

VERSION 5.16.02

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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

<u>Using This Guide</u> - Suggestions for reading the handbook

<u>Conventions</u> - Text formats in the handbook

Required Products

g®.ECGtoolbox uses:

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

 $\ensuremath{\textbf{MATLAB}}\xspace -$ as basic matrix operation platform

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

Using This Guide

Chapter "<u>Running g.BSanalyze</u>" shows how to start the Data Editor.

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

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

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

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

Chapter "<u>Batch-Mode</u>" 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	<pre>set(P_C, 'PropertyName',)</pre>
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





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:

🕢 Complex Detector	—		×
Search for complexes (e.g. QRS) in a specific channel and assign markers markers as input to generate a new re-sampled feature channel in the Data	to the data-set. Editor.	Use compl	ex
Select INPUT-CHANNEL or MARKER:			
O Use complex marker: BEGIN V O Use input channel	Select input c	hannel	
_ Specify DETECTION METHOD:			
QRS detector BP	Advanced se	ettings	
- Specify OPTIONS:			
Generate marker names: 🗹 Detected events: QRS			
Generate feature channel Scaling: interval length [ms]	~		
Result procedure: Add new channels Replace all channels	emakeris: er	abled	
Save result data Filename:	enter file	name	
Help Ca	ancel	Start	

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.

承 Select channels		_	
Select channels for further and channel name on the le right list box.	processing. Currently available ch ft. Calculations are applied only on	annels are listed by c the selected channel	hannel number Is shown in the
Select CHANNELS:			
Available channels: number / name		Selected channels: number / name	
2 TRG	Add to list -> <- Remove from list Select all ->> < Remove all	1 ECG1	~
	Help	Cancel	OK !

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

承 Advanced settings		_ [×	
Specify the bandpass filter and threshold for the QRS complex detection. Specify error correction values.				
_ QRS DETECTION:				
Bandpass filter:				
Lower cutoff frequency: 10 [Hz]				
Upper cutoff frequ	ency:	60	[Hz]	
Three	shold:	0.5	[mV]	
Specify ERROR CORRECTION:				
Accepted heart rate				
Min. : 60 [%]				
1	Max. :	140	[%]	
Highest accepted heart rate: 180 [1/min]				
Help	Cancel		ОК	

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.



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

Marker
The window shows all markers contained in your current data file. Add new markers or delete/modify the markers. To remove one type of marker in general use the right panel (Counter). It is not allowed to delete the BEGIN and END markers. MARKERS in the data file: Name / Sample # / Trial # / Time [ms]
Name / Sample # / Trial # / Time [ms] BEGIN / 1 / 1/3.9063 QRS / 264 / 1 / 1031.25 QRS / 546 / 1 / 2132.8125 QRS / 848 / 1 / 3312.5 QRS / 1152 / 1 / 4500 QRS / 120 / 1 / 6718.75 QRS / 2295 / 1 / 8964.8438 QRS / 2295 / 1 / 8964.8438 QRS / 2295 / 1 / 8964.8438 QRS / 2287 / 1 / 10105.4688 QRS / 3166 / 1 / 12367.1875 QRS / 3166 / 1 / 12367.1875 QRS / 3390 / 1 / 1588.9375 QRS / 3990 / 1 / 15689.8438 QRS / 3990 / 1 / 15689.8438 QRS / 4247 / 1 / 16589.8438
Name / Sample # / Hal # / Hine [His] Counter: BEGIN / 1 / 1031.25 Sort by name QRS / 264 / 1 / 2132.8125 Sort by name QRS / 848 / 1 / 3312.5 Sort by name QRS / 152 / 1 / 4500 Sort by time/trial QRS / 1429 / 1 / 5582.0313 Sort by time/trial QRS / 120 / 1 / 6718.75 Sort by time/trial QRS / 2295 / 1 / 8964.8438 QRS / 2287 / 1 / 10105.4688 QRS / 3166 / 1 / 12367.1875 QRS / 3166 / 1 / 12367.1875 QRS / 3390 / 1 / 15585.9375 QRS / 3990 / 1 / 15585.9375 QRS / 4247 / 1 / 16589.8438 RS / 2291 / 1 / 4592.75
BEGIN / 1 / 1 / 3.9063 A QRS / 264 / 1 / 1031.25 A QRS / 546 / 1 / 2132.8125 Sort by name QRS / 848 / 1 / 3312.5 Sort by name QRS / 1152 / 1 / 4500 QRS / 1152 / 1 / 4500 QRS / 129 / 1 / 5582.0313 QRS / 120 / 1 / 6718.75 QRS / 2019 / 1 / 7886.7188 Sort by time/trial QRS / 2295 / 1 / 8964.8438 QRS / 2287 / 1 / 10105.4688 QRS / 2887 / 1 / 1105.4688 QRS / 2887 / 1 / 11277.3438 QRS / 3166 / 1 / 12367.1875 QRS / 3736 / 1 / 14593.75 QRS / 3990 / 1 / 15585.9375 QRS / 3990 / 1 / 15585.9375 QRS / 4247 / 1 / 16589.8438 QRS / 4247 / 1 / 16589.8438
QRS / 264 / 1 / 1031.25 Sort by name BEGIN / 1 QRS / 546 / 1 / 2132.8125 Sort by name END / 1 QRS / 848 / 1 / 3312.5 Sort by time/trial END / 1 QRS / 1152 / 1 / 4500 Sort by time/trial QRS / 1670 QRS / 1429 / 1 / 5582.0313 Sort by time/trial QRS / 1670 QRS / 2019 / 1 / 7886.7188 QRS / 2295 / 1 / 8964.8438 QRS / 2295 / 1 / 8964.8438 QRS / 2287 / 1 / 10105.4688 QRS / 2887 / 1 / 11277.3438 GRS / 3166 / 1 / 12367.1875 QRS / 376 / 1 / 14593.75 QRS / 3990 / 1 / 15585.9375 QRS / 3990 / 1 / 15585.9375 QRS / 4247 / 1 / 16589.8438 QRS / 4247 / 1 / 16589.8438 GRS / 4247 / 1 / 16589.8438
URS / 546 / 1 / 2/32.8125 Image: Constraint of the second sec
QRS / 1152 / 1 / 4500 QRS / 1152 / 1 / 4500 QRS / 1429 / 1 / 5582.0313 Sort by time/trial QRS / 1720 / 1 / 6718.75 QRS / 2019 / 1 / 7886.7188 QRS / 2295 / 1 / 8964.8438 QRS / 2587 / 1 / 10105.4688 QRS / 3166 / 1 / 12367.1875 QRS / 3166 / 1 / 12367.1875 QRS / 3736 / 1 / 14593.75 QRS / 3736 / 1 / 14593.75 QRS / 4247 / 1 / 16589.8438 QRS / 4247 / 1 / 16589.8438
QRS / 1429 / 1 / 5582.0313 QRS / 1720 / 1 / 6718.75 QRS / 2019 / 1 / 7886.7188 QRS / 2295 / 1 / 8964.8438 QRS / 2587 / 1 / 10105.4688 QRS / 3166 / 1 / 12367.1875 QRS / 3766 / 1 / 12367.1875 QRS / 3736 / 1 / 14593.75 QRS / 3990 / 1 / 15585.9375 QRS / 4247 / 1 / 16589.8438
QRS / 1720 / 1 / 6718.75 QRS / 2019 / 1 / 7886.7188 QRS / 2295 / 1 / 8964.8438 QRS / 2587 / 1 / 10105.4688 QRS / 2887 / 1 / 11277.3438 QRS / 3166 / 1 / 12367.1875 QRS / 3736 / 1 / 14593.75 QRS / 3736 / 1 / 14593.75 QRS / 3990 / 1 / 15585.9375 QRS / 4247 / 1 / 16589.8438
QRS / 2019 / 1 / 7886.7188 QRS / 2295 / 1 / 8964.8438 QRS / 2587 / 1 / 10105.4688 QRS / 2887 / 1 / 11277.3438 QRS / 3166 / 1 / 12367.1875 QRS / 3461 / 1 / 13519.5313 QRS / 3736 / 1 / 14593.75 QRS / 3736 / 1 / 14593.75 QRS / 3990 / 1 / 15585.9375 QRS / 4247 / 1 / 16589.8438 PRS / 4247 / 1 / 16589.8438
QRS / 2295 / 1 / 8964.8438 QRS / 2587 / 1 / 10105.4688 QRS / 2887 / 1 / 11277.3438 QRS / 3166 / 1 / 12367.1875 QRS / 3461 / 1 / 13519.5313 QRS / 3736 / 1 / 14593.75 QRS / 3990 / 1 / 15585.9375 QRS / 4247 / 1 / 16589.8438 QRS / 4247 / 1 / 16589.8438
QRS / 2587 / 1 / 10105.4688 QRS / 2887 / 1 / 11277.3438 QRS / 3166 / 1 / 12367.1875 QRS / 3461 / 1 / 13519.5313 QRS / 3736 / 1 / 14593.75 QRS / 3990 / 1 / 15585.9375 QRS / 4247 / 1 / 16589.8438 QRS / 4247 / 1 / 16589.8438
QRS / 2887 / 1 / 11277.3438 QRS / 3166 / 1 / 12367.1875 QRS / 3461 / 1 / 13519.5313 QRS / 3736 / 1 / 14593.75 QRS / 3990 / 1 / 15585.9375 QRS / 4247 / 1 / 16589.8438
QRS / 3166 / 1 / 12367.1875 QRS / 3461 / 1 / 13519.5313 QRS / 3736 / 1 / 14593.75 QRS / 3990 / 1 / 15585.9375 QRS / 4247 / 1 / 16589.8438
QRS / 3736 / 1 / 14593.75 QRS / 3990 / 1 / 15585.9375 QRS / 4247 / 1 / 16589.8438 QRS / 4247 / 1 / 16589.8438
QRS / 3990 / 1 / 15585.9375 QRS / 4247 / 1 / 16589.8438 QRS / 4247 / 1 / 16589.8438
QRS / 4247 / 1 / 16589.8438
000 / / 500 / / / / 7040 0040
QRS7450971717613.2613
QRS / 4785 / 1 / 18691.4063
QRS / 5068 / 1 / 19796.875
QRS / 5341 / 1 / 20863.2813
ASCII export Markers (total): 1672
QRS / 6134 / 1 / 23960 9375
QRS / 6397 / 1 / 24988.2813 View AScill export Remove selected marker
QRS / 6674 / 1 / 26070.3125
Edit (selected) marker:
Name: Sample #: Trial #: Time [ms]:DeleteAdd new
BEGIN 1 1 3.9063 Modify
Help Cancel OK !

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.

承 Advanced settings	—	×		
Specify the bandpass filter and threshold for the QRS complex detection. Specify error correction values.				
GRS DETECTION:				
Bandpass filter:				
Lower cutoff frequency:	10	[Hz]		
Upper cutoff frequency:	60	[Hz]		
Threshold:	0.2	[mV]		
Specify ERROR CORRECTION:				
Accepted heart rate				
Min. :	60	[%]		
Max. :	140	[%]		
Highest accepted heart rate:	180	[1/min]		
Help Cancel		ОК		

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

Open the **Marker** window from the **Heade**r menu:

🗼 Marker	
The window shows all markers co markers. To remove one type of ma the BEGIN and END markers.	ontained in your current data file. Add new markers or delete/modify the arker in general use the right panel (Counter). It is not allowed to delete
MARKERS in the data file:	
Name / Sample # / Trial # / Time [ms]	Counter:
BEGIN / 1 / 1 / 3.9063	Name / Number
QRS / 264 / 1 / 1031.25	DECIMAL DECIMAL
QRS / 546 / 1 / 2132.8125	Sort by name BEGIN / 1
QRS / 848 / 1 / 3312.5	END / 1
QRS / 1152 / 1 / 4500	Sort by time/trial
QRS / 1429 / 1 / 5582.0313	
QRS / 1720 / 1 / 6718.75	
QRS / 2019 / 1 / 7886.7188	
QRS / 2295 / 1 / 8964.8438	
QRS / 2587 / 1 / 10105.4688	
QRS / 2887 / 1 / 11277.3438	
QRS / 3166 / 1 / 12367.1875	
QRS / 3461 / 1 / 13519.5313	
QRS / 3736 / 1 / 14593.75	
QRS / 3990 / 1 / 15585.9375	
QRS / 4247 / 1 / 16589.8438	
QRS / 4509 / 1 / 17613.2813	
QRS / 4785 / 1 / 18691.4063	
QRS / 5068 / 1 / 19796.875	
QRS / 5341 / 1 / 20863.2813	
QRS / 5606 / 1 / 21898.43/5	ASCII export Markers (total): 1660
QRS / 58/5 / 1 / 22949.2188	
UK5 / 6134 / 1 / 23960.93/5	view ASCII export
QRS / 639/ / 1 / 24966.2613	Remove selected marker
QR37007471720070.3123	
Edit (selected) marker:	
Name: Sample #: Trial #:	Time [me]: Delete Add new
Name. Sample #. Mar#.	Time [ms].
BEGIN 1 1	3.9063 Modify
	Help Cancel OK !

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.

Kunters and attributes		_	
Choose a marker, channel attribute or trial attri the mouse to assign markers or to assign attrit data in the Data Editor. If a trial or channel has	bute you wish to edit outes. Markers and at more than one attribu	or add a new one. Pro ttribute colors will be a ute the segment appea	ess 'OK' and use issigned to the rs in blue.
Edit MARKER O Edit TRIA	L ATTRIBUTE	O Edit CHANNE	L ATTRIBUTE
BEGIN /red END /blue IQRS /green		BAD /red CUT /blue	
Create new: Create new:		Create new:	
Add to list Remove Add to list	Remove	Add to list	Remove
Change COLOR to: red blue green yellow pink	orange purple	olive brown	n grey
	Help	Cancel	OK !

- 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 \quad 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.

SH	ow
Chan. attr.	Vert. scale
Trial attr.	Hor. scale
Separators	Grid Grid
Markers	Ch. name

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

DISPLAY				
1490	-	Seconds		
3	-	Channels		
1		Trials		
Sel	ect	Undo		

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] = qBScomplexdetector(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

 $\label{eq:tachogram} \begin{array}{l} \textbf{Tachogram unit} - \textit{the unit of the calculated tachogram can be in ms, samples or beats} \\ \texttt{per minute} \end{array}$

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

承 HRV Time Domain	- 🗆 X
Compute heart rate and heart rate variability measures from a QRS complex marker "Complex Detector" to generate the complex markers. For SDANN and SDNNindex time series is used. All other measures are computed of the non-uniform sampled F Select the COMPLEX MARKER:	er. Use the function calculations a resampled RR intervals. ex QRS ~
Specify DATA INTERVAL:	
Start interval at: 3.90625 [ms] End at: 632 1 [samples] 161	2000 [ms] 1792 [samples
_ Specify TIME DOMAIN MEASURES:	
Tachogram unit: bpm V Resample tachogram	
Segmented Interval length: 5000 [ms] 1280 [samples	
Histogram unit: bpm V Bin 7.8125	
Correct RR-intervals: Min: 60 [%] Max: 140 [%]	
Result procedure: Show with Result2D Automatic treemaker	r is: enabled V
Save results Filename:estdata\TiltTable\hr	vtd\TiltTable.mat
Help Cancel	Start

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.

🕢 HRV Time Domain – 🗆 🗙
Compute heart rate and heart rate variability measures from a QRS complex marker. Use the function "Complex Detector" to generate the complex markers. For SDANN and SDNNindex calculations a resampled time series is used. All other measures are computed of the non-uniform sampled RR intervals.
Specify DATA INTERVAL:
Start interval at: 634000 [ms] End at: 1.4905e+06 [ms] 162304 [samples] 381568 [samples]
Specify TIME DOMAIN MEASURES:
Tachogram unit: bpm 🗸 🔽 Resample tachogram
Segmented Interval length: 5000 [ms] 1280 [samples
Histogram unit: bpm V Bin 7.8125
Correct RR-intervals: Min: 60 [%] Max: 140 [%]
Result procedure: Show with Result2D Automatic treemaker is: enabled ~
Save results Filename:stdata\TiltTable\hrvtd\TiltTable2.mat
Help Cancel Start



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 [ms²]

VLF...very low frequency components in [ms²]

LF...low frequency components in $[ms^2]$

HF...high frequency components in [ms²]

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.

承 HRV Frequency Domain	– 🗆 X				
Compute heart rate variability frequency domain parameters from complex markers.					
Select the COMPLEX MARKER:	Use complex QRS ~				
- Specify DATA INTERVAL:					
Start interval at: 3.90625	[ms] End at: 632000 [ms] [samples] 161792 [samples]				
Specify FREQUENCY-DOMAIN MEASURES	:				
Tachogram sampling frequency: 2 [Hz]				
Correct RR-intervals: Min: 60	[%] Max: 140 [%]				
ULF: 0.003 [Hz]	Method: Burg ~				
VLF: 0.04 [Hz]	NFFT: 256 [samples]				
LF: 0.15 [Hz]	Overlap: 0 [samples]				
HF: 0.4 [Hz]	Windowing hanning				
Result procedure: Show with Result2D Automatic treemaker is: enabled ~					
Save results Filen	ame:estdata\TiltTable\hrvfd\TiltTable.mat				
	Help Cancel Start				

- 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.

🕢 HRV Frequency Domain —					
Compute heart rate variability frequency domain parameters from complex markers.					
Use complex	ars 🗸				
Specify DATA INTERVAL:					
Start interval at: 634000 [ms] End at: 1.4905e+06 162304 [samples] 381568	[ms] [samples]				
Specify FREQUENCY-DOMAIN MEASURES:					
Tachogram sampling frequency: 2 [Hz]					
Correct RR-intervals: Min: 60 [%] Max: 140 [%]					
ULF: 0.003 [Hz] Method: Burg ~					
VLF: 0.04 [Hz] NFFT: 256 [samples]					
LF: 0.15 [Hz] Order: 10					
HF: 0.4 [Hz] Windowing hanning ~					
Result procedure: Show with Result2D Automatic treemaker is: e	nabled ~				
Save results Filename:stdata\TiltTable\hrvfd\TiltT	able1.mat				
Help Cancel	Start				

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];
                       0.15
                                     0.41;
F=[0.003
               0.04
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 0]=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
                           0.15
                                      0.41;
               0.04
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 0]=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).

 $\ensuremath{\textbf{NFFT}}$ – 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

 $\label{eq:windowing function-select a hanning, hamming or boxcar window for the FFT analysis$

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.

承 HRV Map				X
Compute the power spectral density (PSD) of the heart rate using complex markers. The PSD interval defines the data segment used for the calculation for each time step.				
Select the COMPLEX MARKER:				
		U	se complex	QRS V
Specify DATA INTERVAL:				
Start interval at:	3.90625	[ms] End at:	1.4905e+0	6 [ms]
	1	[samples	381568	[samples
Specify PSD INTERVAL:				
Interval length:	64000	[ms] Stepsize:	500	[ms]
	128	[samples	1	[samples
Specify FREQUENCY DOMAIN N Tachogram sampling Correct RR-intervals: Min: ULF: 0.003 [Hz]	AEASURES: 2 [Hz] 60 [%] Ma Metho NFF	ax: 140 [%] d: Burg T: 256 [sam)	∽ bles]	
VLF: 0.04 [HZ]	Overla	ip: 0 [sam;	oles]	
LF: 0.15 [Hz]	Orde	er: 10		
HF: 0.4 [Hz]	Windowir	ng hanning 🗸		
Result procedure: Show with Re Show with Re	esult2D esult3D	Automatic	treemaker is:	enabled 🗸
Save results	Filename:	stdata\Tilt1	[able\hrvmap\T	itTable.mat
		Help	Cancel	Start

- 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 ms². 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: MEDIAN:	mean of the heart rate [bpm] 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 \mathbf{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:

承 Event Related ECG				-	_	×
This function of after a trigger of event. QRS ma	alculates different Hea event. With the delays i irker represents the he	rt Rate Variability (HRV) p t is also possible to shift t art beats, Trigger marker	arameters he time wi the events	s for a defined indow before s of interest.	I time before a and after the	and trigger
Time before stimulus:	10000 [ms] 2560 [samples]	Time after stimulus:	10000 2560	[ms] [samples]	Accep incomp interva	t ilete Is
Delay before	0 [ms] 0 [samples]	Delay after stimulus:	0	[ms] [samples]		
Specify MARKER:						
Trigger marker: TRIGG	ER	Trigger marker time points [s]:	47.531 633.563 841.77			
QRS marker: QRS	~					~
- Specify METHOD:						
Method: MEAN	N 🗹 RMSSD AN 🗹 SDSD	✓ NNx ✓ pNNx x: 50	[ms]			
Result procedure:	✓ Open with editor	4	Automatic	treemaker is:	enabled	~
	Save as:	Filename:	enter	filename		
		Help		Cancel	Sta	rt

- 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
                [mqd]
_____
  1 | 47.531 | 12168 |
                                              57.75 |
52.78
   2 | 633.563 | 162192 |
                                             59.11 I
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, ...
```

User Manual g.ECGtoolbox

```
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 ${\tt mybatch.m}$ 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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- Downloads
- Troubleshooting
- Additional demonstrations



contact information

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