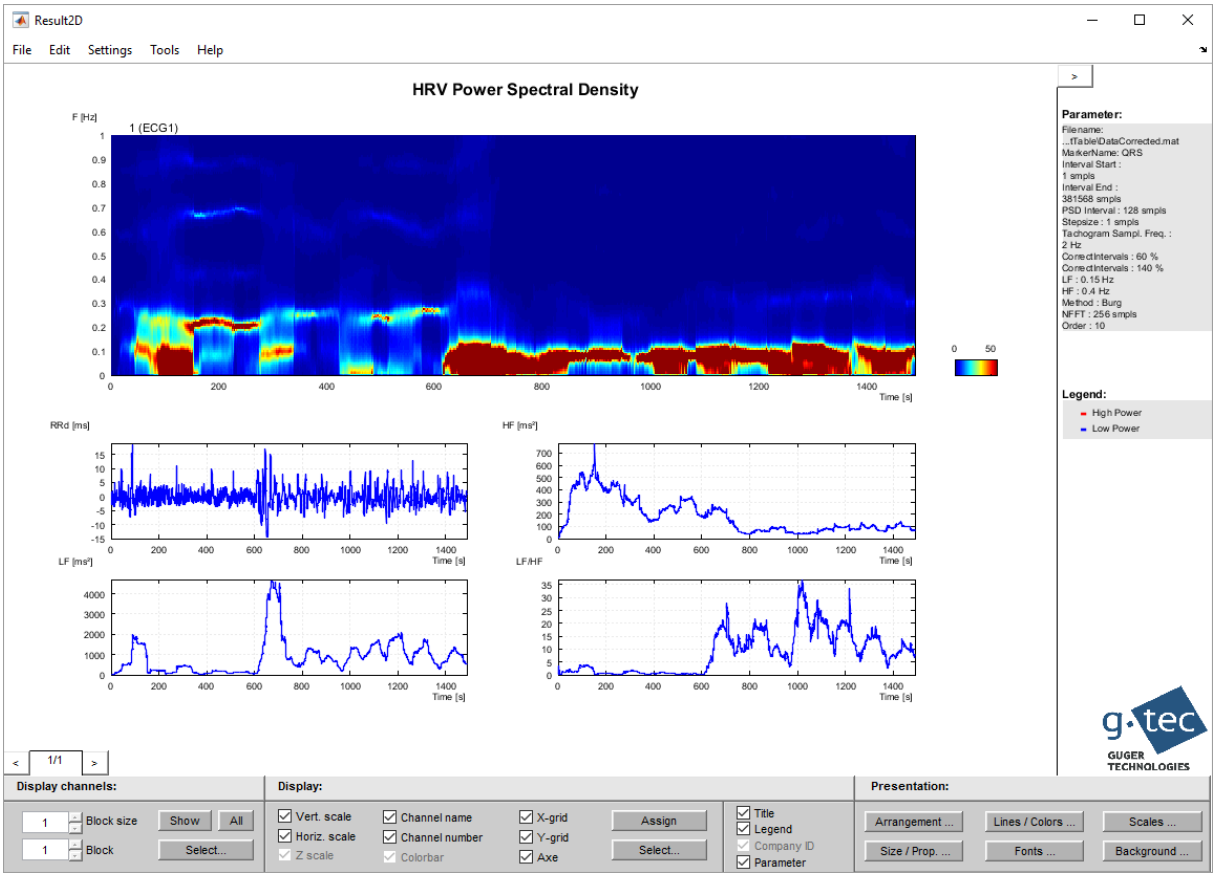
6. Enter under **ULF** `0.003` Hz, under **VLF** `0.04` Hz, under **LF** `0.15` Hz and under **HF** `0.4` Hz.

7. Select the parametric **Method** `Burg` with an **NFFT** length of `256` samples and an **Order** of `10`.

8. Check **Show with Result2D** to open the graphical output of the calculation with g.Result2D.

9. Check **Save results** to save the calculation result to harddisk. The **Automatic treemaker** creates a subdirectory `hrvmap`. Enter `TiltTable.mat` as filename.

10. **Start** the calculation. g.Result2D opens automatically with the calculation result:



The top plot shows the power spectral density evolution from second 0 to second 1490. The subject was standing up at second 620 which can clearly be seen in the data. The middle-left plot is the de-trended RR interval curve in ms. The bottom-left curve and the middle right curve are the time courses of the LF and HF parameters in ms^2. The bottom right curve is the LF/HF quotient.

The following code show how to perform the example demonstrated above from the MATLAB command line.

```
%Load data
P_C=data;
File=['C:\Users\' getenv('USERNAME')
'\Documents\gtec\gBSanalyze\testdata\TiltTable\DataCorrected.mat'];
P_C=load(P_C,File);

%HRV map
MarkerName='QRS';
Interval=[1  381568];
IntervalLength=[128];
StepSize=[1];
TachogramSampling=[2];
CorrectIntervals=[60  140];
F=[0.003        0.04        0.15         0.4];
Method='Burg';
NFFT=[256];
Overlap=[0];
Order=[10];
Window=['hanning'];
FileName=['C:\Users\' getenv('USERNAME')
'\Documents\gtec\gBSanalyze\testdata\TiltTable\TiltTable.mat'];
ProgressBarFlag=0;
[H_O]=gBShrvmap(P_C,MarkerName,Interval,CorrectIntervals,...
TachogramSampling,Method,NFFT,Overlap,Window,Order,F,...
IntervalLength,StepSize,FileName,ProgressBarFlag);
```

Event Related ECG

This function calculates heart rate variability parameters before and after trigger events for a certain interval With **Time before stimulus** and **Time after stimulus** the time range for the calculation can be defined. Additionally a delay can be defined with **Delay before stimulus** and **Delay after stimulus**.

If incomplete intervals defined with the settings above should be considered for calculation, select the **Accept incomplete intervals** checkbox.

The function need assigned QRS markers and markers that indicate the trigger points. The corresponding trigger marker respectively QRS marker can be selected with the popup menus **Trigger marker** for the stimulus and **QRS marker** for the marked QRS complexes.

The user can select:

Heart rate Parameters

- **MEAN:** mean of the heart rate [bpm]
- **MEDIAN:** median of the heat rate [bpm]
- **STD:** standard deviation of the heart rate [bpm]
- **RMSSD:** the square root of the mean of the square of differences between adjacent RR intervals [ms]
- **SDSD:** the standard deviation of differences between adjacent RR intervals [ms]
- **NNx**: number of RR intervals differing by more than x ms to the next RR interval
- **pNNx**: NNx divided by the total number of RR intervals [%]

The time **x** is set in ms, for humans the value is usually 50 ms.

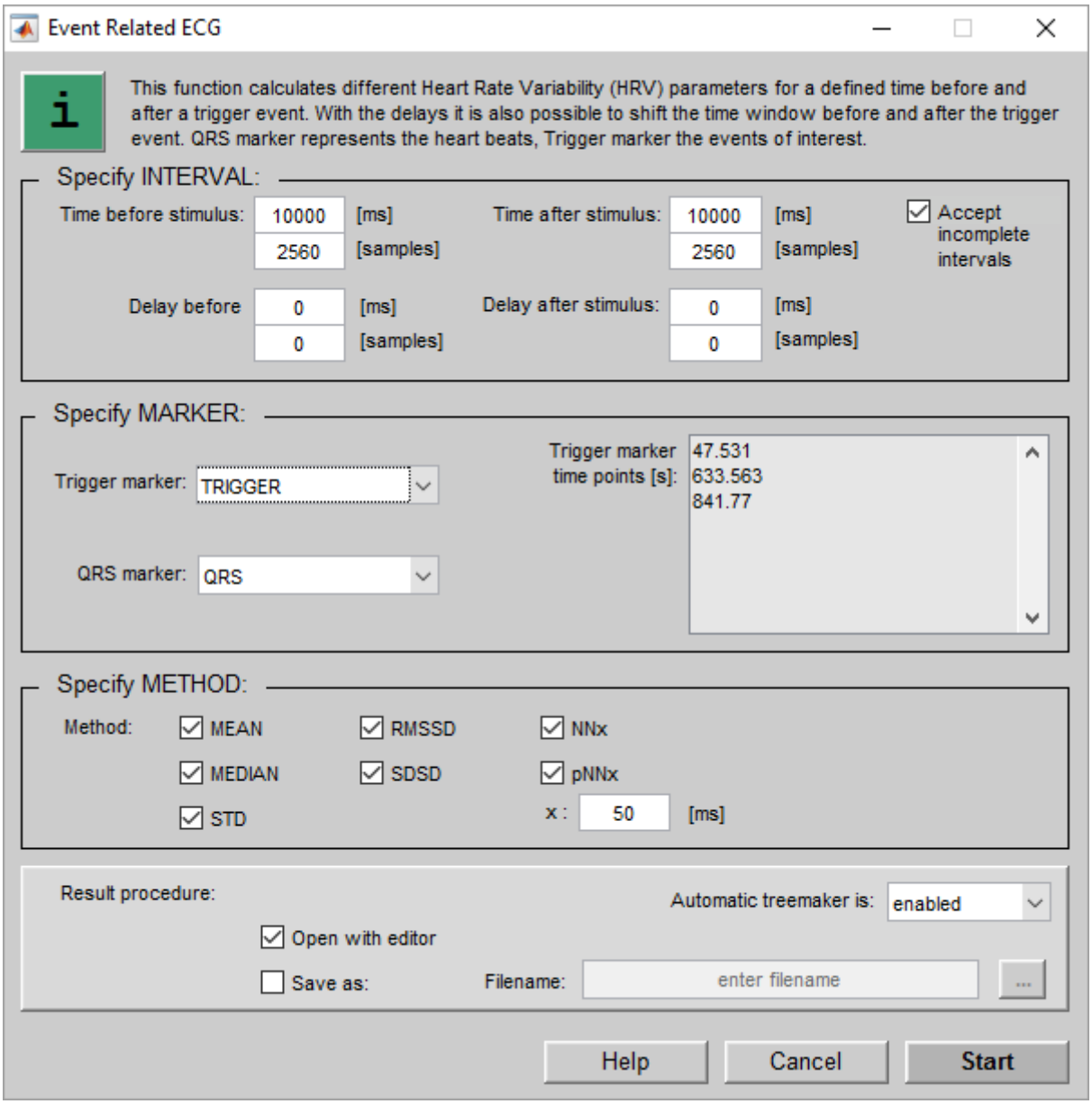
Example:

Perform the following steps:

1. Load data-set `DataCorrected.mat` under

   `Documents\gtec\gBSanalyze\testdata\TiltTable`

2. Click on **Event Related ECG** under the **ECG** menu to open the following window:



3. Specify the **Interval**. Set the **Time before stimulus** to `10000` **ms** and the **Time after stimulus** to `10000` **ms**.
4. Select **Accept incomplete intervals.**
5. Select as **Trigger marker** `TRIGGER` and as **QRS marker** `QRS`.
6. Check all checkboxes in the **Specify METHOD** section and select for **x** `50` ms.
7. Press **Start**.

The MATLAB Editor shows the ASCII description of the result. The first and second columns of the matrix show the **Trigger marker** time point in seconds and samples. The third column represents the calculated values of the selected **Method** (e.g. **MEAN**) of all reference intervals. The next column shows the calculated values of all active intervals.

```
Event related ECG Results:

Input File: Z:\Guger\gBSanalyze\testdata\TiltTable\DataCorrected.mat
Generated: 29-Apr-2011 17:6:4

QRS Marker Name:     QRS
Trigger Marker Name: TRIGGER

Time before stimulus (reference interval):   10.000 s  (2560 samples)
Time after stimulus (active intervall):      10.000 s  (2560 samples)

Delay before stimulus:    0.000 s  (0 samples)
Delay after stimulus:     0.000 s  (0 samples)

Accept incomplete calculation intervals is enabled

Calculation Method: MEAN

Trigger |  Time [s] | Time [samples] |     Mean of reference |     Mean of
active
Number  |           |                |        interval [bpm] |     interval
[bpm]
-------------------------------------------------------------------------
------
      1 |    47.531 |          12168 |                 57.75 |
52.78
      2 |   633.563 |         162192 |                 59.11 |
78.14
      3 |   841.770 |         215493 |                 72.71 |
73.80
```

The following code show how to perform the example demonstrated above from the MATLAB command line.

```
%Load Data

P_C=data;

File=['C:\Users\' getenv('USERNAME')
'\Documents\gtec\gBSanalyze\testdata\TiltTable\DataCorrected.mat'];
P_C=load(P_C,File);

%Event Related ECG:
SamplesBefore = [2560];
SamplesAfter = [2560];
DelayBefore = [0];
DelayAfter = [0];
AcptIncomplete = [1];
TriggerMarkerName = 'TRIGGER';
QRSMarkerName = 'QRS';
Method = {'MEAN';'MEDIAN';'STD';'RMSSD';'SDSD';'NN50';'pNN50'};
FileName = '';
ProgressBarFlag = [1];
E_O = gBSeventrelatedecg(P_C,SamplesBefore,SamplesAfter,DelayBefore,...
```

```
DelayAfter,AcptIncomplete,TriggerMarkerName,QRSMarkerName,Method,...
FileName,ProgressBarFlag);
```

Help

g.BSanalyze and the g.ECGtoolbox provide a printable documentation and a function help.

The printable documentation is stored under

```
C:\Program Files\gtec\gBSanalyze\Help
```

as `gECGtoolbox.pdf`. Use Acrobat Reader to view the documentation.

To view the function help type

```
help gBSfunctionname
```

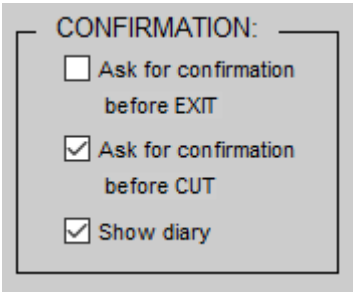
under the MATLAB command window.

To view all functions that are available in batch mode type

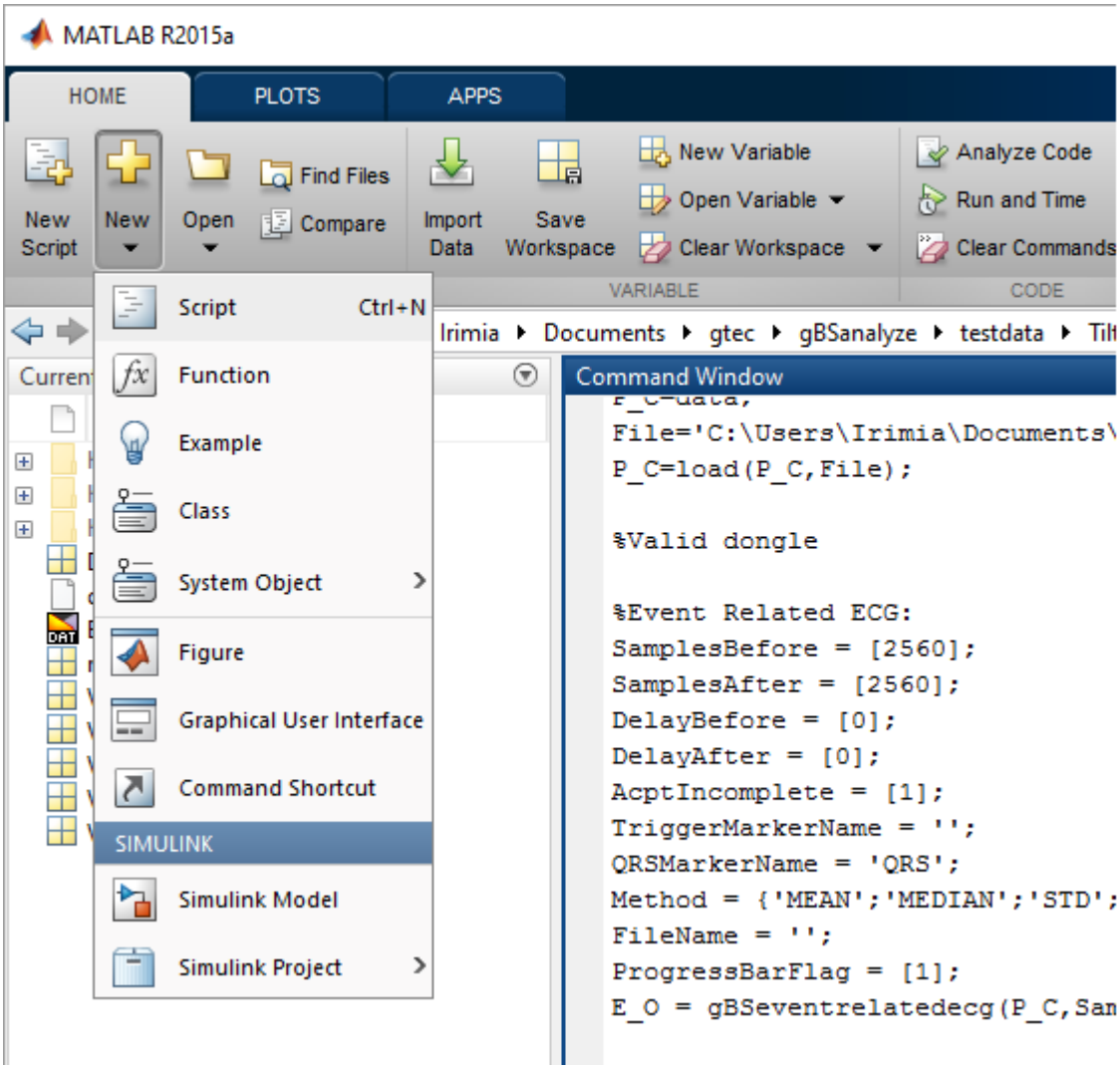
```
gBSfunctions
```

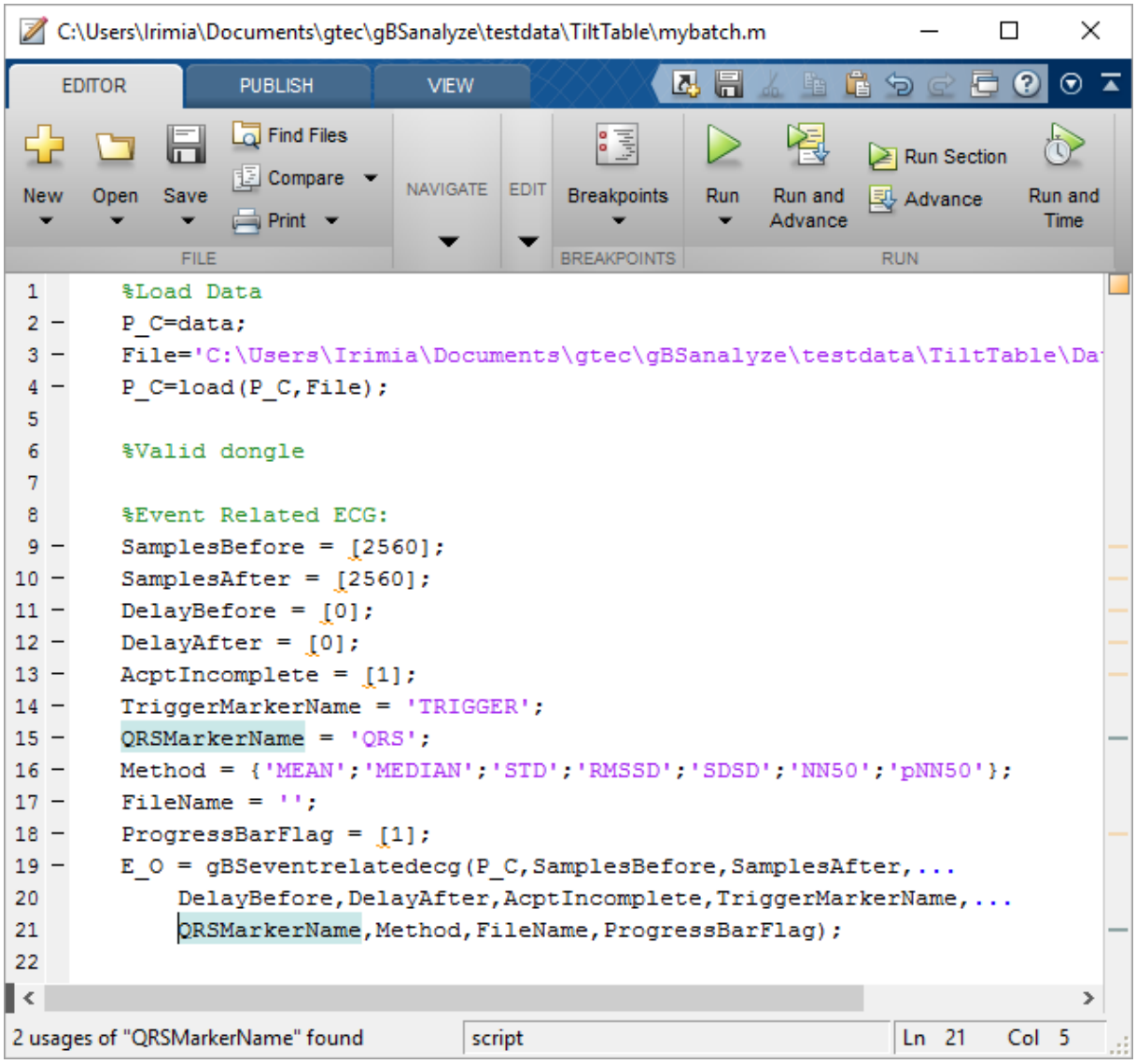
Batch Mode

The easiest way to create a batch for data processing is to perform the analysis under the Data Editor using the graphical user interfaces. Make sure that the **Show diary** checkbox is enabled in **Appearance Settings** under the **Options** menu.



This forces g.BSanalyze to report all calculations in the MATLAB command window. After finishing the analysis open a **New Script** and copy and paste all commands into the file.





Save the batch in your own directory as `mybatch.m` and start the batch under the MATLAB command window with

```
mybatch
```

In order to investigate further data-sets just replace the input data file by the new data file to perform the same analysis.

Product Page

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