STATISTICAL DATA ANALYSIS: RECURRENCE PLOT

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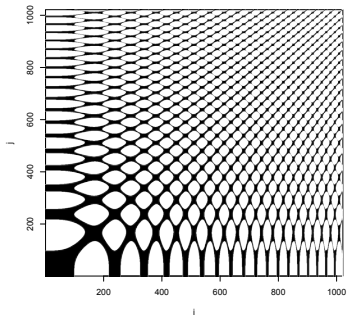

Contents

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1. Background

1.1. **Takens' Recurrence States.** Recurrence plots have been introduced in an attempt to understand near periodic behaviour in hydrodynamics, in particular the transition to turbulence. On the one hand, and extended theory on dynamical systems was available, covering deterministic models. A fundamental concept is that at a certain time a system is in some state, and developing from this. Defining the proper state space is a critical step in modelling.

The other toolkit is that of stochastics processes, in particular Markov models. Classical time series assumes stationarity, and this is obviously not the way to go. A fundamental idea for Markov models is that the system state is seen in a temporal context: you have a Markov process, if you can define a (non-anticipating) state that has sufficient information for prediction: given this state, the future is independent from the past.

Recurrence, coming back to some state, is often a key to understand a near periodic system. A classical field is the movement of celestial bodies.

Hydrodynamics is a challenging problem. Understanding planetary motion is a historical challenge, and may be useful as an illustration.

As a simple illustration, let $x = (x_i)$ be a sequence, maybe near periodic. For now, think of i as a time index.

Recurrence plots have two steps. The first was a bold step by Floris Takens. If you do not know the state space of a system, for a choice of "dimension" d, take the sequence of d tuples taken from your data to define the states.

$$u_i = (x_i, \ldots, x_{i+(d-1)})$$

This is Takens' delay embedding state (re)construction Takens [1981].

As a mere technical refinement: you may know that your data are a flattened representation of m dimensional data. So you take

$$u_i = (x_i, x_{i+m} \ldots, x_{i+(d-1)*m}).$$

ToDo: add support for higher dimensional signals

This may be a relict of FORTRAN times, where it was common to flatten two-dimensional structures by case.

Conceptually, you define states by observed histories. For classical Markov setup, the state is defined by the previous information x_{i-1}, but for more complex situations you may have to step back in the past. Finding the appropriate d is the challenge. So it may be appropriate to view the Takens states as a family, indexed by the time scope d. The rest is structural information how to arrange items.

Of course it is possible to compress information here, sorting states and removing duplicates. Keeping the original definition as the advantage that we have the index i, so that u_i is the state at index position i.

But the states may have an inherent structure, which we may take into account or ignore. Since for this example, we are just in 4-dimensional space, marginal scatterplots may give enough information.

Takens states are vectors in M dimensions. There are standard statistical techniques to visiualize aspects of M dimensional vectors, at least for not too high dimension. One is the draftsman's plot, a scatterplot matrix by marginals. For Takens states, this is

implemented as *statepairs()*. The other is coplots, a variant of scatterplot matrix by marginals, conditionend by one or two additional variables. For Takens states, this is implemented as *statecoplots()*

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

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

By convention, the states are defined using overlapping sliding windows. This imposes considerable dependence between the states: one state is the shifted previous states, with only the end sub-state replaced. As an option, the states can be subsampled, using only non-overlapping ranges.

The Takens states may be stationary, that is asymptotically the states starting at i do not depend on i. In this case, the first row (or column) contains all information, and pairs plot form an inclusion sequence by. In general, we will use state plots in 4 or 8 dimensions, where the limits are suggested by the print area.

ToDo: consider dimension-adjusted radius

1.2. **Recurrence Plots.** The next step, taken in Eckmann *et al.* [1987] was to use a two dimensional display. Take a scatterplot with the Taken's states a marginal. Take a sliding window of your process data, and for each i, find the "distance" of u_i from and to any of the collected states. If the distance is below some chosen threshold, mark the point (i, j) for which u(j) is in the ball of radius r(i) centred at u(i).

The original publication Eckmann *et al.* [1987] actually used a nearest neighbourhood environment to cover about 10 data points.

The construction has considerable arbitrary choices. The critical radius may depend on the point i. In practical applications, using a constant radius is a common first step. Using a dichotomous marking was what presumably was necessary when the idea was introduced. With todays technology, we can allow a markup on a finer scale, as has been seen in Orion-1.

ToDo: support distance instead of 0/1 indicators

We can gain additional freedom by using a correlation view: instead of looking from one axis, we can walk along the diagonal, using two reference axis.

Helpful hints how to interpret recurrence plots are in "Recurrence Plots At A Glance" `<http://www.recurrence-plot.tk/glance.php>`.

1.3. **Recurrence Quantification Analysis.** While visual inspection is the prime way to assess recurrence plots, quantification of some aspects revealed of the plot may be helpful. A collection of indices is provided by a recurrence quantification analysis (RQA) Zbilut and Webber [2006], Webber Jr and Zbilut [2005].

See Table 1 on the following page.

2. R Setup

Input

```
save.RNGseed <- 87149 #.Random.seed
save.RNGkind <- RNGkind()
set.seed(save.RNGseed, save.RNGkind[1])
save.RNGkind
```

Output

TABLE 1. Recurrence Quantification Analysis (RQA)

REC	Recurrence. Percentage of recurrence points in a recurrence Plot.
DET	Determinism. Percentage of recurrence points that form diagonal lines.
LAM	Percentage of recurrent points that form vertical lines.
RATIO	Ratio between *DET* and *RR*.
Lmax	Length of the longest diagonal line.
Lmean	Mean length of the diagonal lines. The main diagonal is not taken into account.
DIV	Inverse of *Lmax*.
Vmax	Longest vertical line.
Vmean	Average length of the vertical lines. This parameter is also referred to as the Trapping time.
ENTR	Shannon entropy of the diagonal line lengths distribution
TREND	Trend of the number of recurrent points depending on the distance to the main diagonal
diagonalHistogram	Histogram of the length of the diagonals.
recurrenceRate	Number of recurrent points depending on the distance to the main diagonal.

```
[1] "Mersenne-Twister" "Inversion"
```

Input

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

Input

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

2.0.1. *Takens States.* Takens states are represented as a matrix, one state per row. The number of colums is the imbedding dimension. If present, the *time.lag* attribute is the lag parameter, *id* an identification string for the basic data set.

ToDo: improve choice of alpha

Input

```
alpha=0.5
```

statepairs *Show marginal scatterplots of Takens states*

Usage.

```
statepairs(states, main,
range  = NULL,
rank = FALSE, nooverlap = FALSE,
col, \ldots)
```

Arguments.

states	A matrix: Takens states by dimension, one state per row.
main	Optional: the main header.
range	Optional: an interval selecting values to be displayd.
rank	An experimental variant. If *rank*, the values are rank transformed.
nooverlap	An experimental variant. If *nooverlap*, the cases are subsampled by dimension.
col	The current choice is $rgb(0,0,0,\alpha = \sqrt{\frac{1}{nr\ states}})$ as a default.

ToDo: colour by time

Input

```
statepairs <- function(states, main,
                rank=FALSE, nooverlap= FALSE, range=NULL,
                col = rgb(1,0,0, 1/sqrt(dim(states)[1])),  ...){
        n <- dim(states)[1]; dim <-  dim(states)[2]
        time.lag <- attr(states,"time.lag"); if (is.null(time.lag)) time.lag <- 1

        if (missing(main)) {
                        stateid <- attr(states, "id")
                        if (is.null(stateid)) stateid <- deparse(substitute(states))
                        main <- paste("Takens states:", stateid, "\n",
                                "n:", n," dim:", dim)
                        if (time.lag != 1) main <- paste(main, " time lag:", time.lag)
                }

        if (nooverlap) {states <- states[ seq(1,n, by=dim),]
        main <- paste(main," no overlap")}

        if (!is.null(range)) { states[states[]< range[1]] <- NA;
                states[states[]> range[2]] <- NA
                main <- paste(main," trimmed")}

        if (rank) {states <- apply(states, 2, rank, ties.method="random")
        main <- paste(main," ranked")}

        pairs(states, main=main,
#        col=rgb(0,0,0, alpha), pch=19, ...)
        col=        col, pch=19, ...)
        #title(main=main, outer=TRUE, line=-2, cex.main=0.8)
}
```

Assuming the index is time, the *statecoplot()* is layed out to show the highest index as response, i.e. $(x_{t-1}, x_t | x_{t-2}, x_{t-3})$.

ToDo: extend for low dimensions, extend parameters

statecoplot	*Show conditioning marginal scatterplots of Takens states*

Usage.

```
statecoplot(states, main,
range  = NULL,
rank = FALSE, nooverlap = FALSE,
 col= rgb(0, 0, 0, \alpha = \sqrt{\frac{1}{nr\ states}})$,
number = c(5,5))
```

Arguments.

states	A matrix: Takens states by dimension, one state per row.
main	Optional: the main header.
range	Optional: an interval selecting values to be displayd.
rank	An experimental variant. If *rank*, the values are rank transformed.
nooverlap	An experimental variant. If *nooverlap*, the cases are subsampled by dimension.
alpha	
col	The current choice is $rgb(0,0,0,\alpha = \sqrt{\frac{1}{nr\ states}})$, as a default.
number	integer; the number of conditioning intervals, for a and b, possibly of length 2.

Input

```
statecoplot <- function(states, main,
                rank = FALSE, nooverlap = FALSE, range = NULL,
                col = rgb(1,0,0, 1/sqrt(dim(states)[1])),
                number = c(5,5), ...){
        n <- dim(states)[1]; dim <-  dim(states)[2]
        time.lag <- attr(states,"time.lag")
        if (is.null(time.lag)) time.lag <- 1
        if (missing(main)) {
        stateid <- attr(states, "id")
        if (is.null(stateid)) stateid <- deparse(substitute(states))
        main <- paste("Takens states:", stateid, "\n",
                "n=", n," dim=", dim)
        if (time.lag != 1) main <- paste(main, " time lag=", time.lag)
                }

        if (nooverlap) {states <- states[ seq(1,n, by=dim),]
        main <- paste(main," no overlap")}


        if (!is.null(range)) { states[states[]< range[1]] <- NA; states[states[]> range[2]] <- NA
        main <- paste(main," trimmed")}

        if (rank) {states <- apply(states, 2, rank, ties.method="random")
        main <- paste(main," ranked")}

        coplot((states[,4]~states[,3]|states[,1]+ states[,2]),
        number=number, main=main,
        col=rgb(0,0,0, alpha), pch=19, ...)
        #title(main=main, outer=TRUE, line=-2, cex.main=0.8)
}
```

2.0.2. *Local Bottleneck: Recurrence Plots.* To allow experimental implementations, functions from *nonlinearTseries* are aliased here.

Input

```
local.buildTakens <- function (time.series,
        embedding.dim, time.lag=1,
        id=deparse(substitute(time.series)))
{
        takens <- nonlinearTseries:::buildTakens(time.series, embedding.dim, time.lag)
        attr(takens,"time.lag") <- time.lag
        attr(takens,"embedding.dim") <- embedding.dim
        attr(takens,"id") <- id
        return(takens)
}
```

Input

```
local.findAllNeighbours <- function (takens, radius, number.boxes = NULL)
{
        allneighs <- nonlinearTseries:::findAllNeighbours(takens, radius, number.boxes = NULL)
        mostattributes(allneighs) <- attributes(takens)
        attr(allneighs, "radius") <- radius
        return(allneighs)
}
```

minor cosmetics added to recurrencePlotAux

ToDo: propagate parameters from *buildTakens* and *findAllNeighbours* in a slot of the result, instead of using explicit parameters in recurrencePlotAux.

Input

```
#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
              }
            }
          }

#! clean up. only one main id should be presentes
        main <- paste("Recurrence Plot: ",
                        deparse(substitute(neighs))
                        )
        id <-  attr(neighs, "id"); if (!is.null(id)) main <- paste(main," id:",id)

        more <- NULL
```

```
        more <- paste(more," n:",length(neighs))

        #use components of neights if available
        embedding.dim <- attr(neighs, "embedding.dim")
        if (is.null(embedding.dim)) embedding.dim <- dim
        if (!is.null(dim)) {
                if (embedding.dim != dim) warning(paste("Embedding dim:", embedding.dim,
                " does not match dim argument=", dim))
                more <- paste(more," dim:",dim)
        }


        attrradius <- attr(neighs, "radius")
        if (!is.null(lag)) more <- paste(more," lag:",lag)
        if (is.null(radius)) radius <- attrradius
        if (!is.null(radius)) {
                more <- paste(more," radius:",radius)
                if (!is.null(attrradius) && (attrradius != radius)) warning(paste("Radius attribute:", a
                " does not match radius argument=", radius))
                }
        # if (!is.null(attrradius)) more <- paste(more," radius attr:",attrradius)
        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
                )
 #        )

}
```

ToDo: improve feedback for data structures in *nonlinearTseries*

2.0.3. *Recurrence Plots: RQA Information.* This is a hack to report RQA information. $dim = NULL$ is added to align calling with other functions.

ToDo: improve to a full *show* method for class *rqa*.

Needs improvement.

Input

```
showrqa <- function(takens, dim=NULL, radius,
                digits=3,
                do.hist = TRUE, rm.hist = TRUE, log = TRUE ,...)
{
        xxrqa <- rqa(takens=takens,radius=radius)
        xxrqa$radius <- radius
        id <- attr(takens,"id")
        if (is.null(id)) id <- deparse(substitute(takens))
        xxrqa$id<- id
        xxrqa$time.lag <- attr(takens,"time.lag")
        cat(id, " n:", dim(takens)[1], " Dim:", dim(takens)[2], "\n")
        xxrqa$n <- dim(takens)[1]
        xxrqa$dim <- dim(takens)[2]
        #str(xxrqa)
        #str(digits)
```

```
        #browser()
        cat(paste("Radius:", radius,
                " Recurrence coverage REC:", round(xxrqa$REC, digits),
                " log(REC)/log(R):", round(log(xxrqa$REC)/log(radius), digits), "\n"))
        xxrqa$logratio <- log(xxrqa$REC)/log(radius)
        cat(paste("Determinism:", round(xxrqa$DET, digits),
                " Laminarity:",round(xxrqa$LAM, digits), "\n"))
        cat(paste("DIV:", round(xxrqa$DIV, digits), "\n"))
        cat(paste("Trend:", round(xxrqa$TREND, digits),
                " Entropy:",round(xxrqa$ENTR, digits), "\n"))
        cat(paste("Diagonal lines max:", round(xxrqa$Lmax, digits),
                 " Mean:",round(xxrqa$Lmean, digits),
                " Mean off main:",round(xxrqa$LmeanWithoutMain, digits), "\n"))
        cat(paste("Vertical lines max:", round(xxrqa$Vmax, digits),
                " Mean:",round(xxrqa$Vmean, digits), "\n"))
                # str(xxrqa[4:12])

        if (do.hist){
        if (log==TRUE) log<-"y"
        oldpar <- par(mfrow=c(2,1))

                xxrqa$diagonalHistogram[xxrqa$diagonalHistogram==0] <- NA # hack for log zero counts
                dh<- xxrqa$diagonalHistogram
                #if (log=="y")  {dh <- dh+1}

                id <- attr(takens,"id"); if (is.null(id) ) id <- deparse(substitute(takens))
                pars <- paste("\n n=", dim(takens)[1], " Dim:",
                        dim(takens)[2])
                lag<- attr(takens,"time.lag")
                  if (!is.null(lag) && (lag !=1) ) pars <- paste(pars, " Lag:", lag)
                plot(dh, type="h", main=paste( id, " Diagonal:",
                        pars," Radius: ",radius, " REC:", round(xxrqa$REC, digits)),
                        xlab="length of diagonals",
                        log = log, ...)

        xxrqa$recurrenceRate[xxrqa$recurrenceRate==0] <- NA # hack for log zero counts
        drR<- xxrqa$recurrenceRate
                #if (log=="y")  {drR <- drR+1}

                id <- attr(takens,"id"); if (is.null(id) ) id <- deparse(substitute(takens))
                pars <- paste("\n n=", dim(takens)[1], " Dim:",
                        dim(takens)[2])
                lag<- attr(takens,"time.lag")
                  if (!is.null(lag) && (lag !=1) ) pars <- paste(pars, " Lag:", lag)
        plot(drR, type="h",
                 main=paste( id," Recurrence Rate",
                        pars," Radius: ",radius, " REC:", round(xxrqa$REC, digits)),
                        xlab="distance to diagonal",
                        #ylim=c(1,3),
                        log = log, ...)
        par(oldpar)
                }

        if (rm.hist) { xxrqa$recurrenceRate <- NULL; xxrqa$diagonalHistogram <- NULL }
        invisible(xxrqa)
}
```

3. Test Signals

We set up a small series of test signals. Some synthetic test signals are introduced here. More test cases used later are the Geyser data set (Section 8 on page 66) and two examples of heart rate data sets (Section 9 on page 67 and Section 10 on page 89) from *library(rhrv)*.

For convenience, some source code from other libraries is included to make this self-contained.

As a global constant, we set up the length of the series to be used for test signals.

Input

```
#nsignal <- 256
nsignal <- 1024
#nsignal <- 4096
system.time.start <- proc.time()
```

For signal representation, we use a common layout.

Input

```
plotsignal <- function(signal, main, ylab) {
        #! alpha level should depend on expected number of overlaps

        if (missing(ylab)) { ylab <- deparse(substitute(signal)) }

        par(mfrow = c(1,
                2))
        plot(signal,
                main = "", xlab = "index",  ylab = ylab,
                col = rgb(0, 0, 1, 0.3), pch = 20)

        plot(signal, type = "l",
                main = "",  xlab = "index", ylab = ylab,
                col = rgb(0, 0, 0, 0.4))
        points(signal,
                col = rgb(0, 0, 1, 0.3), pch = 20)
        if (missing(main)) { main = deparse(substitute(signal)) }
        title(main = main,
                outer = TRUE, line = -2, cex.main = 1.2)
}
```

3.1. **Sinus.**

Input

```
sin10 <- function(n=nsignal) {sin( (1:n)/n* 2*pi*10)}
plotsignal(sin10())
```

See Figure 1 on the facing page.

3.2. **Uniform Random Numbers.**

Input

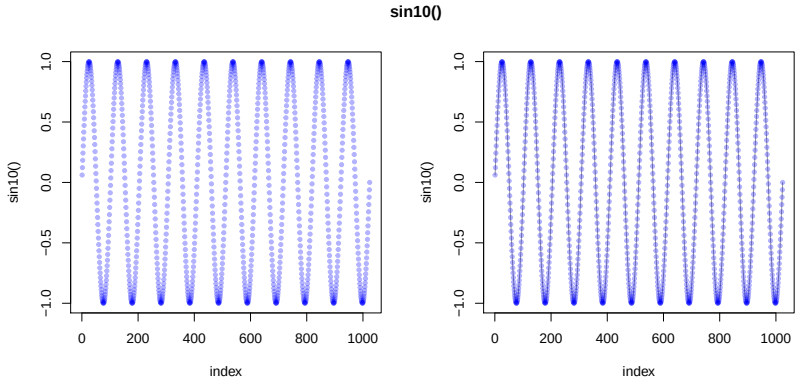


FIGURE 1. Test case: sin10. Signal and linear interpolation.

```
unif <- function(n=nsignal) {runif(n)}
xunif<-unif()
plotsignal(xunif)
```

See Figure 2,

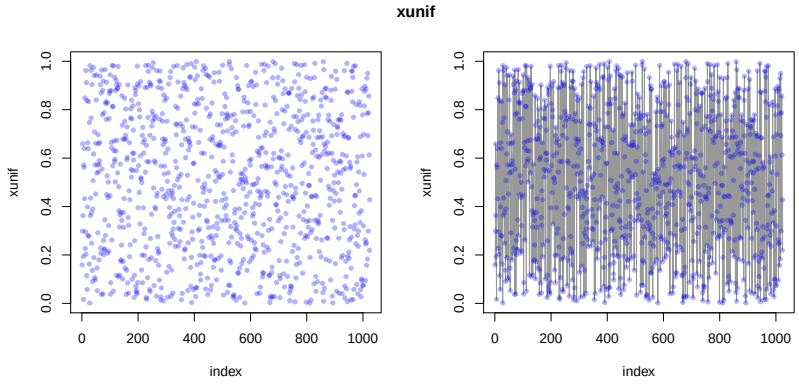


FIGURE 2. Test case: unif - uniform random numbers. Signal and linear interpolation.

3.3. **Chirp Signal.**

Input

```
chirp <- function(n=nsignal)       # this is copied from library(signal)
{signal.chirp <- function(t, f0 = 0, t1 = 1, f1 = 100,
                  form = c("linear", "quadratic", "logarithmic"),
                  phase = 0){

  form <- match.arg(form);  phase <- 2*pi*phase/360

  switch(form,
    "linear" = {
        a <- pi*(f1 - f0)/t1;        b <- 2*pi*f0
        cos(a*t^2 + b*t + phase)
    },
    "quadratic" = {
```

```
        a <- (2/3*pi*(f1-f0)/t1/t1);        b <- 2*pi*f0
        cos(a*t^3 + b*t + phase)
    },
    "logarithmic" = {
        a <- 2*pi * t1 / log(f1 - f0);        b <- 2*pi * f0
        x <- (f1-f0)^(1/t1)
        cos(a*x^t + b*t + phase)
    })
}

signal.chirp(seq(0, 0.6, len=nsignal))
}
plotsignal(chirp())
```

See Figure 3,

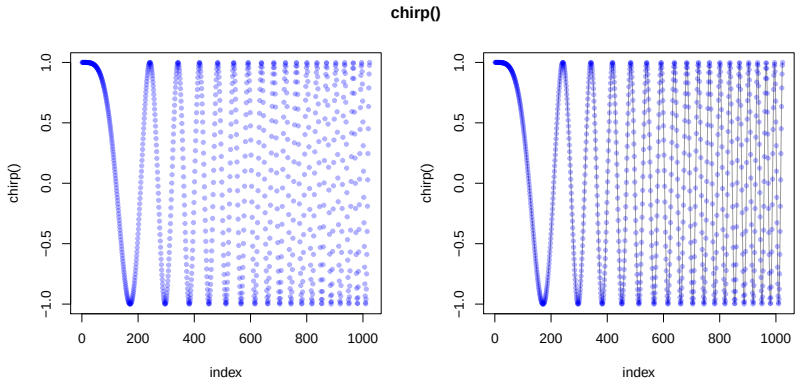


FIGURE 3. Test case: chirp signal. Signal and linear interpolation.

3.4. **Doppler signal.**

Input

```
doppler <- function(n=nsignal) {

dopplersignal  <- function(x) { sqrt(x*(1-x))* sin((2.1*pi)/(x+0.05))}
dopplersignal((1:nsignal)/nsignal)
}
plotsignal(doppler())
```

See Figure 4 on the next page,

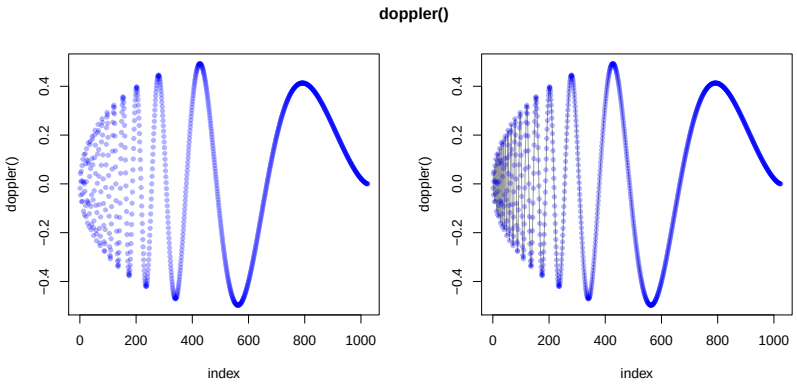


FIGURE 4. Test case: Doppler signal. Signal and linear interpolation.

4. nonlinearTseries Quick-Start

Input

```
#suppressMessages(library('nonlinearTseries'))
library('plot3D')
# by default, the simulation creates a RGL plot of the system's phase space
```

4.1. **Sinus.**

Input

```
sinN <- sin10()
oldpar <-  par(mfrow=c(1,2))
# taudelay estimation based on the autocorrelation function
tau.acf = timeLag(sinN, technique = "acf", do.plot = T,
main=paste("acf\n",deparse(substitute(x))))
cat("tau.acf:",tau.acf)
```

Output

```
tau.acf: 20
```

Input

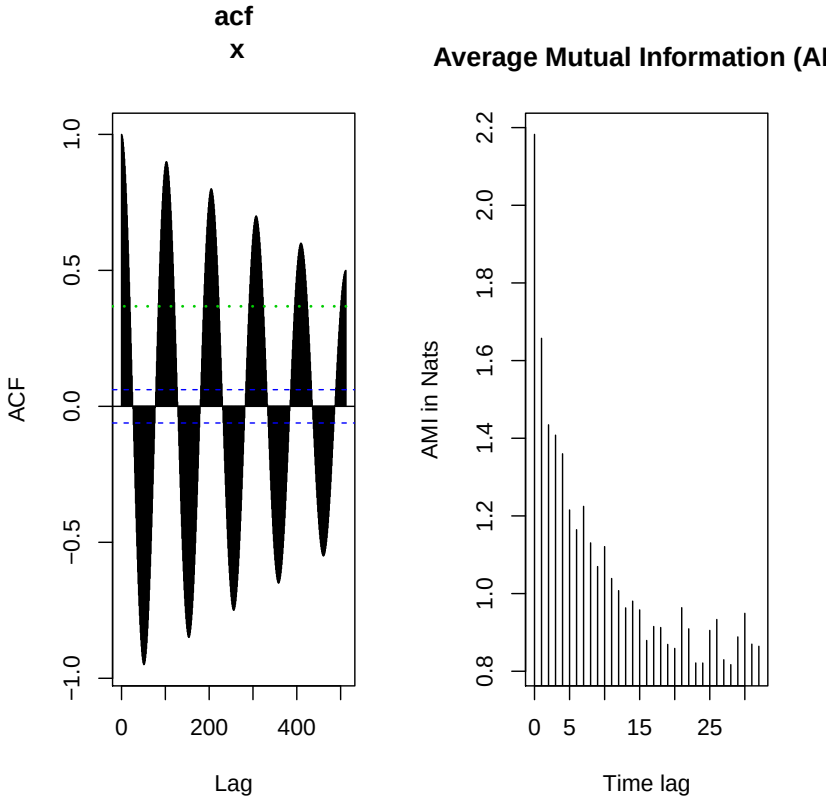
```
# taudelay estimation based on the mutual information function
tau.ami=NA
try(tau.ami <- timeLag(sinN, technique = "ami", do.plot = T,
main=paste("ami\n",deparse(substitute(x)))))
cat("tau.ami:",tau.ami)
```

Output

```
tau.ami: NA
```

Input

```
par(oldpar)
```



Note: fails. See Rnw source code.

4.2. **Uniform Random Numbers.**

Input

```
unifN <- unif()
oldpar <-  par(mfrow=c(1,2))
# taudelay estimation based on the autocorrelation function
tau.acf = timeLag(unifN, technique = "acf", do.plot = T,
main=paste("acf\n",deparse(substitute(x))))
cat("tau.acf:",tau.acf)
```

Output

```
tau.acf: 1
```

Input

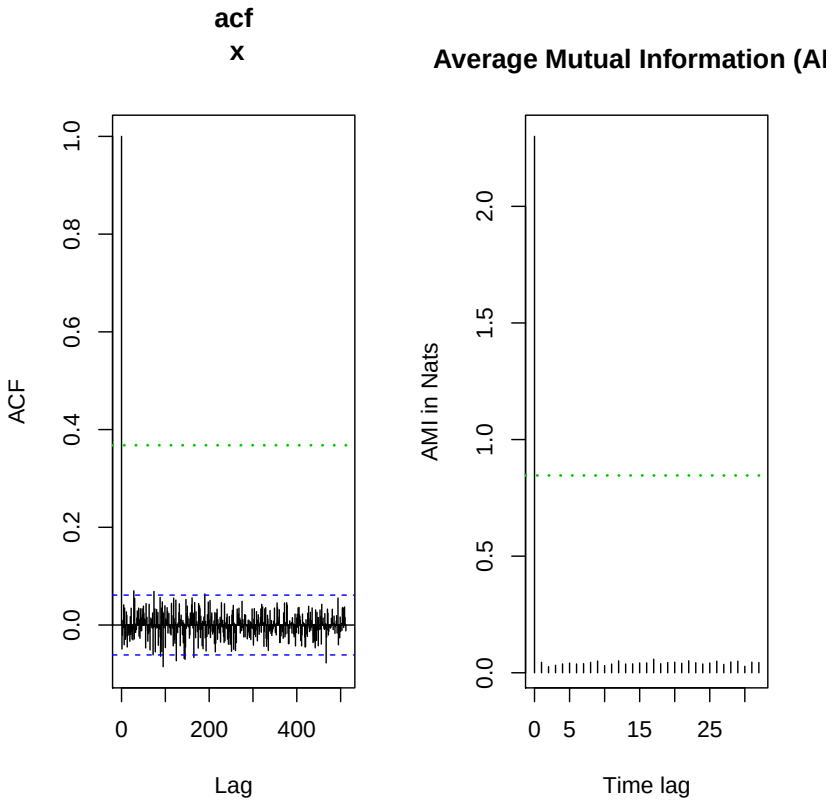
```
# taudelay estimation based on the mutual information function
tau.ami = timeLag(unifN, technique = "ami", do.plot = T,
main=paste("ami\n",deparse(substitute(x))))
cat("tau.ami:",tau.ami)
```

Output

```
tau.ami: 1
```

Input

```
par(oldpar)
```



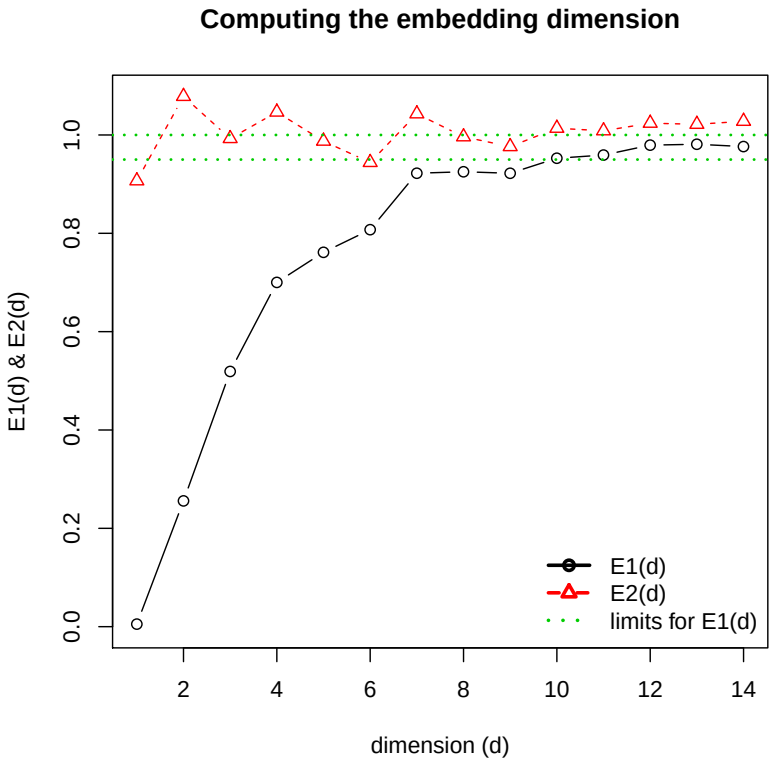
Input

```
if (is.numeric(tau.ami)) {
emb.dim = estimateEmbeddingDim(unifN, time.lag = tau.ami,
max.embedding.dim = 15)}  else  {
emb.dim = estimateEmbeddingDim(unifN, time.lag = tau.acf,
max.embedding.dim = 15)}
cat("Estimated embedding dim:", emb.dim)
```

Output

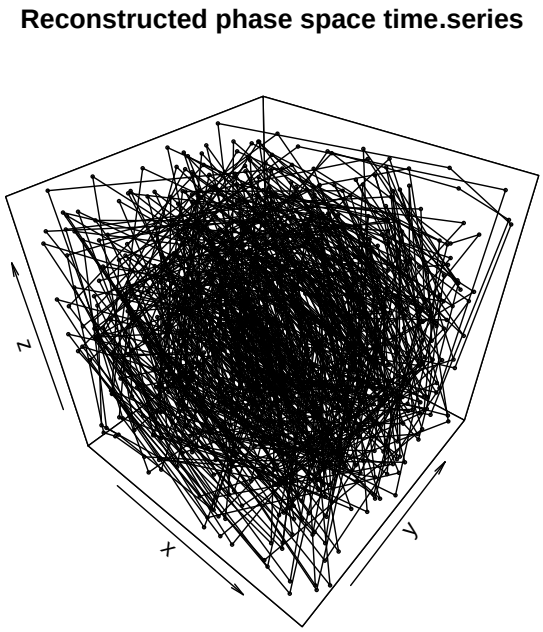
```
Estimated embedding dim: 10
```

Input



Input

```
tak = buildTakens(unifN,embedding.dim = emb.dim, time.lag = tau.ami)
scatter3D(tak[,1], tak[,2], tak[,3],
main = paste("Reconstructed phase space",deparse(substitute(time.series))),
col = 1, type="o",cex = 0.3)
```



4.3. **Chirp.**

Input

```
chirpN <- chirp()
oldpar <-  par(mfrow=c(1,2))
# taudelay estimation based on the autocorrelation function
tau.acf = timeLag(chirpN, technique = "acf", do.plot = T,
main=paste("acf\n",deparse(substitute(x))))
cat("tau.acf:",tau.acf)
```

Output

```
tau.acf: 11
```

Input

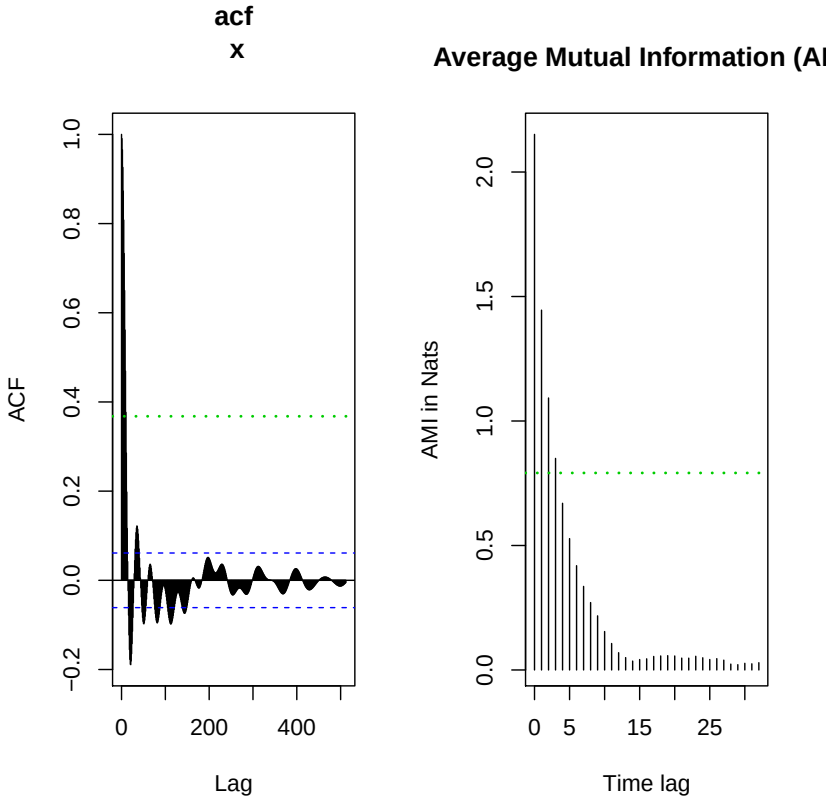
```
# taudelay estimation based on the mutual information function
tau.ami = timeLag(chirpN, technique = "ami", do.plot = T,
main=paste("ami\n",deparse(substitute(x))))
cat("tau.ami:",tau.ami)
```

Output

```
tau.ami: 4
```

Input

```
par(oldpar)
```



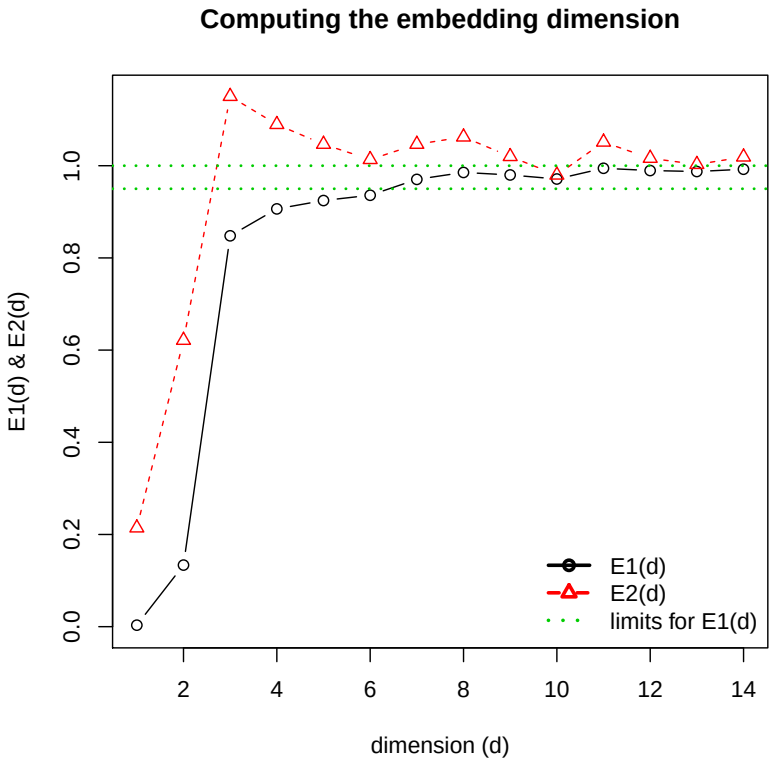
Input

```
if (is.numeric(tau.ami)) {
emb.dim = estimateEmbeddingDim(chirpN, time.lag = tau.ami,
max.embedding.dim = 15)}  else  {
emb.dim = estimateEmbeddingDim(chirpN, time.lag = tau.acf,
max.embedding.dim = 15)}
cat("Estimated embedding dim:", emb.dim)
```

Output

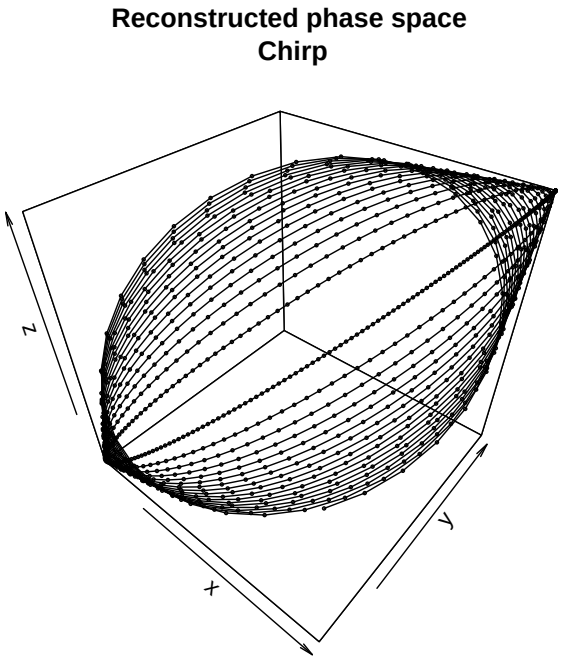
```
Estimated embedding dim: 7
```

Input



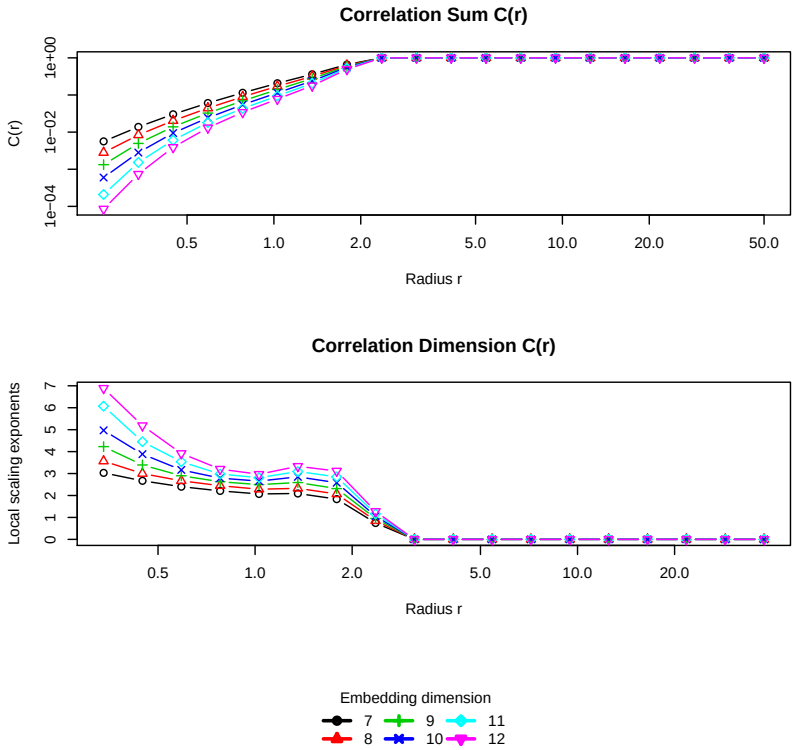
Input

```
tak = buildTakens(chirpN,embedding.dim = emb.dim, time.lag = tau.ami)
scatter3D(tak[,1], tak[,2], tak[,3],
main = paste("Reconstructed phase space\n","Chirp"),
col = 1, type="o",cex = 0.3)
```



Input

```
cd = corrDim(chirpN,
min.embedding.dim = emb.dim,
max.embedding.dim = emb.dim + 5,
time.lag = tau.ami,
min.radius = 0.001, max.radius = 50,
n.points.radius = 40,
do.plot=FALSE)
plot(cd)
```



Input

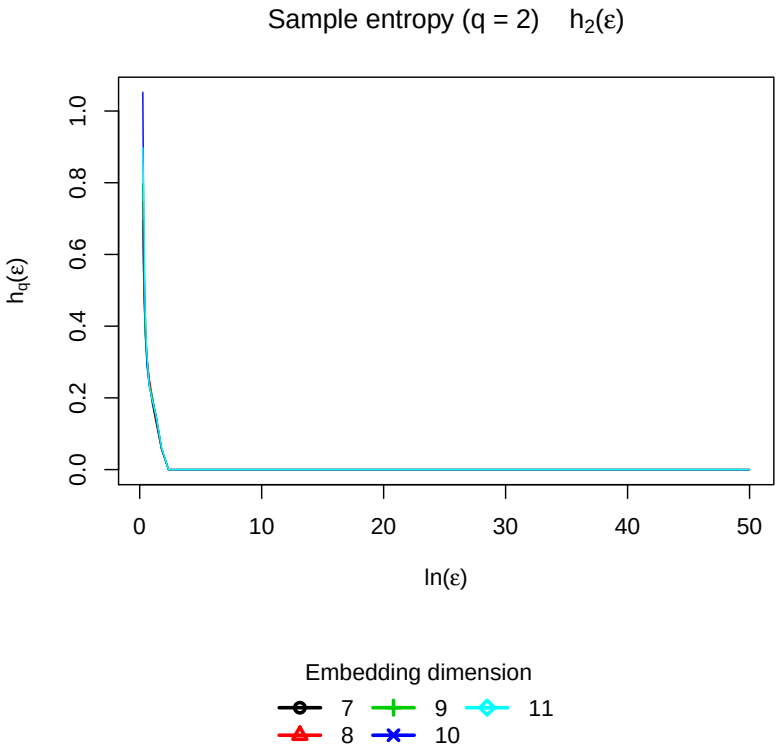
```
oldpar <- par(mfrow=c(1,2))
se = sampleEntropy(cd, do.plot =T)
se.est = estimate(se, do.plot = T,
regression.range = c(8,15))
cat("Sample entropy estimate: ", mean(se.est), "\n")
```

Output

```
Sample entropy estimate:  0
```

Input

```
par(oldpar)
```



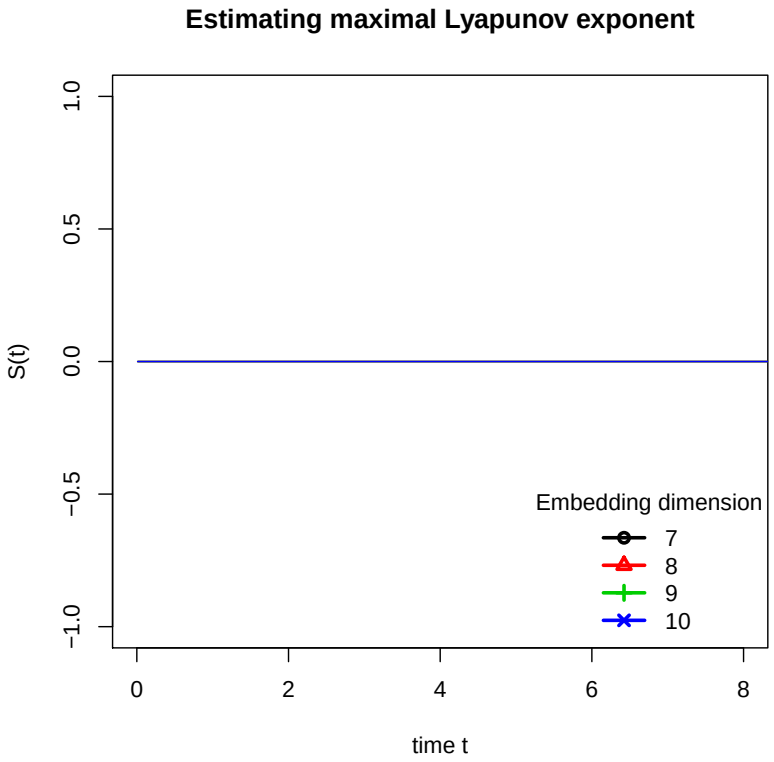
Input

```
#sampling.period = diff(lor$time)[1]
ml = maxLyapunov(chirpN,
sampling.period=0.01,
min.embedding.dim = emb.dim,
max.embedding.dim = emb.dim + 3,
time.lag = tau.ami,
radius=1,
max.time.steps=1000,
do.plot=FALSE)
plot(ml,type="l", xlim = c(0,8))
ml.est = estimate(ml, regression.range = c(0,3),
do.plot = T,type="l")
#cat("expected: 0.906 estimate:", ml.est,"\n")
cat("estimate:", ml.est,"\n")
```

Output

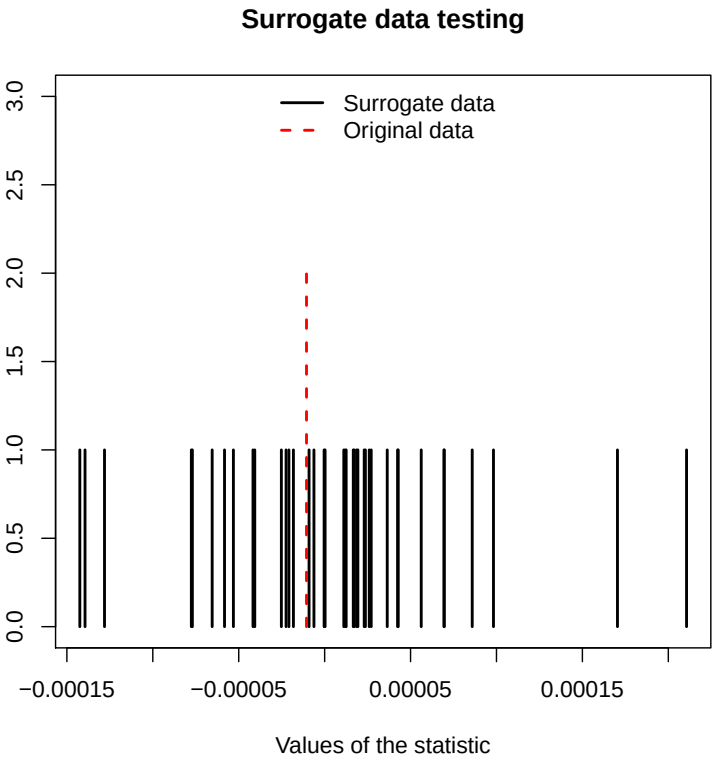
```
estimate: 0
```

Input



Input

```
st = surrogateTest(chirpN,significance = 0.05,one.sided = F,
FUN = timeAsymmetry, do.plot=F)
## Computing statistics
##
## Null Hypothesis: Data comes from a linear stochastic process
## Reject Null hypothesis:
## Original data's stat is significant larger than surrogates' stats
plot(st)
```


Surrogate data testing
Surrogate data
Original data
0.0
0.5
1.0
1.5
2.0
2.5
3.0
−0.00015
−0.00005
0.00005
0.00015
Values of the statistic

4.4. **Doppler.**

Input

```
dopplerN <- doppler()
oldpar <-  par(mfrow=c(1,2))
# taudelay estimation based on the autocorrelation function
tau.acf = timeLag(dopplerN, technique = "acf", do.plot = T,
main=paste("acf\n",deparse(substitute(x))))
cat("tau.acf:",tau.acf)
```

Output

```
tau.acf: 45
```

Input

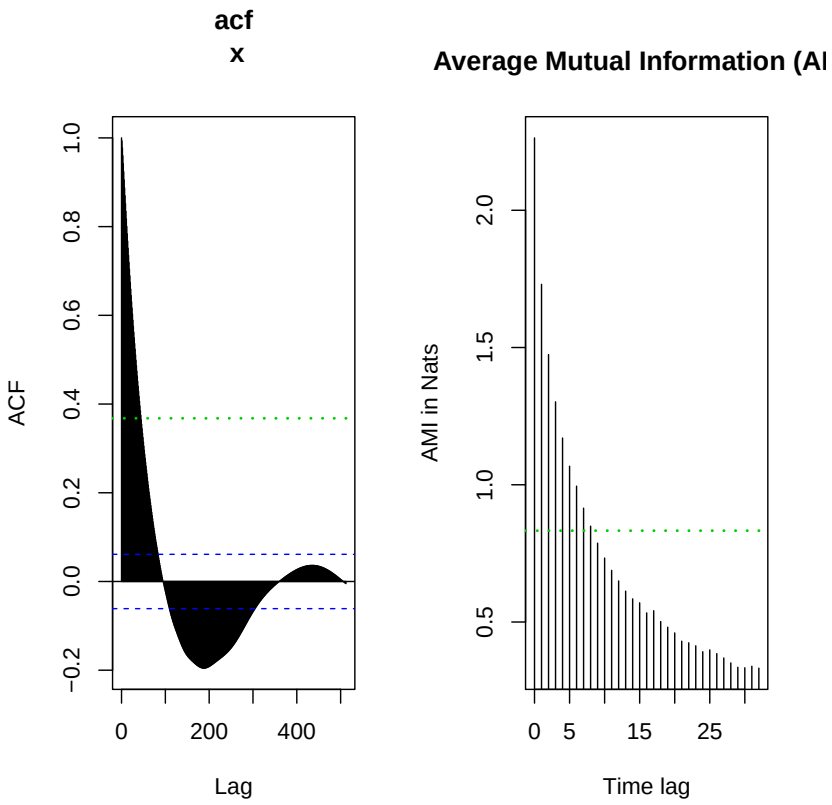
```
# taudelay estimation based on the mutual information function
tau.ami = timeLag(dopplerN, technique = "ami", do.plot = T,
main=paste("ami\n",deparse(substitute(x))))
cat("tau.ami:",tau.ami)
```

Output

```
tau.ami: 9
```

Input

```
par(oldpar)
```



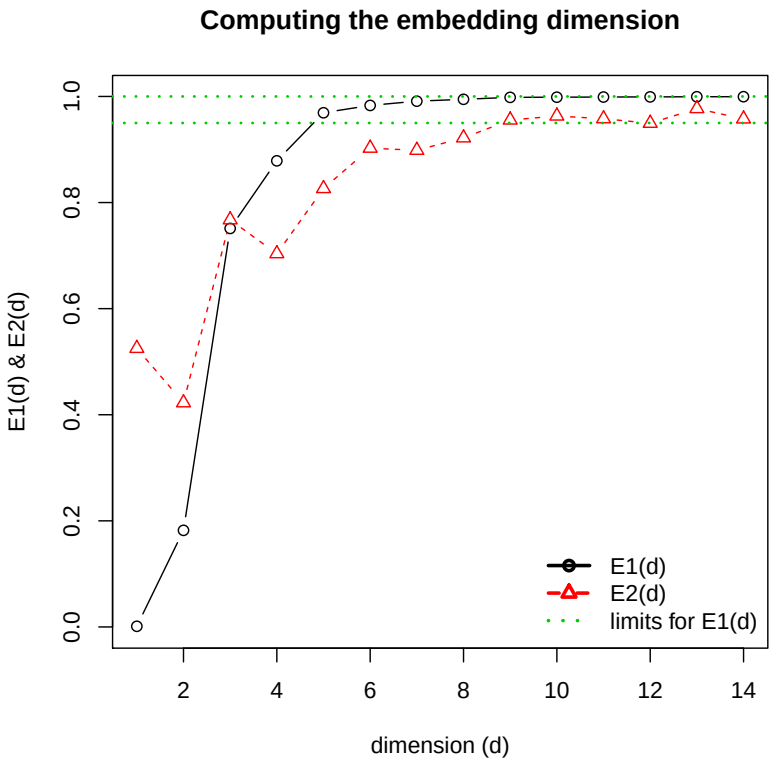
Input

```
if (is.numeric(tau.ami)) {
emb.dim = estimateEmbeddingDim(dopplerN, time.lag = tau.ami,
max.embedding.dim = 15)}  else  {
emb.dim = estimateEmbeddingDim(dopplerN, time.lag = tau.acf,
max.embedding.dim = 15)}
cat("Estimated embedding dim:", emb.dim)
```

Output

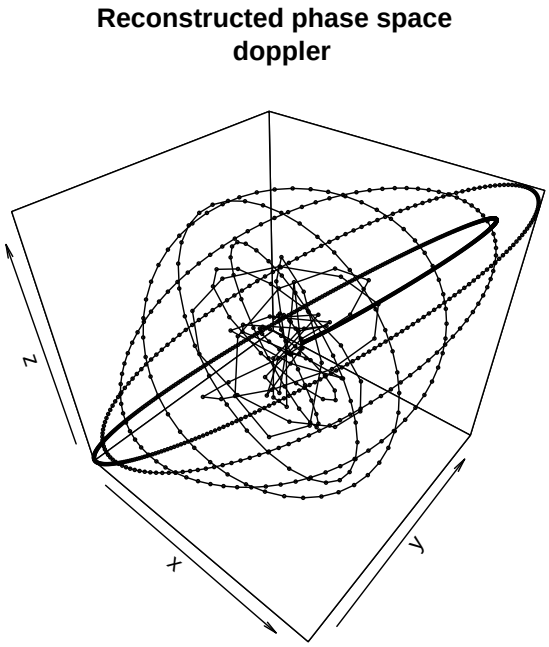
```
Estimated embedding dim: 5
```

Input



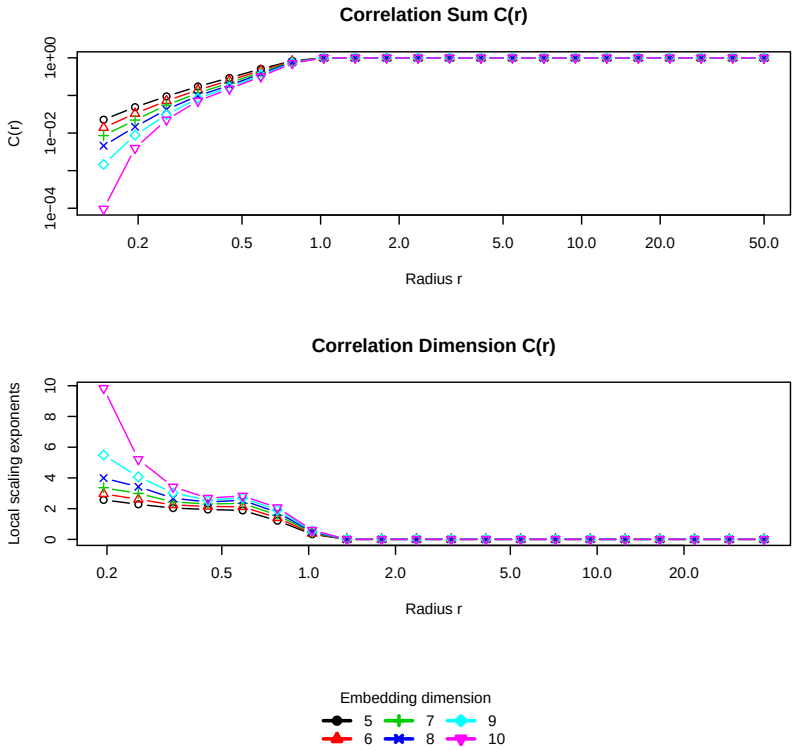
Input

```
tak = buildTakens(dopplerN,embedding.dim = emb.dim, time.lag = tau.ami)
scatter3D(tak[,1], tak[,2], tak[,3],
main = "Reconstructed phase space \n doppler" ,
col = 1, type="o",cex = 0.3)
```



Input

```
cd = corrDim(dopplerN,
min.embedding.dim = emb.dim,
max.embedding.dim = emb.dim + 5,
time.lag = tau.ami,
min.radius = 0.001, max.radius = 50,
n.points.radius = 40,
do.plot=FALSE)
plot(cd)
```



Input

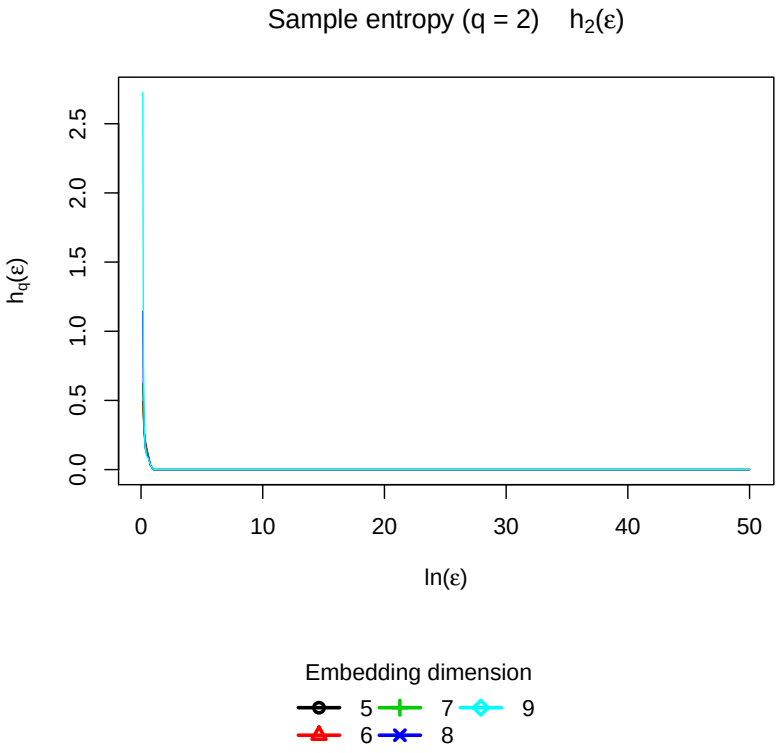
```
oldpar <- par(mfrow=c(1,2))
se = sampleEntropy(cd, do.plot = T)
se.est = estimate(se, do.plot = T,
regression.range = c(8,15))
cat("Sample entropy estimate: ", mean(se.est), "\n")
```

Output

```
Sample entropy estimate:  0
```

Input

```
par(oldpar)
```



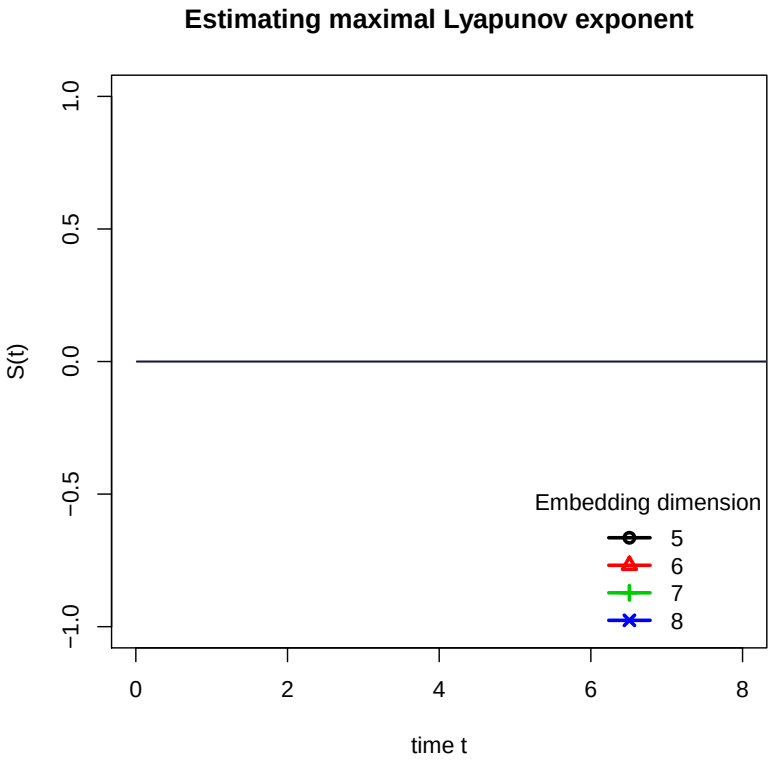
Input

```
#sampling.period = diff(lor$time)[1]
ml = maxLyapunov(dopplerN,
sampling.period=0.01,
min.embedding.dim = emb.dim,
max.embedding.dim = emb.dim + 3,
time.lag = tau.ami,
radius=1,
max.time.steps=1000,
do.plot=FALSE)
plot(ml,type="l", xlim = c(0,8))
ml.est = estimate(ml, regression.range = c(0,3),
do.plot = T,type="l")
#cat("expected: 0.906 estimate:", ml.est,"\n")
cat("estimate:", ml.est,"\n")
```

Output

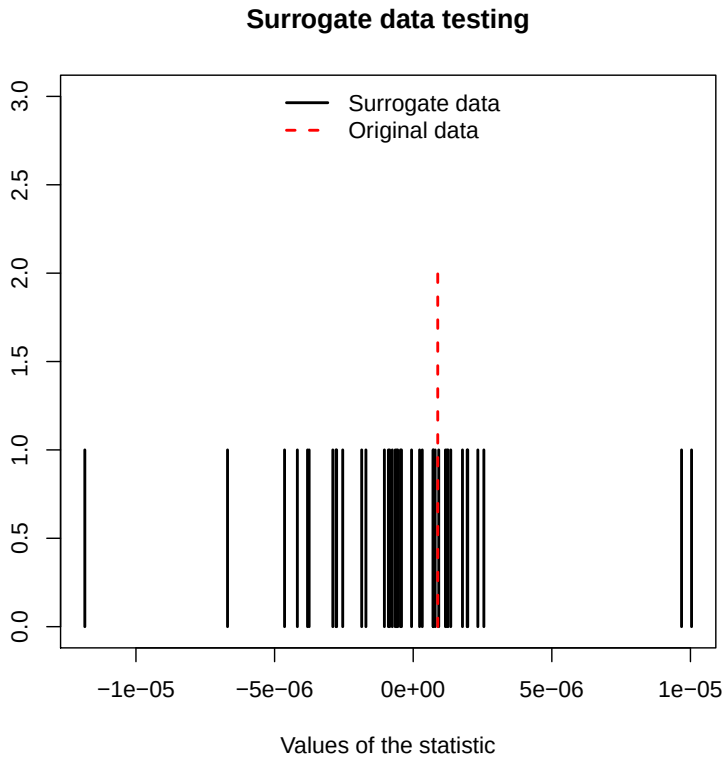
```
estimate: 0
```

Input



Input

```
st = surrogateTest(dopplerN,significance = 0.05,one.sided = F,
FUN = timeAsymmetry, do.plot=F)
## Computing statistics
##
## Null Hypothesis: Data comes from a linear stochastic process
## Reject Null hypothesis:
## Original data's stat is significant larger than surrogates' stats
plot(st)
```


Surrogate data testing
Surrogate data
Original data
0.0
0.5
1.0
1.5
2.0
2.5
3.0
−1e−05
−5e−06
0e+00
5e−06
1e−05
Values of the statistic

5. Takens' States for Test Signals

Input
```
sintakens <- local.buildTakens(time.series=sin10(),
        embedding.dim=4, time.lag=1)
statepairs(sintakens) #4
```

See Figure 5.

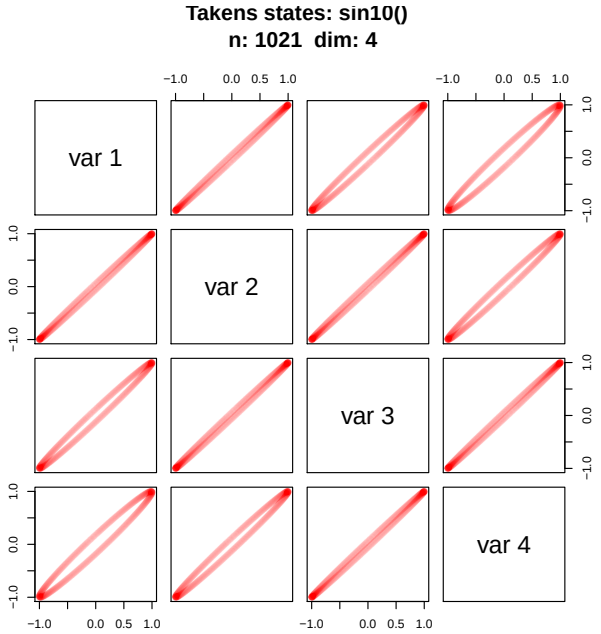


Figure 5. Takens states. Test case: sinus. Note that $2 - dim$ marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 1.255 sec.

The states only catch the local behaviour, where "local" depends on the sampling rate and the variation of the signal. For the sinus signal, we get a better picture if we subsample the signal.

Input
```
sintakenslag16 <- local.buildTakens(time.series=sin10(),
        embedding.dim=4, time.lag=16)
statepairs(sintakenslag16) #4
```

See Figure 6 on the next page.

Input
```
statepairs(sintakens, nooverlap=TRUE) #dim=4
```

See Figure 7 on the following page.

Input
```
statecoplot(sintakens) #4
```

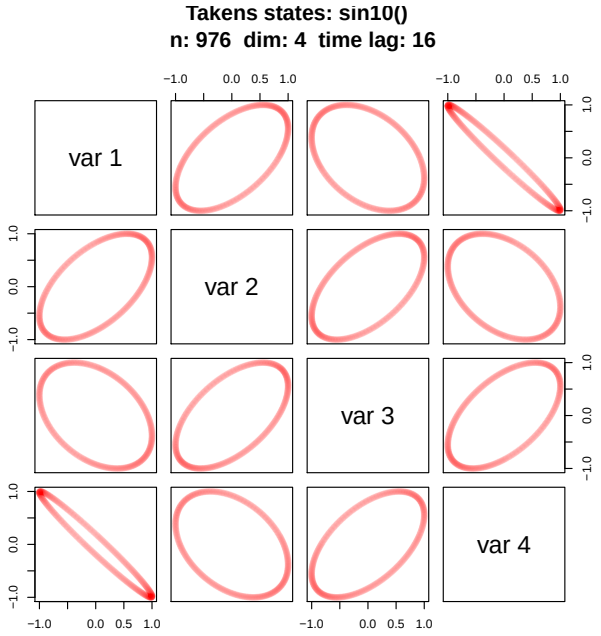


FIGURE 6. Takens states. Test case: sinus at time lag 16. Note that $2-dim$ marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.74 sec.

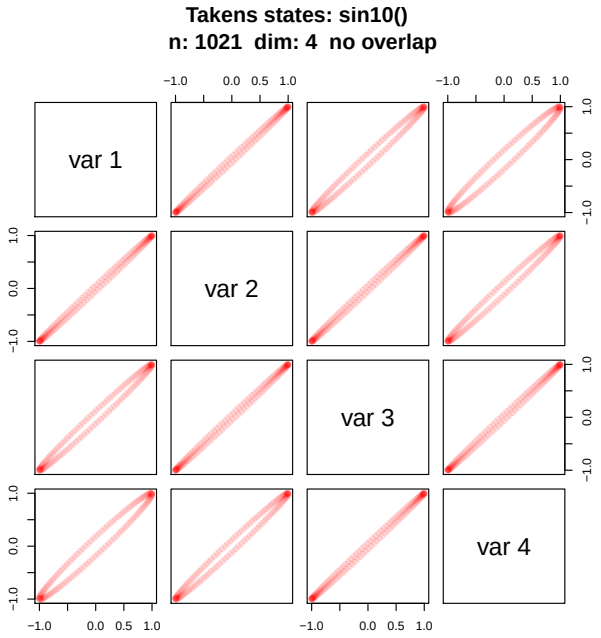


FIGURE 7. Takens states. Test case: sinus, no overlap. Note that $2-dim$ marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.978 sec.

See Figure 8.

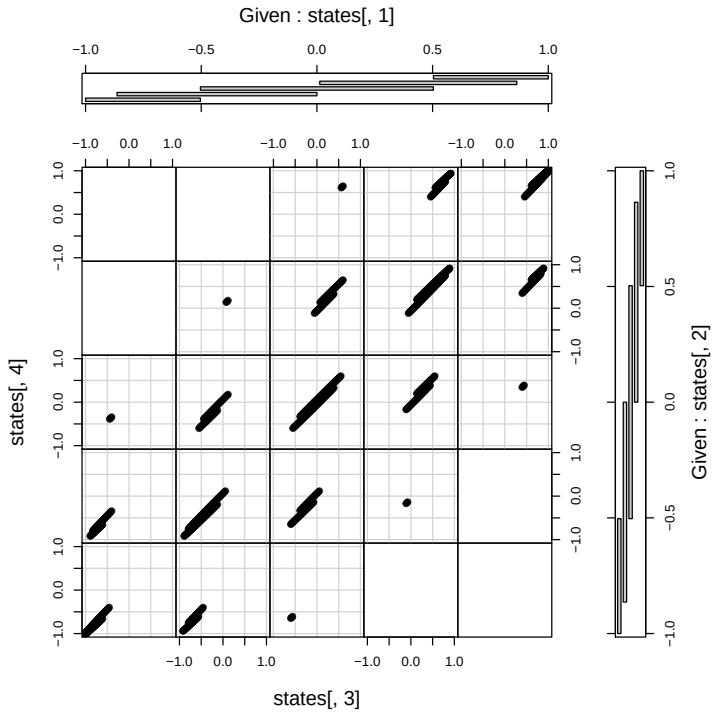


FIGURE 8. State coplot. Test case: sinus. Note that $2 - dim$ marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.268 sec.

Input

```
statecoplot(sintakenslag16) #4
```

See Figure 9 on the following page.

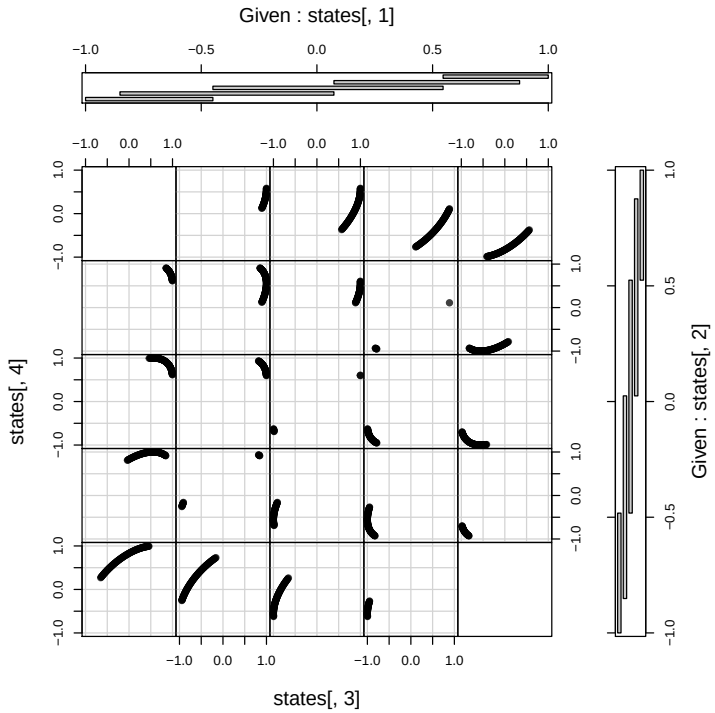


FIGURE 9. State coplot. Test case: sinus, time lag 16. Note that $2-dim$ marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.366 sec.

Input

```
uniftakens <- local.buildTakens( time.series=xunif,
        embedding.dim=4, time.lag=1)
statepairs(uniftakens) #dim=4
```

See Figure 10.

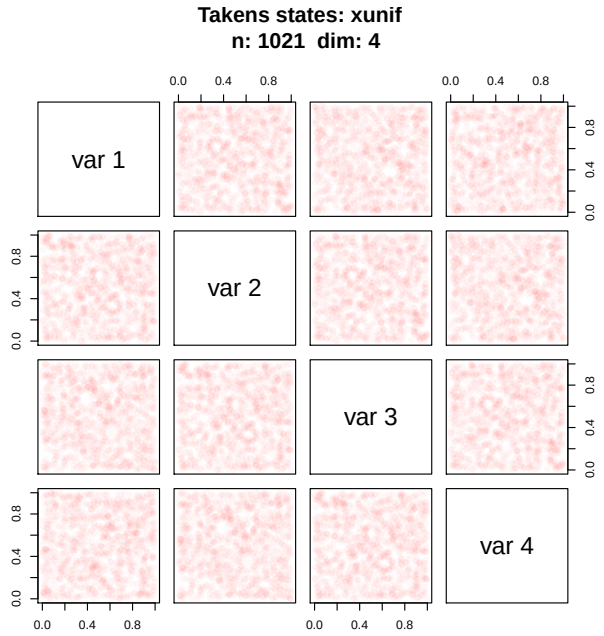


FIGURE 10. Takens states. Test case: uniform random numbers. Time used: 0.969 sec.

Input

```
statecoplot(uniftakens) #dim=4
```

See Figure 11 on the following page.

Input

```
statepairs(uniftakens, nooverlap=TRUE) #dim=4
```

See Figure 12 on the next page.

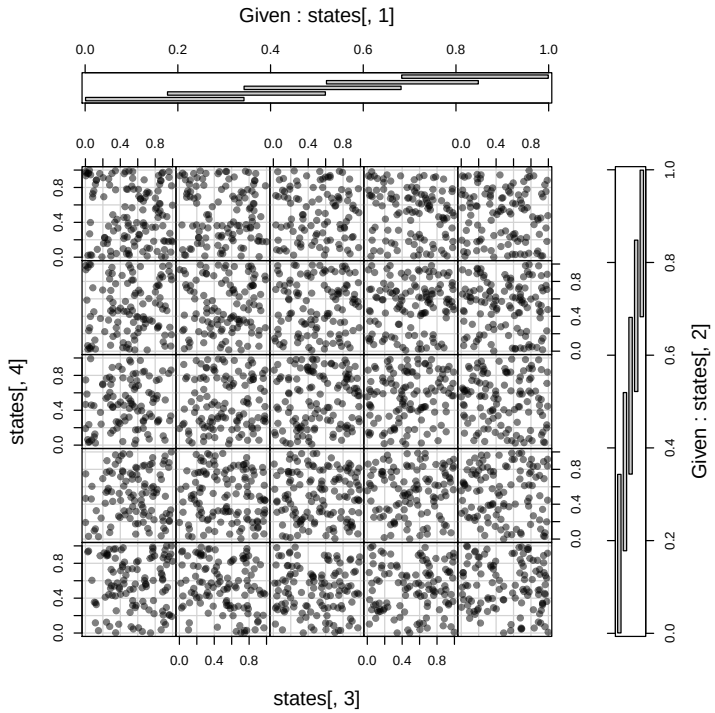


FIGURE 11. State coplot. Test case: uniform random numbers. Time used: 1.21 sec.

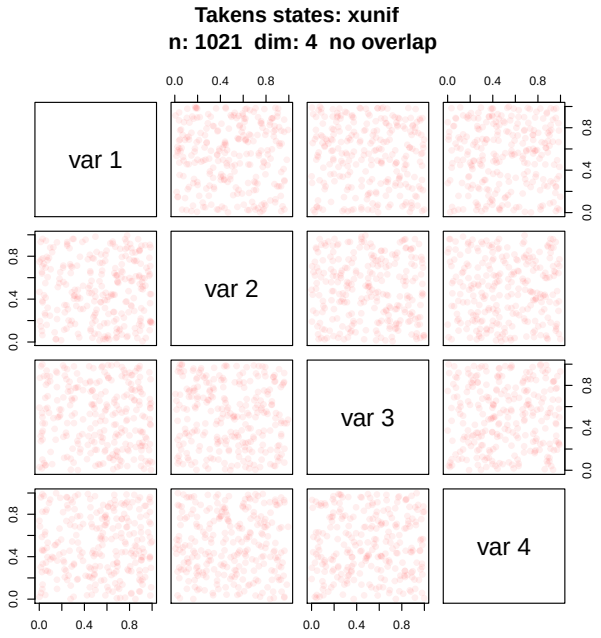


FIGURE 12. Takens states. Test case: uniform random numbers. Time used: 1.426 sec.

Input

```
chirptakens <- local.buildTakens( time.series=chirp(),
        embedding.dim=4,time.lag=1)
statepairs(chirptakens) #dim=4
```

See Figure 13.

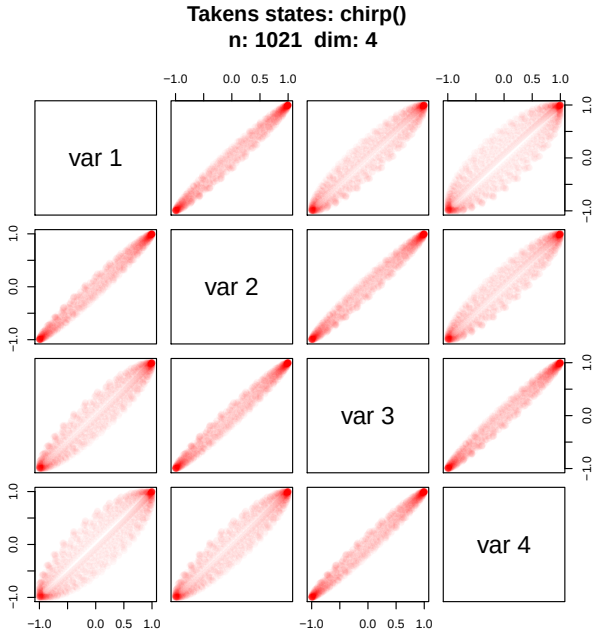


FIGURE 13. Takens states. Test case: chirp signal. Time used: 0.95 sec.

Input

```
statecoplot(chirptakens) #dim=4
```

See Figure 14 on the next page.

Input

```
statepairs(chirptakens, nooverlap=TRUE) #dim=4
```

See Figure 15 on the following page.

Input

```
dopplertakens <- local.buildTakens(time.series=doppler(),
        embedding.dim=4, time.lag=1)
statepairs(dopplertakens) #4
```

See Figure 16 on page 41.

The states only catch the local behaviour, where “local” depends on the sampling rate and the variation of the signal. For the doppler signal, we get a better picture if we subsample the signal.

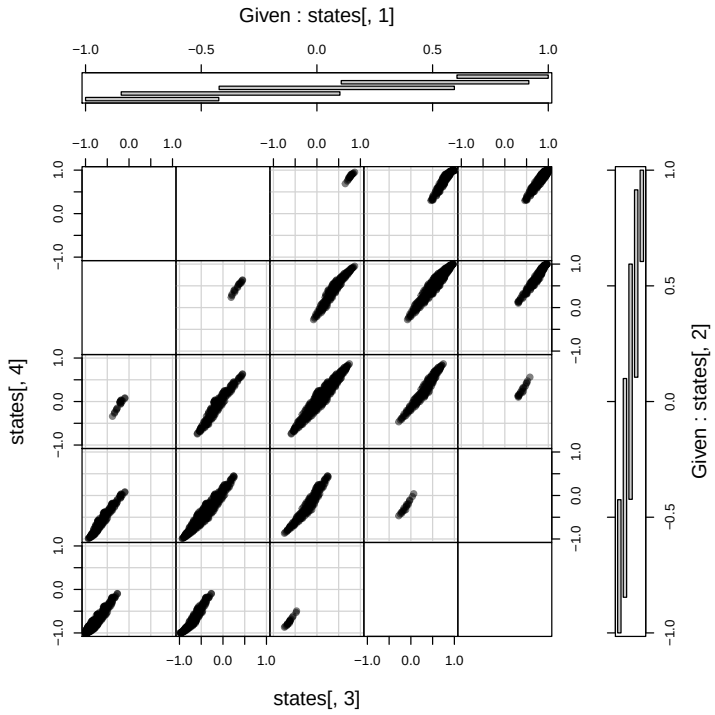


FIGURE 14. State coplot. Test case: chirp signal. Time used: 1.487 sec.

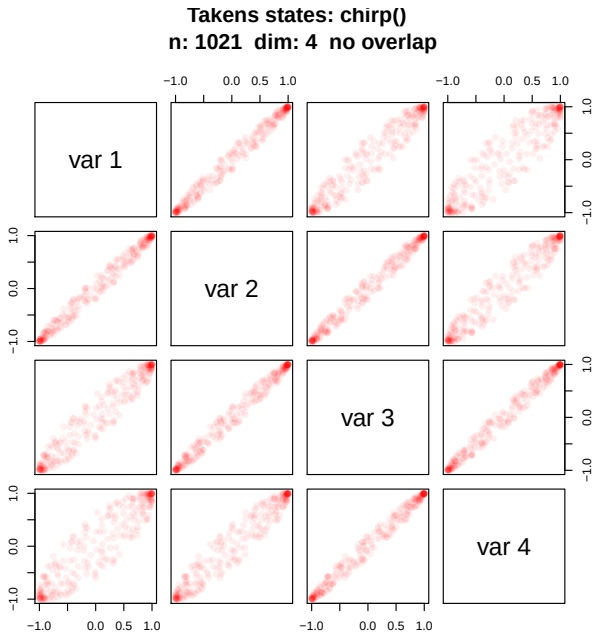


FIGURE 15. Takens states. Test case: chirp signal. Time used: 2.029 sec-

Input

```
dopplertakenslag16 <- local.buildTakens(time.series=doppler(),
        embedding.dim=4, time.lag=16)
statepairs(dopplertakenslag16) #4
```

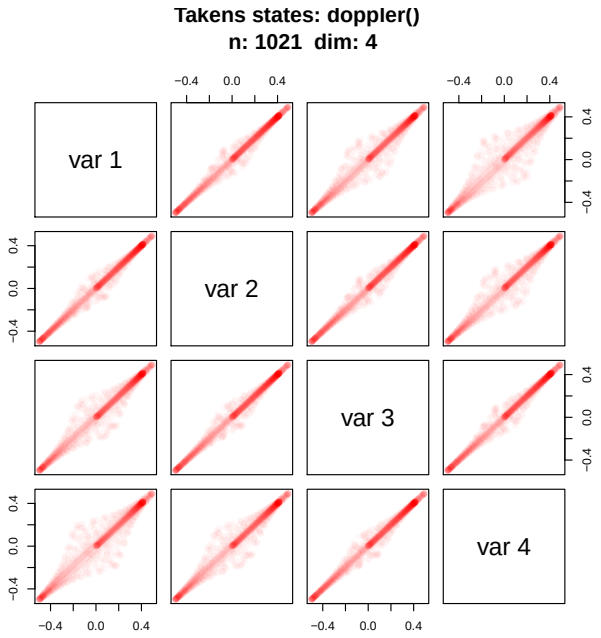


FIGURE 16. Takens states. Test case: Doppler. Note that $2 - dim$ marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.967 sec.

See Figure 17.

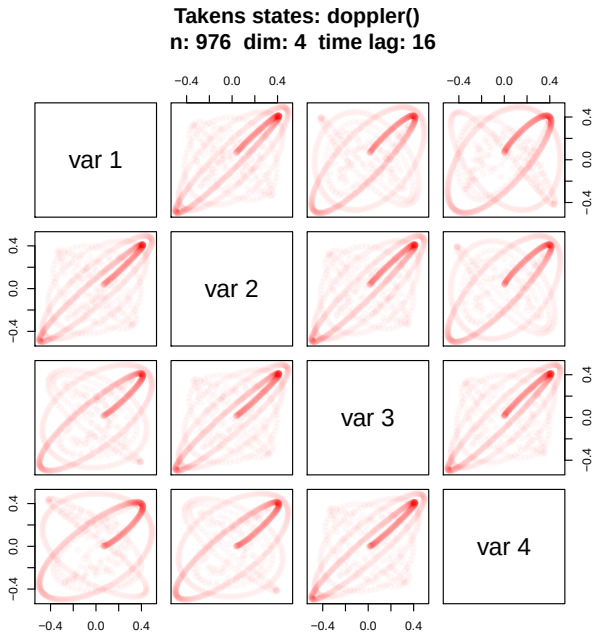


FIGURE 17. Takens states. Test case: doppler at time lag 16. Note that $2 - dim$ marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.95 sec.

Input

```
statepairs(dopplertakens, nooverlap=TRUE) #dim=4
```

See Figure 18.

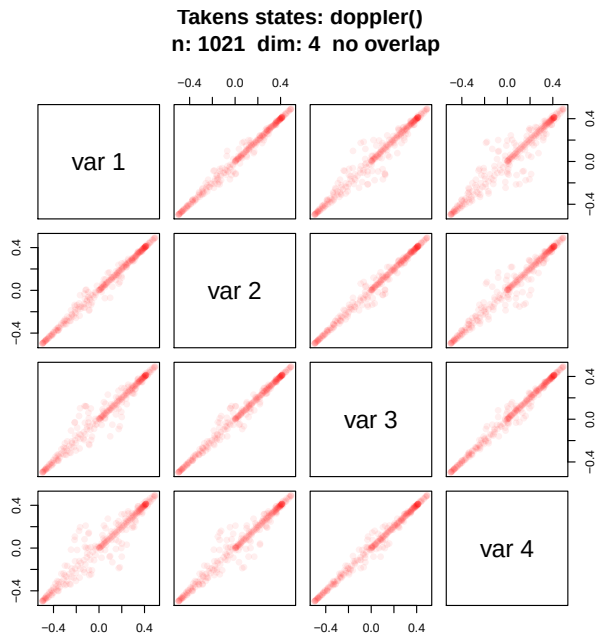


FIGURE 18. Takens states. Test case: doppler, no overlap. Note that $2-dim$ marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 1.351 sec.

Input

```
statecoplot(dopplertakens) #4
```

See Figure 19 on the facing page.

Input

```
statecoplot(dopplertakenslag16) #4
```

See Figure 20 on the next page.

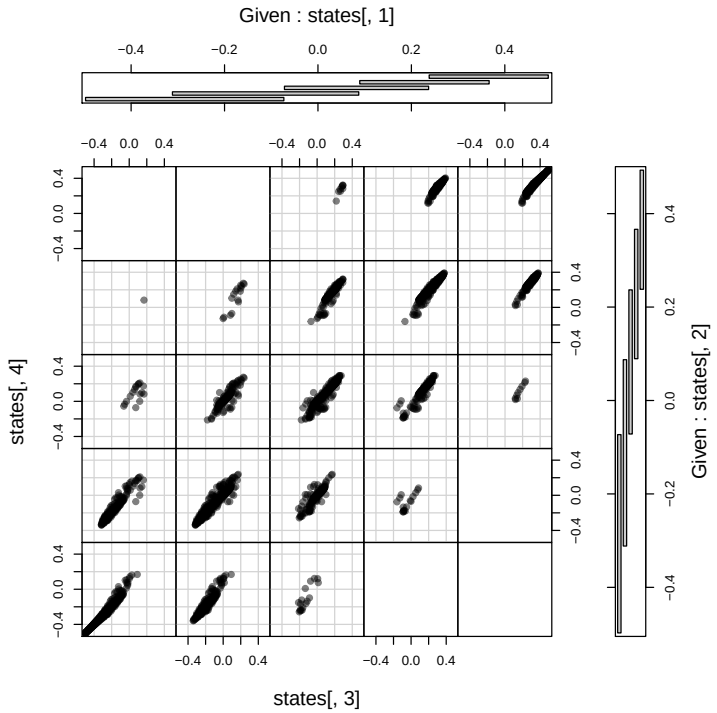


FIGURE 19. State coplot. Test case: Doppler. Note that $2-dim$ marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.256 sec.

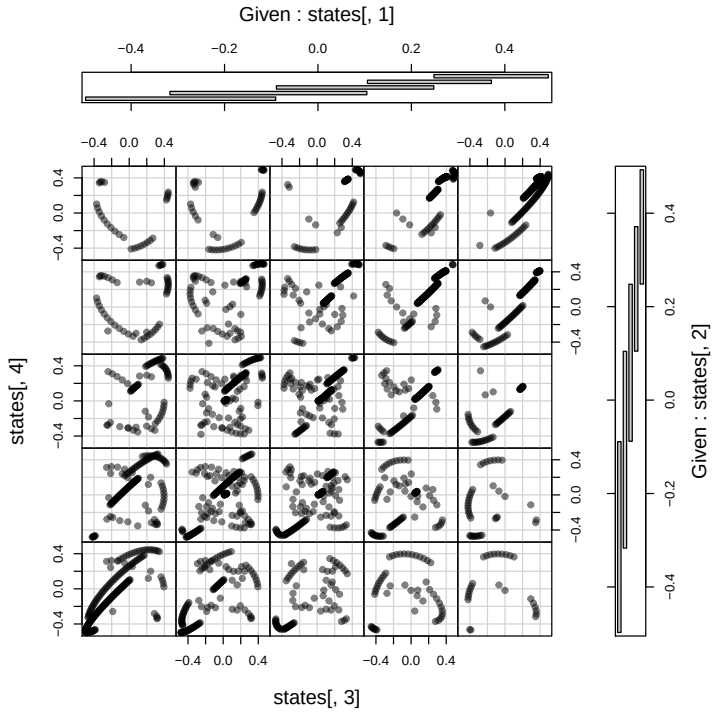


FIGURE 20. State coplot. Test case: Doppler, time lag 16. Note that $2-dim$ marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.244 sec.

6. Recurrence Plots for Test Signals

6.0.1. *Sinus Recurrence Plots.*

Input

```
sin10neighs <- local.findAllNeighbours(sintakens, radius=0.8)
save(sin10neighs, file="sin10neighs.Rdata")
# load(file="sin10neighs.RData")
local.recurrencePlotAux(sin10neighs, dim=dim(sintakens)[2], radius=0.8)
```

See Figure 21.

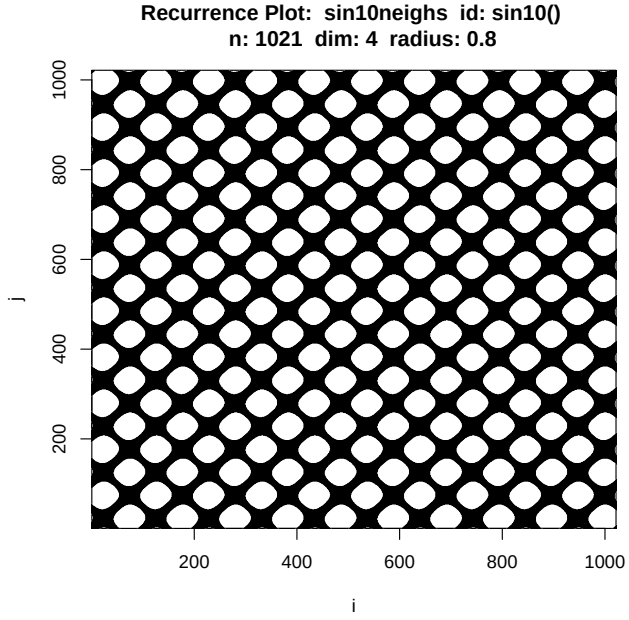


Figure 21. Recurrence plot. Test case: sinus curve. Time used: 1.563 sec.

Input

```
sin10rqa <- showrqa(sintakens, radius=0.8, log=TRUE)
```

Output

```
sin10()  n: 1021  Dim: 4
Radius: 0.8  Recurrence coverage REC: 0.496  log(REC)/log(R): 3.143
Determinism: 1  Laminarity: 1
DIV: 0.001
Trend: 0  Entropy: 3.213
Diagonal lines max: 1020  Mean: 32.712  Mean off main: 32.65
Vertical lines max: 66  Mean: 41.479
```

See Figure 22 on the next page.

Input

```
sin10lag16neighs <- local.findAllNeighbours(sintakenslag16, radius=0.2)
save(sin10lag16neighs, file="sin10lag16neighs.Rdata")
```

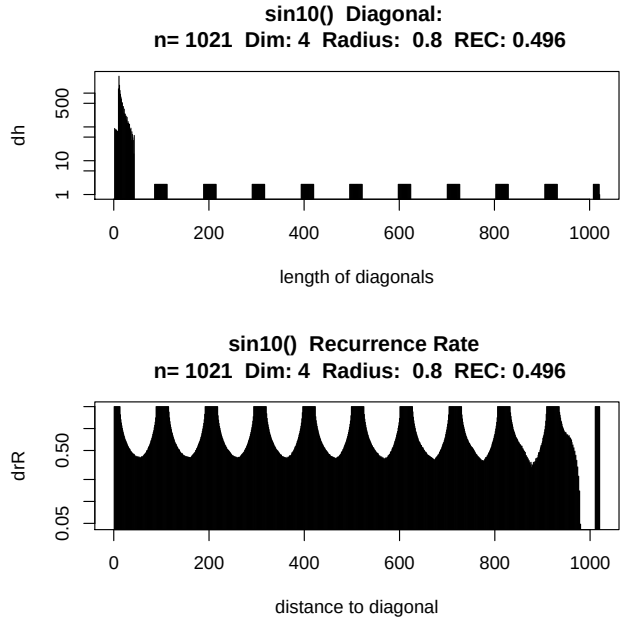


FIGURE 22. RQA. Test case: sinus curve. Time used: 1.023 sec.

```
# load(file="sin10lag16neighs.RData")
local.recurrencePlotAux(sin10lag16neighs, dim=4, radius=0.2)
```

See Figure 23.

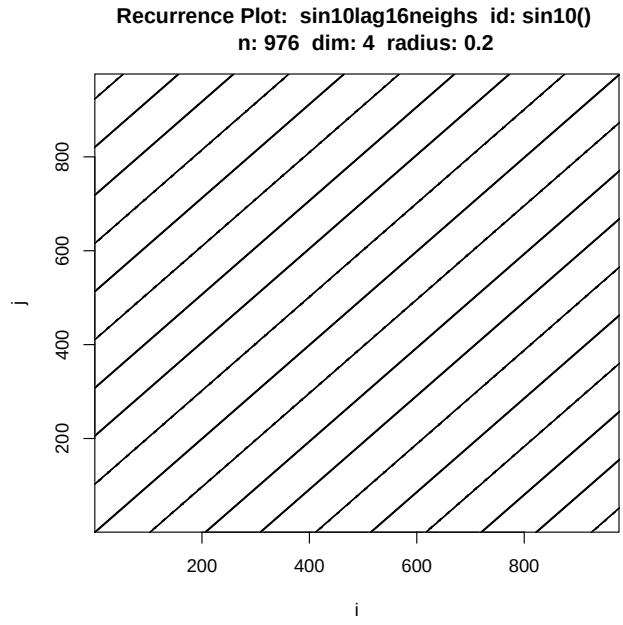


FIGURE 23. Recurrence plot. Recurrence Plot. Test case: sinus curve, time lag 16. Time used: 1.566 sec.

Input
```
sin10lag16rqa <- showrqa(sintakenslag16, radius=0.2)
```

Output
```
sin10()  n: 976  Dim: 4
Radius: 0.2  Recurrence coverage REC: 0.067  log(REC)/log(R): 1.683
Determinism: 0.999  Laminarity: 1
DIV: 0.001
Trend: 0  Entropy: 2.316
Diagonal lines max: 975  Mean: 124.503  Mean off main: 122.827
Vertical lines max: 8  Mean: 6.774
```

See Figure 24.

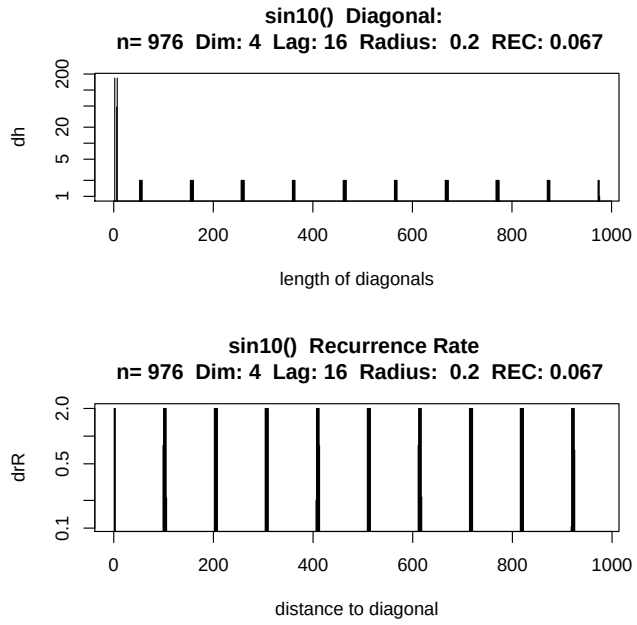


FIGURE 24. RQA. Test case: sinus curve, time lag 16. Time used: 2.249 sec.

6.0.2. *Uniform Random Numbers Recurrence Plots.*

Input

```
unifneighs <- local.findAllNeighbours(uniftakens, radius=0.6)#0.4
save(unifneighs, file="unifneighs.RData")
# load(file="unifneighs.RData")
local.recurrencePlotAux(unifneighs, radius=0.6)
```

See Figure 25.

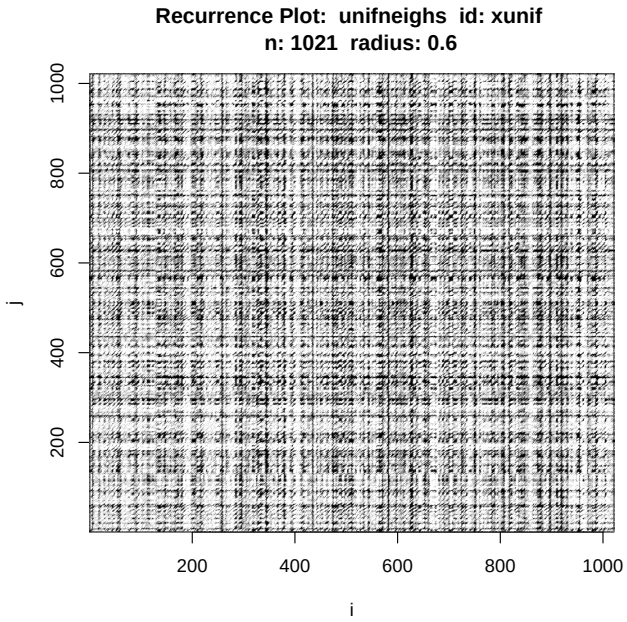


FIGURE 25. Recurrence plot. Test case: uniform random numbers. Time used: 2.084 sec.

Input

```
showrqa(uniftakens, radius=0.6, log=TRUE)
```

Output

```
xunif  n: 1021  Dim: 4
Radius: 0.6  Recurrence coverage REC: 0.491  log(REC)/log(R): 1.392
Determinism: 0.973  Laminarity: 0.785
DIV: 0.017
Trend: 0  Entropy: 2.716
Diagonal lines max: 60  Mean: 7.092  Mean off main: 7.078
Vertical lines max: 1021  Mean: 3.867
```

See Figure 26 on the next page.

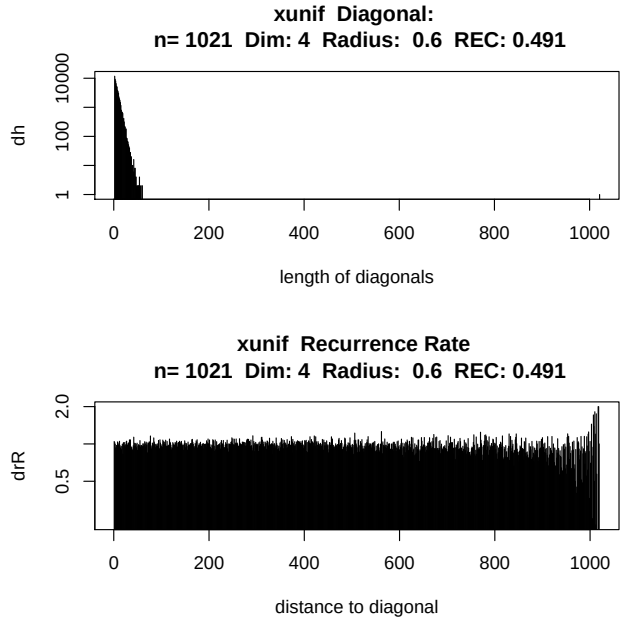


FIGURE 26. RQA. Test case: uniform random numbers, radius=0.6. Time used: 3.358 sec.

6.0.3. *Chirp Signal Recurrence Plots.*

Input

```
chirpneighs <- local.findAllNeighbours(chirptakens, radius=0.6)
save(chirpneighs, file="chirpneighs.RData")
# load(file="chirpneighs.RData")
local.recurrencePlotAux(chirpneighs, radius=0.6)
```

See Figure 27.

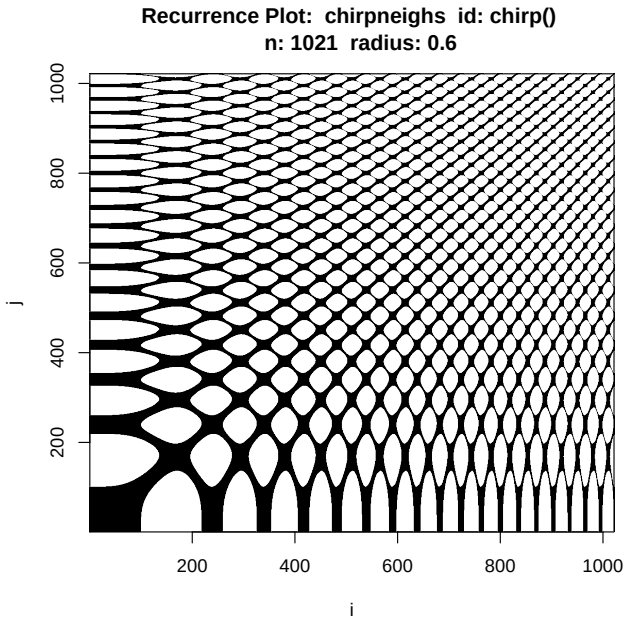


FIGURE 27. Recurrence plot. Test case: chirp signal. Time used: 1.124 sec.

Input

```
showrqa(chirptakens, radius=0.6)
```

Output

```
chirp()  n: 1021  Dim: 4
Radius: 0.6  Recurrence coverage REC: 0.341  log(REC)/log(R): 2.108
Determinism: 0.988  Laminarity: 0.998
DIV: 0.001
Trend: 0  Entropy: 3.254
Diagonal lines max: 1020  Mean: 12.496  Mean off main: 12.46
Vertical lines max: 125  Mean: 14.721
```

See Figure 28 on the next page.

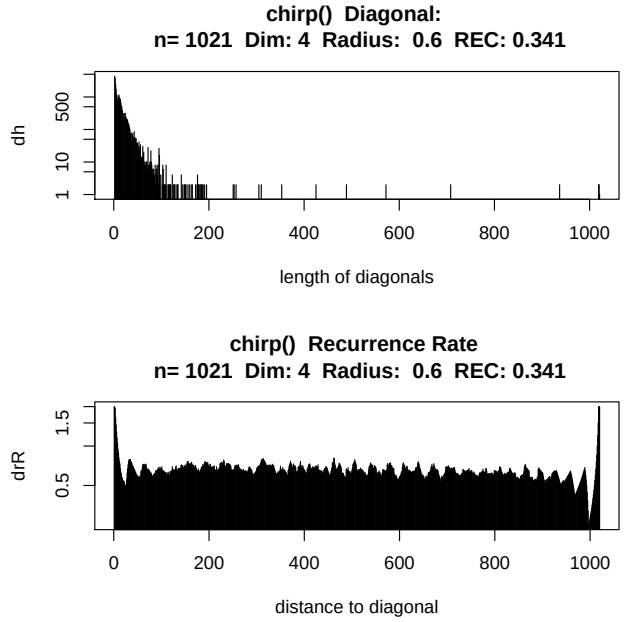


FIGURE 28. RQA. Test case: chirp signal. Time used: 2.165 sec.

6.0.4. *Doppler Recurrence Plots.*

Input

```
dopplerneighs <- local.findAllNeighbours(dopplertakens, radius=0.2)
save(dopplerneighs, file="dopplerneighs.Rdata")
```

Input

```
load(file="dopplerneighs.RData")
local.recurrencePlotAux(dopplerneighs, dim=4, radius=0.2)
```

See Figure 29.

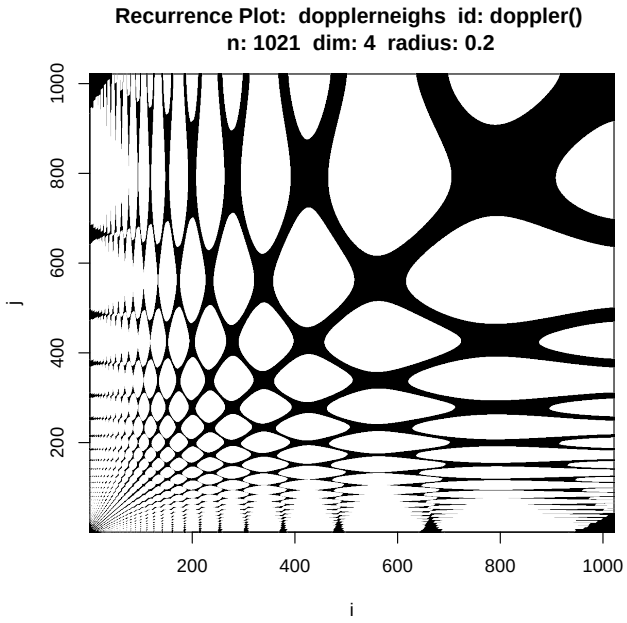


FIGURE 29. Recurrence plot. Test case: Doppler. Time used: 0.997 sec.

Input

```
showrqa(dopplertakens, radius=0.2)
```

Output

```
doppler()  n: 1021  Dim: 4
Radius: 0.2  Recurrence coverage REC: 0.299  log(REC)/log(R): 0.75
Determinism: 0.991  Laminarity: 0.995
DIV: 0.001
Trend: 0  Entropy: 3.445
Diagonal lines max: 1020  Mean: 17.496  Mean off main: 17.439
Vertical lines max: 329  Mean: 24.835
```

See Figure 30 on the next page.

Input

```
dopplerlag16neighs <- local.findAllNeighbours(dopplertakenslag16, radius=0.2)
save(dopplerlag16neighs, file="dopplerlag16neighs.Rdata")
```

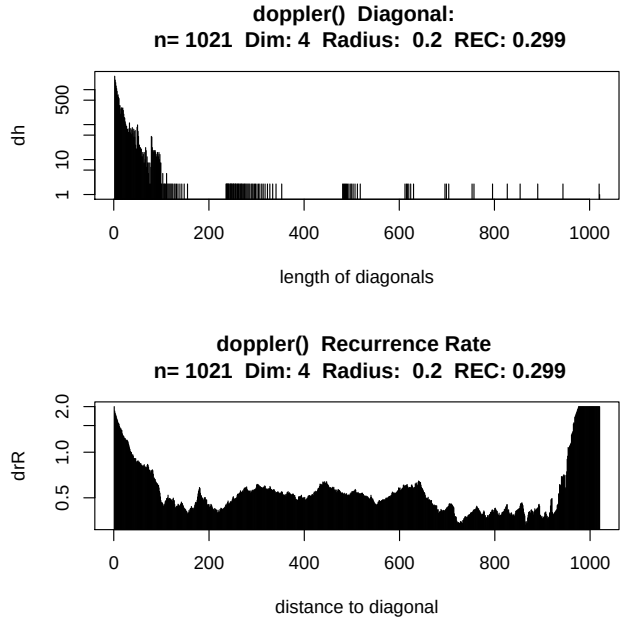


FIGURE 30. RQA. Test case: Doppler. Time used: 0.689 sec.

```
# load(file="dopplerlag16neighs.RData")
local.recurrencePlotAux(dopplerlag16neighs, dim=4, radius=0.2)
```

See Figure 31.

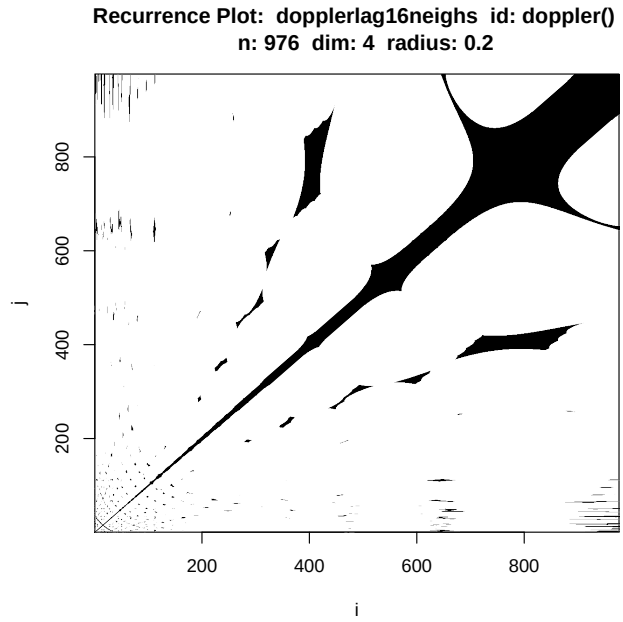


FIGURE 31. Recurrence plot. Test case: Doppler. Time used: 0.91 sec.

Input

```
showrqa(dopplertakenslag16, radius=0.2)
```

Output

```
doppler()  n: 976  Dim: 4
Radius: 0.2  Recurrence coverage REC: 0.098  log(REC)/log(R): 1.443
Determinism: 0.98  Laminarity: 0.989
DIV: 0.001
Trend: 0  Entropy: 2.815
Diagonal lines max: 975  Mean: 28.978  Mean off main: 28.678
Vertical lines max: 256  Mean: 31.539
```

See Figure 32.

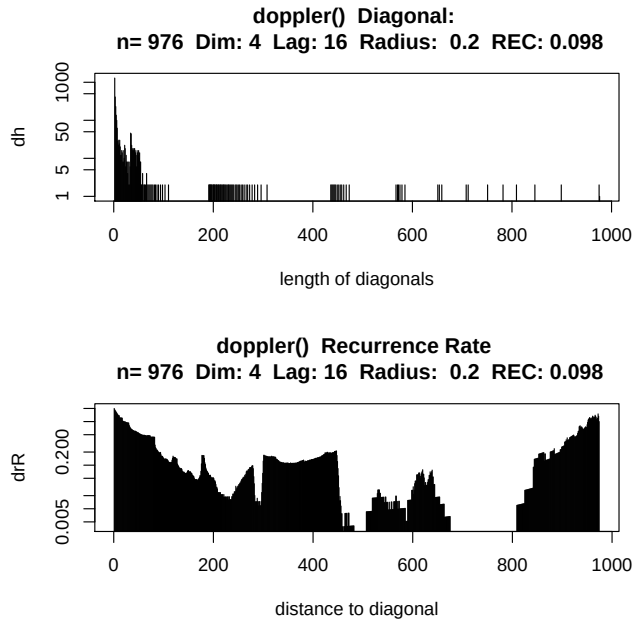


FIGURE 32. RQA. RQA. Test case: Doppler. Time used: 1.447 sec.

7. Bivariate recurrence plots

ToDo: double check: *MASS:::geyser* should be used, not *faithful*

This is a classical data set with a two dimensional structure, *duration* and *waiting*.

More specific it is a marked point process, with points marked as duration and waiting.

Decomposing it, we get two sequences, duration and waiting. Both sequences have (at least) bi-moddal structures. The main application problem is to predict waiting, base on the available information from the past.

Afer decomposition, both sequences can be handled separately.

Input

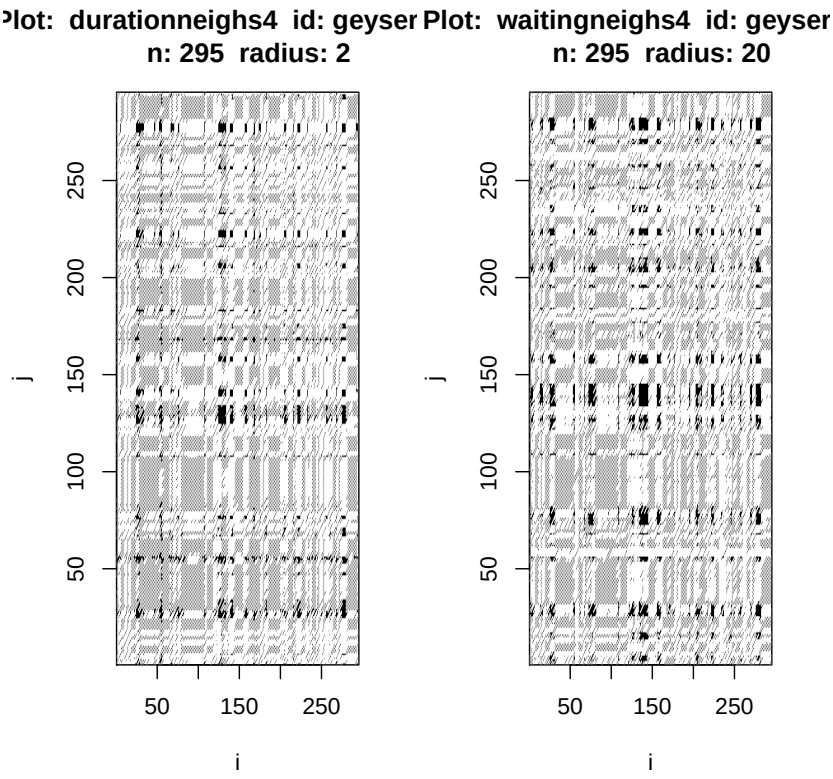
```
try(detach("package:MASS" ), silent=TRUE)
try(detach(faithful), silent=TRUE)
try(detach(geyser), silent=TRUE)
library(MASS)
data(geyser)
```

Input

```
attach(geyser)
takens.duration4 <- buildTakens( time.series=duration[-1], embedding.dim=4, time.lag=1)
takens.waiting4 <- buildTakens( time.series=waiting[-1], embedding.dim=4, time.lag=1)
takens.duration4 <- buildTakens( time.series=geyseradj$duration[-1], embedding.dim=4, time.lag=1)
takens.waiting4 <- buildTakens( time.series=geyseradj$waiting[-1], embedding.dim=4, time.lag=1)
durationneighs4<- findAllNeighbours(takens.duration4, radius=2.0)
waitingneighs4<-findAllNeighbours(takens.waiting4, radius=20.0)
```

Input

```
oldpar <- par(mfrow=c(1,2))
local.recurrencePlotAux(durationneighs4)
local.recurrencePlotAux(waitingneighs4)
par(oldpar)
```



Assuming that labels etc. are propragated as attributes, we can use a modified version of *recureencePlot()*

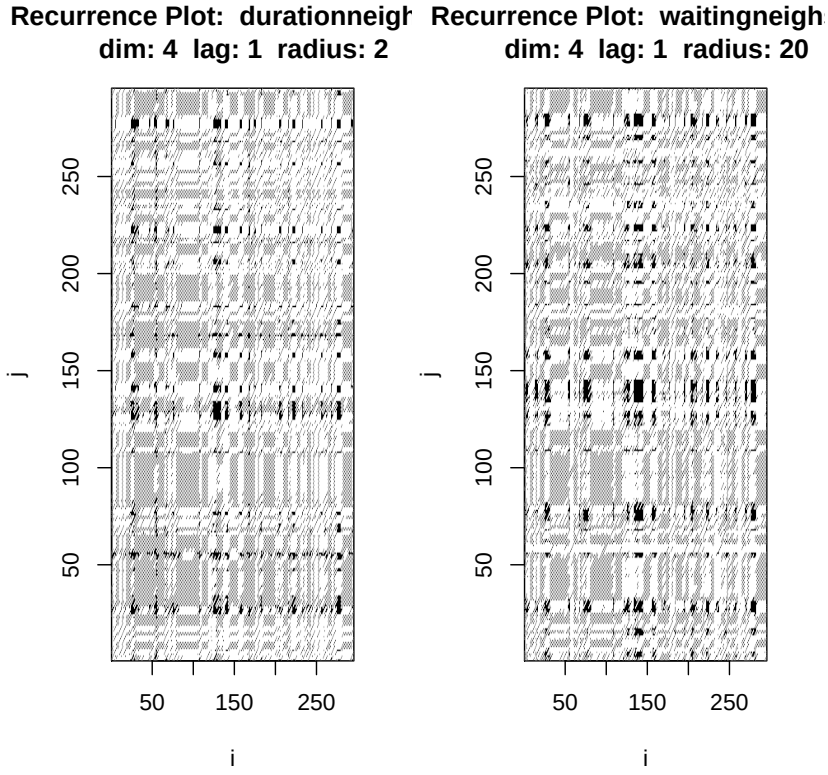
Input

```
# univariate variant, assuming attributes
local.recurrencePlot1=function(neighs){
    dim <- attr(neighs,"embedding.dim")
    lag <- attr(neighs,"time.lag")
    radius <- attr(neighs,"radius")
        # 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
                )
 #        )

}
```

Input

```
oldpar <- par(mfrow=c(1,2))
local.recurrencePlot1(durationneighs4)
local.recurrencePlot1(waitingneighs4)
par(oldpar)
```



Each plot shows a symmetric matrix. Since dimensions match, we can use the upper and ower triangle to allow comparison of both series in one plot, comparing the upper and lower triangle.

Input

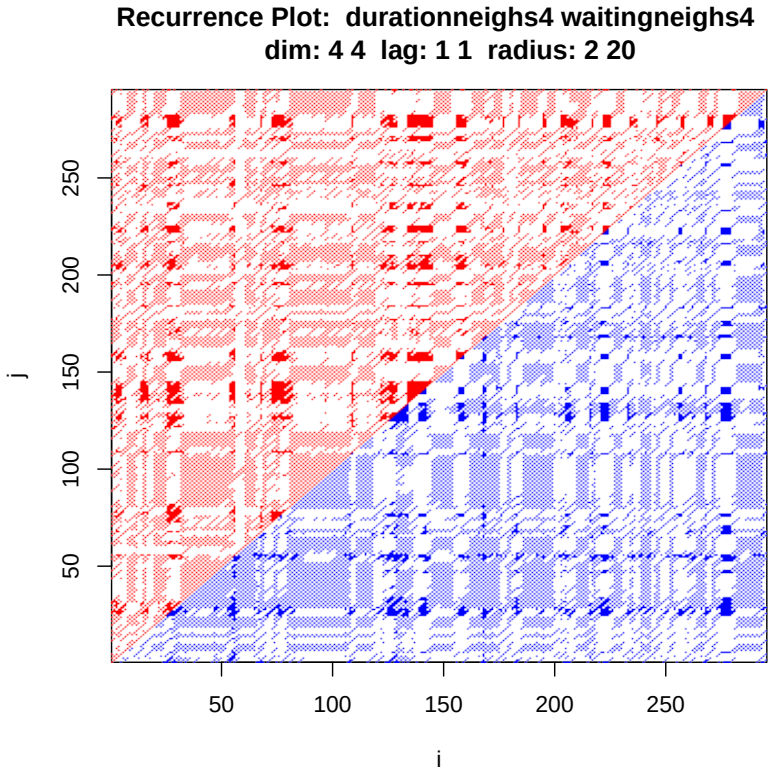
```
# bivariate variant, assuming attributes
# same dimension and size required
local.recurrencePlot2=function(neighs1, neighs2){
    dim1 <- attr(neighs1,"embedding.dim")
    lag1 <- attr(neighs1,"time.lag")
    radius1 <- attr(neighs1,"radius")

    dim2 <- attr(neighs2,"embedding.dim")
    lag2 <- attr(neighs2,"time.lag")
    radius2 <- attr(neighs2,"radius")

        # 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)
        }

#1
```

```
  ntakens1=length(neighs1)
  neighs1.matrix <- matrix(nrow=ntakens1,ncol=ntakens1)
  #neighbourListNeighbourMatrix()
    #neighs.matrix = Diagonal(ntakens)
          for (i in 1:ntakens1){
                  neighs1.matrix[i,i] = 1 # do we want the diagonal fixed to 1
            if (length(neighs1[[i]])>0){
              for (j in neighs1[[i]]){
                neighs1.matrix[i,j] = 1
              }
            }
          }
#2
  ntakens2=length(neighs2)
  neighs2.matrix <- matrix(nrow=ntakens2,ncol=ntakens2)
  #neighbourListNeighbourMatrix()
    #neighs.matrix = Diagonal(ntakens)
          for (i in 1:ntakens2){
                  neighs2.matrix[i,i] = 1 # do we want the diagonal fixed to 1
            if (length(neighs2[[i]])>0){
              for (j in neighs2[[i]]){
                neighs2.matrix[i,j] = 1
              }
            }
          }
# merge
neighs.matrix <- neighs1.matrix
# replace upper triangle by neighs2.matrix
for (i in 1:ntakens2){
        for (j in i:ntakens2)
        neighs.matrix[i,j] <- - neighs2.matrix[i,j]  #for colour
}


        main <- paste("Recurrence Plot: ",
                      deparse(substitute(neighs1)),
                      deparse(substitute(neighs2))
                      )
        more <- NULL

        #use compones of neights if available
        if (!is.null(dim1)) more <- paste(more," dim:",dim1, dim2)
        if (!is.null(lag1)) more <- paste(more," lag:",lag1, lag2)
        if (!is.null(radius1)) more <- paste(more," radius:",radius1, radius2)

        if (!is.null(more)) main <- paste(main,"\n",more)
#

ntakens <- ntakens1

  # 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=c("red","blue"),
                #xlim=c(1,ntakens), ylim=c(1,ntakens),
                useRaster=TRUE,  #? is this safe??
                main=main
                )
 #        )
```

```
}
```

Input

```
oldpar <- par(mfrow=c(1,1))
local.recurrencePlot2(durationneighs4,waitingneighs4)
par(oldpar)
```



So far, the data have been handled as a pair of one-dimensional problems. Looking at the data as a bivariate problem requires to use a bivariate distance to define neighbours.

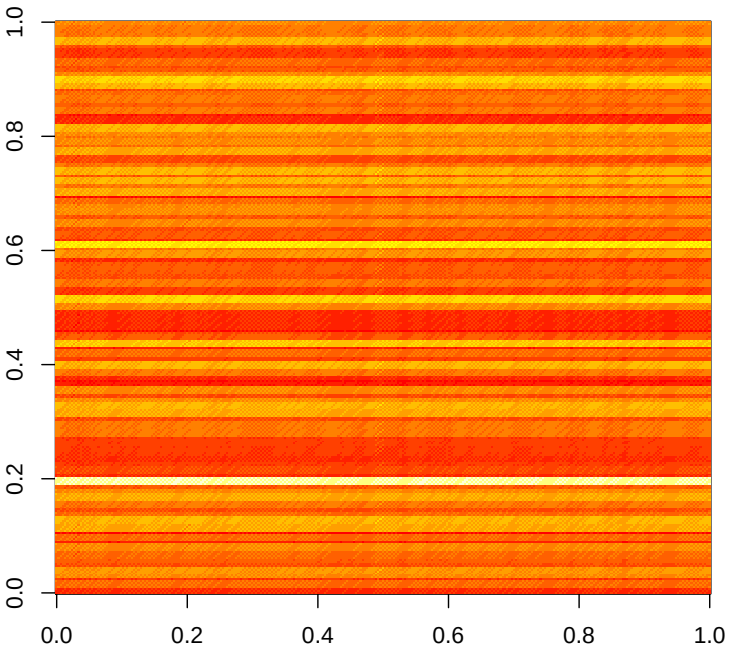
Input

```
#
# covariance
# see \cite{marwan2002nonlinear}
# CR[i,j] = \Theta( \epsilon - \norm( xv[i] - yv[j] ))

# Brute force

# signed distances may be used for experiments.
maxdist <- function (x){ max(abs(x))} # works on delta
cordist <- function (x, y){ suppressWarnings(cor(x,y))} # using signed. Warnings for zero #
# variances are suppressed

# epsilon/radius and heaviside not use here - may be added in image rendering.

# propagate names from takens
```

```
CR0 <- function (xtakens, ytakens, sdist= maxdist) {
        xl <- nrow(xtakens); yl <- nrow(ytakens)
        xname <- deparse(substitute(xtakens))
        yname <- deparse(substitute(ytakens))
        cr <- matrix(nrow=xl, ncol=yl)
        for (i in 1:xl)
         for (j in 1:yl)
        {
        cr[i,j] <- sdist(xtakens[i,]- ytakens[j,])
        }
        return(cr)
}
CR2 <- function (xtakens, ytakens, cdist= cordist) {
        xl <- nrow(xtakens); yl <- nrow(ytakens)
        xname <- deparse(substitute(xtakens))
        yname <- deparse(substitute(ytakens))
        cr <- matrix(nrow=xl, ncol=yl)
        for (i in 1:xl)
         for (j in 1:yl)
        {
        cr[i,j] <- cdist(xtakens[i,], ytakens[j,])
        }
        return(cr)
}
## for experiments only. do not copy large matrices
crossrecurrencePlotFromMatrix <- function(neighs.matrix,
                                                                    zlim= range(neighs.matrix, na.rm
                                                                    main="Cross Recurrence plot",
                                  xlab="x Takens vector's index",
                                  ylab="y Takens vector's index",...){
  # need a print because it is (possibly) a trellis object!!
  rec.plot = image(neighs.matrix,
                                        zlim= zlim,
                                        x = 1: ncol(neighs.matrix),
                                        y = 1: nrow(neighs.matrix),
                   main = main, xlab = xlab, ylab = ylab,
                   ...)
  print(rec.plot)
  rec.plot
}
# raw data may give a poor impression. Adjust e.g. for scale and location
cr4 <- CR0(takens.duration4,takens.waiting4)
cr4C <- CR2(takens.duration4,takens.waiting4)
```

Input

```
image(cr4)
# neighs.matrix <- cr4;range(cr4) #  70.5500 107.1667
```

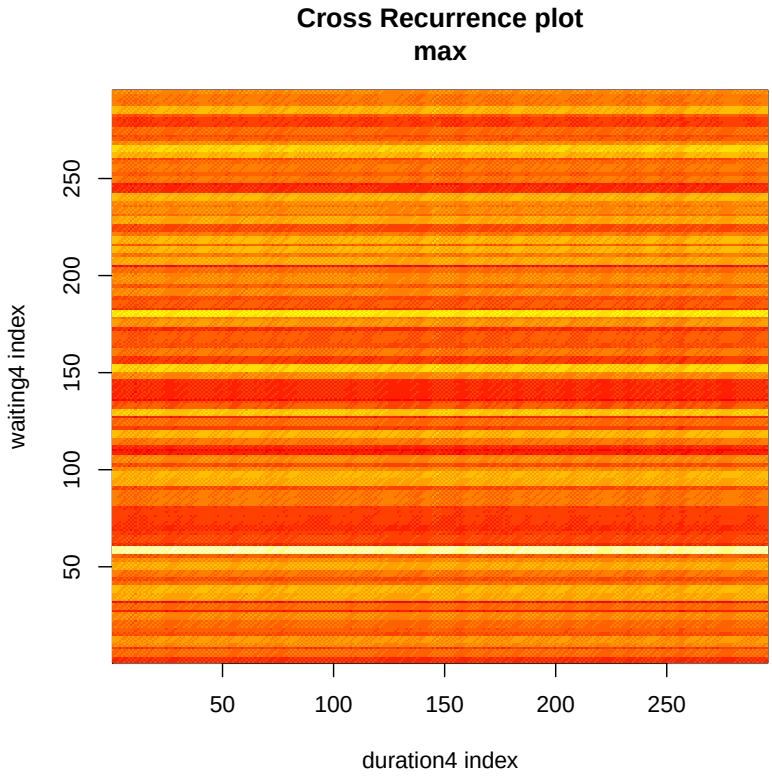


Input

```
# a max distance
crossrecurrencePlotFromMatrix(cr4,
main="Cross Recurrence plot\nmax",
xlab="duration4 index", ylab="waiting4 index")  # ugly heat matrix
```

Output

```
NULL
NULL
```



Input

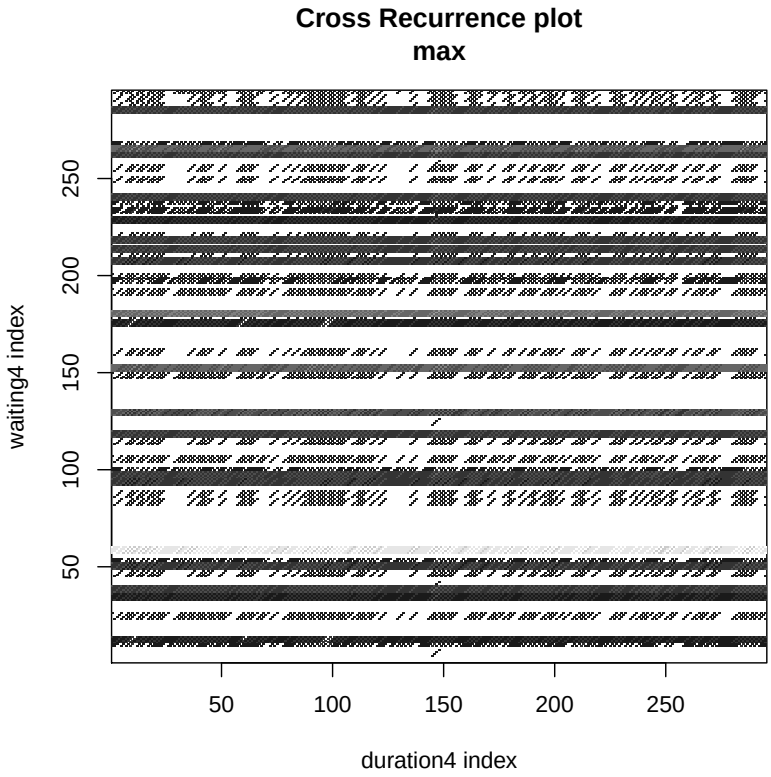
```
crossrecurrencePlotFromMatrix(cr4, zlim=c(85,108), col=grey((1:10)/10),
main="Cross Recurrence plot\nmax",
xlab="duration4 index", ylab="waiting4 index")
```

Output

```
NULL
NULL
```

Input

```
# near conventional bw,
# introducing radius/cut by zlim
```

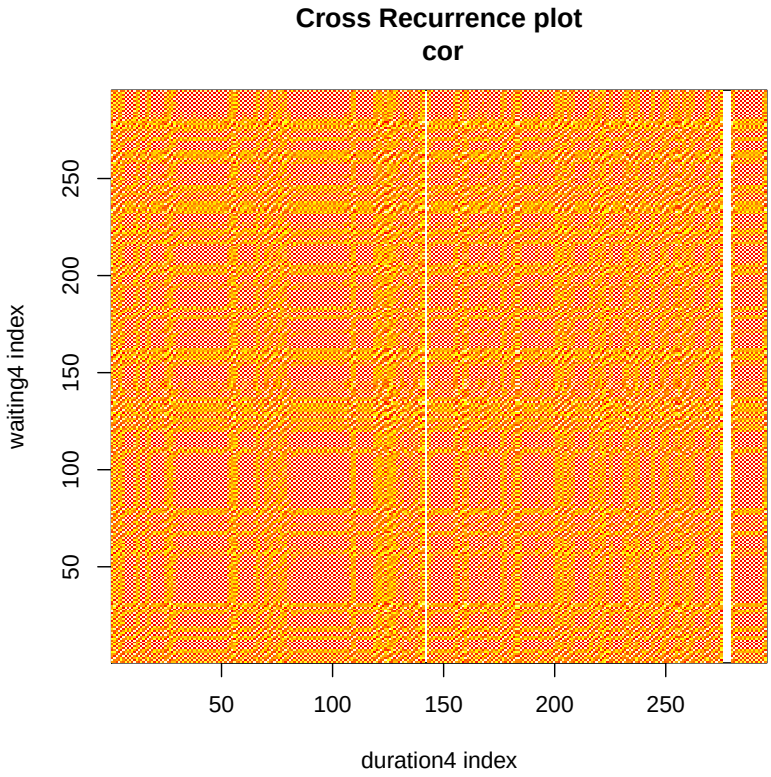


Input

```
# a correlation distance
crossrecurrencePlotFromMatrix(cr4C,
main="Cross Recurrence plot\n cor",
xlab="duration4 index", ylab="waiting4 index")  # ugly heat matrix
```

Output

```
NULL
NULL
```



Input

```
quantile(cr4C, na.rm=TRUE)
```

Output

```
         0%         25%         50%         75%        100%
-1.00000000 -0.68871962 -0.03456356  0.72305306  1.00000000
```

Input

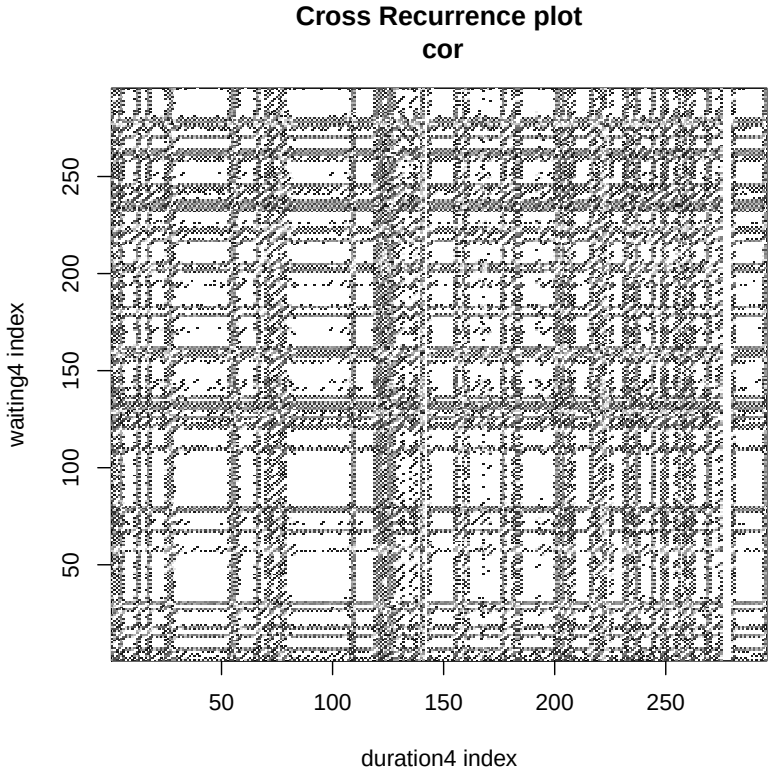
```
crossrecurrencePlotFromMatrix(cr4C, zlim=c(-0.7,0.7), col=grey((1:10)/10),
main="Cross Recurrence plot\n cor",
xlab="duration4 index", ylab="waiting4 index")
```

Output

```
NULL
NULL
```

Input

```
# near conventional
# introducing radius/cut by zlim
```


Cross Recurrence plot
cor
waiting4 index
50
100
150
200
250
duration4 index
50
100
150
200
250

8. Case Study: Geyser data –defunct

Defunct. hopefully completely replaced by bivariate analysis in previous chapter.

This is a classical data set with a two dimensional structure, *duration* and *waiting*.

The data structure asks for a variant of the recurence plot, adapted to a two dimensional series.

ToDo: double check: `MASS:::geyser` should be used, not `faithful`

ToDo: Geyser: extended to two-dimensional data in `geyserlin`. Experimental only. Check.

9. Case Study: HRV data example.beats

Only 1024 data points used in recurrence plots in this section

Input

```
#stop("Stopping before RHRV")

#install.packages("RHRV",repos="http://r-forge.r-project.org",type="source")
if (!require("RHRV")) {
install.packages("RHRV")
library(RHRV)
}
load("/users/gs/projects/rforge/rhrv/pkg/data/HRVData.rda")
load("/users/gs/projects/rforge/rhrv/pkg/data/HRVProcessedData.rda")
#####################################################
### code chunk number 1: creation
#####################################################
hrv.data  = CreateHRVData()
hrv.data = SetVerbose(hrv.data, TRUE )
#####################################################
### code chunk number 3: loading
#####################################################
hrv.data = LoadBeatAscii(hrv.data, "example.beats",
       RecordPath = "/users/gs/projects/rforge/rhrv/tutorial/beatsFolder")
#       RecordPath = "beatsFolder")


#####################################################
### code chunk number 4: derivating
#####################################################
hrv.data = BuildNIHR(hrv.data)
```

Input

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

See Figure 33.

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

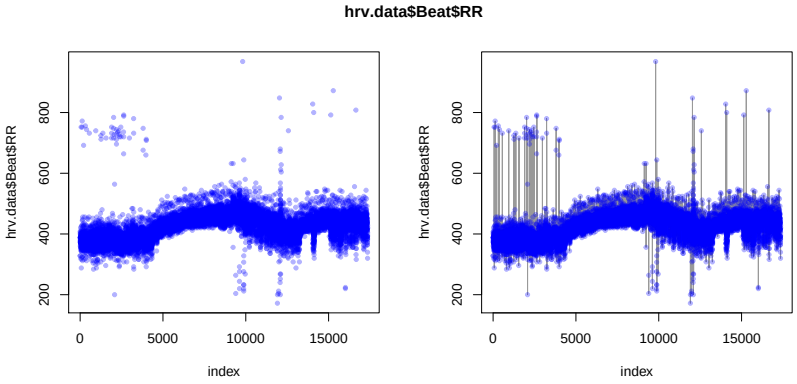


Figure 33. RHRV tutorial example.beats. Signal and linear interpolation.

Input

```
hrvRRtakens4 <- local.buildTakens( time.series=hrv.data$Beat$RR[1:nsignal],
        embedding.dim=4,time.lag=1)
statepairs(hrvRRtakens4) #dim=4
```

See Figure 34.

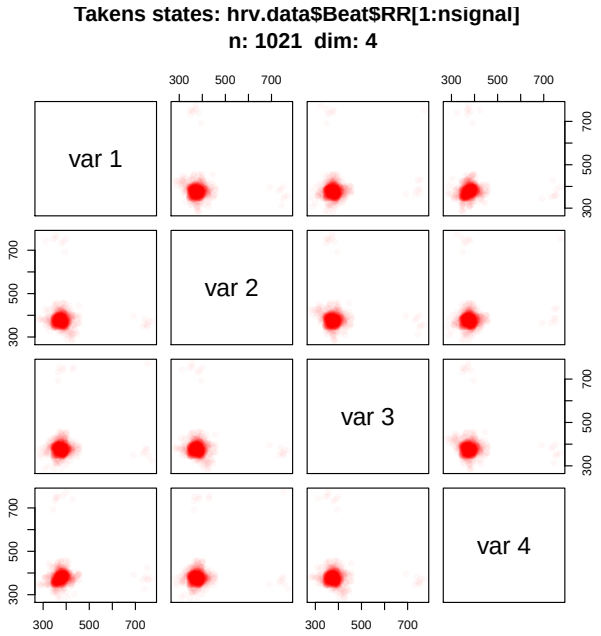


FIGURE 34. Recurrence plot. RHRV tutorial example.beats. Time used: 0.872 sec.

Input

```
statepairs(hrvRRtakens4, rank=TRUE) #dim=4
```

See Figure 35 on the facing page.

Input

```
statecoplot(hrvRRtakens4) #dim=4
```

See Figure 36 on page 70.

See Figure 37 on page 70.

Input

```
hrvRRneighs4  <- local.findAllNeighbours(hrvRRtakens4, radius=16)
save(hrvRRneighs4, file="hrvRRneighs4.Rdata")
```

Time used: 0.072 sec.

Input

```
load(file="hrvRRneighs4.RData")
local.recurrencePlotAux(hrvRRneighs4)
```

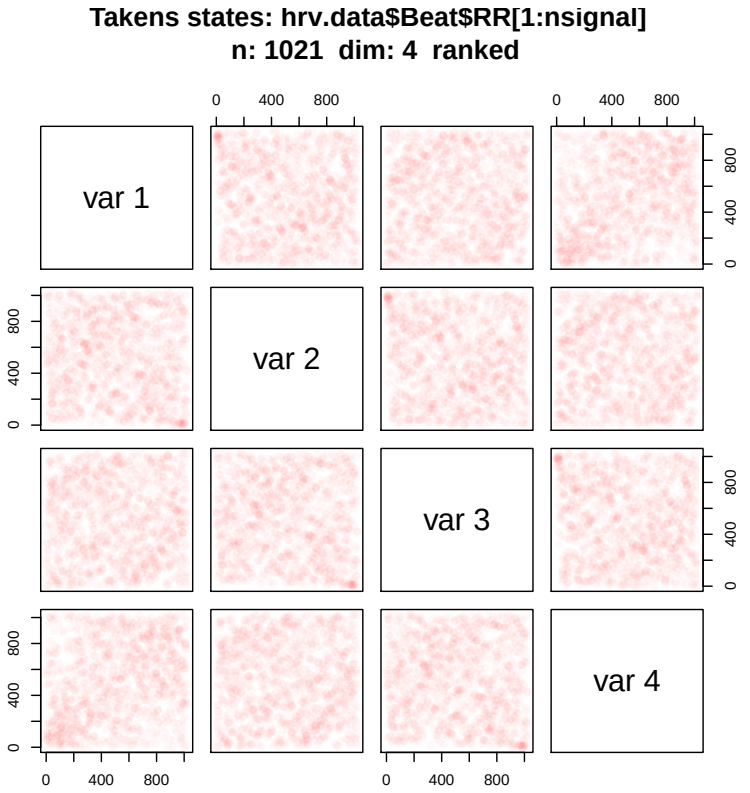


FIGURE 35. RHRV tutorial example.beats. Ranked data. Time used: 1.681 sec.

See Figure 38 on page 71.

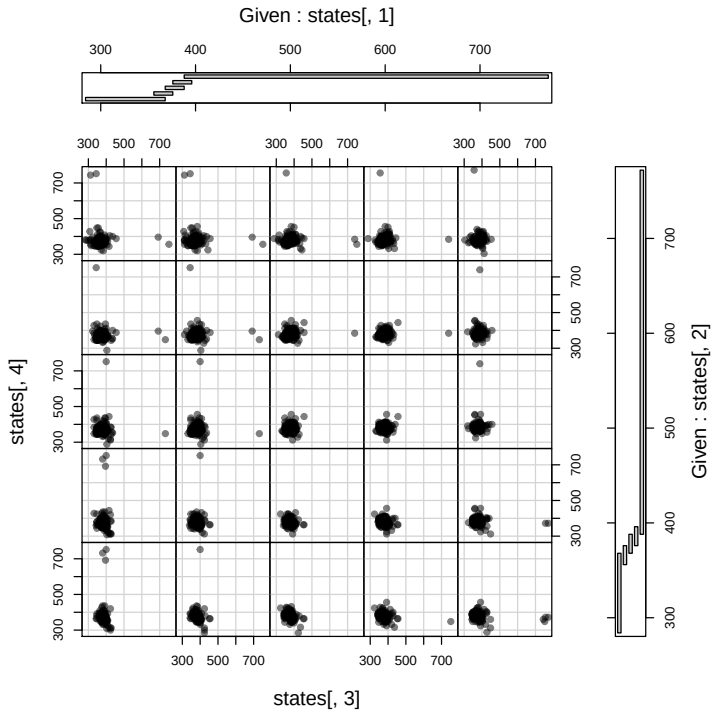


FIGURE 36. State coplot. RHRV tutorial example.beats. Time used: 0.22 sec.

FIGURE 37. Recurrence plot. RHRV tutorial example.beats. Time used: 0.002 sec.

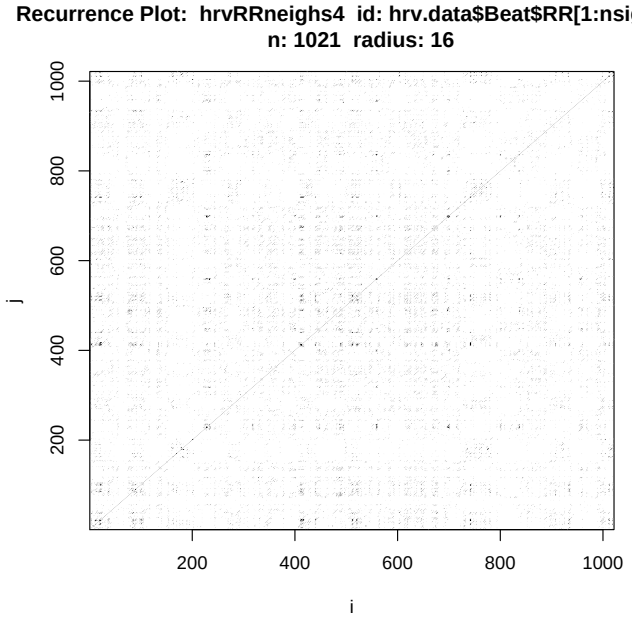


FIGURE 38. Recurrence plot. Recurrence Plot. Example case: RHRV tutorial example.beats. Dim=4. Time used: 0.822 sec.

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

9.0.1. *RHRV: example.beats - Comparison by Dimension.*

Input

```
hrvRRtakens2 <- local.buildTakens( time.series=hrv.data$Beat$RR[1:nsignal],
        embedding.dim=2,time.lag=1)
hrvRRneighs2  <- local.findAllNeighbours(hrvRRtakens2, radius=16)
save(hrvRRneighs2, file="hrvRRneighs2.Rdata")
# load(file="hrvRRneighs2.RData")
local.recurrencePlotAux(hrvRRneighs2)
showrqa(hrvRRtakens2, do.hist=FALSE, radius=16)
```

Output

```
hrv.data$Beat$RR[1:nsignal]  n: 1023  Dim: 2
Radius: 16  Recurrence coverage REC: 0.165  log(REC)/log(R): -0.65
Determinism: 0.651  Laminarity: 0.376
DIV: 0.056
Trend: 0  Entropy: 1.248
Diagonal lines max: 18  Mean: 2.841  Mean off main: 2.816
Vertical lines max: 14  Mean: 2.463
```

See Figure 39.

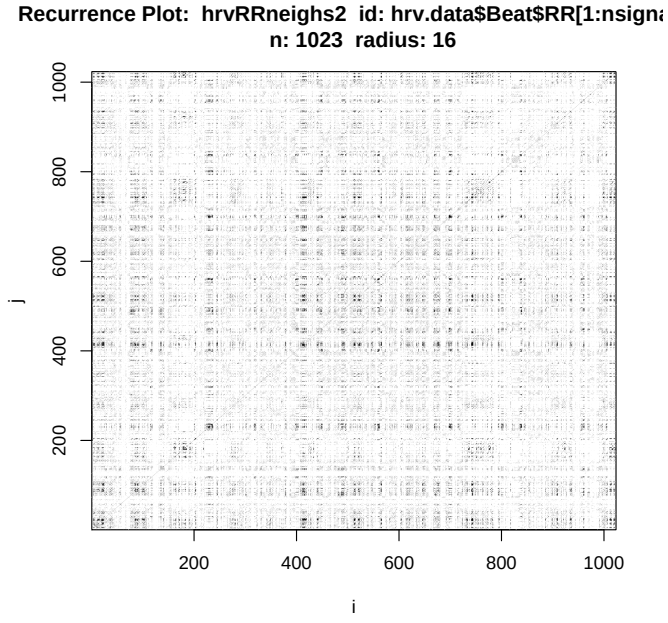


FIGURE 39. Recurrence plot. Dim=2. Time used: 1.356 sec.

Input

```
hrvRRtakens6 <- local.buildTakens( time.series=hrv.data$Beat$RR[1:nsignal],
        embedding.dim=6,time.lag=1)
hrvRRneighs6  <- local.findAllNeighbours(hrvRRtakens6, radius=16)
save(hrvRRneighs6, file="hrvRRneighs6.Rdata")
# load(file="hrvRRneighs6.RData")
local.recurrencePlotAux(hrvRRneighs6)
```

Dim=6. Time used: 0.877 sec.

Input

```
hrvRRtakens8 <- local.buildTakens( time.series=hrv.data$Beat$RR[1:nsignal],
        embedding.dim=8,time.lag=1)
hrvRRneighs8  <- local.findAllNeighbours(hrvRRtakens8, radius=32)
save(hrvRRneighs8, file="hrvRRneighs8.Rdata")
# load(file="hrvRRneighs8.RData")
local.recurrencePlotAux(hrvRRneighs8)
```

Dim=8. Time used: 1.356 sec.

Input

```
hrvRRtakens12 <- local.buildTakens( time.series=hrv.data$Beat$RR[1:nsignal],
        embedding.dim=2,time.lag=1)
hrvRRneighs12  <- local.findAllNeighbours(hrvRRtakens12, radius=16)
save(hrvRRneighs12, file="hrvRRneighs12.Rdata")
# load(file="hrvRRneighs12.RData")
local.recurrencePlotAux(hrvRRneighs12)
```

Dim=12. Time used: 2.621 sec.

Input

```
hrvRRtakens16 <- local.buildTakens(
        time.series=hrv.data$Beat$RR[1:nsignal],
        embedding.dim=16,time.lag=1)
hrvRRneighs16  <- local.findAllNeighbours(hrvRRtakens16, radius=32)
save(hrvRRneighs16, file="hrvRRneighs16.Rdata")
# load(file="hrvRRneighs16.RData")
local.recurrencePlotAux(hrvRRneighs16)
```

Dim=16. Time used: 0.771 sec.

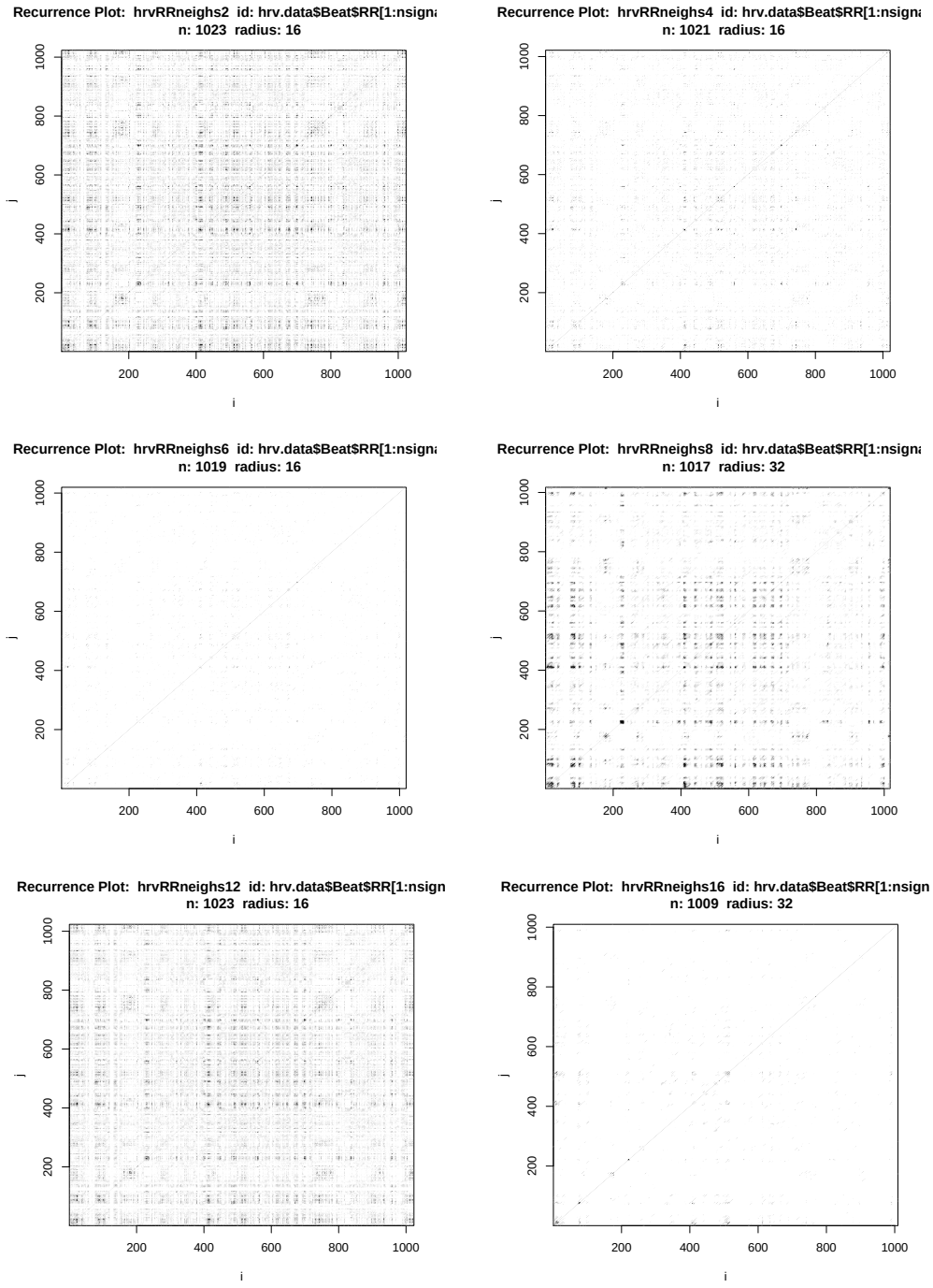


FIGURE 40. Recurrence Plot. Example case: RHRV tutorial example.beats. Dim=2, 4, 6, 8, 12, 16. Time used: 0.772 sec.

ToDo: This is an experimental proposal

9.1. **RHRV: example.beats - Hart Rate Variation.** Since we are not interested in heart rate (or pulse), but in heart rate variation, a proposal is to use scaled differences.

Input

```
# source('/users/gs/projects/rforge/rhrv/pkg/R/BuildNIHR2.R', chdir = TRUE)
BuildNIDHR <-
function(HRVData, verbose=NULL) {
#------------------------------------------------------
# Obtains instantaneous heart rate variation from beats positions
# D for difference. The scaled difference is recorded as variation HRRV
#------------------------------------------------------
        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
        # end addition gs
        return(HRVData)
}
```

differences for HRV

Input

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

Output

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

Input

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

These are the displays of the Takens state space we used before, now for HRRV:

Input
```
plotsignal(HRRV)
```

See Figure 41,

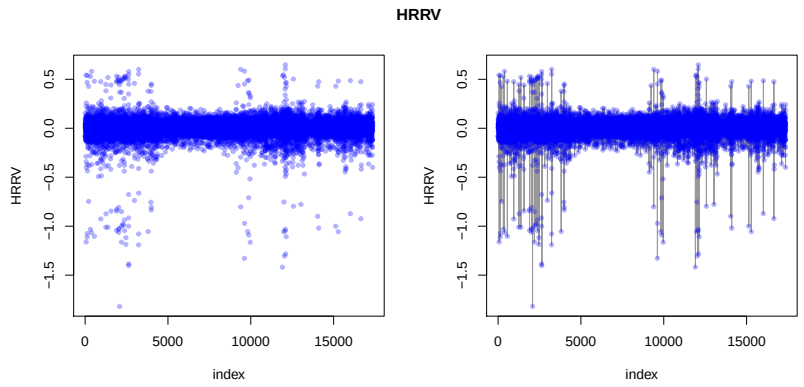


FIGURE 41. RHRV tutorial example.beats. HRRV Signal and linear interpolation.

Only 1024 data points used in this section

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

See Figure 42 on the facing page

Input
```
statepairs(hrvRRVtakens4, rank=TRUE) #dim=4
```

ToDo: findAllNeighbours does not handle NAs

See Figure 43 on page 78

Input
```
#use hack: findAllNeighbours does not handle NAs
hrvRRVneighs4  <- local.findAllNeighbours(hrvRRVtakens4[-(1:2),], radius=0.125)
save(hrvRRVneighs4, file="hrvRRVneighs4.Rdata")
```

Time used: 0.152 sec.

Input
```
load(file="hrvRRVneighs4.RData")
local.recurrencePlotAux(hrvRRVneighs4,dim=4, radius=0.125)
```

ToDo: check. There seem to be strange artefacts.

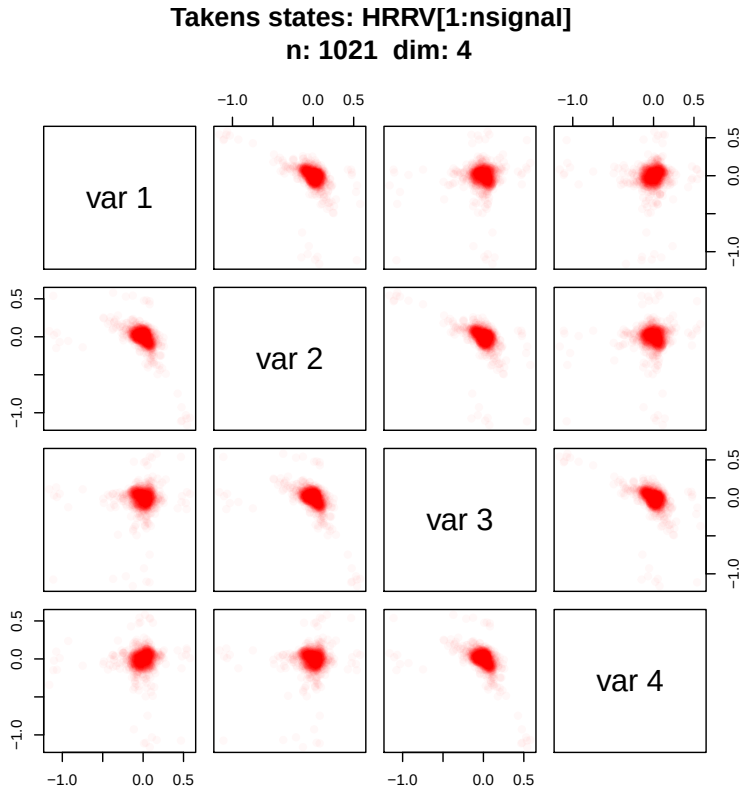


FIGURE 42. RHRV tutorial example.beats. HRRV Time used: 0.804 sec.

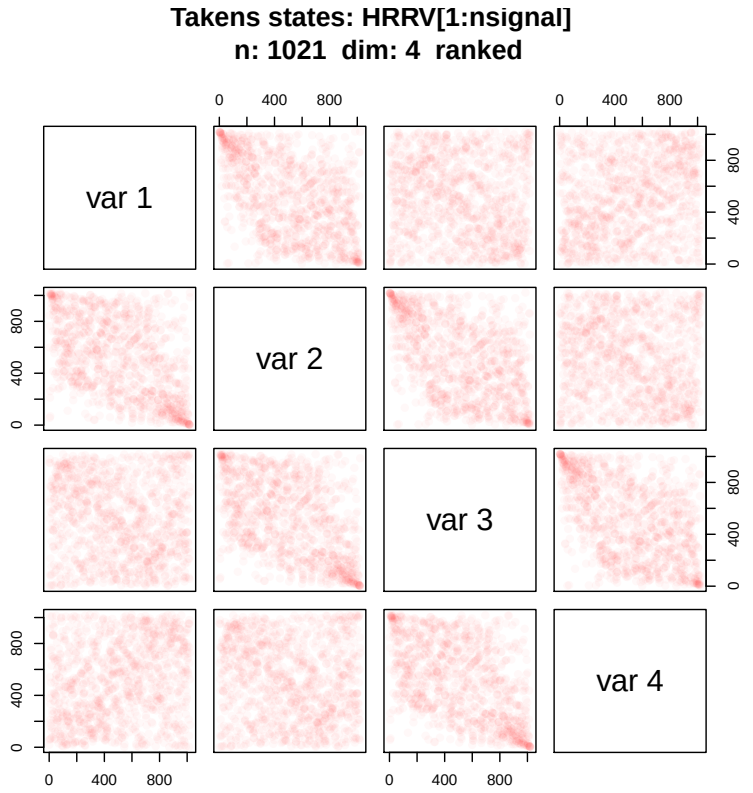


FIGURE 43. RHRV tutorial example.beats. Ranked HRRV data. Time used: 1.588 sec.

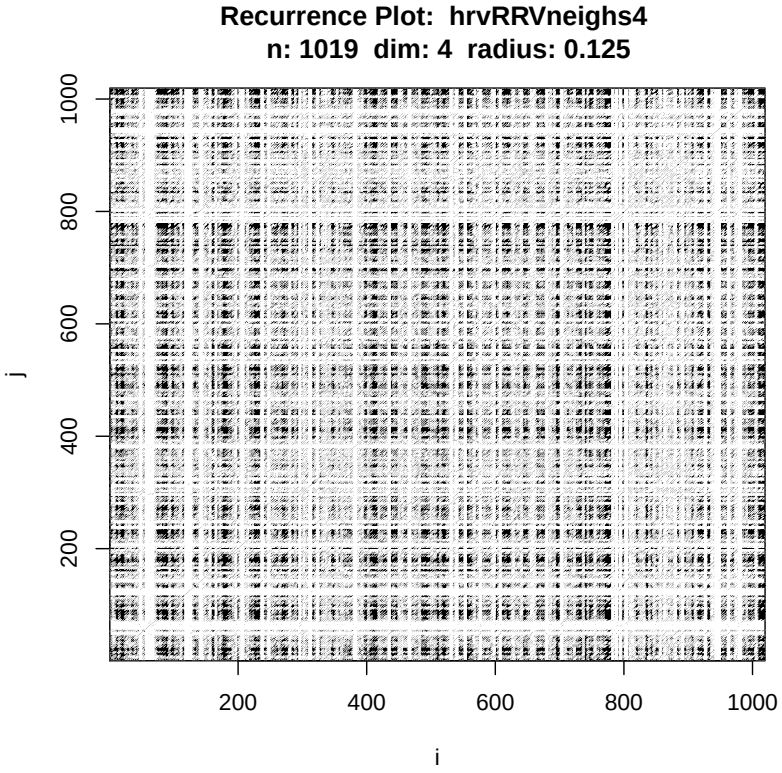


FIGURE 44. Recurrence Plot. Example case: RHRV tutorial example.beats. HRRV Dim=4. Time used: 1.289 sec.

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

9.1.1. *RHRV: example.beats - RR Variation: Comparison by Dimension.*

Input

```
hrvRRVtakens2 <- local.buildTakens( time.series=HRRV[1:nsignal],
        embedding.dim=2, time.lag=1)
hrvRRVneighs2  <- local.findAllNeighbours(hrvRRVtakens2[-(1:2),],
        radius=0.125)
save(hrvRRVneighs2, file="hrvRRVneighs2.Rdata")
# load(file="hrvRRVneighs2.RData")
local.recurrencePlotAux(hrvRRVneighs2, dim=2,  radius=0.125)
showrqa(hrvRRVtakens2[-(1:2),], radius=0.125, do.hist=FALSE)
```

Output

```
hrvRRVtakens2[-(1:2), ]  n: 1021  Dim: 2
Radius: 0.125  Recurrence coverage REC: 0.515  log(REC)/log(R): 0.319
Determinism: 0.939  Laminarity: 0.81
DIV: 0.027
Trend: 0  Entropy: 2.346
Diagonal lines max: 37  Mean: 5.373  Mean off main: 5.362
Vertical lines max: 48  Mean: 3.998
```

Dim=2. Time used: 3.186 sec.

Input

```
hrvRRVtakens6 <- local.buildTakens( time.series=HRRV[1:nsignal],
        embedding.dim=6,time.lag=1)
hrvRRVneighs6  <- local.findAllNeighbours(hrvRRVtakens6[-(1:2),], radius=0.125)
save(hrvRRVneighs6, file="hrvRRVneighs6.Rdata")
# load(file="hrvRRVneighs6.RData")
local.recurrencePlotAux(hrvRRVneighs6, dim=6, radius=0.125)
showrqa(hrvRRVtakens6[-(1:2),], radius=0.125, do.hist=FALSE)
```

Output

```
hrvRRVtakens6[-(1:2), ]  n: 1017  Dim: 6
Radius: 0.125  Recurrence coverage REC: 0.179  log(REC)/log(R): 0.827
Determinism: 0.943  Laminarity: 0.451
DIV: 0.03
Trend: 0  Entropy: 2.305
Diagonal lines max: 33  Mean: 5.243  Mean off main: 5.213
Vertical lines max: 22  Mean: 2.887
```

Dim=6. Time used: 1.868 sec.

Input

```
hrvRRVtakens8 <- local.buildTakens( time.series=HRRV[1:nsignal],
        embedding.dim=8,time.lag=1)
hrvRRVneighs8  <- local.findAllNeighbours(hrvRRVtakens8[-(1:2),], radius=0.125)
save(hrvRRVneighs8, file="hrvRRVneighs8.Rdata")
# load(file="hrvRRVneighs8.RData")
local.recurrencePlotAux(hrvRRVneighs8, dim=8, radius=0.125)
showrqa(hrvRRVtakens8[-(1:2),], radius=0.125, do.hist=FALSE)
```

Output

```
hrvRRVtakens8[-(1:2), ]  n: 1015  Dim: 8
Radius: 0.125  Recurrence coverage REC: 0.105  log(REC)/log(R): 1.084
Determinism: 0.943  Laminarity: 0.337
DIV: 0.032
Trend: 0  Entropy: 2.329
Diagonal lines max: 31  Mean: 5.361  Mean off main: 5.308
Vertical lines max: 17  Mean: 2.715
```

Dim=8. Time used: 1.993 sec.

Input

```
hrvRRVtakens12 <-
        local.buildTakens( time.series=HRRV[1:nsignal],
                embedding.dim=12,time.lag=1)
hrvRRVneighs12 <-
        local.findAllNeighbours(hrvRRVtakens12[-(1:2),], radius=3/16)
save(hrvRRVneighs12, file="hrvRRVneighs12.Rdata")
# load(file="hrvRRVneighs12.RData")
local.recurrencePlotAux(hrvRRVneighs12, dim=12,  radius=3/16)
showrqa(hrvRRVtakens12[-(1:2),], radius=3/16, do.hist=FALSE)
```

Output

```
hrvRRVtakens12[-(1:2), ]  n: 1011  Dim: 12
Radius: 0.1875  Recurrence coverage REC: 0.235  log(REC)/log(R): 0.865
Determinism: 0.988  Laminarity: 0.635
DIV: 0.015
Trend: 0  Entropy: 3.075
Diagonal lines max: 68  Mean: 9.775  Mean off main: 9.733
Vertical lines max: 52  Mean: 3.656
```

Dim=12: Time used: 2.445 sec.

Input

```
hrvRRVtakens16 <- local.buildTakens( time.series=HRRV[1:nsignal],
        embedding.dim=16,time.lag=1)
hrvRRVneighs16  <- local.findAllNeighbours(hrvRRVtakens16[-(1:2),], radius=3/16)
save(hrvRRVneighs16, file="hrvRRVneighs16.Rdata")
# load(file="hrvRRVneighs16.RData")
local.recurrencePlotAux(hrvRRVneighs16, dim=16, radius=3/16)
showrqa(hrvRRVtakens16[-(1:2),], radius=3/16, do.hist=FALSE)
```

Output

```
hrvRRVtakens16[-(1:2), ]  n: 1007  Dim: 16
Radius: 0.1875  Recurrence coverage REC: 0.147  log(REC)/log(R): 1.144
Determinism: 0.99  Laminarity: 0.527
DIV: 0.016
Trend: 0  Entropy: 3.163
Diagonal lines max: 64  Mean: 10.594  Mean off main: 10.523
Vertical lines max: 40  Mean: 3.114
```

Dim=16. Time used: 2.335 sec.

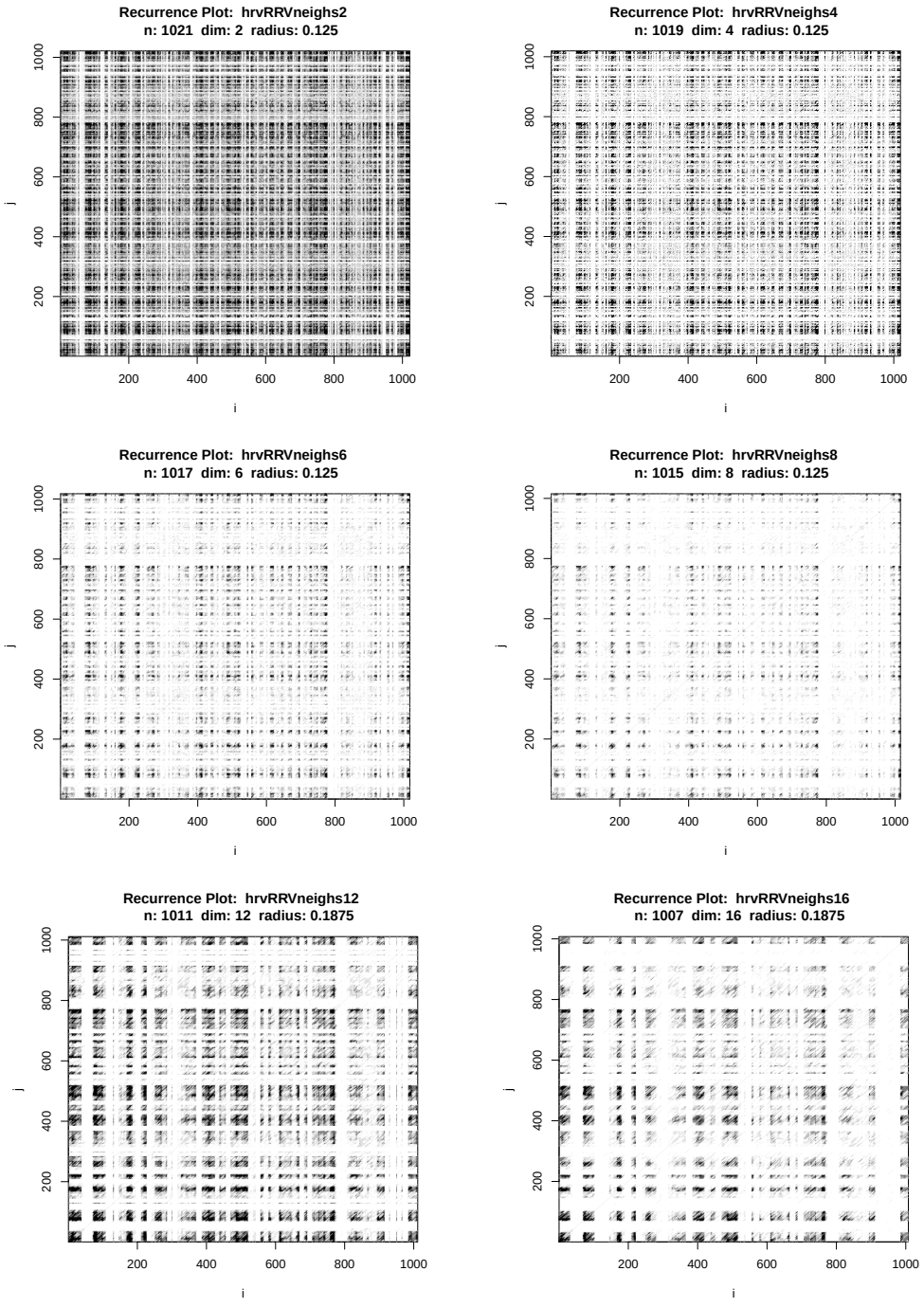


FIGURE 45. Recurrence Plot. Example case: RHRV tutorial example.beats variation. Dim=2, 4, 6, 8, 12, 16. Time used: 2.336 sec.

9.1.2. *RHRV: example.beats - RR Variation: Comparison by Dimension, Time.Lag = 8.*

Input

```
hrvRRVtakens2Lag08 <- local.buildTakens( time.series=HRRV[1:nsignal],
        embedding.dim=2, time.lag=8)
hrvRRVneighs2Lag08  <- local.findAllNeighbours(hrvRRVtakens2Lag08[-(1:2),],
        radius=0.125)
save(hrvRRVneighs2Lag08, file="hrvRRVneighs2Lag08.Rdata")
# load(file="hrvRRVneighs2Lag08.RData")
local.recurrencePlotAux(hrvRRVneighs2Lag08, dim=2,  radius=0.125)
showrqa(hrvRRVtakens2Lag08[-(1:2),], radius=0.125, do.hist=FALSE)
```

Output

```
hrvRRVtakens2Lag08[-(1:2), ]  n: 1014  Dim: 2
Radius: 0.125  Recurrence coverage REC: 0.469  log(REC)/log(R): 0.364
Determinism: 0.809  Laminarity: 0.792
DIV: 0.033
Trend: 0  Entropy: 1.637
Diagonal lines max: 30  Mean: 3.451  Mean off main: 3.442
Vertical lines max: 41  Mean: 3.445
```

Dim=2. Time used: 2.948 sec.

Input

```
hrvRRVtakens4Lag08 <- local.buildTakens( time.series=HRRV[1:nsignal],
        embedding.dim=4, time.lag=8)
hrvRRVneighs4Lag08  <- local.findAllNeighbours(hrvRRVtakens4Lag08[-(1:2),],
        radius=0.125)
save(hrvRRVneighs4Lag08, file="hrvRRVneighs4Lag08.Rdata")
# load(file="hrvRRVneighs4Lag08.RData")
local.recurrencePlotAux(hrvRRVneighs4Lag08, dim=2,  radius=0.125)
showrqa(hrvRRVtakens2Lag08[-(1:2),], radius=0.125, do.hist=FALSE)
```

Output

```
hrvRRVtakens2Lag08[-(1:2), ]  n: 1014  Dim: 2
Radius: 0.125  Recurrence coverage REC: 0.469  log(REC)/log(R): 0.364
Determinism: 0.809  Laminarity: 0.792
DIV: 0.033
Trend: 0  Entropy: 1.637
Diagonal lines max: 30  Mean: 3.451  Mean off main: 3.442
Vertical lines max: 41  Mean: 3.445
```

Dim=4. Time used: 2.607 sec.

Input

```
statepairs(hrvRRVtakens4Lag08)
```

Input

```
statecoplot(hrvRRVtakens4Lag08)
```

Output

```
Missing rows: 1, 2
```

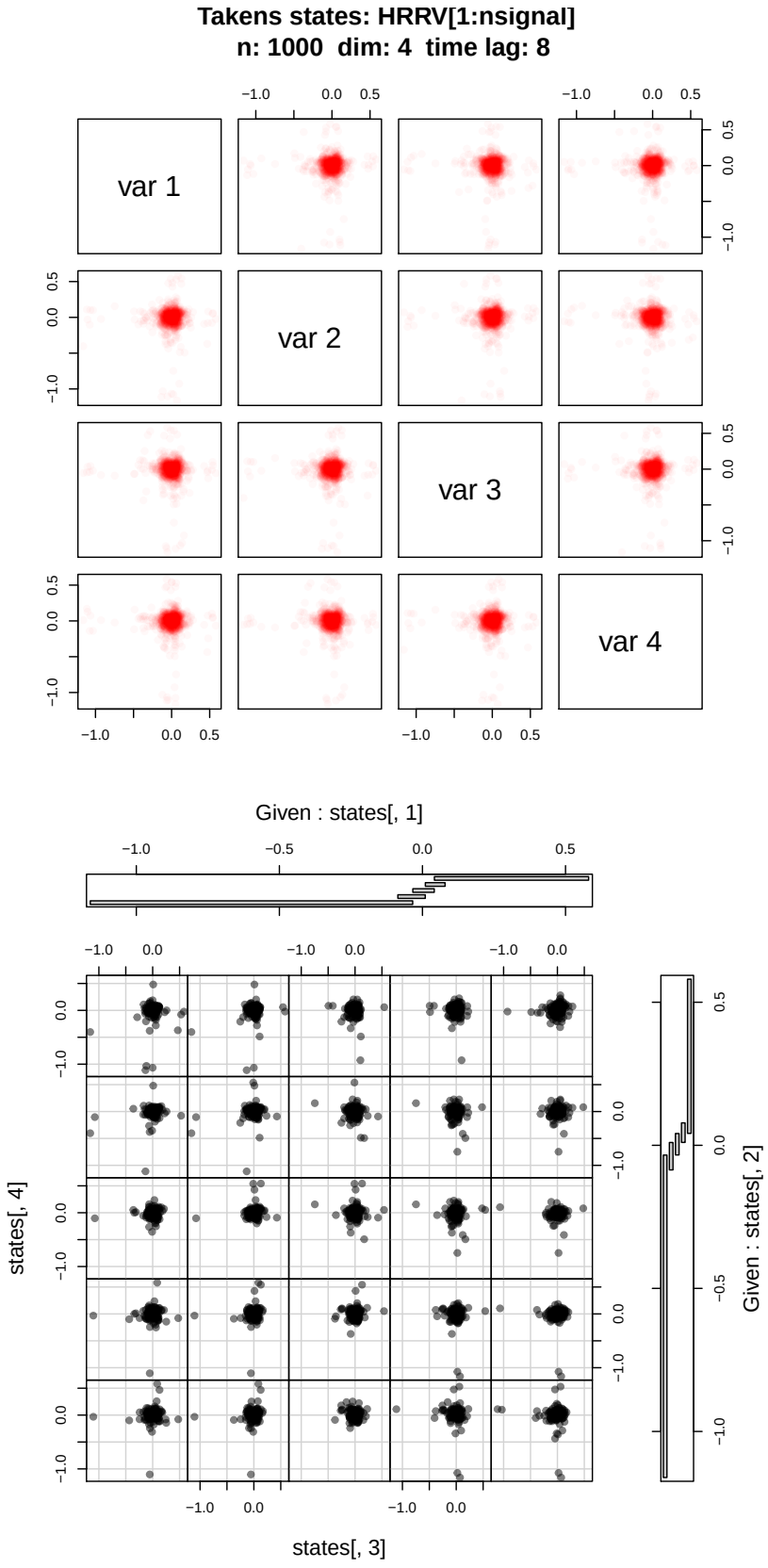


FIGURE 46. Takens states. Example case: RHRV tutorial example.beats variation. Dim=4, time.lag=8. Time used: 4.077 sec.

Input

```
statepairs(hrvRRVtakens4Lag08, range=c(-0.5, 0.5))
```

Input

```
statecoplot(hrvRRVtakens4Lag08, range=c(-0.5, 0.5))
```

Output

```
Missing rows: 1, 2, 38, 39, 46, 47, 54, 55, 62, 63, 100, 101, 102, 108, 109, 110, 116, 117, 118, 124, 125
```

Input

```
hrvRRVtakens6Lag08 <- local.buildTakens( time.series=HRRV[1:nsignal],
        embedding.dim=6,time.lag=8)
hrvRRVneighs6Lag08  <- local.findAllNeighbours(hrvRRVtakens6Lag08[-(1:2),], radius=0.125)
save(hrvRRVneighs6Lag08, file="hrvRRVneighs6Lag08.Rdata")
# load(file="hrvRRVneighs6Lag08.RData")
local.recurrencePlotAux(hrvRRVneighs6Lag08, dim=6, radius=0.125)
showrqa(hrvRRVtakens6Lag08[-(1:2),], radius=0.125, do.hist=FALSE)
```

Output

```
hrvRRVtakens6Lag08[-(1:2), ]  n: 982  Dim: 6
Radius: 0.125  Recurrence coverage REC: 0.1  log(REC)/log(R): 1.107
Determinism: 0.357  Laminarity: 0.311
DIV: 0.143
Trend: 0  Entropy: 0.604
Diagonal lines max: 7  Mean: 2.302  Mean off main: 2.237
Vertical lines max: 8  Mean: 2.234
```

Dim=6. Time used: 6.907 sec.

Input

```
hrvRRVtakens8Lag08 <- local.buildTakens( time.series=HRRV[1:nsignal],
        embedding.dim=8,time.lag=8)
hrvRRVneighs8Lag08  <- local.findAllNeighbours(hrvRRVtakens8Lag08[-(1:2),], radius=0.125)
save(hrvRRVneighs8Lag08, file="hrvRRVneighs8Lag08.Rdata")
# load(file="hrvRRVneighs8Lag08.RData")
local.recurrencePlotAux(hrvRRVneighs8Lag08, dim=8, radius=0.125)
showrqa(hrvRRVtakens8Lag08[-(1:2),], radius=0.125, do.hist=FALSE)
```

Output

```
hrvRRVtakens8Lag08[-(1:2), ]  n: 966  Dim: 8
Radius: 0.125  Recurrence coverage REC: 0.045  log(REC)/log(R): 1.488
Determinism: 0.223  Laminarity: 0.161
DIV: 0.2
Trend: 0  Entropy: 0.354
Diagonal lines max: 5  Mean: 2.348  Mean off main: 2.108
Vertical lines max: 5  Mean: 2.089
```

Dim=8. Time used: 1.313 sec.

Input

```
hrvRRVtakens12Lag08 <-
        local.buildTakens( time.series=HRRV[1:nsignal],
                embedding.dim=12,time.lag=8)
hrvRRVneighs12Lag08 <-
```

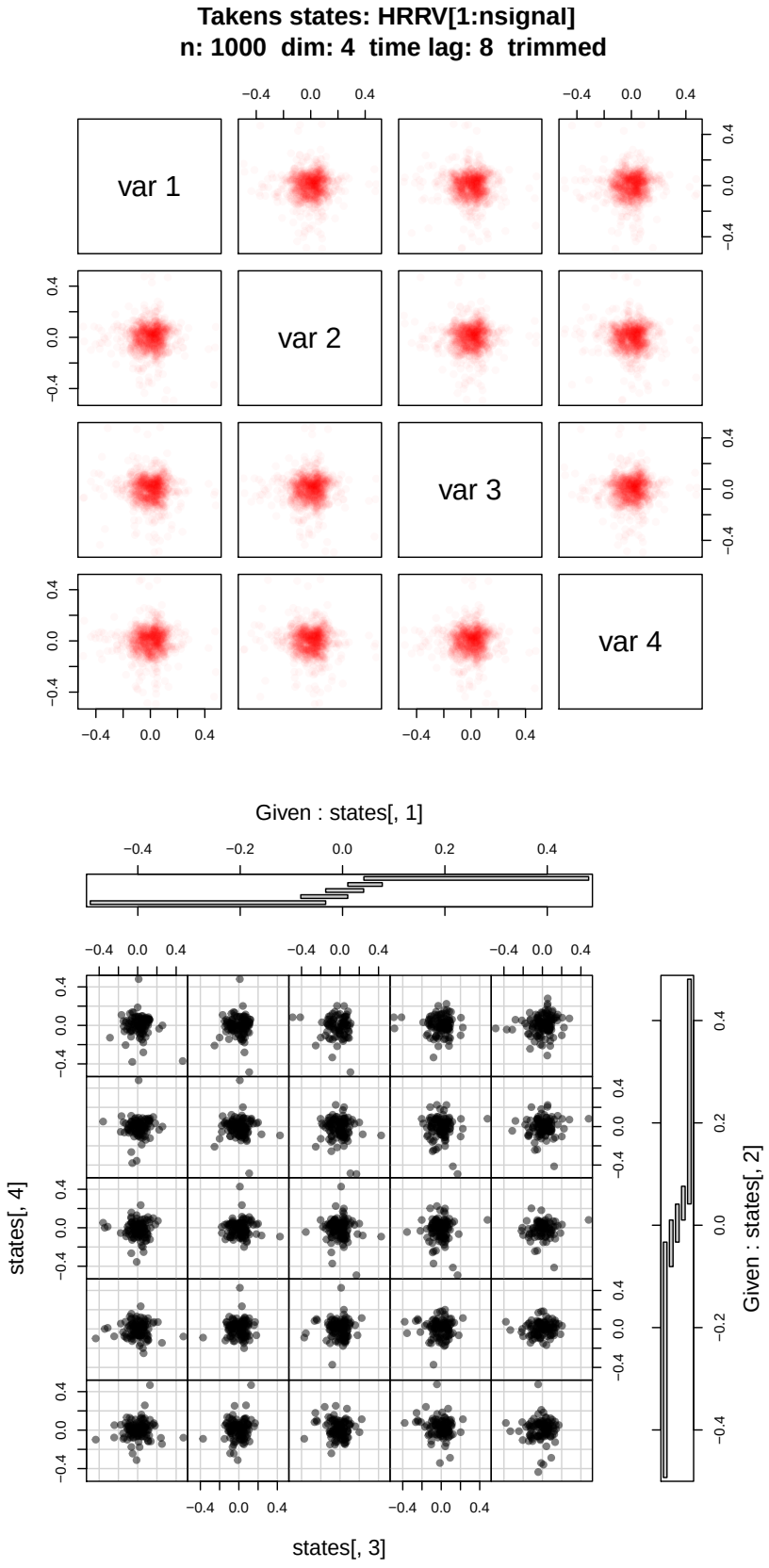


FIGURE 47. Takens states. Example case: RHRV tutorial example.beats variation, trimmed. Dim=4, time.lag=8. Time used: 5.235 sec.

```
        local.findAllNeighbours(hrvRRVtakens12Lag08[-(1:2),], radius=3/16)
save(hrvRRVneighs12Lag08, file="hrvRRVneighs12Lag08.Rdata")
# load(file="hrvRRVneighs12Lag08.RData")
local.recurrencePlotAux(hrvRRVneighs12Lag08, dim=12,  radius=3/16)
showrqa(hrvRRVtakens12Lag08[-(1:2),], radius=3/16, do.hist=FALSE)
```

Output

```
hrvRRVtakens12Lag08[-(1:2), ]  n: 934  Dim: 12
Radius: 0.1875  Recurrence coverage REC: 0.133  log(REC)/log(R): 1.207
Determinism: 0.472  Laminarity: 0.443
DIV: 0.143
Trend: 0  Entropy: 0.77
Diagonal lines max: 7  Mean: 2.39  Mean off main: 2.349
Vertical lines max: 7  Mean: 2.457
```

Dim=12: Time used: 1.649 sec.

Input

```
hrvRRVtakens16Lag08 <- local.buildTakens( time.series=HRRV[1:nsignal],
        embedding.dim=16,time.lag=8)
hrvRRVneighs16Lag08  <- local.findAllNeighbours(hrvRRVtakens16Lag08[-(1:2),], radius=3/16)
save(hrvRRVneighs16Lag08, file="hrvRRVneighs16Lag08.Rdata")
# load(file="hrvRRVneighs16Lag08.RData")
local.recurrencePlotAux(hrvRRVneighs16Lag08, dim=16, radius=3/16)
showrqa(hrvRRVtakens16Lag08[-(1:2),], radius=3/16, do.hist=FALSE)
```

Output

```
hrvRRVtakens16Lag08[-(1:2), ]  n: 902  Dim: 16
Radius: 0.1875  Recurrence coverage REC: 0.071  log(REC)/log(R): 1.581
Determinism: 0.339  Laminarity: 0.31
DIV: 0.167
Trend: 0  Entropy: 0.608
Diagonal lines max: 6  Mean: 2.347  Mean off main: 2.239
Vertical lines max: 6  Mean: 2.321
```

Dim=16. Time used: 1.782 sec.

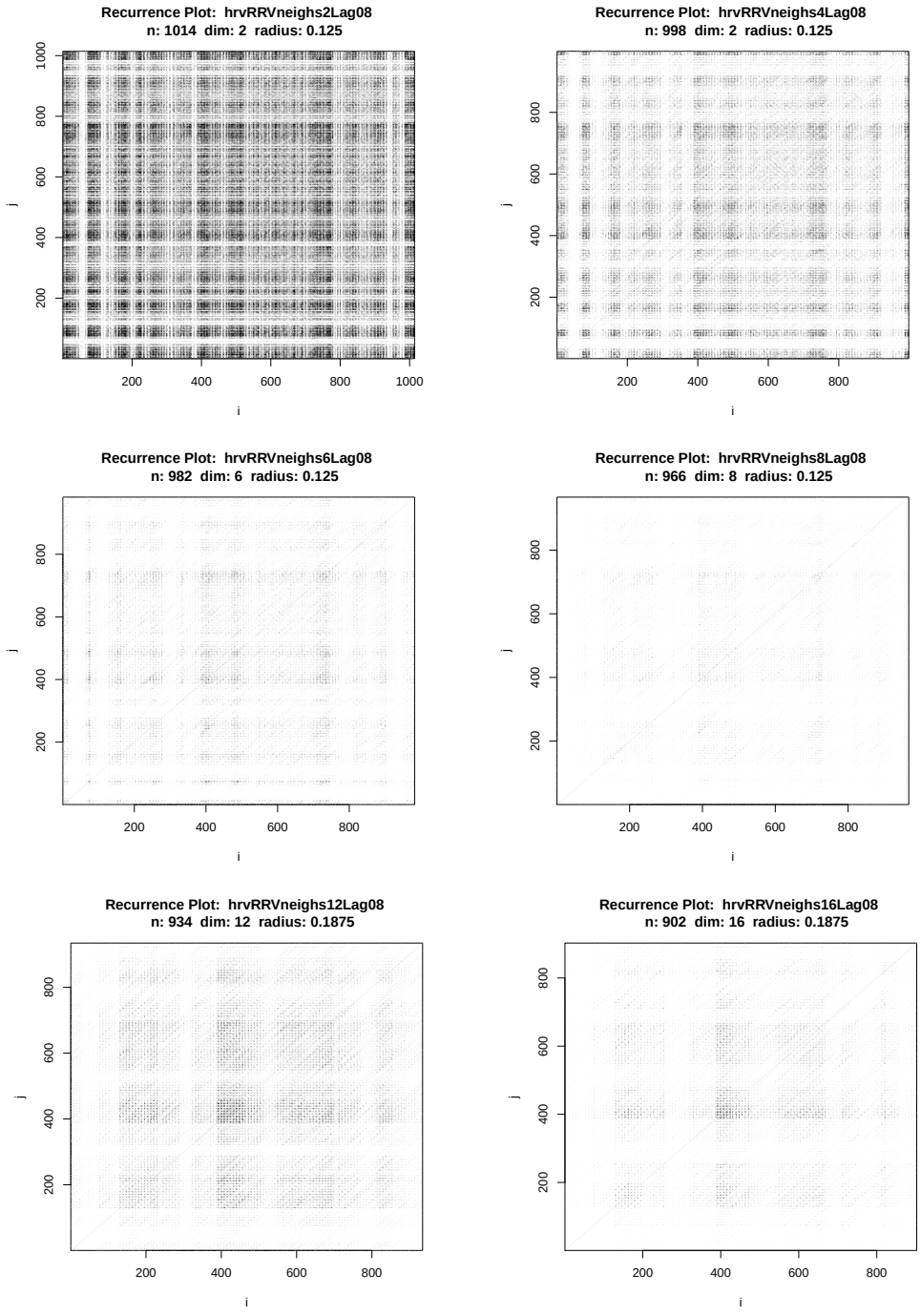


FIGURE 48. Recurrence Plot. Example case: RHRV tutorial example.beats variation. Dim=2, 4, 6, 8, 12, 16. Time.lag=8. Time used: 1.783 sec.

10. Case Study: HRV data example2.beats

This is a copy of the previous section, now applied to HRV data example2.beats.

Input

```
library(RHRV)
load("/users/gs/projects/rforge/rhrv/pkg/data/HRVData.rda")
load("/users/gs/projects/rforge/rhrv/pkg/data/HRVProcessedData.rda")
#####################################################
### code chunk number 1: creation
#####################################################
hrv2.data  = CreateHRVData()
hrv2.data = SetVerbose(hrv2.data, TRUE )
#####################################################
### code chunk number 3: loading
#####################################################
hrv2.data = LoadBeatAscii(hrv2.data, "example2.beats",
       RecordPath = "/users/gs/projects/rforge/rhrv/tutorial/beatsFolder")
#       RecordPath = "beatsFolder")


#####################################################
### code chunk number 4: derivating
#####################################################
hrv2.data = BuildNIHR(hrv2.data)
```

Input

```
plotsignal(hrv2.data$Beat$RR)
```

See Figure 49.

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

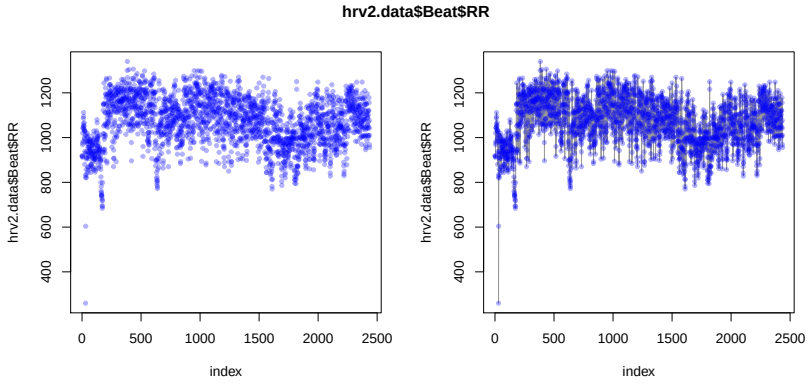


Figure 49. RHRV tutorial example2.beats. Signal and linear interpolation.

Input

```
hrv2RRtakens4 <- local.buildTakens( time.series=hrv2.data$Beat$RR[1:nsignal],
        embedding.dim=4, time.lag=1)
statepairs(hrv2RRtakens4) #dim=4
```

See Figure 50 on the next page.

Only 1024 data points used in this plot

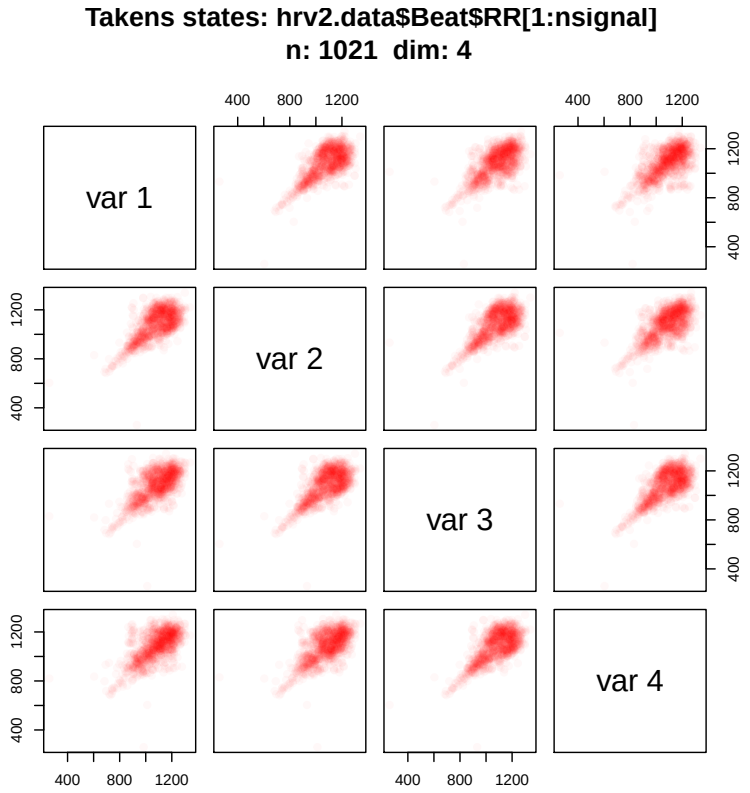


FIGURE 50. RHRV tutorial example2.beats. Time used: 0.982 sec.

Input
```
statepairs(hrv2RRtakens4, rank=TRUE) #dim=4
```

See Figure 51 on the facing page.

Input
```
statecoplot(hrv2RRtakens4) #dim=4
```

See Figure 52 on page 92.

Input
```
hrv2RRneighs4  <- local.findAllNeighbours(hrv2RRtakens4, radius=12*16)
save(hrv2RRneighs4, file="hrv2RRneighs4.Rdata")
# load(file="hrv2RRneighs4.RData")
local.recurrencePlotAux(hrv2RRneighs4, radius=12*16)
showrqa(hrv2RRtakens4[-(1:2),], radius=12*16, do.hist=FALSE)
```

Output
```
hrv2RRtakens4[-(1:2), ]  n: 1019  Dim: 4
Radius: 192  Recurrence coverage REC: 0.493  log(REC)/log(R): -0.135
Determinism: 0.982  Laminarity: 0.906
DIV: 0.005
Trend: 0  Entropy: 3.158
Diagonal lines max: 191  Mean: 10.396  Mean off main: 10.375
Vertical lines max: 136  Mean: 7.145
```

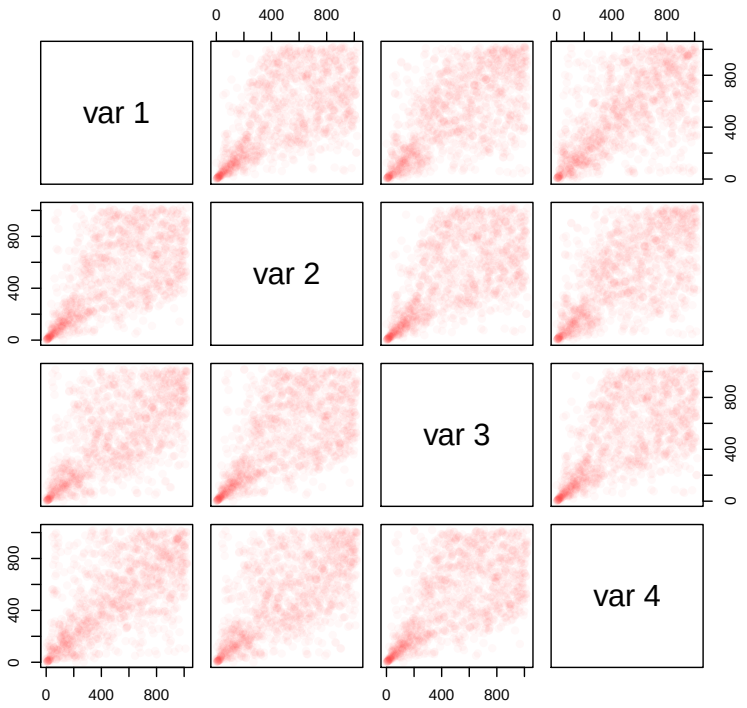


FIGURE 51. RHRV tutorial example2.beats. Ranked data. Time used: 2.295 sec.

Dim=4. Time used: 2.822 sec.

See Figure 53 on page 93.

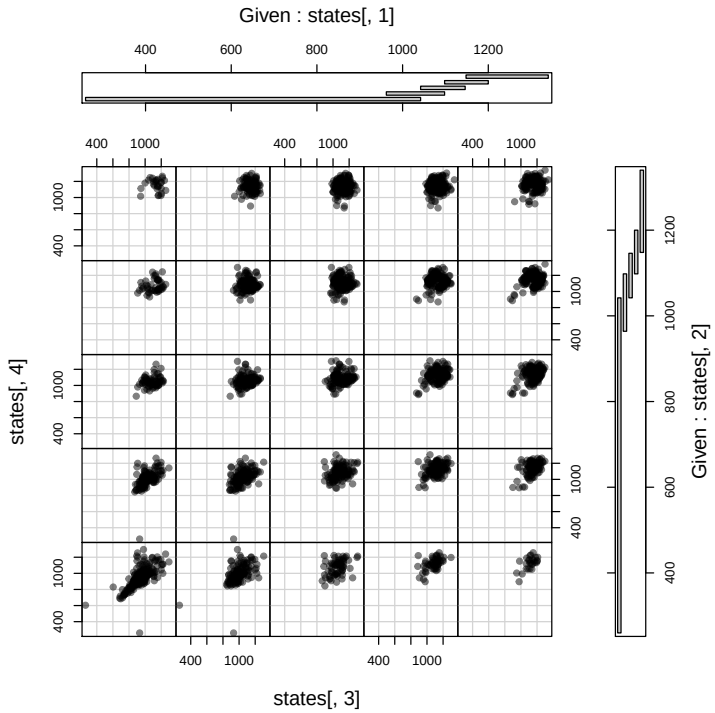


FIGURE 52. State coplot. RHRV tutorial example2.beats. Time used: 0.243 sec.

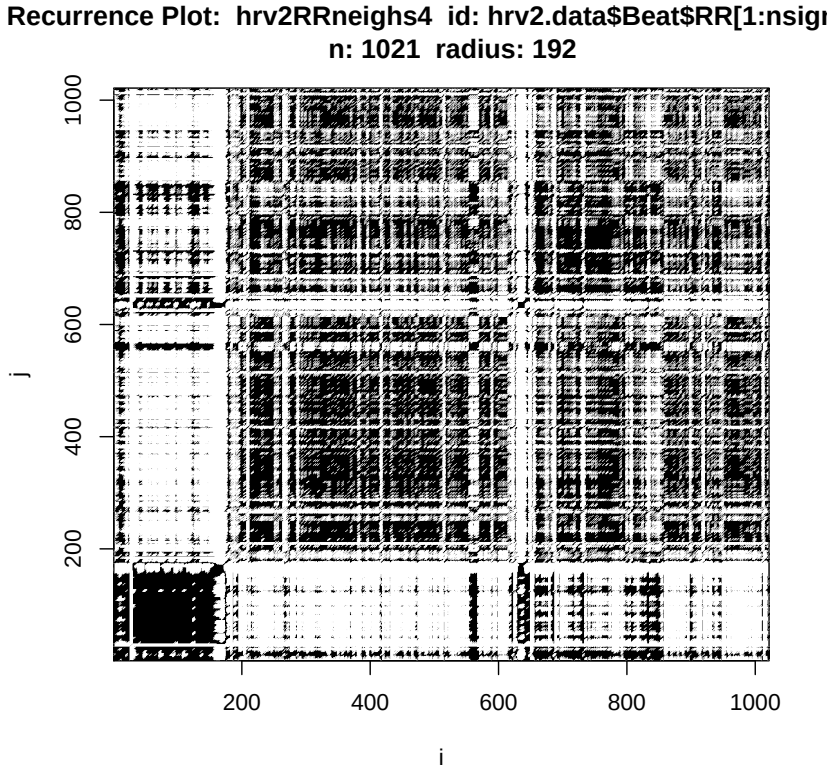


FIGURE 53. Recurrence Plot. Example case: RHRV tutorial example2.beats. Dim=4. Time used: 2.823 sec.

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

10.0.1. *RHRV: example2.beats, RR-intervals. Comparison by Dimension.*

Input

```
hrv2RRtakens2 <- local.buildTakens( time.series=hrv2.data$Beat$RR[1:nsignal],
        embedding.dim=2,time.lag=1)
hrv2RRneighs2  <- local.findAllNeighbours(hrv2RRtakens2, radius=10*16)
save(hrv2RRneighs2, file="hrv2RRneighs2.Rdata")
# load(file="hrv2RRneighs2.RData")
local.recurrencePlotAux(hrv2RRneighs2, radius=10*16)
showrqa(hrv2RRtakens2[-(1:2),], radius=10*16, do.hist=FALSE)
```

Output

```
hrv2RRtakens2[-(1:2), ]  n: 1021  Dim: 2
Radius: 160  Recurrence coverage REC: 0.52  log(REC)/log(R): -0.129
Determinism: 0.948  Laminarity: 0.91
DIV: 0.007
Trend: 0  Entropy: 2.691
Diagonal lines max: 152  Mean: 7.057  Mean off main: 7.043
Vertical lines max: 130  Mean: 6.607
```

Dim=2. Time used: 3.27 sec.

See Figure 54 on page 96.

Input

```
hrv2RRtakens6 <- local.buildTakens( time.series=hrv2.data$Beat$RR[1:nsignal],
        embedding.dim=6,time.lag=1)
hrv2RRneighs6  <- local.findAllNeighbours(hrv2RRtakens6, radius=14*16)
save(hrv2RRneighs6, file="hrv2RRneighs6.Rdata")
# load(file="hrv2RRneighs6.RData")
local.recurrencePlotAux(hrv2RRneighs6, radius=14*16)
showrqa(hrv2RRtakens6[-(1:2),], radius=14*16, do.hist=FALSE)
```

Output

```
hrv2RRtakens6[-(1:2), ]  n: 1017  Dim: 6
Radius: 224  Recurrence coverage REC: 0.528  log(REC)/log(R): -0.118
Determinism: 0.993  Laminarity: 0.925
DIV: 0.004
Trend: 0  Entropy: 3.584
Diagonal lines max: 225  Mean: 15.258  Mean off main: 15.23
Vertical lines max: 167  Mean: 9.007
```

Dim=6. Time used: 2.746 sec.

See Figure 54 on page 96.

Input

```
hrv2RRtakens8 <- local.buildTakens( time.series=hrv2.data$Beat$RR[1:nsignal],
        embedding.dim=8,time.lag=1)
hrv2RRneighs8  <- local.findAllNeighbours(hrv2RRtakens8, radius=16*16)
save(hrv2RRneighs8, file="hrv2RRneighs8.Rdata")
# load(file="hrv2RRneighs8.RData")
local.recurrencePlotAux(hrv2RRneighs8, radius=16*16)
showrqa(hrv2RRtakens8[-(1:2),], radius=16*16, do.hist=FALSE)
```

Output

```
hrv2RRtakens8[-(1:2), ]  n: 1015  Dim: 8
Radius: 256  Recurrence coverage REC: 0.584  log(REC)/log(R): -0.097
Determinism: 0.997  Laminarity: 0.942
DIV: 0.004
Trend: 0  Entropy: 3.986
Diagonal lines max: 241  Mean: 22.506  Mean off main: 22.469
Vertical lines max: 310  Mean: 11.256
```

Dim=8. Time used: 3.584 sec.

See Figure 54 on the next page.

Input

```
hrv2RRtakens12 <- local.buildTakens( time.series=hrv2.data$Beat$RR[1:nsignal],
        embedding.dim=12,time.lag=1)
hrv2RRneighs12  <- local.findAllNeighbours(hrv2RRtakens12, radius=16*16)
save(hrv2RRneighs12, file="hrv2RRneighs12.Rdata")
# load(file="hrv2RRneighs12.RData")
local.recurrencePlotAux(hrv2RRneighs12, radius=16*16)
showrqa(hrv2RRtakens12[-(1:2),], radius=16*16, do.hist=FALSE)
```

Output

```
hrv2RRtakens12[-(1:2), ]  n: 1011  Dim: 12
Radius: 256  Recurrence coverage REC: 0.488  log(REC)/log(R): -0.129
Determinism: 0.997  Laminarity: 0.914
DIV: 0.004
Trend: 0  Entropy: 4.062
Diagonal lines max: 237  Mean: 24.127  Mean off main: 24.079
Vertical lines max: 299  Mean: 8.972
```

Dim=12. Time used: 3.847 sec.

Input

```
hrv2RRtakens16 <- local.buildTakens(
        time.series=hrv2.data$Beat$RR[1:nsignal],
        embedding.dim=16,time.lag=1)
hrv2RRneighs16  <- local.findAllNeighbours(hrv2RRtakens16, radius=18*16)
save(hrv2RRneighs16, file="hrv2RRneighs16.Rdata")
# load(file="hrv2RRneighs16.RData")
local.recurrencePlotAux(hrv2RRneighs16, radius=18*16)
showrqa(hrv2RRtakens16[-(1:2),], radius=18*16, do.hist=FALSE)
```

Output

```
hrv2RRtakens16[-(1:2), ]  n: 1007  Dim: 16
Radius: 288  Recurrence coverage REC: 0.544  log(REC)/log(R): -0.107
Determinism: 0.999  Laminarity: 0.932
DIV: 0.003
Trend: 0  Entropy: 4.372
Diagonal lines max: 346  Mean: 34.916  Mean off main: 34.854
Vertical lines max: 297  Mean: 9.929
```

Dim=16. Time used: 3.655 sec.

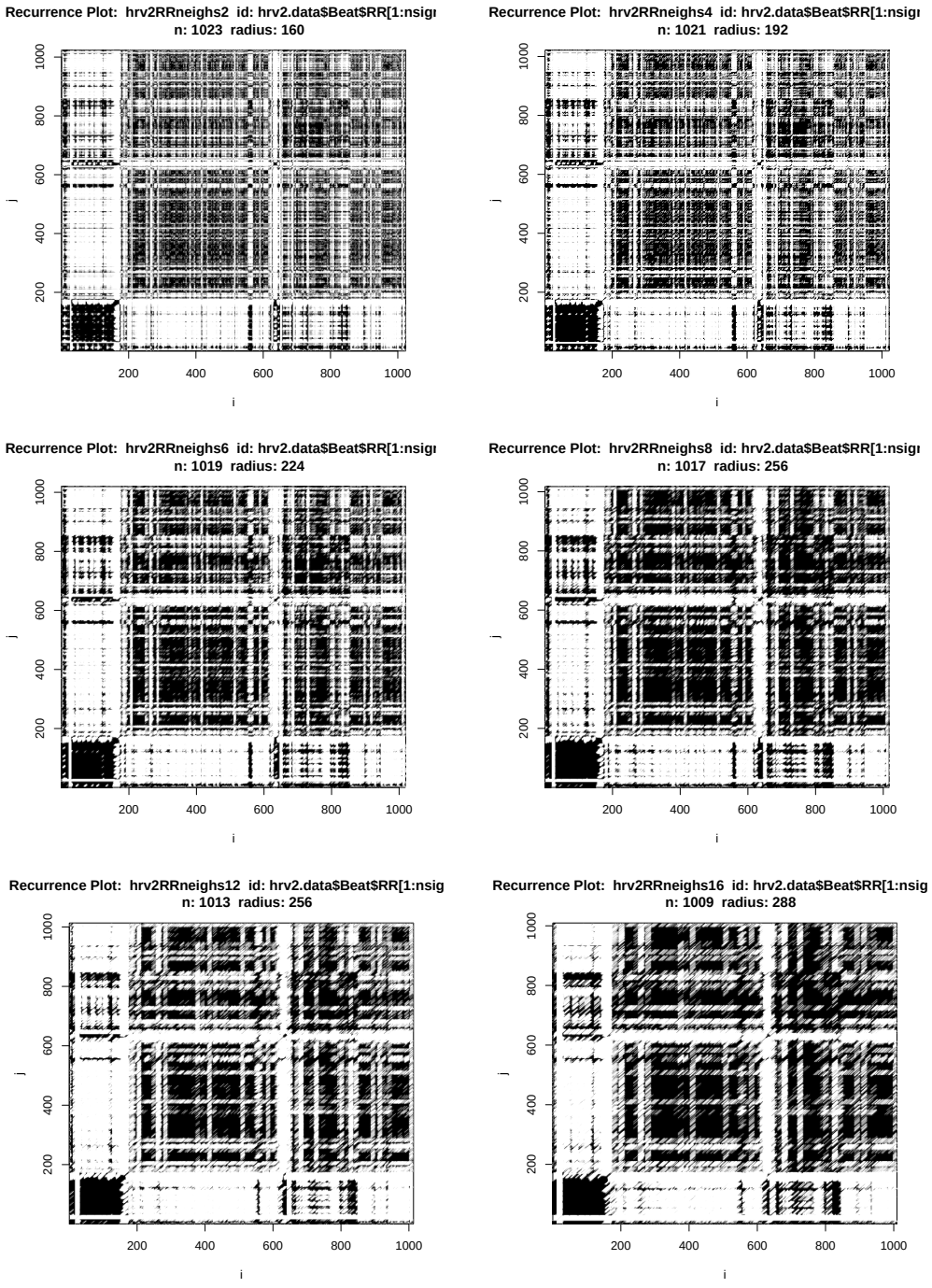


FIGURE 54. Recurrence Plot. Example case: RHRV tutorial example2.beats. Dim=2, 4, 6, 8, 12, 16. Time used: 3.656 sec.

ToDo: Consider using differences

differences for HRV

10.1. **RHRV: example2.beats - Hart Rate Variation.** Since we are not interested in heart rate (or pulse), but in heart rate variation, a proposal is to use scaled differences.

Input

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

Output

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

Input

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

These are the displays of the Takens state space we used before, now for HRRV:

Input

```
plotsignal(HRRV)
```

See Figure 55,

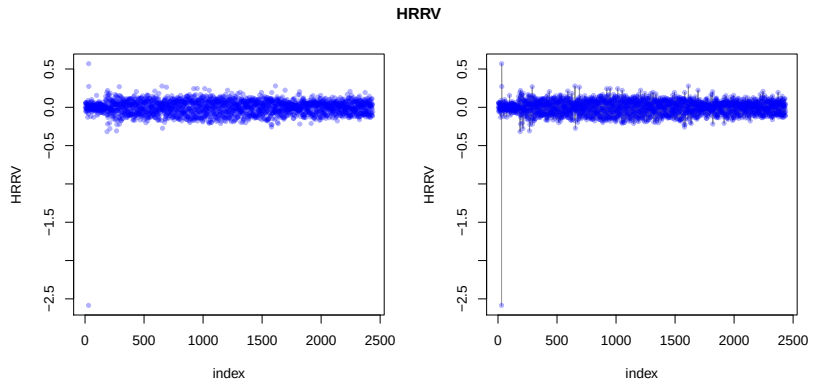


FIGURE 55. RHRV tutorial example2.beats. HRRV Signal and linear interpolation.

Only 1024 data points used in these plots

Input

```
hrv2RRVtakens4 <-
        local.buildTakens( time.series=HRRV[1:nsignal],
                embedding.dim=4,time.lag=1)
statepairs(hrv2RRVtakens4) #dim=4
```

See Figure 56 on the next page.

Input

```
        statecoplot(hrv2RRVtakens4) #dim=4
```

Output

```
Missing rows: 1, 2
```

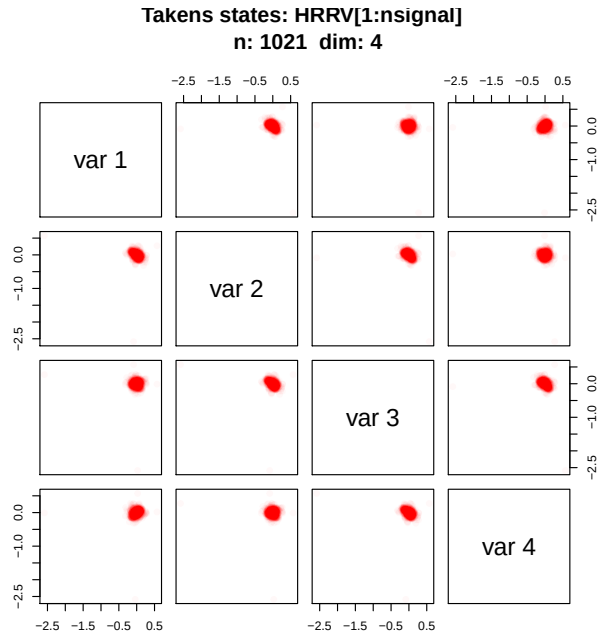


FIGURE 56. Recurrence plot. RHRV tutorial example2.beats. HRRV Time used: 0.848 sec.

See Figure 57.

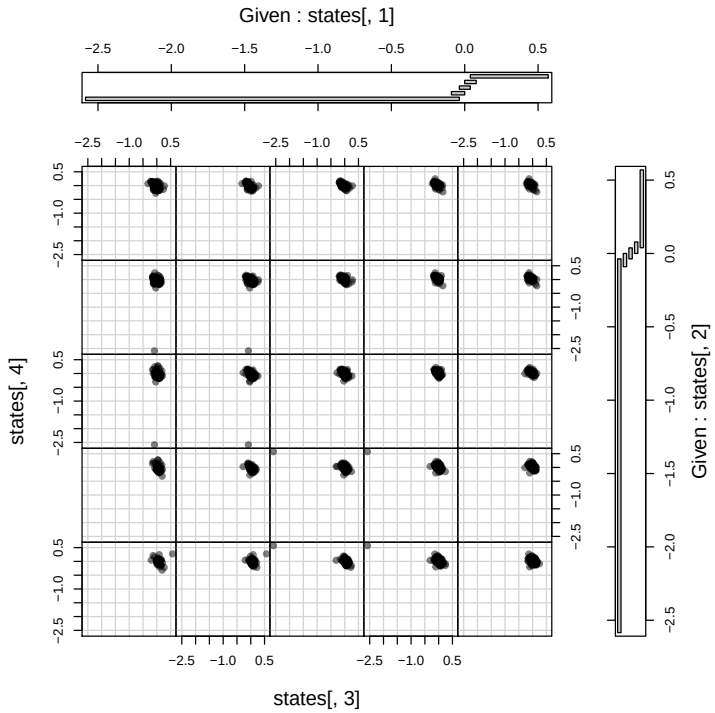


FIGURE 57. State coplot. RHRV tutorial example2.beats. HRRV. Time used: 1.092 sec.

```
statepairs(hrv2RRVtakens4, rank=TRUE) #dim=4
```

See Figure 58

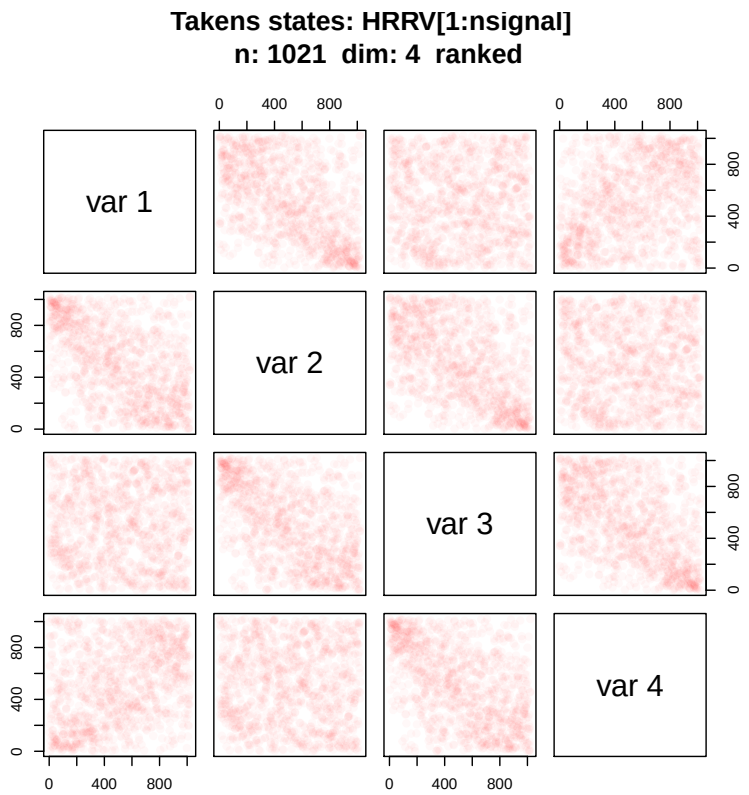


FIGURE 58. RHRV tutorial example2.beats. Ranked HRRV data. Time used: 1.896 sec.

Input

```
hrv2RRVtakens41 <- hrv2RRVtakens4
hrv2RRVtakens41[hrv2RRVtakens41 < -1.5] <- NA
hrv2RRVtakens41[hrv2RRVtakens41 > 0.45] <- NA
statepairs(hrv2RRVtakens41) #dim=4
```

See Figure 59 on the following page.

Input

```
statecoplot(hrv2RRVtakens41) #dim=4
```

Output

```
Missing rows: 1, 2, 27, 28, 29, 30, 31
```

See Figure 60 on the next page.

ToDo: findAllNeighbours does not handle NAs

Input

```
#use hack: findAllNeighbours does not handle NAs
hrv2RRVneighs4  <- local.findAllNeighbours(hrv2RRVtakens4[-(1:2),], radius=0.125)
save(hrv2RRVneighs4, file="hrv2RRVneighs4.Rdata")
```

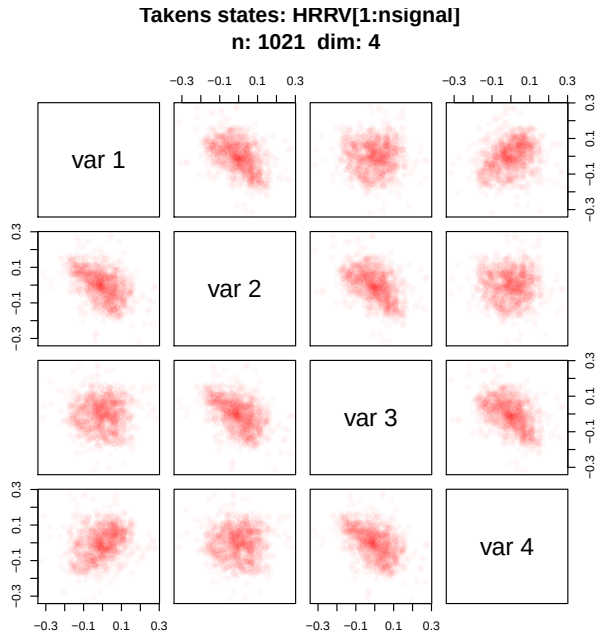


FIGURE 59. Recurrence plot. RHRV tutorial example2.beats. HRRV Time used: 2.71 sec.

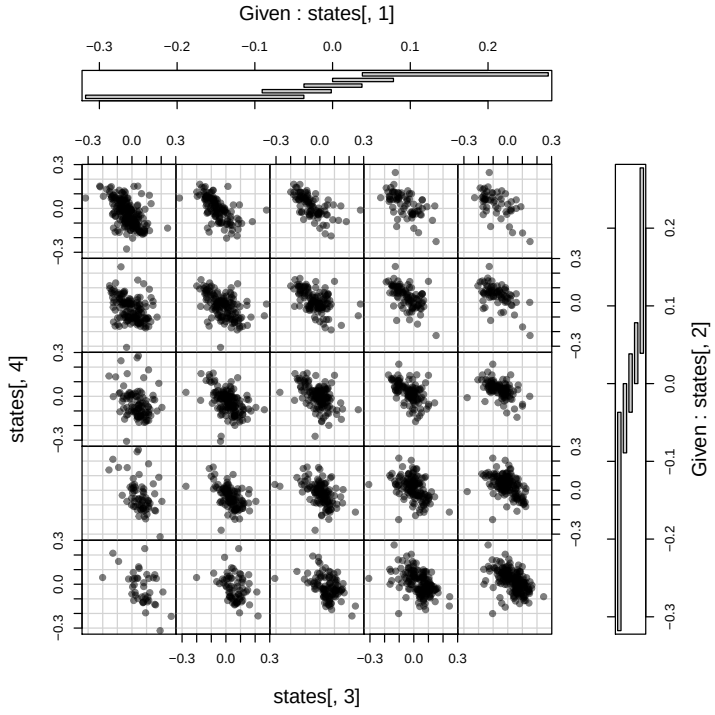


FIGURE 60. State coplot. RHRV tutorial example2.beats. HRRV. Time used: 2.949 sec.

Time used: 0.182 sec.

Input

```
load(file="hrv2RRVneighs4.RData")
local.recurrencePlotAux(hrv2RRVneighs4,dim=4, radius=0.125)
```

ToDo: check. There seem to be strange artefacts.

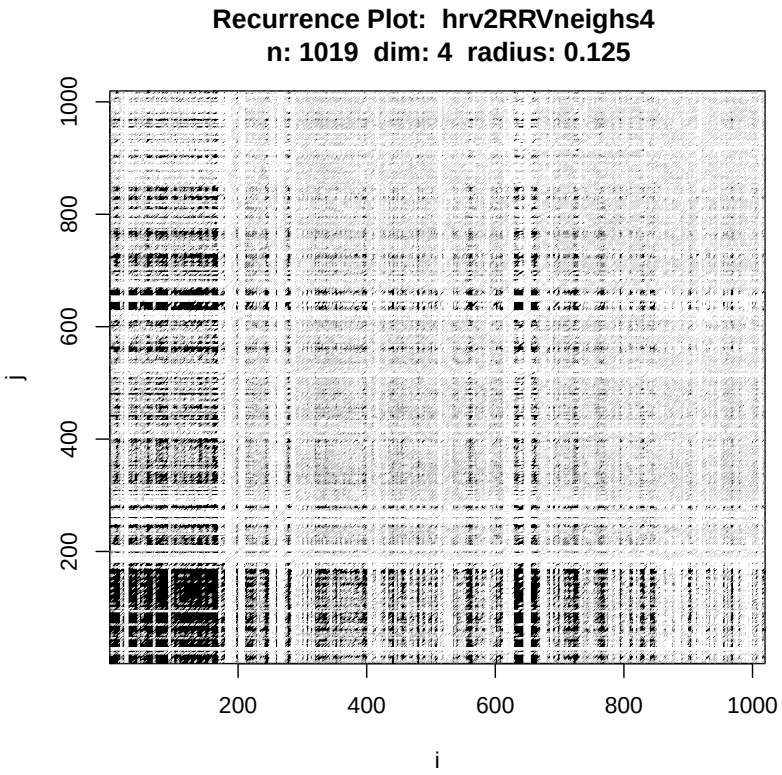


FIGURE 61. Recurrence Plot. Example case: RHRV tutorial example2.beats. HRRV Dim=4. Time used: 1.34 sec.

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

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

10.1.1. *RHRV: example2.beats - RR Variation: Comparison by Dimension.*

Input

```
hrv2RRVtakens2 <- local.buildTakens( time.series=HRRV[1:nsignal],
        embedding.dim=2, time.lag=1)
hrv2RRVneighs2  <- local.findAllNeighbours(hrv2RRVtakens2[-(1:2),],
        radius=0.125)
save(hrv2RRVneighs2, file="hrv2RRVneighs2.Rdata")
# load(file="hrv2RRVneighs2.RData")
local.recurrencePlotAux(hrv2RRVneighs2, dim=2,  radius=0.125)
hrv2RRVrqa2 <- showrqa(hrv2RRVtakens2[-(1:2),], radius=0.125, do.hist=FALSE)
```

Output

```
hrv2RRVtakens2[-(1:2), ]  n: 1021  Dim: 2
Radius: 0.125  Recurrence coverage REC: 0.508  log(REC)/log(R): 0.326
Determinism: 0.913  Laminarity: 0.712
DIV: 0.009
Trend: 0  Entropy: 2.289
Diagonal lines max: 117  Mean: 5.305  Mean off main: 5.294
Vertical lines max: 86  Mean: 3.923
```

Time used: 2.934 sec.

Input

```
hrv2RRVtakens6 <- local.buildTakens( time.series=HRRV[1:nsignal],
        embedding.dim=6,time.lag=1)
hrv2RRVneighs6  <- local.findAllNeighbours(hrv2RRVtakens6[-(1:2),], radius=0.125*1.5)
save(hrv2RRVneighs6, file="hrv2RRVneighs6.Rdata")
# load(file="hrv2RRVneighs6.RData")
local.recurrencePlotAux(hrv2RRVneighs6, dim=6, radius=0.125*1.5)
hrv2RRVrqa6 <- showrqa(hrv2RRVtakens6[-(1:2),], radius=0.125*1.5, do.hist=FALSE)
```

Output

```
hrv2RRVtakens6[-(1:2), ]  n: 1017  Dim: 6
Radius: 0.1875  Recurrence coverage REC: 0.516  log(REC)/log(R): 0.395
Determinism: 0.992  Laminarity: 0.736
DIV: 0.007
Trend: 0  Entropy: 3.355
Diagonal lines max: 147  Mean: 12.475  Mean off main: 12.452
Vertical lines max: 193  Mean: 4.902
```

Dim=6. Time used: 3.178 sec.

Input

```
hrv2RRVtakens8 <- local.buildTakens( time.series=HRRV[1:nsignal],
        embedding.dim=8,time.lag=1)
hrv2RRVneighs8  <- local.findAllNeighbours(hrv2RRVtakens8[-(1:2),], radius=3/16)
save(hrv2RRVneighs8, file="hrv2RRVneighs8.Rdata")
# load(file="hrv2RRVneighs8.RData")
local.recurrencePlotAux(hrv2RRVneighs8, dim=8, radius=3/16)
hrv2RRVrqa8 <- showrqa(hrv2RRVtakens8[-(1:2),], radius=3/16, do.hist=FALSE)
```

Output

```
hrv2RRVtakens8[-(1:2), ]  n: 1015  Dim: 8
Radius: 0.1875  Recurrence coverage REC: 0.432  log(REC)/log(R): 0.501
Determinism: 0.992  Laminarity: 0.679
DIV: 0.007
Trend: 0  Entropy: 3.369
Diagonal lines max: 145  Mean: 12.714  Mean off main: 12.685
Vertical lines max: 147  Mean: 4.628
```

Dim=8. Time used: 2.934 sec.

Input

```
hrv2RRVtakens12 <-
        local.buildTakens( time.series=HRRV[1:nsignal],
                embedding.dim=12,time.lag=1)
hrv2RRVneighs12 <-
        local.findAllNeighbours(hrv2RRVtakens12[-(1:2),], radius=3.5/16)
save(hrv2RRVneighs12, file="hrv2RRVneighs12.Rdata")
# load(file="hrv2RRVneighs12.RData")
local.recurrencePlotAux(hrv2RRVneighs12, dim=12,  radius=3.5/16)
hrv2RRVrqa12 <- showrqa(hrv2RRVtakens12[-(1:2),], radius=3.5/16, do.hist=FALSE)
```

Output

```
hrv2RRVtakens12[-(1:2), ]  n: 1011  Dim: 12
Radius: 0.21875  Recurrence coverage REC: 0.479  log(REC)/log(R): 0.484
Determinism: 0.997  Laminarity: 0.746
DIV: 0.006
Trend: 0  Entropy: 3.803
Diagonal lines max: 156  Mean: 19.62  Mean off main: 19.58
Vertical lines max: 192  Mean: 5.298
```

Dim=12. Time used: 3.56 sec.

Input

```
hrv2RRVtakens16 <- local.buildTakens( time.series=HRRV[1:nsignal],
        embedding.dim=16,time.lag=1)
hrv2RRVneighs16  <- local.findAllNeighbours(hrv2RRVtakens16[-(1:2),], radius=4/16)
save(hrv2RRVneighs16, file="hrv2RRVneighs16.Rdata")
# load(file="hrv2RRVneighs16.RData")
local.recurrencePlotAux(hrv2RRVneighs16, dim=16, radius=4/16)
hrv2RRVrqa16 <- showrqa(hrv2RRVtakens16[-(1:2),], radius=4/16, do.hist=FALSE)
```

Output

```
hrv2RRVtakens16[-(1:2), ]  n: 1007  Dim: 16
Radius: 0.25  Recurrence coverage REC: 0.568  log(REC)/log(R): 0.408
Determinism: 0.999  Laminarity: 0.816
DIV: 0.005
Trend: 0  Entropy: 4.186
Diagonal lines max: 221  Mean: 30.105  Mean off main: 30.054
Vertical lines max: 220  Mean: 6.145
```

Dim=16. Time used: 3.857 sec.

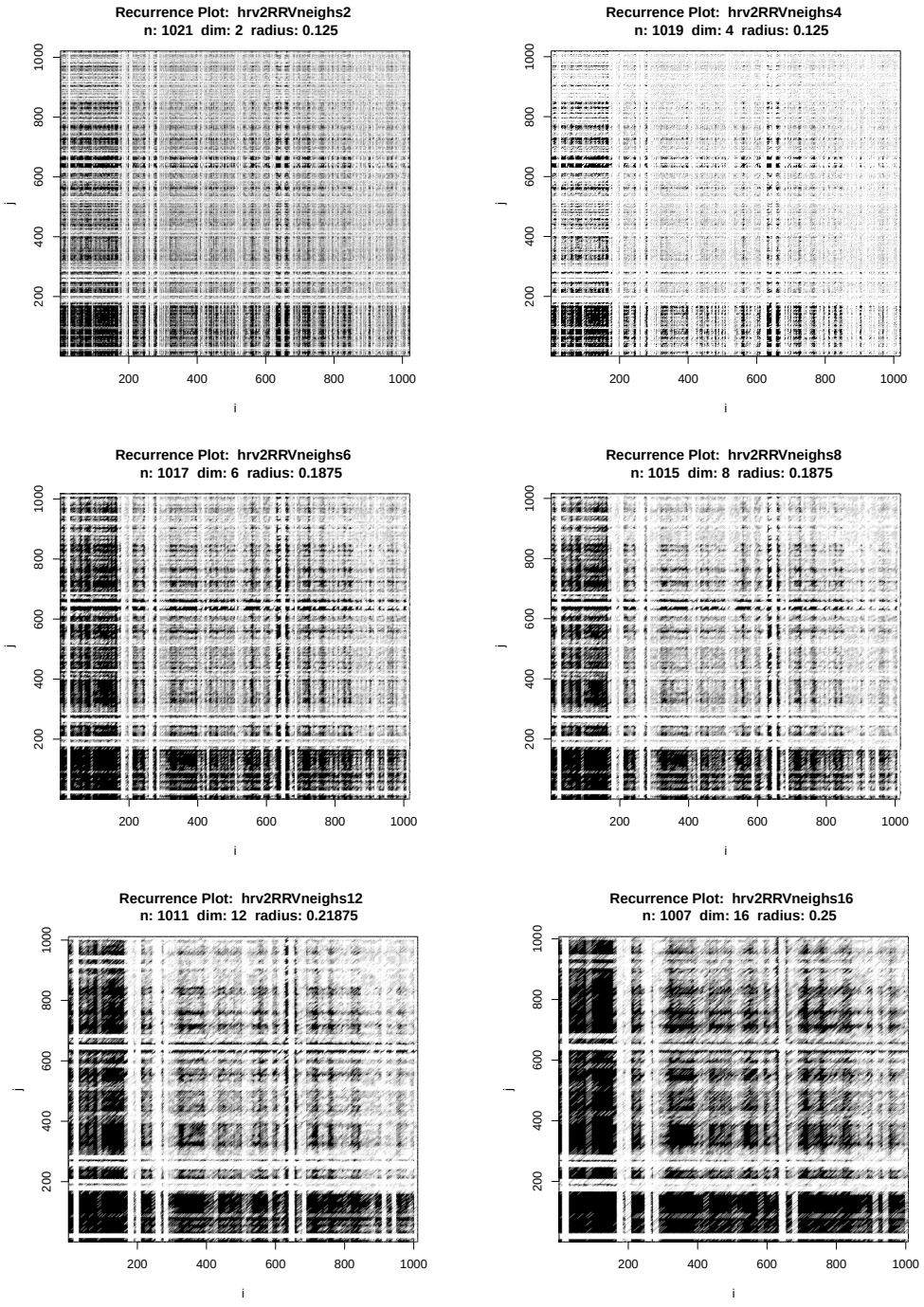


FIGURE 62. Recurrence Plot. Example case: RHRV tutorial example2.beats. Dim=2, 4, 6, 8, 12, 16. Time used: 3.857 sec.

References

Eckmann JP, Kamphorst SO, Ruelle D (1987). "Recurrence plots of dynamical systems." *Europhys. Lett*, **4**(9), 973–977.

Takens F (1981). "Detecting strange attractors in turbulence." In *Dynamical systems and turbulence, Warwick 1980*, pp. 366–381. Springer.

Webber Jr CL, Zbilut JP (2005). "Recurrence quantification analysis of nonlinear dynamical systems." *Tutorials in contemporary nonlinear methods for the behavioral sciences*, pp. 26–94.

Zbilut JP, Webber CL (2006). "Recurrence quantification analysis." *Wiley encyclopedia of biomedical engineering*. URL `http://onlinelibrary.wiley.com/doi/10.1002/9780471740360.ebs1355/full`.

Index

R session info:

Total Sweave time used: 163.69 sec. at Sun May 28 19:52:39 2017.

- R version 3.4.0 (2017-04-21), x86_64-apple-darwin15.6.0
- Locale: en_GB.UTF-8/en_GB.UTF-8/en_GB.UTF-8/C/en_GB.UTF-8/en_GB.UTF-8
- Running under: macOS Sierra 10.12.5
- Matrix products: default
- BLAS: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRblas.0.dylib
- LAPACK: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRlapack.dylib
- Base packages: base, datasets, graphics, grDevices, methods, stats, tcltk, utils
- Other packages: leaps 3.0, locfit 1.5-9.1, lomb 1.0, MASS 7.3-47, Matrix 1.2-9, mgcv 1.8-17, nlme 3.1-131, nonlinearTseries 0.2.3, plot3D 1.1, Rcpp 0.12.10, rgl 0.98.1, RHRV 4.2.3, sintro 0.1-6, tkrplot 0.0-23, TSA 1.01, tseries 0.10-40, waveslim 1.7.5
- Loaded via a namespace (and not attached): compiler 3.4.0, digest 0.6.12, grid 3.4.0, htmltools 0.3.6, htmlwidgets 0.8, httpuv 1.3.3, jsonlite 1.4, knitr 1.15.1, lattice 0.20-35, magrittr 1.5, mime 0.5, misc3d 0.8-4, quadprog 1.5-5, R6 2.2.0, shiny 1.0.3, tools 3.4.0, xtable 1.8-2, zoo 1.8-0

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Bibliography style: jss

CVS/Svn repository information:

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copied to r-forge

$HeadURL: svn+ssh://gsawitzki@scm.r-forge.r-project.org/svnroot/rhrv/gs/Rnw/recurrence.Rnw $

$Revision: 245 $

$Date: 2017-05-28 19:45:01 +0200 (Sun, 28 May 2017) $

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