

# ESTIMATING HEART RATE VARIABILITY

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## CONTENTS

1. Purpose	1
2. RHRV Data Import	3
3. Support Functions	4
3.1. Plotsignal	4
3.2. BuildNIDHR	5
4. First Inspection: example.beats	7
4.1. Hart Rate: example.beats	7
4.2. Hart Rate Variation: example beats	7
5. First Inspection: example2.beats	8
5.1. Hart Rate example 2	9
5.2. Hart Rate Variation: example2.beats	10
6. Exercises	11
References	13
Index	18

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*Corrections and comments are welcome.*

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*A waist book. These notes are internal RFC for the R project RHRV, available from R-Forge. Material from RHRV may be used without explicit quotation.*

*For more details on recurrence plots, see Sawitzki [2013b].*

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## 1. PURPOSE

Heart rate variation is a non-invasive indicator of the physical state. However, heart rate variation is a derived variable, based on heart rate, and heart rate by itself is not an observable variable, but a derived construct.

There are several sources that can be used to derive the heart rate. The quality of the heart rate data, and hence the possibilities to assess the heart rate, depends on the quality of the original data and the preprocessing steps.

The classical means is to register some form of pulse. In all of these, classical methods the basic information is some local blood pressure, and the pulse is derived from it. Typically this information is collected as an average over a small number of beats ( $\approx 15$  beats) or a small time interval (e.g. 15 s).

More precise information can be derived from ECG information. The ECG records the potential difference between two or more electrodes at a chosen sampling rate. Typical amplitudes range from -0.5mV to 2 mv. As of 2014, the standard seems to be recording at 1024 Hz with 3 to 12 electrodes for clinical measurements. Technical facilities allow ambulatory sampling for continuous time, typically using two electrodes.

In clinical environment, the ECG recording is usually commented, and the commenting annotations are an additional source of information (Figure figure 1).



FIGURE 1. Annotated ECG

Heart rate, and heart rate variation are only means to judge the physical state, and oxygen supply ported by the blood may be one of the better indicators. Advanced devices can provide non-invasive measure of the oxygen concentration. This combines information circulation and respiration effects.

At present, we concentrate on ECG based data. These are common in clinical environment, and in ambulatory devices as the Polar series of monitors.

For evaluation, we concentrate on the RHRV package for R (version 4.0) Mendez *et al.* [2014].

These technical notes concentrate on data preparation. Takens states and recurrence plots, with a view to heart rate variability, are discussed in a separate technical note Sawitzki [2013b].

## 2. RHRV DATA IMPORT

The data source for all ECG based data is an ECG recording. From this ECG recording, a beats data set is generated. Usually, pattern recognition is applied to detect QRS signals, and the time of the R component is reported as the beat time. This step may already include additional filtering.

RHRV can import various data formats. Section 5.2: “Reading several file formats” of the RHRV tutorial gives some of the common facilities. The *LoadBeat* function is a common interface for loading heart beat data. In particular, *LoadBeatAscii* loads an ASCII file with the time of beats, one beat per line. The time scale can be specified by the *scale* parameter of *LoadBeatAscii*.

The internal data is added to an extensible R list, a *HRVData* structure in terms of the RHRV tutorial (García *et al.* [2014]). At this point, the data are a vector of beat times [s], stored as a data frame (one variable) in component *\$Beat*.

---

*Input*

```
hrv.data = CreateHRVData()
hrv.data = SetVerbose(hrv.data, TRUE )
hrv.data = LoadBeatAscii(hrv.data, "../beatsFolder/example.beats",
RecordPath = "../beatsFolder")
```

---

*Output*

```
** Loading beats positions for record: ../beatsFolder/example.beats **
Path: ../beatsFolder
Scale: 1
Date: 01/01/1900
Time: 00:00:00
Number of beats: 17360
```

The data structure is augmented by derived information in a second step (see Section 4.1.2 “Calculating HR and filtering” of García *et al.* [2014]).

---

*Input*

```
hrv.data = BuildNIHR(hrv.data)
```

---

*Output*

```
** Calculating non-interpolated heart rate **
Number of beats: 17360
```

At this point, the data are as given in Table table 1 and contained in the *Beat* component of the *HRVData* list. The data structure maintained by *RHRV* may contain additional information.

There may be beats missing, due to the previous processing steps, and there may be gremlins that are generated by false events from the signal detection. An additional step may remove some of the gremlins. *FilterNIHR* uses adaptive thresholds for rejecting those beats different from the given threshold more than a certain value.

Name	Variable	Unit, Remarks
Time	beat time	[s]
niHR	(single beat) heart rate	[beats/min] (rounded?)
RR	beat duration	[ms] (rounded?)

TABLE 1. Raw data inventory

Name	Variable	Unit, Remarks
Time	beat time. Note: some beats have been filtered.	[s]
niHR	(single beat) heart rate	[beats/min] (??? rounded?)
RR	beat duration	[ms] (??? rounded?)

TABLE 2. Data inventory for filtered data

The rule for beat acceptance or rejection is to compare with previous, following and with the updated mean. It also applies a comparison with acceptable physiological values (default values 25 and 200 bpm). Details can be controlled by parameters for *FilterNIHR*. The data structure is similar to Table table 1 on the previous page, but the semantics has changed (Table table 2).

```
Input
hrvfilt.data = FilterNIHR(hrv.data)

Output
** Filtering non-interpolated Heart Rate **
Number of original beats: 17360
Number of accepted beats: 17259
```

As a convenience, an interpolated version of the data can be provided to allow frequency domain analysis. But note: we are not dealing with stationary processes.

```
Input
# Note that it is not necessary to specify freqhr since it matches with
# the default value: 4 Hz
hrvipl.data = InterpolateNIHR (hrvfilt.data, freqhr = 4)

Output
** Interpolating instantaneous heart rate **
Frequency: 4Hz
Number of beats: 17259
Number of points: 29594
```

The data may be imbedded in a *RHRVData* structure as outlined in Figure figure 2 on the next page.

### 3. SUPPORT FUNCTIONS

These functions could go to RHRV.

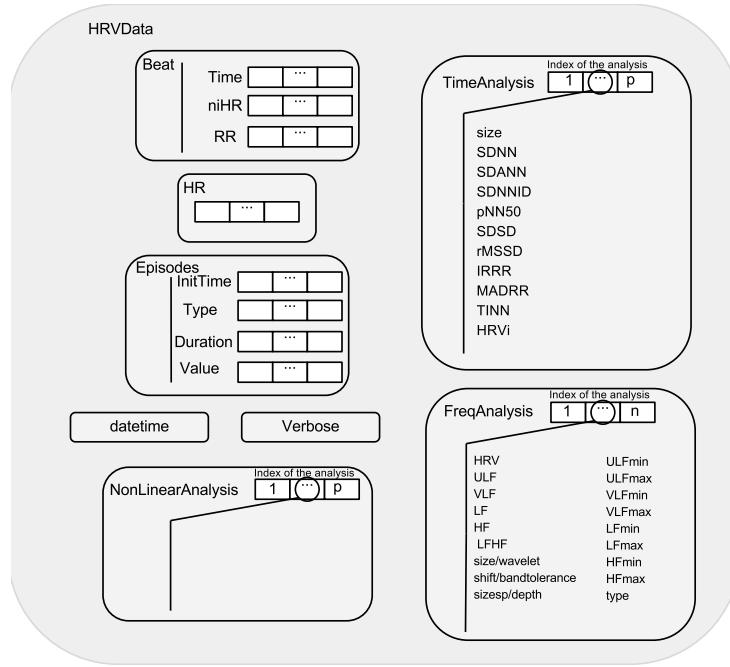


FIGURE 2. RHRV data structure: overview

**To Do:** handle Beat    3.1. **Plotsignal.** For signal representation, we use a common layout.  
not avail in plot

---

*Input*

```

plotsignal <- function (signal) {
  #! alpha level should depend on expected number of overlaps
  par(mfrow=c(1,2))
  plot(signal, col=rgb(0,0,1,0.4), pch=20, xlab="t" )

  plot(signal, type="l",
       xlab="t", col=rgb(0,0,0,0.4))
  points(signal, col=rgb(0,0,1,0.4), pch=20 )
  main=deparse(substitute(signal))
  title(main=main, outer=TRUE, line=-2, cex.main=1.2)
}
```

---

3.2. **BuildNIDHR.** Since we are not interested in heart rate (or pulse), but in heart rate variation, a proposal is to use scaled differences

$$HRRV_i = \frac{RR_i - RR_{i-1}}{(RR_i + RR_{i-1})/2}$$

where  $RR_i$  is the  $i^{th}$  RR interval length. Taking these differences removes the mere pulse effects which otherwise may dominate the variation. There is no information loss, since the original RR sequence can be reconstructed, given initial conditions.

The residuals form this construct isolate structural influence from heart rate variation.

Note: if we think of online monitoring, statistics should be non-anticipating. We can take information from the past, as above, and should avoid assumptions about future data.

```

# source('.../.../pkg/R/BuildNIHR2.R', chdir = TRUE)
BuildNIDHR <-
function(HRVData, verbose=NULL) {
#-----
# Obtains instantaneous heart rate variation from beats positions
# D for difference
#-----
if (!is.null(verbose)) {
  cat(" --- Warning: deprecated argument, using SetVerbose() instead ---\n",
      "--- See help for more information!! ---\n")
  SetVerbose(HRVData,verbose)
}

if (HRVData$Verbose) {
  cat("** Calculating non-interpolated heart rate differences **\n")
}

if (is.null(HRVData$Beat$Time)) {
  cat(" --- ERROR: Beats positions not present... ",
      "Impossible to calculate Heart Rate!! ---\n")
  return(HRVData)
}

NBeats=length(HRVData$Beat$Time)
if (HRVData$Verbose) {
  cat("    Number of beats:",NBeats,"\\n");
}

# addition gs
#using NA, not constant extrapolation as else in RHRV
#drr=c(NA,NA,1000.0*       diff(HRVData$Beat$Time, lag=1 , differences=2))
HRVData$Beat$dRR=c(NA, NA,
                  1000.0*diff(HRVData$Beat$Time, lag=1, differences=2))

HRVData$Beat$avRR=(c(NA,HRVData$Beat$RR[-1])+HRVData$Beat$RR)/2

HRVData$Beat$HRRV <- HRVData$Beat$dRR/HRVData$Beat$avRR

return(HRVData)
}

```

## 4. FIRST INSPECTION: EXAMPLE.BEATS

## 4.1. Hart Rate: example.beats.

---

*Input*

```
plotsignal(hrv.data$Beat$RR)
```

---



---

*Input*

```
plotsignal(hrvfilt.data$Beat$RR)
```

---

See Figure figure 3 for the unfiltered and Figure figure 4 for the filtered version.

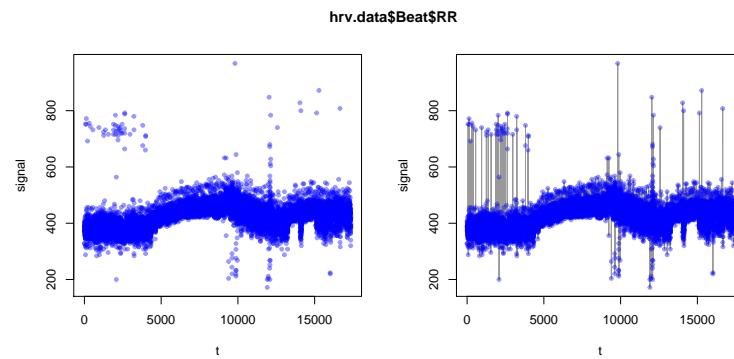


FIGURE 3. RHRV tutorial example.beats. Signal and linear interpolation.

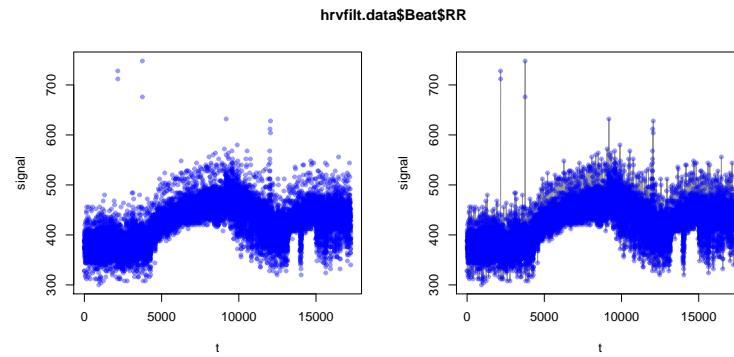


FIGURE 4. RHRV tutorial example.beats filtered. Signal and linear interpolation.

4.2. Hart Rate Variation: example beats. If we are interested in heart rate variation, we may prefer starting with (scaled) differences.

---

*Input*

```
hrv.data <- BuildNIDHR(hrv.data)
```

---



---

*Output*

```
** Calculating non-interpolated heart rate differences **
Number of beats: 17360
```

---

**ToDo:** We have outliers at approximately  $2 \times \text{RR}$ . Could this be an artefact of preprocessing, filtering out too many impulses?

**ToDo:** Consider using differences differences for HRV

---

*Input*

```
HRRV <- hrv.data$Beat$HRRV
```

---



---

*Input*

```
plotsignal(HRRV)
```

---

See Figure figure 5,

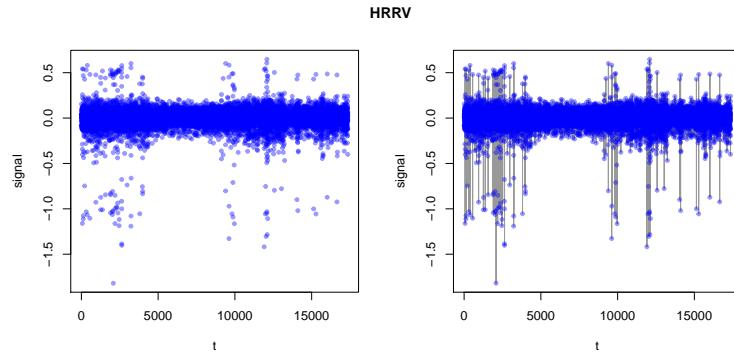


FIGURE 5. RHRV tutorial example.beats. HRRV Signal (differences) and linear interpolation.

---

*Input*

```
hrvfilt.data <- BuildNIDHR(hrvfilt.data)
```

---

*Output*

```
** Calculating non-interpolated heart rate differences **
Number of beats: 17259
```

---



---

*Input*

```
HRRVfilt <- hrvfilt.data$Beat$HRRV
```

---



---

*Input*

```
plotsignal(HRRVfilt)
```

---

See Figure figure 6 on the next page,

## 5. FIRST INSPECTION: EXAMPLE2.BEATS

---

*Input*

```
hrv2.data = CreateHRVData()
hrv2.data = SetVerbose(hrv2.data, TRUE )
hrv2.data = LoadBeatAscii(hrv2.data, "example2.beats",
RecordPath = "../beatsFolder")
```

---



---

*Output*

```
** Loading beats positions for record: example2.beats **
Path: ../beatsFolder
Scale: 1
```

---

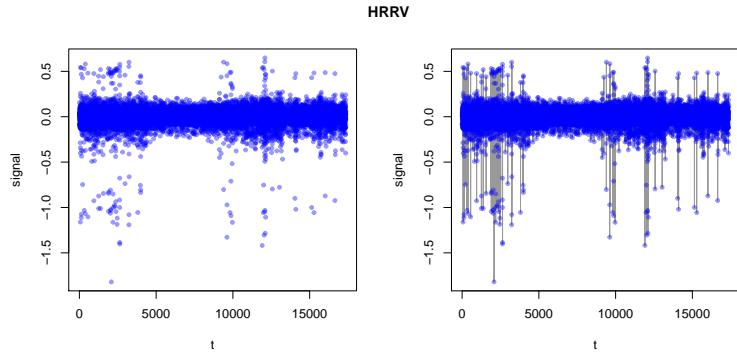


FIGURE 6. RHRV tutorial example.beats, filtered. HRRV Signal (differences) and linear interpolation.

```
Removed 2437 duplicated beats
Date: 01/01/1900
Time: 00:00:00
Number of beats: 2437
```

```


---

Input  
hrv2.data = BuildNIHR(hrv2.data)

---

Output  
** Calculating non-interpolated heart rate **  
Number of beats: 2437

---

Input  
hrv2filt.data = FilterNIHR(hrv2.data)

---

Output  
** Filtering non-interpolated Heart Rate **  
Number of original beats: 2437  
Number of accepted beats: 2434
```

### 5.1. Hart Rate example 2.

```


---

Input  
plotsignal(hrv2.data$Beat$RR)

---

Input  
plotsignal(hrv2filt.data$Beat$RR)
```

See Figure figure 7 on the following page for the unfiltered and Figure figure 8 on the next page for the filtered version.

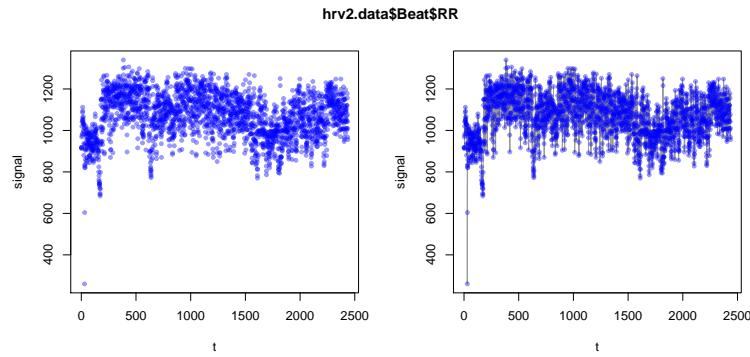


FIGURE 7. RHRV tutorial example2.beats. Signal and linear interpolation.

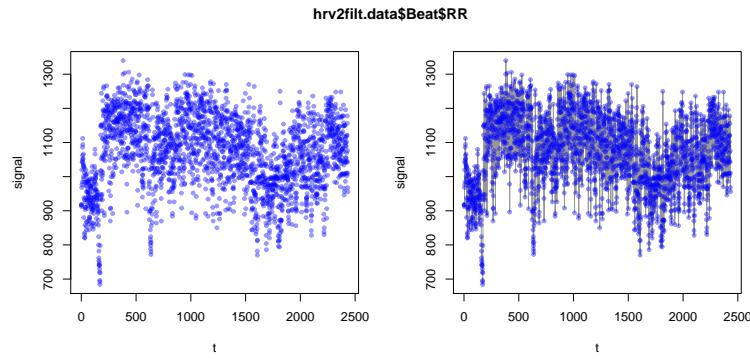


FIGURE 8. RHRV tutorial example2.beats filtered. Signal and linear interpolation.

### 5.2. Hart Rate Variation: example2.beats.

```
Input
hrv2.data <- BuildNIDHR(hrv2.data)

Output
** Calculating non-interpolated heart rate differences **
Number of beats: 2437
```

---

```
Input
HRRV2 <- hrv2.data$Beat$HRRV
```

---

```
Input
plotsignal(HRRV2)
```

See Figure figure 9 on the facing page,

---

```
Input
hrv2filt.data <- BuildNIDHR(hrv2filt.data)
```

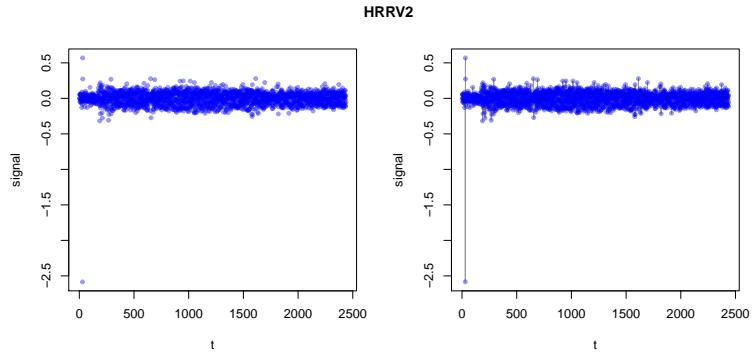


FIGURE 9. RHRV tutorial example2.beats. HRRV Signal (differences) and linear interpolation.

---

```
** Calculating non-interpolated heart rate differences **
Number of beats: 2434
```

---



---

```
HRRV2filt <- hrv2filt.data$Beat$HRRV
```

---



---

```
plotsignal(HRRV2filt)
```

---

See Figure figure 10,

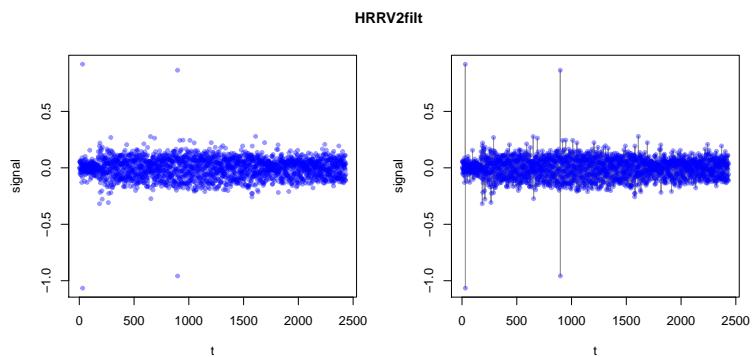


FIGURE 10. RHRV tutorial example2.beats, filtered. HRRV2 Signal (differences) and linear interpolation.

## 6. EXERCISES

---

**Exercise 1.** *Augment the data structure to reflect filtering.*

---

**Exercise 2.** For analysis of heart rate variability, we are interested in effect in the range of less than 10s.

Can you modify the displays to focus on this range?

---

---

**Exercise 3.** For analysis of recovery effects, we are interested in effect in the range of less about 5 min (??).

Can you modify the displays to focus on this range?

---

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## INDEX

### ToDo

- 3: handle Beat not avail in plot, 4
- 4: Consider using differences, 7
- 4: We have outliers at approximately  $2 \times RR$ . Could this be an artefact of preprocessing, filtering out too many impulses?, 7

heart rate variation, 8, 10, 11

**HRVData**, 3

**LoadBeatAscii**, 3

R session info:

Total Sweave time used: 11.046 sec. at Sat Aug 23 18:08:08 2014.

- R version 3.1.1 (2014-07-10), x86\_64-apple-darwin13.1.0
- Locale: en\_GB.UTF-8/en\_GB.UTF-8/en\_GB.UTF-8/C/en\_GB.UTF-8/en\_GB.UTF-8
- Base packages: base, datasets, graphics, grDevices, methods, stats, tcltk, utils
- Other packages: leaps 2.9, locfit 1.5-9.1, MASS 7.3-34, Matrix 1.1-5, mgcv 1.8-2, nlme 3.1-117, nonlinearTseries 0.2.2, rgl 0.94.1118, RHRV 4.0, sintro 0.1-3, tkrplot 0.0-23, TSA 1.01, tsseries 0.10-32, waveslim 1.7.3
- Loaded via a namespace (and not attached): grid 3.1.1, lattice 0.20-29, quadprog 1.5-5, tools 3.1.1, zoo 1.7-12

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Bibliography style: jss

CVS/Svn repository information:

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$HeadURL: svn+ssh://gsawitzki@scm.r-forge.r-project.org/svnroot/rhrv/gs/Rnw/heartrate.Rnw $
$Revision: 152 $
$Date: 2014-08-06 21:48:03 +0200 (Wed, 06 Aug 2014) $
$name: 
$Author: gsawitzki $
```

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