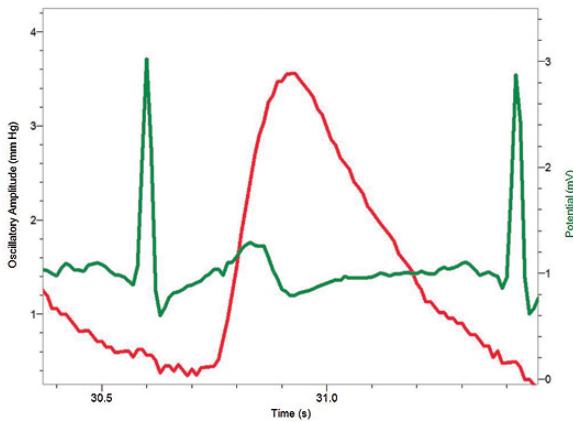


# PULSE AND MORE

GÜNTHER SAWITZKI



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*Corrections and comments are welcome.*

---

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## 1. UTILITIES

---

*Input*

```
system.time.start <- proc.time()
```

---

*Input*

```
# install.packages("sintro",repos="http://r-forge.r-project.org",type="source")
library(sintro) # for modified residual plot
```

---

*Input*

```
text.id <- function(x, y, ind, labels.id=rownames(x), adj.x = TRUE,
cex.id = 1.5, label.pos = c(4,2)) {
  x<-x[ind];y<-y[ind];labels.id<-labels.id[ind]
  labpos <-
    if(adj.x) label.pos[1+as.numeric(x > mean(range(x)))] else 3
  text(x, y, labels.id, cex = cex.id, xpd = TRUE,
        pos = labpos, offset = 0.25)
}
```

## 2. BLOOD PRESSURE

Blood pressure is considered by the WHO as one of the primary concerns Taylor [2013]. This should be put in a frame: the prevalent causes for premature death is that people just starve or do not have clean water. However, an estimated burden of 4.5% if premature deaths is attributed to high blood pressure.

Blood pressure, and related variables, can be evaluated without major intrusion. In developed countries, blood pressure monitors are commonly accessible.



FIGURE 1. Blood pressure monitor.

The definition of hypertension, and the classification are political decisions, laid down by the WHO in Taylor [2013].

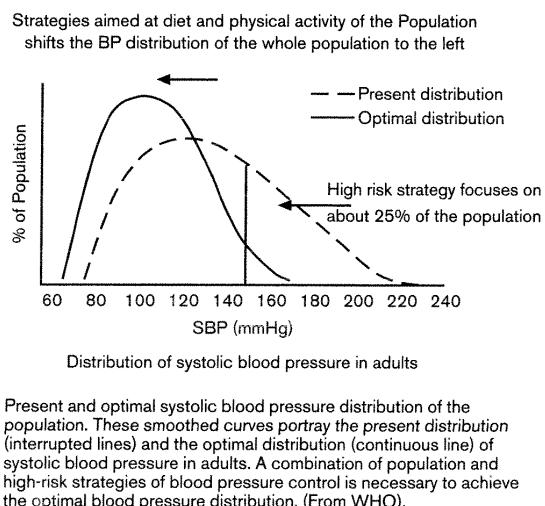


FIGURE 2. WHO suggestion.

Usual blood pressure monitors report three values: systolic and diastolic blood pressure, and pulse rate. It is common to record the time of measurement, and supply a memory for previous measurements.

The basic measurements reported usually are averages, and the sampling scheme is rarely documented.

---

**Exercise 1.** *There are common models, such as using a fixed time, or a fixed number of pulses. The next is adaptive, that is sampling until a good error rate is achieved.*

*Check your blood pressure monitor. Does it have a fixed time?*

*Prepare a record table, recording the basic information date, time, systolic and diastolic pressure, pulse, and the number of breaths during each one measurement.*

---



---

**Exercise 2.** *Record the blood pressure data during one hour, and during one day.*

*Specify a sampling scheme before you do the experiment, give a report and include information about the precision.*

*How many measurements are needed to analyse the within-hour variation?*

*How many measurements are needed to analyse the intra-day variation?*

*Specify sampling schemes for both tasks.*

---



---

**Exercise 3.** *Sample and document your personal within-hour variation.*

*Sample and document your personal intra-day variation.*

---



---

**Exercise 4.** *If you want to use your blood pressure data as a monitor, you have to specify warning limits.*

*Sample and document your personal for  $k = 14$  days, and specify “warning limits” that call you for a rest if exceeded (or the opposite, depending on your personality).*

*What is the history size  $k$  needed to get a warning interval that is covering 90% of the daily data to come?*

---

As always: to analyse data, you have to specify your ideas about the data generating mechanism. This idea may be incorrect, or coarse, but you should specify it.

As far as blood pressure is concerned, there are many ideas that are coarse.

What is circulation good for?

As far as circulation is concerned, this is very complex, and most ideas are just caricatures.

The most prominent idea is that circulation is to transport oxygen. If oxygen transport breaks down, the brain may suffer a major damage.

But this is a major break down which should not dominate the global picture. The common picture behind this is that circulation is to maintain a certain pressure level in the circulation system.

This is blended into other systems. Breathing obviously affects pressure. This is a very interesting influence, because breathing has two modes: it can be autonomous, and it can be controlled: so here is a direct way to exert influence on circulation.

Temperature is another related system, and you have choices from cloth to sauna to influence circulation. But you play on a different scale. If you take a pulse of 60/min as an example, respiration usually takes  $1/10 = 1/s$  as a scale, whereas after a sauna it usually is not in this range.

From a physiology point of view, prime difference is to see sympathetic effects (usually in the scale of over 5 heartbeats) and parasympathetic effects (usually in the scale of 1-2 heartbeats). (See 3).

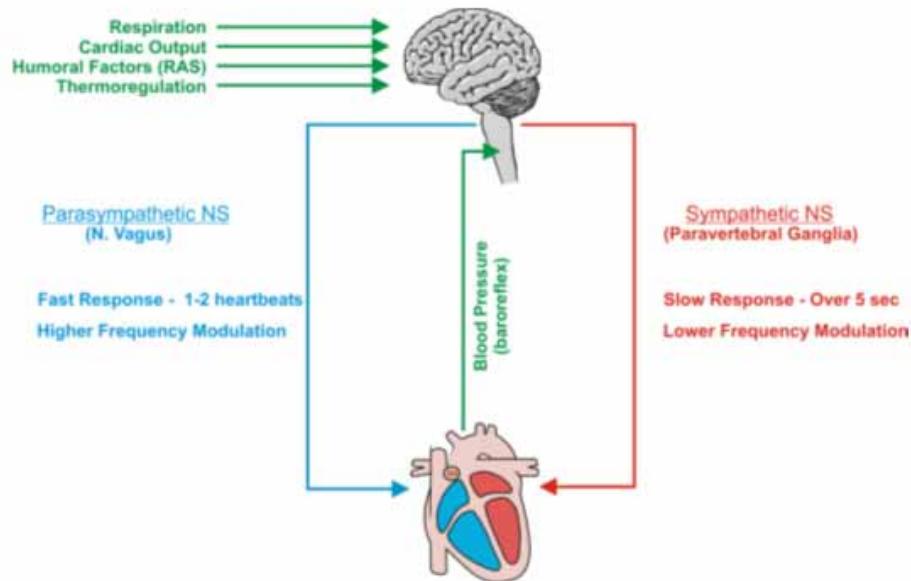


FIGURE 3. Pressure regulation. <http://www.biocomtech.com/hrv-science/heart-rate-variability-basics>

If you are familiar with physiology, parasympathetic and sympathetic nervous system will be familiar concepts. If you are not familiar with these, 4 on the next page may give some orientation.

The combined effect is a dynamically regulated system that tries to give adequate response to varying requirements. From a conceptual view, it may be helpful to think of a target blood pressure, varying corresponding to the requirements, and a response pressure as can be provided by the physiology to meet the requirements.

### 3. MONITORING BLOOD PRESSURE

Taking one sample of blood pressure and pulse values is a starting point. Viewing them as an evolving process is the next step.

From an abstract point, we have a process in time, with three components (systolic and diastolic pressure, pulse) at each time point. Re-thinking it for a moment, these are not component of the state. The basic state under inspection is the (continuous time) pressure. Systolic and diastolic pressure, and pulse, are summaries to be reported per measurement. This is a typical “imbedded instrument” situation. A lot of statistics is already imbedded in the monitor. The data we get are not raw data, but results of this statistics.

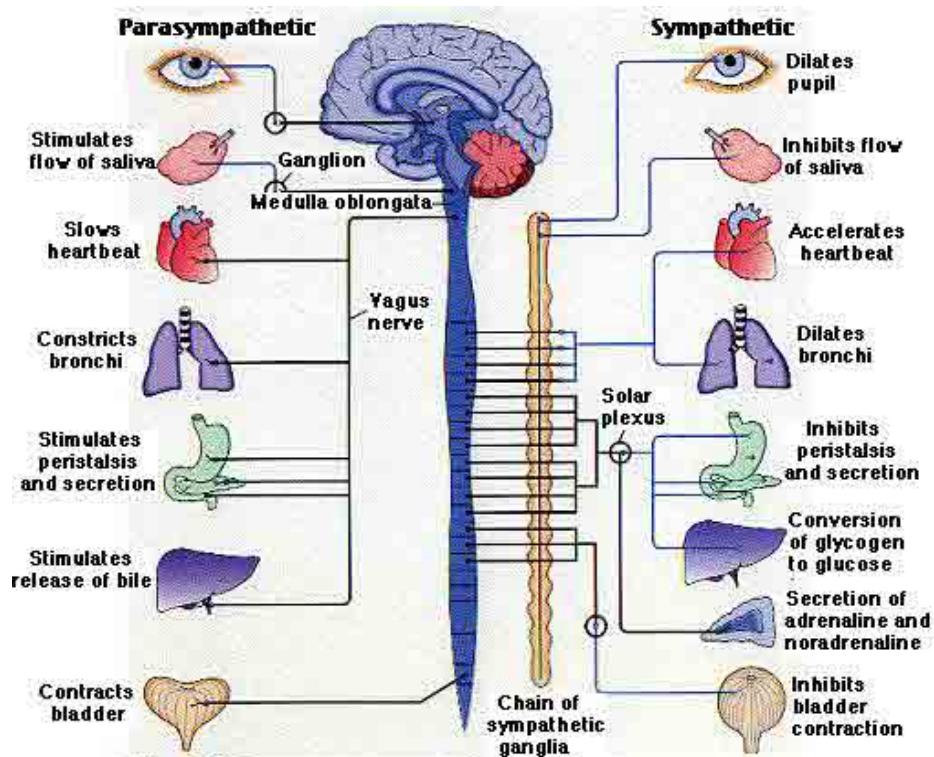


FIGURE 4. from: <http://www.biocomtech.com/hrv-science/heart-rate-variability-basics>

In this section, a standard measurement will mean a tuple

*timestamp      systolic      diastolic      pulse*

Monitoring blood pressure, we get a process sampled at discrete times. Even with good intentions, sampling will not be at regular times. So we are not in the range of time series data.

**Exercise 5.** We rarely get information of the actual interpretation of “pulse”.

Assume you have continuous time information of systolic and diastolic pressure. How would you define “pulse”? Give an algorithm.

However, some concepts from time series may be helpful. We may look at the process in terms of frequencies. A first simplification: heart beat add a first component. Taking 60 beats/minute (to make number simple) we have a beat per second, so a frequency in the order of  $\approx 1$  Hz. There is a very close relation between circulation and respiration. In regulatory aspects, circulation is regulated to support the  $O_2/CO_2$  exchange. By mere mechanic pressure, respiration activity directly interact with the heart muscle. We should be aware of this relation. It would be possible to record respiration by the monitor. Unfortunately, current devices do not support this. Respiration would give a contribution on the order of  $\approx 0.1$  Hz. There is a common well known rhythmic behaviour in the circulation in the 10s range, that is with a frequency of  $\approx 0.01$  Hz. it seems there is a very universal activity rhythm in the range of 30-45 min.

Taking a (not so large) step is the circadian rhythm.

Studying circulation, we should know about these rhythms. Most important, we should not care about them. But we must find ways to handle them.

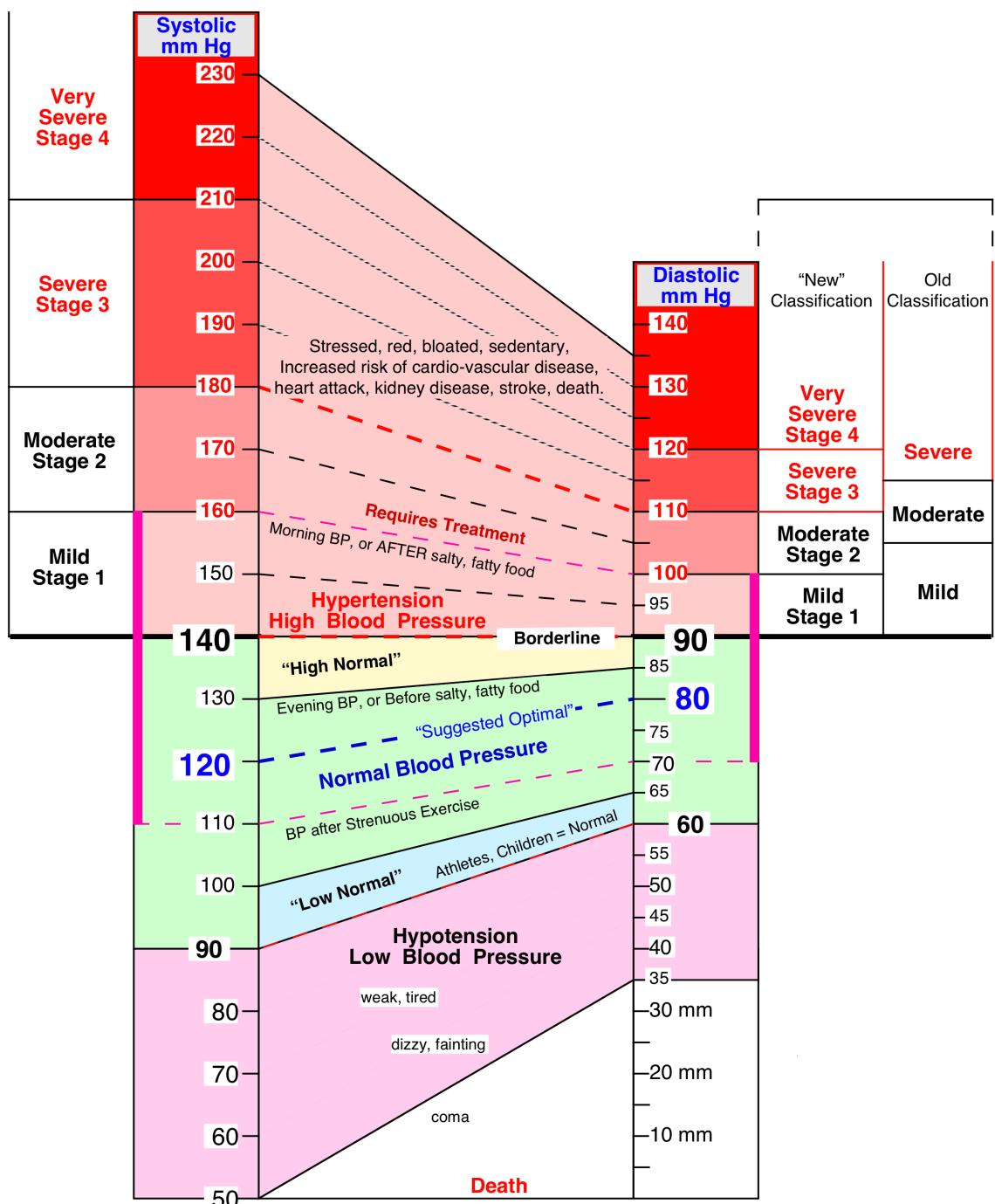


FIGURE 5. Blood pressure chart. Modified from: <http://www.vaughns-1-pagers.com/medicine/blood-pressure.14.pdf>

We start with the idea of circadian rhythm. This is present for everyone. The “internal clock” is a helpful concept. It is more important for people under treatment.

See 6 on the following page.

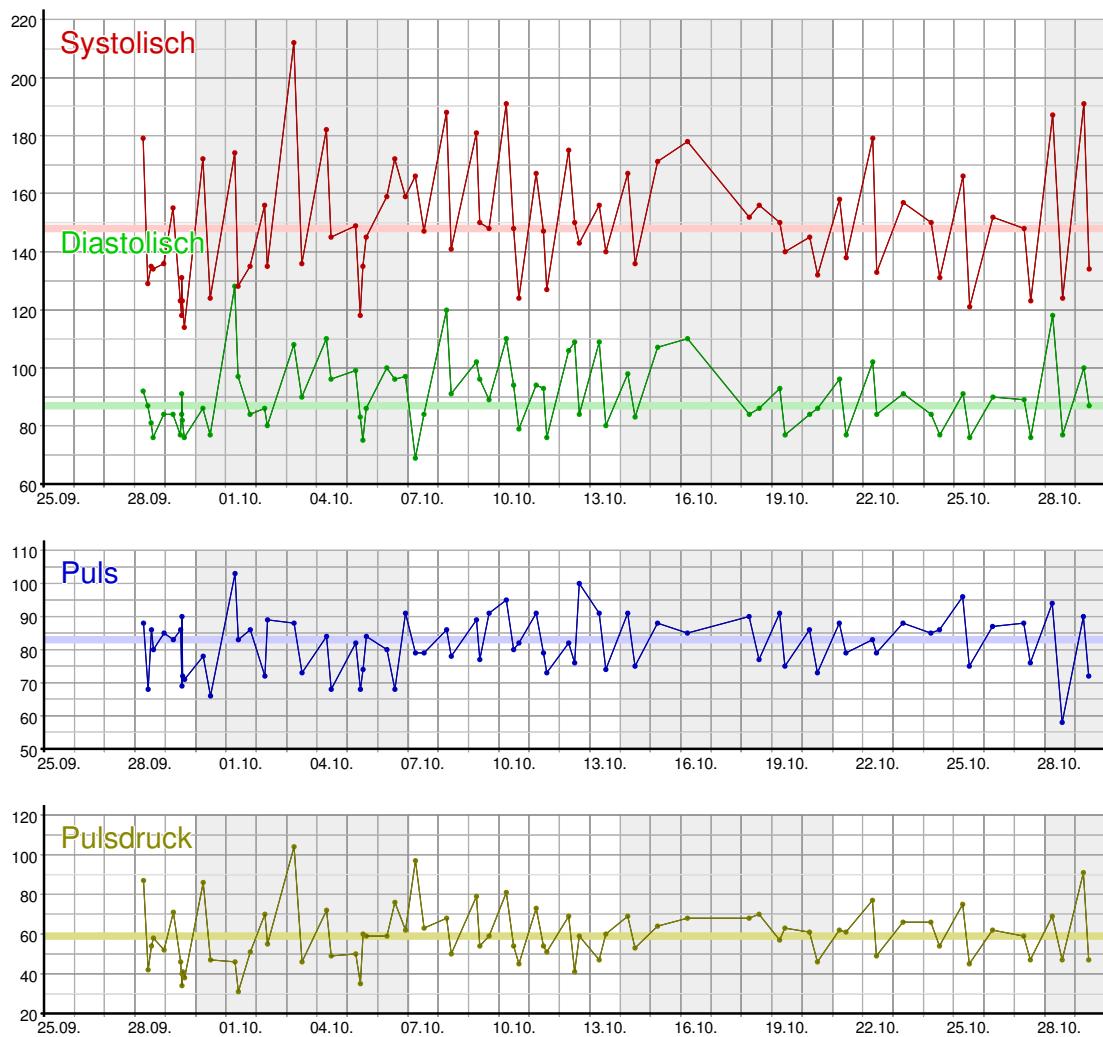


FIGURE 6. Blood pressure monitoring with hypertension in the morning measurements, and under treatment later in the day. Provided by <http://BlutdruckDaten.de>.

**Exercise 6.** Assume you have a series of standard measurements.

Find a rule to identify “morning measurements”.

Hint: First, find a rule to define “morning measurements”. It is not sufficient to take the first measurement on a day. Some people are awake after midnight.

Then: find a rule to define “before first medicamentation”.

These rules could be avoided, if the measurements are annotated. Give a proposal how to formulate this for the user.

**Exercise 7.** Assume you have a series of standard measurements.

Filter the data for “morning measurements”.

The null distribution is now a iid series with three components.

**3.1. Data Sets & Software.** Individual data can be collected easily. Extensive support is available from <http://www.blutdruckdaten.de> (in German) or <http://www.bloodpressuredb.com/> (in English).

See <http://www.statlab.uni-Heidelberg.de/data/pulse/> for more information.

#### 4. ECG

The electrocardiogram (ECG) represents the nervous heart activity by recording the average activity picked up using electrodes.



FIGURE 7. Normal ECG

There is a rather clear picture how various parts of the heart activity contribute to this picture. As always the real image is more complicated. Besides regular systoles triggered by impulses from the sinus node (sinoatrial node) in the heart, the “pacemaker”, there may be ectopic beats of various origin. The regular picture is the exception rather than the rule.

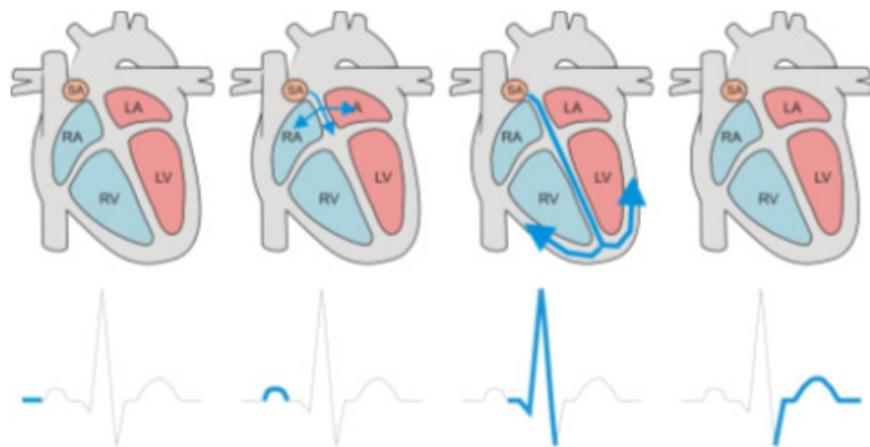


FIGURE 8. Schematic explanation of RA, LA, RV, LV parameters. <http://www.biocomtech.com/hrv-science/heart-rate-variability-basics>

A single ECG event is composed of several components that have a small time delay, so they appear as a distinct pattern. See Figure 9 on the next page.

The core may be simplified. This simplification, the QRS complex, has a typical duration: if synchronisations are working efficiently, the QRS complex is 80 to 120 ms in duration.

The simple picture is that the sinoatrial node responds to information from the autonomous nervous system and other regulatory information. A heart beat is triggered by an impulse originating from the sinoatrial node and then propagating as in Figure 8 resulting in an electrical potential picked up by electrodes, resulting in Figure ?? on page ??.

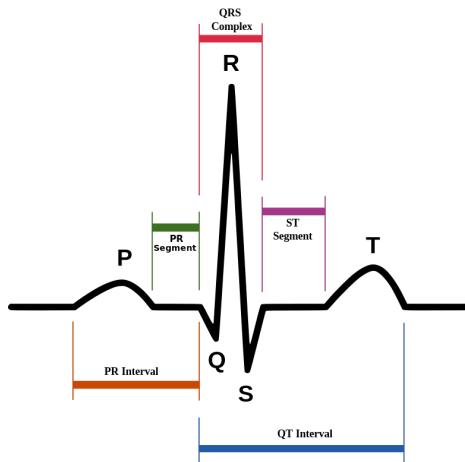


FIGURE 9. Schematic representation of normal ECG

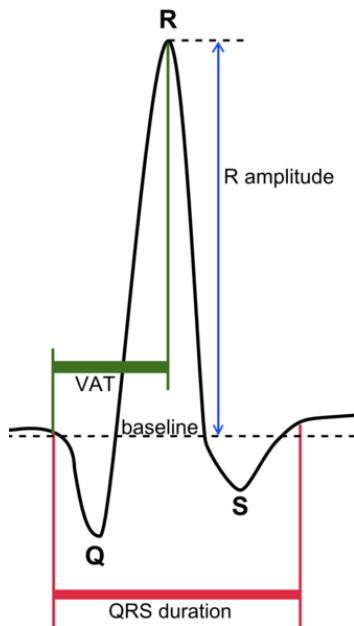


FIGURE 10. Close-up: Simplified schematic representation of QRS metrics

However, the activation wave may be incomplete, or “out of place” (ectopic), or distorted. On a very low level, ECG recordings are first annotated, and only after this the data are evaluated.

In a medical setting, several electrodes are used to get a detailed picture. Careful placement of the electrodes and knowledge of the electrophysiology of the body can help to reconstruct a localised and individualised version of 8 on the facing page. For our purposes, it is enough to look at one pair of electrodes.

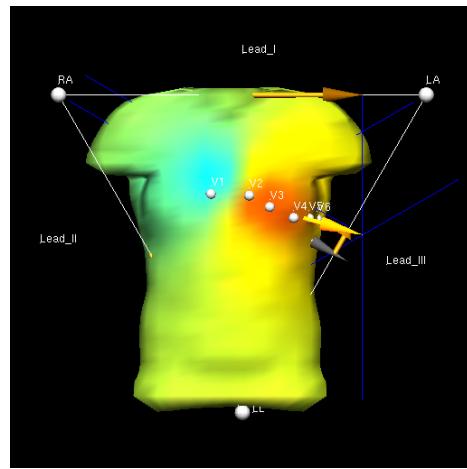


FIGURE 11. ECG: electrode positions and body electrophysiology.  
[http://cmisss.bioeng.auckland.ac.nz/development/examples/a/ecg\\_lab/index.html](http://cmisss.bioeng.auckland.ac.nz/development/examples/a/ecg_lab/index.html)

## 5. HEART RATE VARIABILITY

An average heart rate of 60 beats per minute (bpm) does not mean that the interval between successive heartbeats would be exactly 1.0 sec, instead they may fluctuate/vary from 0.5 sec up to 2.0 sec.

Under healthy conditions, a heart does not beat regularly, but comes with a wealth of rhythms.

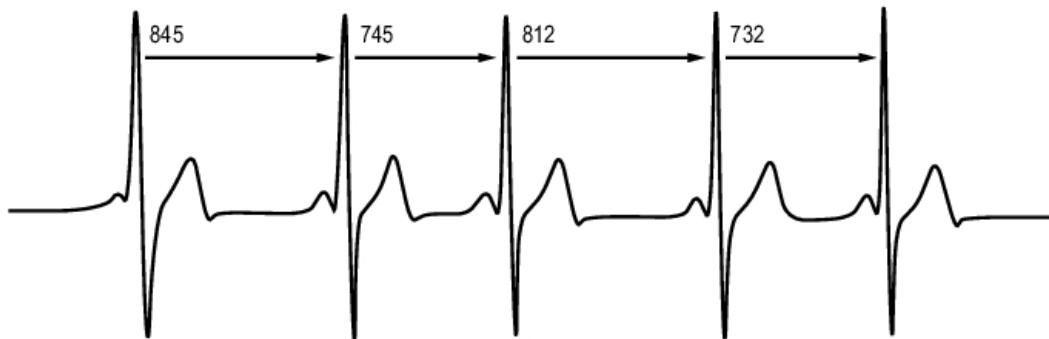


FIGURE 12. Heart rate variability. Time in ms.

**ToDo:**  
et al. [1981]

When studying heart rate variability, the compound signal is reduced to sequence of time differences between two heart beats. Physiologically, in a textbook ECG, the P signal is the first indicator of a new heart beat. So the P-P intervals between onsets of the P wave would be the obvious seduction for studying heart rate variability.

However, the signal to noise ratio for peak to peak P-P in general is very low, and detecting the onset of the P wave brings additional stochastic variation which does not occur for the R component.

By convention, the R-R intervals are used as a base for the analysis of heart rate variability. The signal to noise ratio for P-P in general is very low, compared to the R-R signal to noise ratio. The P-R delay is rather stable. So the peak to peak R-R intervals may be preferable.

**Exercise 8.** How do you filter P-P intervals (or R-R intervals) from the data. Hint. Do no re-invent the wheel. Look up for the keywords “pattern recognition” and “signal detection”

**Exercise 9.** You need information on data access for this exercise. See Subsection 5.1 on the next page. Compare the distribution information from P-P intervals to that from R-R intervals for the data sets accessible to you.

So to study the heart rate variability, the raw ECG data are conceptually reduced to the sequence of R-peaks, or rather the R-R intervals. Technically, the time differences between two consecutive R-peaks is recorded, the RR-interval.

From a mathematical point, this is a random point process. This imposes its own challenges for analysis. A consensus paper, from the application side, is Camm *et al.* [1996]. See in particular Section 3: *Measurement of Heart Rate Variability* with a subsection on statistical methods. A newer review article with an extended summary of available methods is in Acharya *et al.* [2006].

The statistical possibilities depend on the data available. Typically the raw data as recorded are ECG data, that is potential differences by time. Traditional devices recorded it as an analog impulse, that is the convolution of the original impulse with a device dependent kernel. Digital devices provide the signal recorded at a regular intervals, sampled at 128 Hz by first generation devices. 1000 Hz, that is sampled on the ms scale, is common by now. However the data may have been compressed before recording. So you may get the RR intervals sampled by 1 kHz, but these are generated from the original data and you should be aware of potential artefacts.

In principle, you would be interested in the time between subsequent heart beats. Using the ECG however the onset is hard to localize. The main peak, the R component of the signal, is much easier to localize. So the common pragmatic solution is to first clean up the ECG record, removing spurious pulses and other artefacts, preferably with a robust algorithm. The next step is to locate the QRS pattern, or some extensions. Pattern detection algorithms are first choice for this step. Only after the QRS group has been isolated, the R time is read off. Conventionally already at this step the RR differences are taken. The resulting input data set for RR analysis is the sequence of these interval lengths.

The statistical challenge is to represent the variability of the RR point process. This has two aspects. Looking at the abstract side: how do you characterise the variability of a point process? Looking at the physiological side: what are the parameters of the process that are physiologically relevant? Neither the statistical problem nor the application question seems to have a satisfactory answer so far.

Of course there are dumb answers: if quadratic variation were relevant, we could calculate the variance of successive differences, or we could use a frequency approach looking at the power spectrum. Can we do better?

### 5.1. Data Sets & Software. R Heart Rate Variability Project:

[<http://rhrv.r-forge.r-project.org>](http://rhrv.r-forge.r-project.org)

PysioNet Interbeat (RR)Course Material:

[\(http://physionet.org/events/hrv-2006/\)](http://physionet.org/events/hrv-2006/)

PysioNet Interbeat (RR) Data Bases:

[\(http://physionet.incor.usp.br/physiobank/database/#rr\)](http://physionet.incor.usp.br/physiobank/database/#rr)

For signal representation, we use a common layout.

---

	<i>Input</i>	
<pre>plotsignal &lt;- function (signal) {</pre>		
<pre>  par(mfrow=c(1,2))</pre>		
<pre>  plot(signal, col=rgb(0,0,1,0.4), pch=20, xlab="t" )</pre>		
<pre>  plot(signal, type="l",</pre>		
<pre>    main=deparse(substitute(signal)), xlab="t", col=rgb(0,0,0,0.4))</pre>		

---

```
    points(signal, col=rgb(0,0,1,0.4), pch=20 )
}
```

## 5.2. HRV Data.

---

*Input*

```
library(RHRV)
#load("/data/pulse/rhrv/pkg/data/HRVData.rda")
#load("/data/pulse/rhrv/pkg/data/HRVProcessedData.rda")
#####
hrv.data = CreateHRVData()
hrv.data = SetVerbose(hrv.data, FALSE )
hrv.data = LoadBeatAscii(hrv.data, "example.beats",
    RecordPath = "/data/pulse/rhrv/tutorial/beatsFolder")
#      RecordPath = "beatsFolder")

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

---

*Input*

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

See Figure 13.

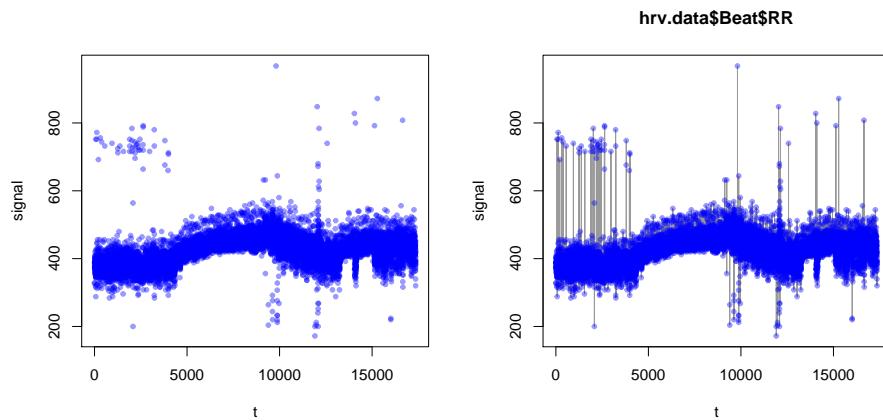


FIGURE 13. RHRV tutorial example.beats. Signal and linear interpolation.

Data based on beat counts are not equidistantly sampled. *RHRV* keeps the time  $t_i$  as a separate component.

**Exercise 10.** Does the sequence  $RR_i$  need a compensation for  $t_i$ . How does an index based evaluation differ from a time based evaluation? Which one is to be preferred?

---

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

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

**ToDo:** What about outliers at approximately  $2*RR$ ? Can this be an indicator of pre-processing or many impulses?

where  $RR_i$  is the  $i^{th}$  RR interval length. Taking this 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.

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.

---

*Input*

```
hrv.data <- BuildNIDHR(hrv.data)
HRRV <- hrv.data$Beat$HRRV
```

---

*Input*

```
plotsignal(HRRV)
```

---

See Figure 14,

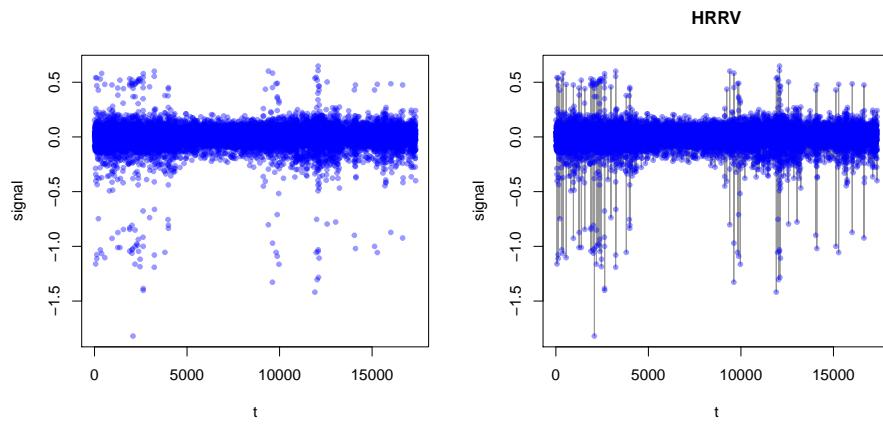


FIGURE 14. RHRV tutorial example.beats. Differences HRRV Signal and linear interpolation.

---

**Exercise 11.** Does the sequence  $HRRV_i$  need a compensation for  $t_i$ . How does an index based evalutaion differ from a time based evaluation? Which one is to be preferred?

---



---

**Exercise 12.** Compare the HRRV with the RR signal. Find an improved way to represent the pulse by comparing both sequences.

---

The process is not stationary or periodic. So we use Takens' delay embedding state (re)construction Takens [1981] and a recurrence plot Eckmann *et al.* [1987] to inspect the process.

To display the Takens state space, we us a variant of pairs().

---

*Input*

```
statepairs <- function(states, rank=FALSE){
  main <- paste("Takens states:", deparse(substitute(states)), "\n",
               "n=", dim(states)[1], " dim=", dim(states)[2])
  if (rank) {states <- apply(uniftakens, 2, rank, ties.method="random")}
  main <- paste(main, " ranked")}
```

---

**ToDo:** the takens state plot may be critically affected by outliers. Find a good rescaling.

```

    pairs(states,
      main=main,
      col=rgb(0,0,0,0.2))
}

```

`showrqa()` is a hack to report RQA information.

To allow experimental implementations, functions from `nonlinearTseries` are aliased here.

	<i>Input</i>	
	local.buildTakens <- buildTakens	
	<i>Input</i>	
	local.findAllNeighbours <- nonlinearTseries:::findAllNeighbours	
	<i>Input</i>	
	#non-sparse variant	
	#local.recurrencePlotAux <- nonlinearTseries:::recurrencePlotAux	
	local.recurrencePlotAux=function(neighs, dim=NULL, lag=NULL, radius=NULL){	
	# just for reference. This function is inlined	
	neighbourListNeighbourMatrix = function(){	
	#neighs.matrix = Diagonal(ntakens)	
	for (i in 1:ntakens){	
	if (length(neighs[[i]])>0){	
	for (j in neighs[[i]]){	
	neighs.matrix[i,j] = 1	
	}	
	}	
	return (neighs.matrix)	
	}	
	ntakens=length(neighs)	
	neighs.matrix <- matrix(nrow=ntakens,ncol=ntakens)	
	#neighbourListNeighbourMatrix()	
	#neighs.matrix = Diagonal(ntakens)	
	for (i in 1:ntakens){	
	neighs.matrix[i,i] = 1 # do we want the diagonal fixed to 1	
	if (length(neighs[[i]])>0){	
	for (j in neighs[[i]]){	
	neighs.matrix[i,j] = 1	
	}	
	}	
	}	
	}	
	main <- paste("Recurrence Plot: ",	
	deparse(substitute(neighs))	
	)	
	more <- NULL	
	#use compones of neights if available	
	if (!is.null(dim)) more <- paste(more," dim:",dim)	
	if (!is.null(lag)) more <- paste(more," lag:",lag)	
	if (!is.null(radius)) more <- paste(more," radius:",radius)	
	if (!is.null(more)) main <- paste(main,"\\n",more)	
	# need no print because it is not a trellis object!!	

```

#print(
  image(x=1:ntakens, y=1:ntakens,
        z=neighs.matrix,xlab="i", ylab="j",
        col="black",
        #xlim=c(1,ntakens), ylim=c(1,ntakens),
        useRaster=TRUE,  #? is this safe??
        main=main
      )
#)
}

```

We should expect the breathing rhythm, so a time lag in the order of 10 is to be expected.

**ToDo:** fix default setting for radius. Eckmann uses nearest neighbours with NN=10

To reduce the computing time used, we limit the analysis to the head of the series.

---

*Input*

```
#nsignal=1024 ## 33s
#nsignal=2*1024 ## 89s
nsignal=4*1024 ## 542.516 s
```

---

*Input*

```
laptme <- function(){
  return(round(structure(proc.time() - chunk.time.start, class = "proc_time")[3],3))
  chunk.time.start <- proc.time()
}
```

---

*Input*

```
hrvRRVtakens2 <- local.buildTakens( time.series=HRRV[1:nsignal], embedding.dim=2, time.lag=1)
load(file="hrvRRVneighs2.RData")
```

---

*Input*

```
hrvRRVneighs2 <-local.findAllNeighbours(hrvRRVtakens2[-(1:2),], radius=0.125)
save(hrvRRVneighs2, file="hrvRRVneighs2.Rdata")
```

Time used: 3.138 sec.

---

*Input*

```
showrqa(hrvRRVtakens2[-(1:2),], radius=0.125, do.hist=FALSE)
```

---

*Output*

```
hrvRRVtakens2[-(1:2), ] n= 4093 Dim: 2
Radius: 0.125 Recurrence coverage REC: 0.531
Determinism: 0.945 Laminarity: 0.816
DIV: 0.014
Trend: 0 Entropy: 2.437
Diagonal lines max: 70 Mean: 5.737 Mean off main: 5.734
Vertical lines max: 78 Mean: 4.539
```

---

*Input*

```
local.recurrencePlotAux(hrvRRVneighs2, dim=2, radius=0.125)
```

Time used: 205.347 sec.

---

*Input*

```
hrvRRVtakens4 <-
  local.buildTakens( time.series=HRRV[1:nseries], embedding.dim=4, time.lag=1)
statepairs(hrvRRVtakens4)
```

See Figure 15

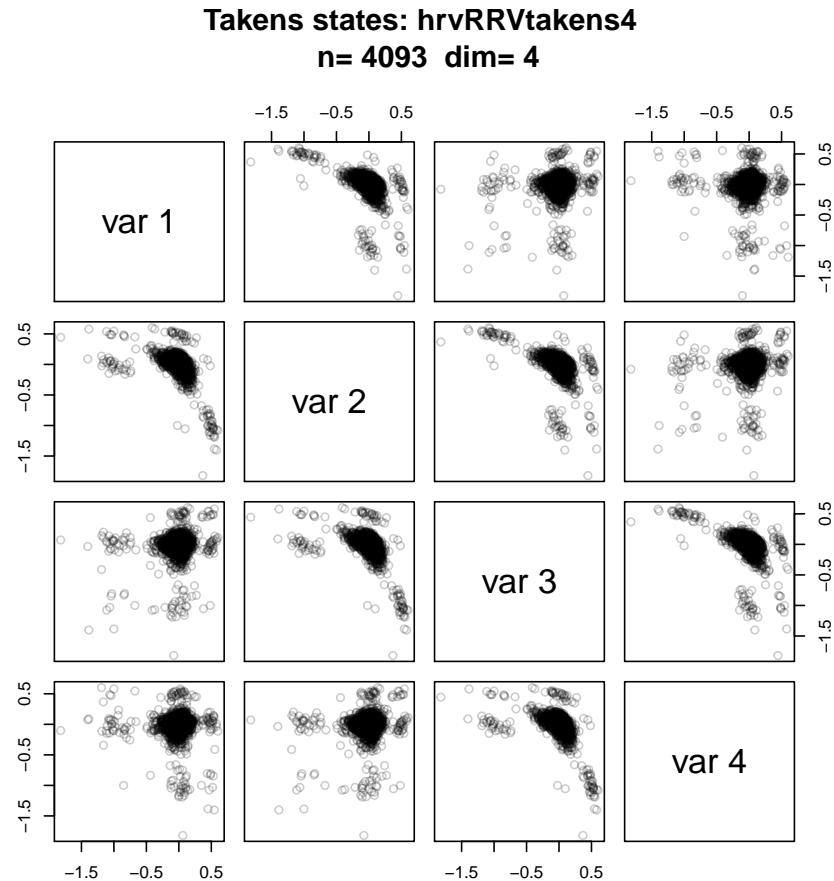


FIGURE 15. RHRV tutorial example.beats. HRRV Differences. Time used: 208.065 sec.

---

**Exercise 13.** Identify the components in the Takens state plot, and trace them in the signal and recurrence plots, using colour and linking.

---



---

`Input`  
`hrvRRVneighs4 <- local.findAllNeighbours(hrvRRVtakens4[-(1:2),], radius=0.125)`

Time used: 209.19 sec.

---

`Input`  
`local.recurrencePlotAux(hrvRRVneighs4, dim=4, radius=0.125)`

Time used: 43.695 sec.

---

`Input`  
`hrvRRVtakens6 <- local.buildTakens( time.series=HRRV[1:nseries], embedding.dim=6, time.lag=1)`  
`load(file="hrvRRVneighs6.RData")`

---

*Input*

```
hrvRRVneighs6 <- local.findAllNeighbours(hrvRRVtakens6[-(1:2),], radius=0.125)
save(hrvRRVneighs6, file="hrvRRVneighs6.Rdata")
```

---

Time used: 0.354 sec.

---

*Input*

```
showrqa(hrvRRVtakens6[-(1:2),], radius=0.125, do.hist=FALSE)
```

---

*Output*

```
hrvRRVtakens6[-(1:2), ] n= 4089 Dim: 6
Radius: 0.125 Recurrence coverage REC: 0.206
Determinism: 0.956 Laminarity: 0.544
DIV: 0.015
Trend: 0 Entropy: 2.52
Diagonal lines max: 66 Mean: 6.108 Mean off main: 6.101
Vertical lines max: 53 Mean: 3.392
```

---

*Input*

```
local.recurrencePlotAux(hrvRRVneighs6, dim=6, radius=0.125)
```

---

Dim=6. Time used: 31.033 sec.

---

*Input*

```
hrvRRVtakens8 <- local.buildTakens( time.series=HRRV[1:nseries], embedding.dim=8, time.lag=1)
load(file="hrvRRVneighs8.RData")
```

---



---

*Input*

```
hrvRRVneighs8 <- local.findAllNeighbours(hrvRRVtakens8[-(1:2),], radius=0.125)
save(hrvRRVneighs8, file="hrvRRVneighs8.Rdata")
```

---

Time used: 0.33 sec.

---

*Input*

```
showrqa(hrvRRVtakens8[-(1:2),], radius=0.125, do.hist=FALSE)
```

---

*Output*

```
hrvRRVtakens8[-(1:2), ] n= 4087 Dim: 8
Radius: 0.125 Recurrence coverage REC: 0.133
Determinism: 0.961 Laminarity: 0.466
DIV: 0.016
Trend: 0 Entropy: 2.568
Diagonal lines max: 64 Mean: 6.329 Mean off main: 6.317
Vertical lines max: 49 Mean: 3.175
```

---

*Input*

```
local.recurrencePlotAux(hrvRRVneighs8, dim=8, radius=0.125)
```

---

Dim=8. Time used: 23.226 sec.

---

*Input*

```
hrvRRVtakens12 <-
  local.buildTakens( time.series=HRRV[1:nseries], embedding.dim=12, time.lag=1)
  load(file="hrvRRVneighs12.RData")
```

---

---

*Input*

```
hrvRRVneighs12 <-
  local.findAllNeighbours(hrvRRVtakens12[-(1:2),], radius=3/16)
  save(hrvRRVneighs12, file="hrvRRVneighs12.Rdata")
```

---

Time used: 23.7 sec.

---

*Input*

```
showrqa(hrvRRVtakens12[-(1:2),], radius=3/16, do.hist=FALSE)
```

---

*Output*

```
hrvRRVtakens12[-(1:2), ] n= 4083 Dim: 12
Radius: 0.1875 Recurrence coverage REC: 0.293
Determinism: 0.992 Laminarity: 0.726
DIV: 0.007
Trend: 0 Entropy: 3.421
Diagonal lines max: 145 Mean: 12.946 Mean off main: 12.935
Vertical lines max: 96 Mean: 4.926
```

---

*Input*

```
local.recurrencePlotAux(hrvRRVneighs12, dim=12, radius=3/16)
```

---

Time used: 38.76 sec.

---

*Input*

```
hrvRRVtakens16 <- local.buildTakens( time.series=HRRV[1:nsignal],embedding.dim=16,time.lag=1)
load(file="hrvRRVneighs16.RData")
```

---



---

*Input*

```
hrvRRVneighs16 <-local.findAllNeighbours(hrvRRVtakens16[-(1:2),], radius=3/16)
  save(hrvRRVneighs16, file="hrvRRVneighs16.Rdata")
```

---

Time used: 39.115 sec.

---

*Input*

```
showrqa(hrvRRVtakens16[-(1:2),], radius=3/16, do.hist=FALSE)
```

---

*Output*

```
hrvRRVtakens16[-(1:2), ] n= 4079 Dim: 16
Radius: 0.1875 Recurrence coverage REC: 0.207
Determinism: 0.994 Laminarity: 0.666
DIV: 0.007
Trend: 0 Entropy: 3.476
Diagonal lines max: 141 Mean: 13.607 Mean off main: 13.59
Vertical lines max: 84 Mean: 4.371
```

---

*Input*

```
local.recurrencePlotAux(hrvRRVneighs16, dim=16, radius=3/16)
```

---

Time used: 89.507 sec.

---

**Exercise 14.** What is the most informative dimension for this data set, based on the recurrence plots and RQA data?

---

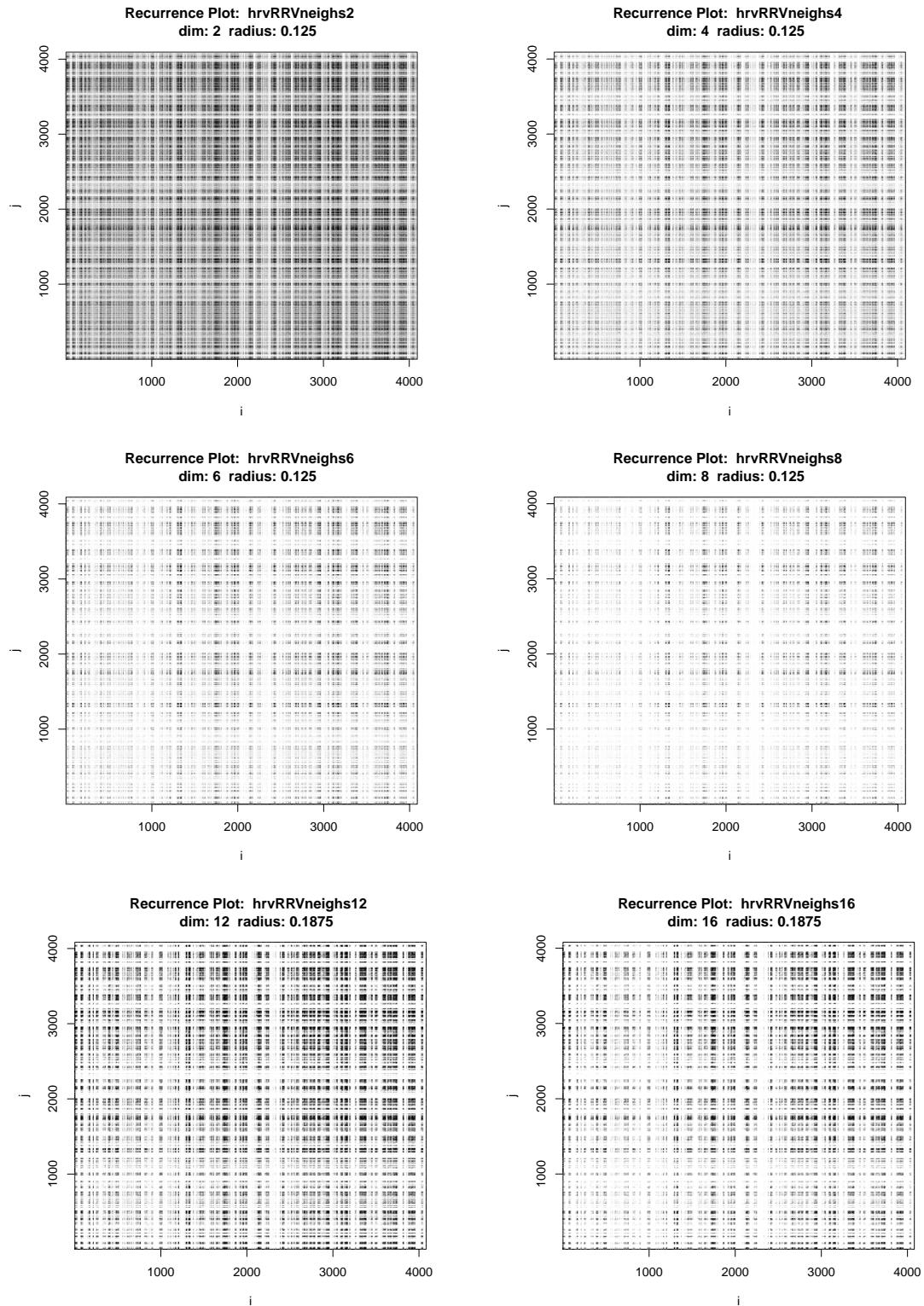


FIGURE 16. Recurrence Plot. Example case: RHRV tutorial example.beats.  
Dim=2, 4, 6, 8, 12, 16. HRRV Differences. Time used: 89.507 sec.

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R session info:

Total Sweave time used: 480.372 sec. at Thu Feb 20 11:44:09 2014.

- R version 3.0.2 (2013-09-25), x86\_64-apple-darwin10.8.0
- 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, Matrix 1.1-2, mgcv 1.7-28, nlme 3.1-113, nonlinearTseries 0.2, rgl 0.93.996, RHRV 4.0, sintro 0.1-3, tkrplot 0.0-23, TSA 1.01, tseries 0.10-32, waveslim 1.7.3
- Loaded via a namespace (and not attached): grid 3.0.2, lattice 0.20-25, quadprog 1.5-5, tools 3.0.2, zoo 1.7-11

LATEX information:

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textheight: 9.21922in
```

Svn repository information:

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Generated by Sweave from:
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Revision: 1.12
Date: 2013/12/12 19:12:37
name:
Author: j40
$Source: /u/math/j40/cvsroot/data/pulse/Rnw/pulse.Rnw.tex,v $
$Revision: 1.12 $
$Date: 2013/12/12 19:12:37 $
$name: $
$Author: j40 $
```

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