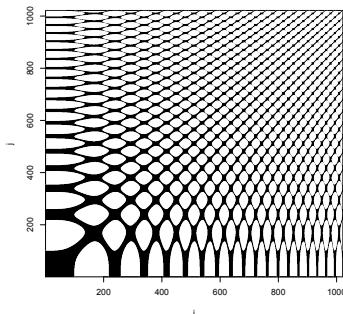


STATISTICAL DATA ANALYSIS: RECURRENCE PLOT

GÜNTHER SAWITZKI



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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 phase space of a system, for a choice of “dimension” d , take the sequence of d tuples taken from your data to define the states.

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

Under mild conditions, this Takens’ delay embedding allows to reconstruct the topology of the phase space from this embedded sequence [Takens, 1981].

The delay imbedding implicitly depends on the sampling rate with which the signal has been sampled. For example, if the rate is sufficiently high, all differentiable dynamics appear to be linear sine linear approximation holds. The imbedding construction allows a sub-sampling using a lag parameter m . So you take

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

ToDo: add support
for higher dimensional signals

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 visualise 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, conditioned 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()`.

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.

The visual impression of recurrence plots are strongly affected by the coverage, controlled by the radius used to determine neighbourhoods. So far, this parameter is chosen visually, and comparison needs some care.

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

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>>, for example Figure 1

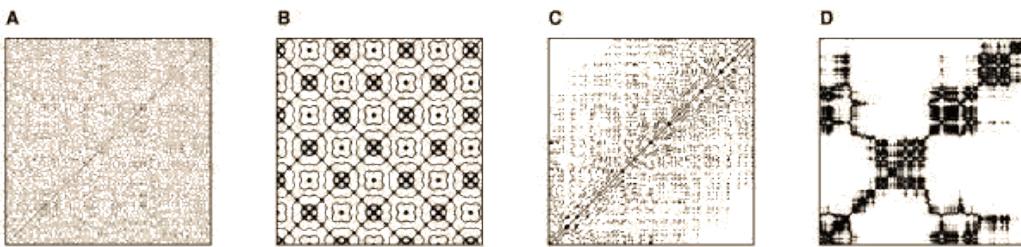


FIGURE 1. Characteristic typology of recurrence plots: (A) homogeneous (uniformly distributed noise), (B) periodic (super-positioned harmonic oscillations), (C) drift (logistic map corrupted with a linearly increasing term) and (D) disrupted (Brownian motion). These examples illustrate how different RPs can be. The used data have the length 400 (A, B, D) and 150 (C), respectively; no embeddings are used; the thresholds are $\epsilon = 0.2$ (A, C, D) and $\epsilon = 0.4$ (B). From <<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). References: [Zbilut and Webber, 2006], [Webber Jr and Zbilut, 2005]. See Table 1 on the next page.

ToDo: check RATIO - remove $RR = ?$
Radius²
ToDo: make scale
independent

2. R SETUP

Input

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

TABLE 1. Recurrence Quantification Analysis (RQA)

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

```

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

options(warn=1)                         Input

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

if (!require("sintro")) {                 Input
  # install.packages("sintro",repos="http://r-forge.r-project.org",type="source")
  library(sintro)
}
if (!require("nonlinearTseries")) {
  install.packages("nonlinearTseries")
  library(nonlinearTseries)
}
#suppressMessages(library('nonlinearTseries'))
library('plot3D')
# by default, the simulation creates a RGL plot of the system's phase space

```

For signal representation, we use a common layout.

Input

```

plotsignal <- function(signal, main, ylab, alpha=0.4) {
  if (missing(ylab)) { ylab <- deparse(substitute(signal)) }

  par(mfrow = c(1, 2))
  plot(signal,
       main = "", xlab = "index", ylab = ylab,
       col = rgb(0, 0, 1, 0.75*alpha), pch = 20)

  plot(signal, type = "l",
       main = "", xlab = "index", ylab = ylab,
       col = rgb(0, 0, 0, alpha))
  points(signal,
         col = rgb(0, 0, 1, 0.75*alpha), pch = 20)
  if (missing(main)) { main = deparse(substitute(signal)) }
  title(main = paste("signal and linear interpolation\n", main),
        outer = TRUE, line = -2, cex.main = 1.2)
}

}

```

2.0.1. *Takens States.* Takens states are represented as a matrix, one state per row. The number of columns 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

<i>Input</i>	
<code>alpha=0.5</code>	
<code>statepairs</code>	<i>Show marginal scatterplots of Takens states</i>

Usage.

```

statepairs(states, main,
range = NULL,
rank = FALSE, nooverlap = FALSE,
col,...)

```

Arguments.

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

ToDo: colour by time

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

```

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

<code>statecoplot</code>	<i>Show conditioning marginal scatterplots of Takens states</i>
--------------------------	---

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.

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

<code>statecoplot <- function(states, main,</code>	<i>Input</i>
---	--------------

```

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.

```

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)
}

```

```

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 recurrence-
PlotAux

ToDo: propagate
parameters from
`buildTakens` and
`findAllNeighbours`
in a slot of the result,
instead of using ex-
plicit parameters in

```

#non-sparse variant
#local.recurrencePlotAux <- nonlinearTseries:::recurrencePlotAux
local.recurrencePlotAux = function(neigs, dim=NULL, lag=NULL, radius=NULL){

  # just for reference. This function is inlined
  neighbourListNeighbourMatrix = function(){
    #neigs.matrix = Diagonal(ntakens)
    for (i in 1:ntakens){
      if (length(neigs[[i]])>0){
        for (j in neigs[[i]]){
          neigs.matrix[i,j] = 1
        }
      }
    }
    return (neigs.matrix)
  }

  ntakens=length(neigs)
  neigs.matrix <- matrix(nrow=ntakens, ncol=ntakens)
  #neighbourListNeighbourMatrix()
  #neigs.matrix = Diagonal(ntakens)
  for (i in 1:ntakens){
    neigs.matrix[i,i] = 1 # do we want the diagonal fixed to 1
    if (length(neigs[[i]])>0){
      for (j in neigs[[i]]){
        neigs.matrix[i,j] = 1
      }
    }
  }
}

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

more <- NULL

more <- paste(more," n:",length(neigs))

#use components of neights if available
embedding.dim <- attr(neigs, "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(neigs, "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:", attrradius,
                  " 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 `non-linearTseries`

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 ,...)
{
  #takens <- takens[!is.na(takens)]
  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]

  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("Ratio", xxrqa$RATIO)
  cat(paste(" Determinism:", round(xxrqa$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"))

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

    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)
    try(plot(dh, type="h", main=paste( id, " Diagonal:",
                                         pars, " Radius: ",radius, " REC:", round(xxrqa$REC, digits)),
              xlab="length of diagonals",
              log = log, ...))
    #needs handling of nan, Inf.

    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",
          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 7 on page 50) and two examples of heart rate data sets (Section 10 on page 81 and Section 11 on page 102) from *library(rhrv)*. The Geyser data set gives an example of a bi-variate point process. The HRV data sets give real live point process examples.

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, if restricting is appropriate.

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

3.1. Sinus.

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

See Figure 2 on page 15.

3.2. Uniform Random Numbers.

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

See Figure 3 on page 15,

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 4 on the next page,

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 5 on the facing page,

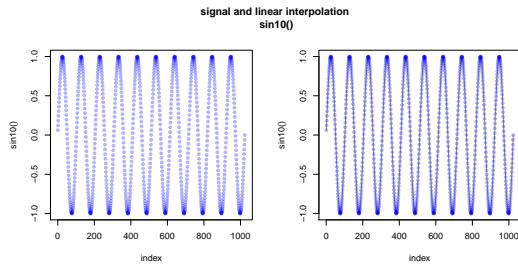
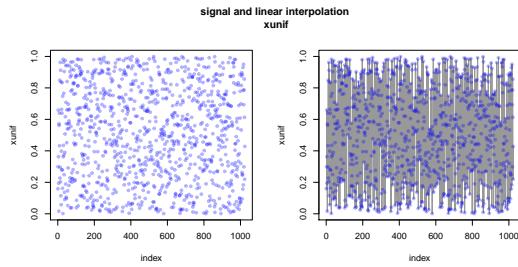
FIGURE 2. Test case: $\sin(10)$. Signal and linear interpolation.

FIGURE 3. Test case: unif - uniform random numbers. Signal and linear interpolation.

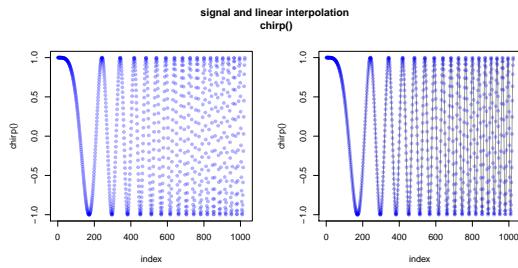


FIGURE 4. Test case: chirp signal. Signal and linear interpolation.

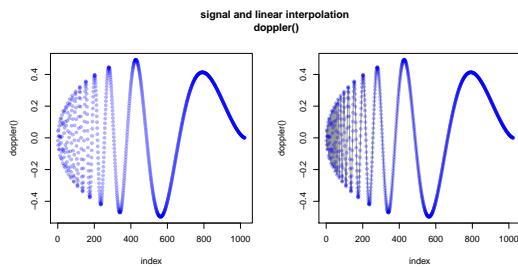


FIGURE 5. Test case: Doppler signal. Signal and linear interpolation.

4. NONLINEARTSERIES QUICK-START

4.1. Sinus.

Input

```

sinN <- sin10()
oldpar <- par(mfrow=c(1,2))
# tau delay estimation based on the autocorrelation function
tau.acf = timeLag(sinN, technique = "acf", do.plot = T,
main=paste("$\tau_{delay}$ estimation based on acf\n","sin()"))
# tau delay estimation based on the mutual information function
tau.ami=NA
try(tau.ami <- timeLag(sinN, technique = "ami",
do.plot = T, selection.method="first.minimum",
main=paste("$\tau_{delay}$ estimation based on ami\n","sin()")))
par(oldpar)
cat("Sinus tau.ami:",tau.ami," tau.acf:",tau.acf)

```

Output

```

Sinus tau.ami: 6  tau.acf: 20

```

See Figure 6.

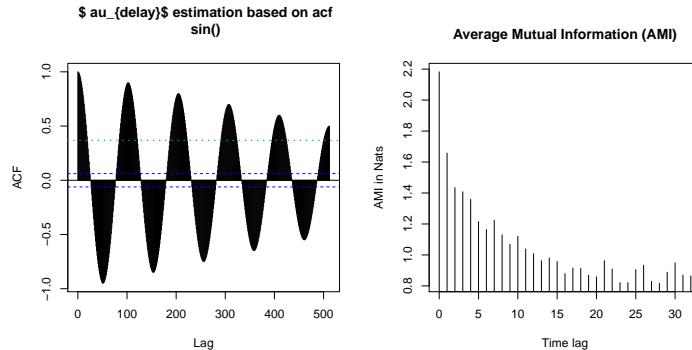


FIGURE 6. τ_{delay} estimation. "Sinus" Left: based on the autocorrelation function ACF. Right: AMI

Input

```

oldpar <- par(mfrow=c(1,2))
if (is.numeric(tau.ami)) {
emb.dim = estimateEmbeddingDim(sinN, time.lag = tau.ami,
max.embedding.dim = 15)
cat("sin() Lag tau.ami", tau.ami,"Estimated embedding dim:", emb.dim)
} else {
emb.dim = estimateEmbeddingDim(sinN, time.lag = tau.acf,
max.embedding.dim = 15)
cat("sin() Lag tau.acf", tau.acf,"Estimated embedding dim:", emb.dim)
}

```

Output

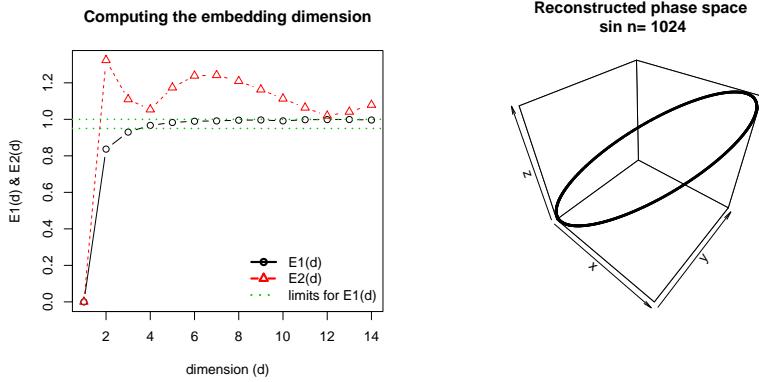
```

sin() Lag tau.ami 6 Estimated embedding dim: 4

```

Input

```
#taksinN = buildTakens(sinN, embedding.dim = 2, time.lag = 1)
taksinN = buildTakens(sinN, embedding.dim = emb.dim, time.lag = tau.ami)
scatter3D(taksinN[,1], taksinN[,2], taksinN[,3],
           main = paste("Reconstructed phase space\n sin n=",length(sinN)),
           col = 1, type="o",cex = 0.3)
par(oldpar)
```



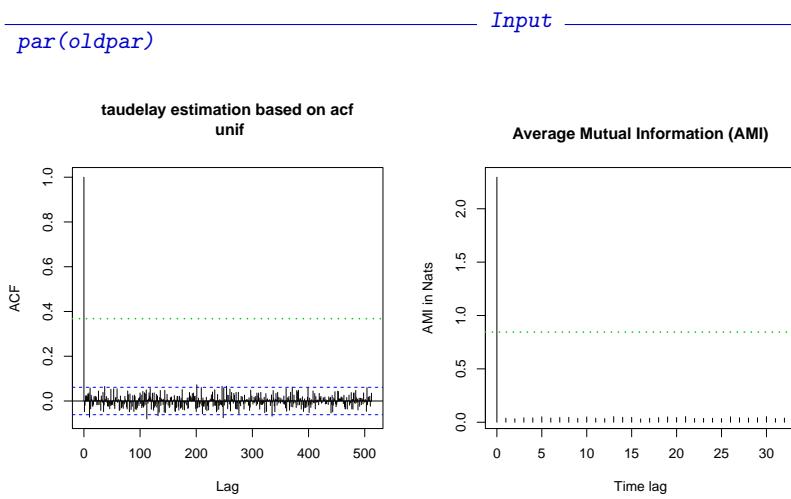
4.2. Uniform Random Numbers.

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

Output

```
Uniform  tau.acf: 1  tau.ami: 1
```



Input

```

oldpar <- par(mfrow=c(1,2))
if (is.numeric(tau.ami)) {
  emb.dim = estimateEmbeddingDim(unifN, time.lag = tau.ami,
    max.embedding.dim = 15)
  cat("unif Lag tau.ami", tau.ami,"Estimated embedding dim:", emb.dim)
} else {
  emb.dim = estimateEmbeddingDim(unifN, time.lag = tau.acf,
    max.embedding.dim = 15)
  cat("unif Lag tau.acf", tau.acf,"Estimated embedding dim:", emb.dim)
}

```

Output

```

unif Lag tau.ami 1 Estimated embedding dim: 11

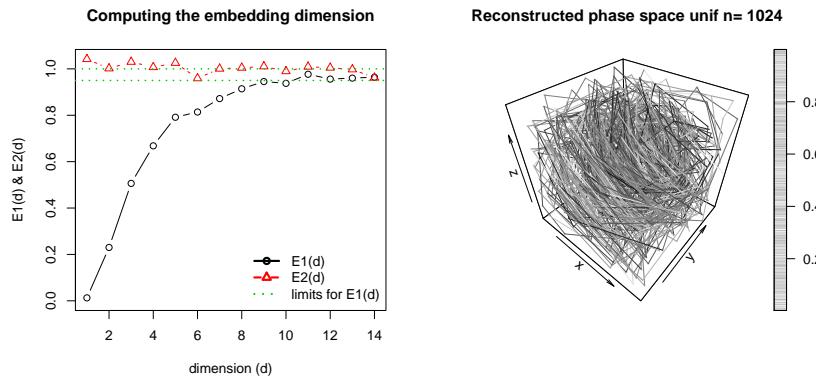
```

Input

```

#<<takfunifN, fig=TRUE>>=
takUnif = buildTakens(unifN, embedding.dim = emb.dim, time.lag = tau.ami)
#range(takUnif[4,])
col4 <- gray((1-takUnif[,4]),0.1)
scatter3D(takUnif[,1], takUnif[,2], takUnif[,3],
  main = paste("Reconstructed phase space","unif n=",length(unifN)),
  col = col4, type="o",cex = 0.3)
par(oldpar)

```



4.3. Chirp.

Input

```

chirpN <- chirp()
oldpar <- par(mfrow=c(1,2))
# tau delay estimation based on the autocorrelation function
tau.acf = timeLag(chirpN, technique = "acf", do.plot = T,
main=paste("tau delay estimation based on acf\n","chirp()"))
# tau delay estimation based on the mutual information function
tau.ami = timeLag(chirpN, technique = "ami", do.plot = T,
main=paste("tau delay estimation based on ami\n n=",length(chirpN),"chirp()"))
cat("Chirp ", "tau.acf:", tau.acf , " tau.ami:",tau.ami)

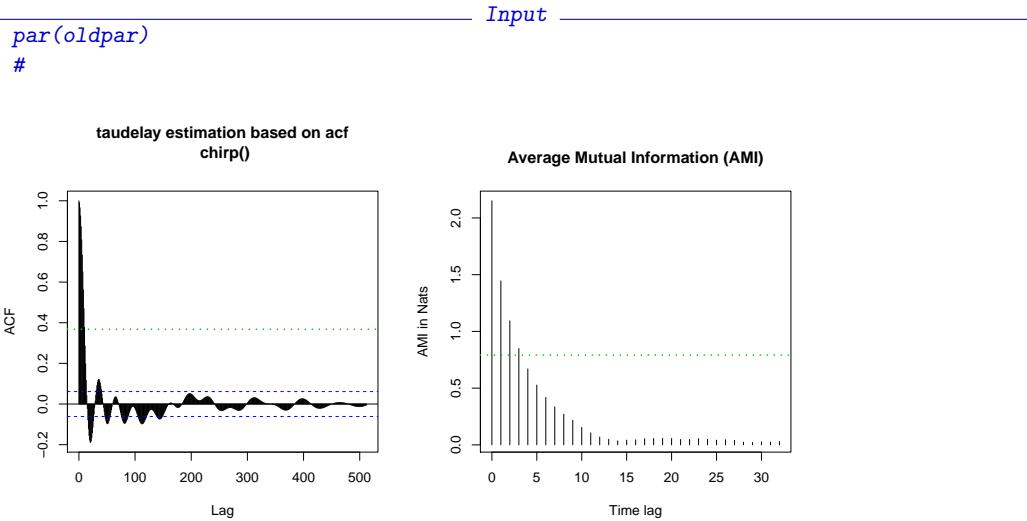
```

Output

```

Chirp  tau.acf: 11  tau.ami: 4

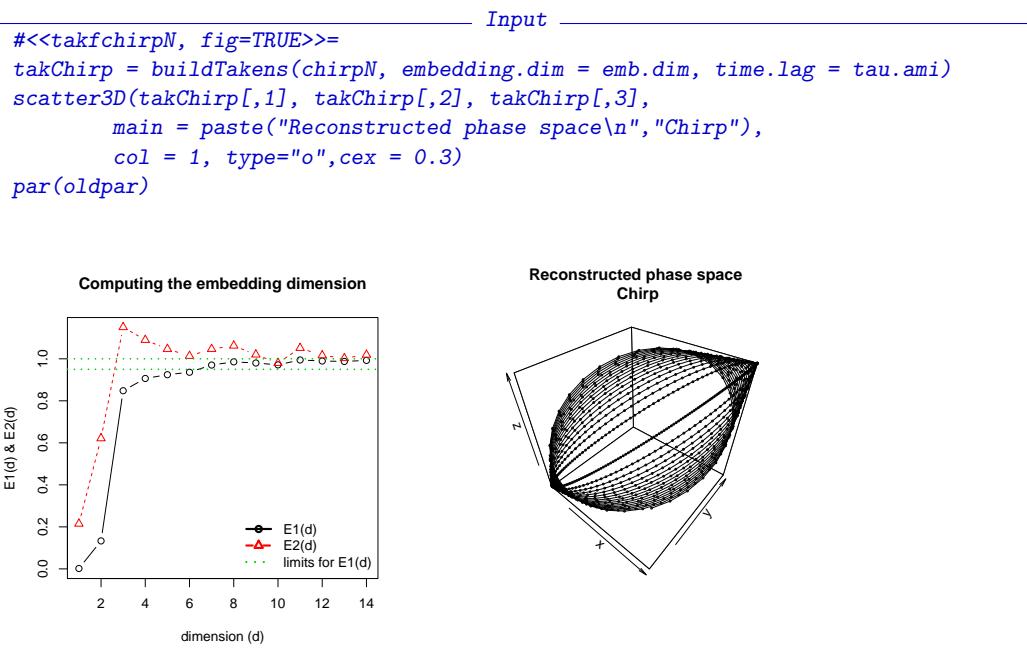
```



```
oldpar <- par(mfrow=c(1,2))
if (is.numeric(tau.ami)) {
  emb.dim = estimateEmbeddingDim(chirpN, time.lag = tau.ami,
    max.embedding.dim = 15)
  cat("chirp Lag tau.ami", tau.ami, "Estimated embedding dim:", emb.dim)
} else {
  emb.dim = estimateEmbeddingDim(chirpN, time.lag = tau.acf,
    max.embedding.dim = 15)
  cat("chirp Lag tau.acf", tau.acf, "Estimated embedding dim:", emb.dim)
}
```

Output

```
chirp Lag tau.ami 4 Estimated embedding dim: 7
```

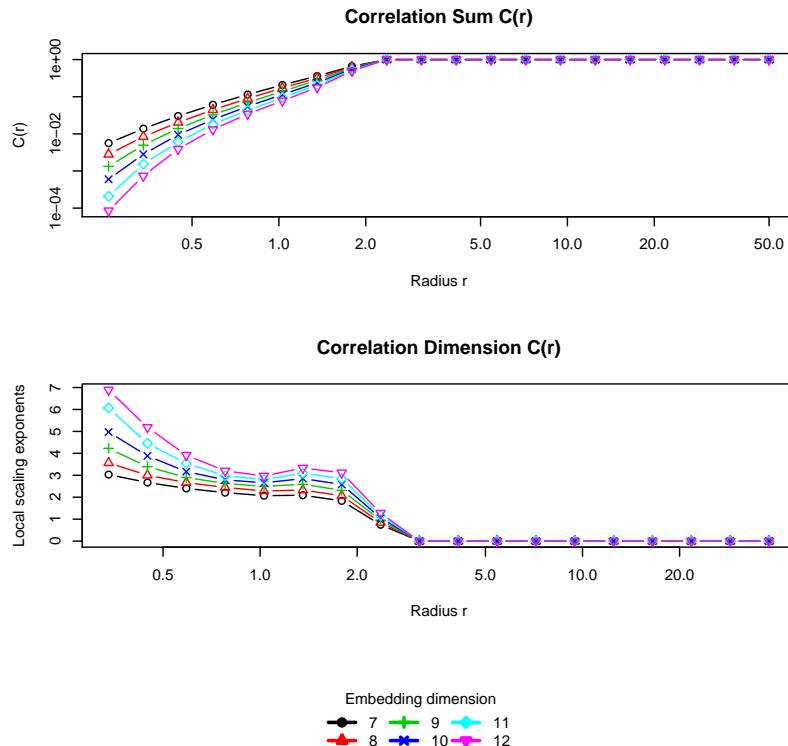


Input

```

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)
par(oldpar)

```



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

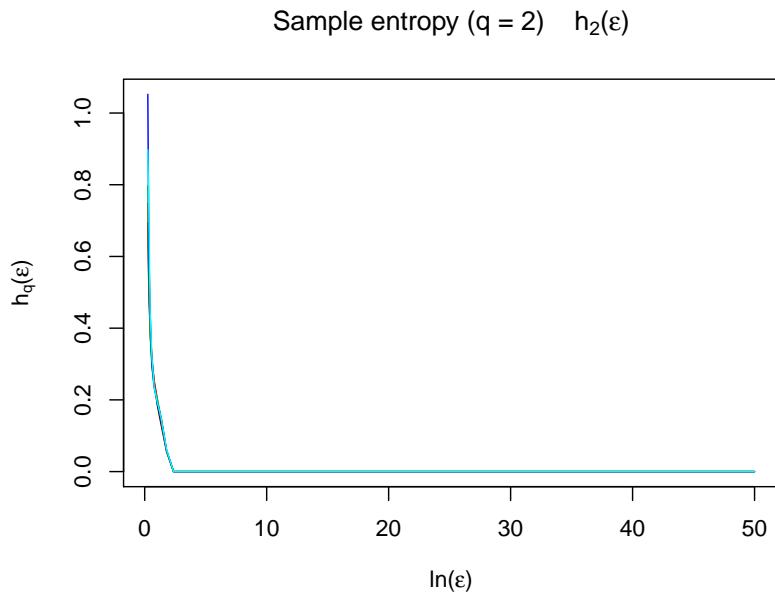
```

Input

```

par(oldpar)

```



Embedding dimension

●	7	+/-	9	diamond	11
▲	8	x	10		

Input

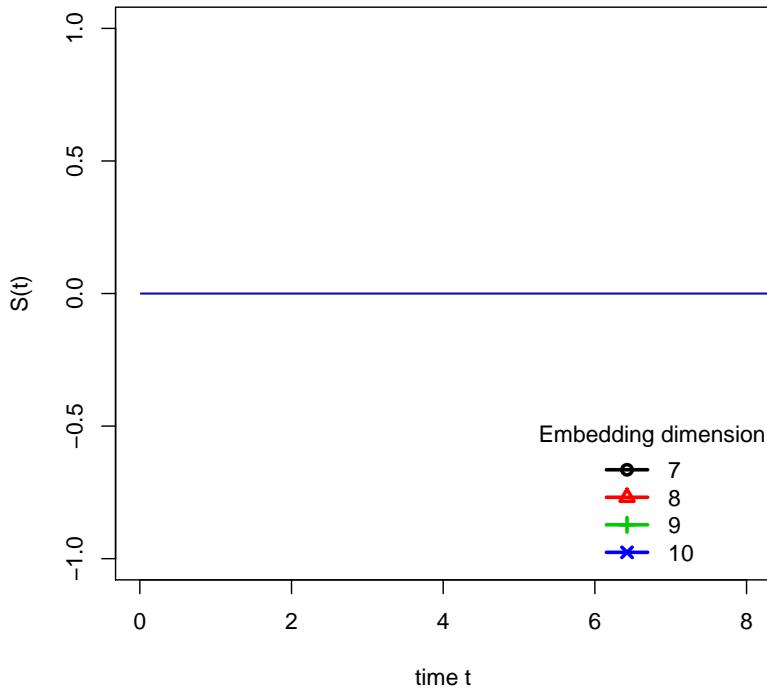
```
#sampling.period = diff(lor$time)[1]
ml = maxLyapunov(chirpN,
  sampling.period=0.01,
  min.embedding.dim = emb.dim,
  max.embedding.dim = emb.dim + 3,
  time.lag = tau.ami,
  radius=1,
  max.time.steps=1000,
  do.plot=FALSE)
plot(ml,type="l", xlim = c(0,8))
ml.est = estimate(ml, regression.range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

Estimating maximal Lyapunov exponent

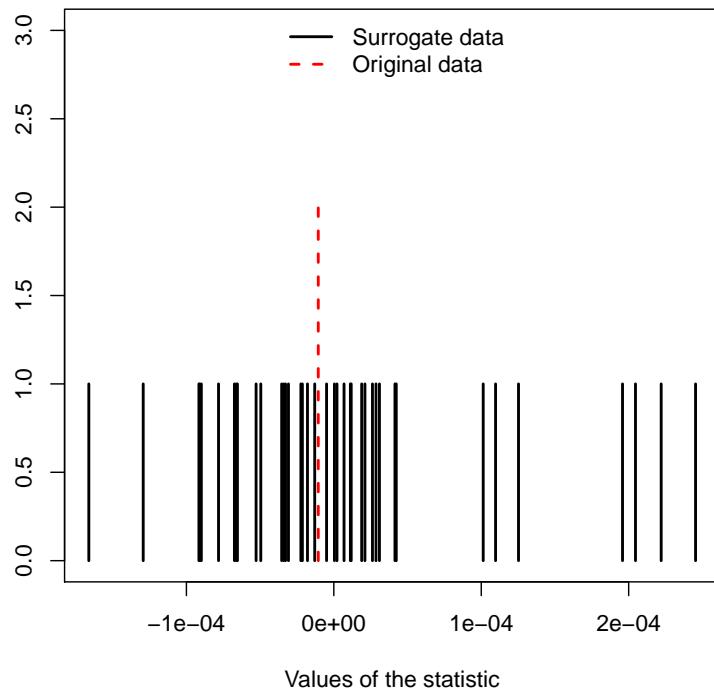


Input

```

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

4.4. Doppler.

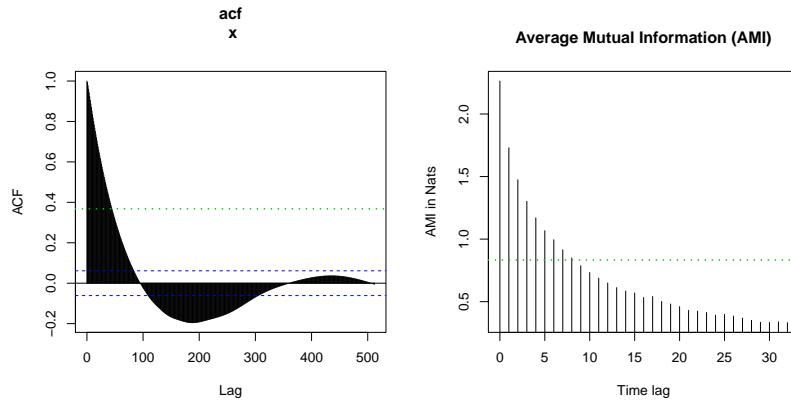
Input

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

Doppler tau.acf: 45 tau.ami: 9

Input

```
par(oldpar)
```



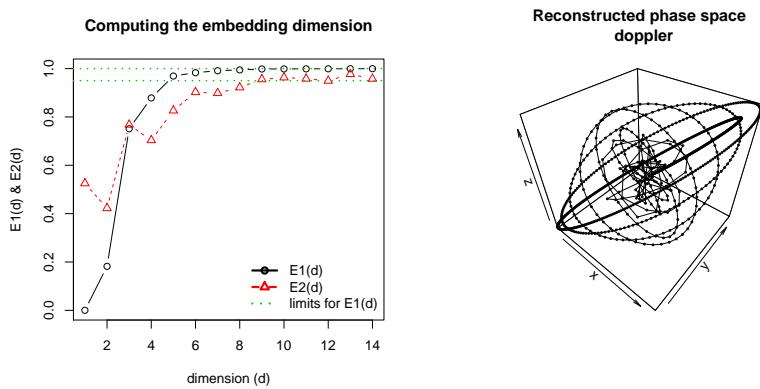
Input

```
oldpar <- par(mfrow=c(1,2))
if (is.numeric(tau.ami)) {
  emb.dim = estimateEmbeddingDim(dopplerN, time.lag = tau.ami,
      max.embedding.dim = 15)
  cat("Doppler lag tau.ami", tau.ami,"Estimated embedding dim:", emb.dim)
} else {
  emb.dim = estimateEmbeddingDim(dopplerN, time.lag = tau.acf,
      max.embedding.dim = 15)
  cat("Doppler lag tau.acf", tau.acf,"Estimated embedding dim:", emb.dim)
}
```

Doppler lag tau.ami 9 Estimated embedding dim: 5

Input

```
#<<takfdopplerN, fig=TRUE>>
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)
par(oldpar)
```

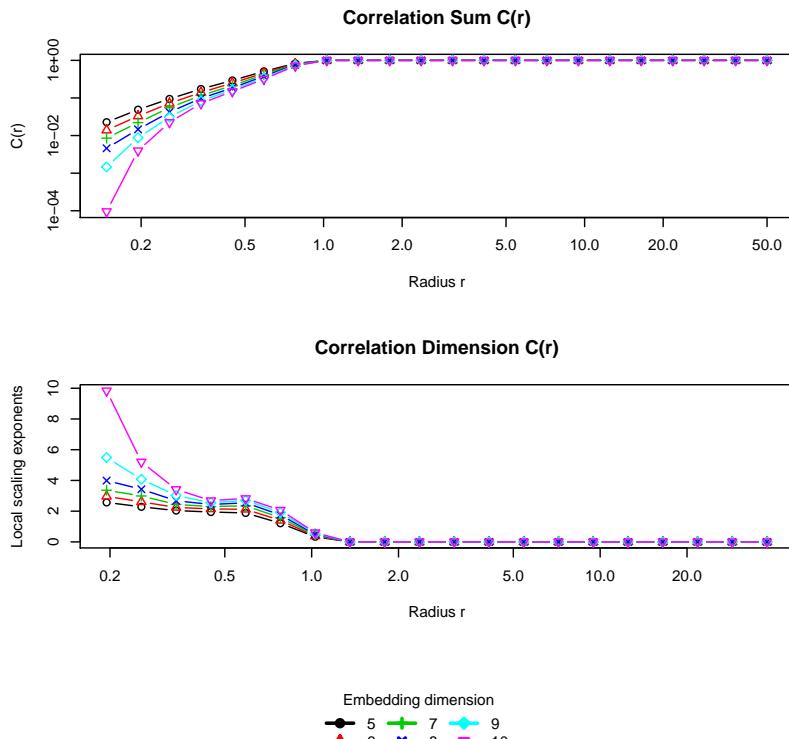


Input

```

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,

```

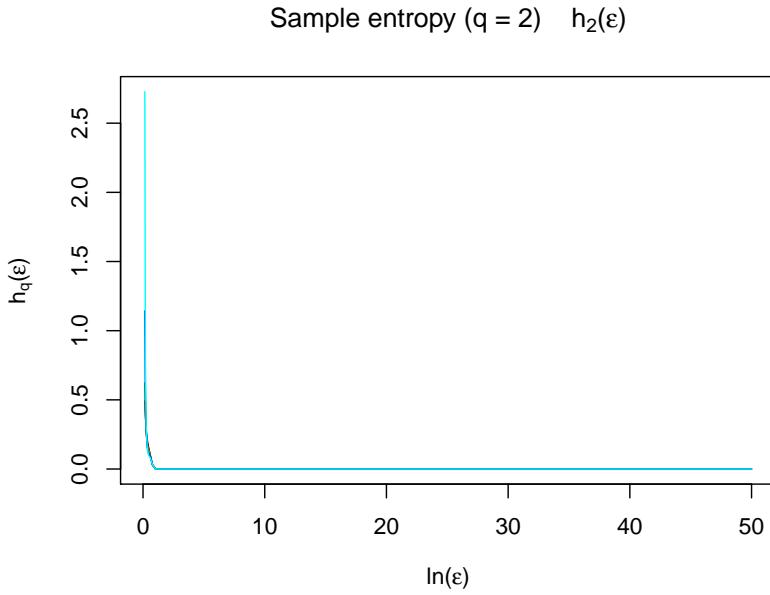
```
regression.range = c(8,15)
cat("Sample entropy estimate: ", mean(se.est), "\n")
```

Output

Sample entropy estimate: 0

Input

par(oldpar)



Embedding dimension

	5		7		9
	6		8		

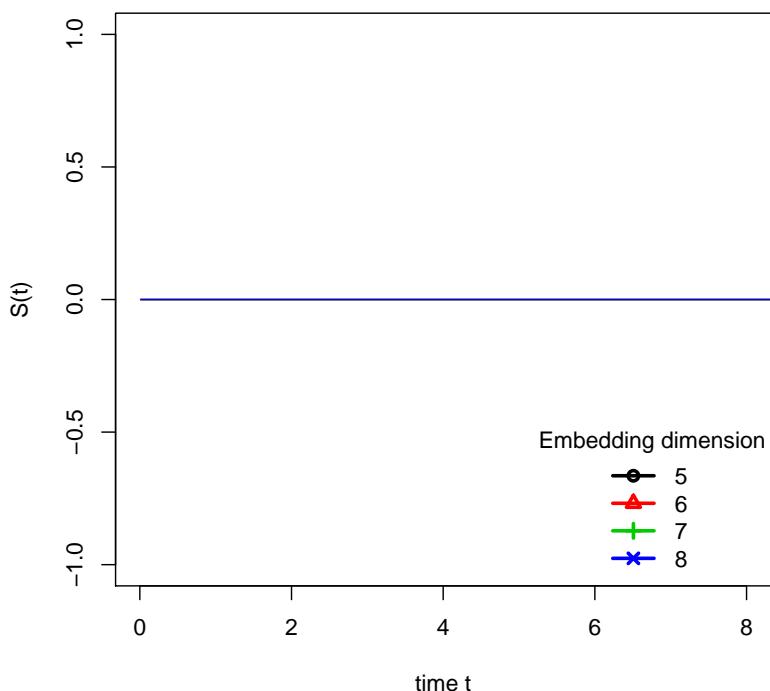
Input

```
#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

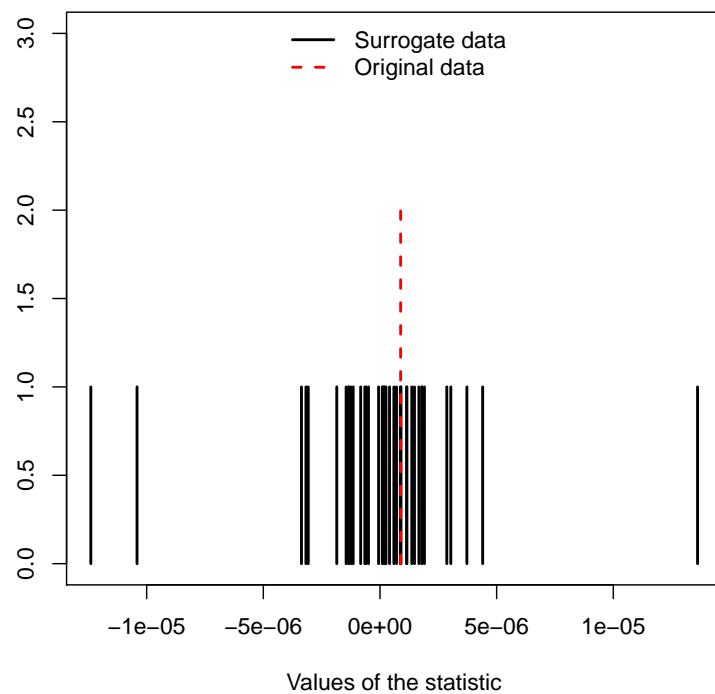
estimate: 0

Input

Estimating maximal Lyapunov exponent

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

5. TAKENS' STATES FOR TEST SIGNALS

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

See Figure 7.

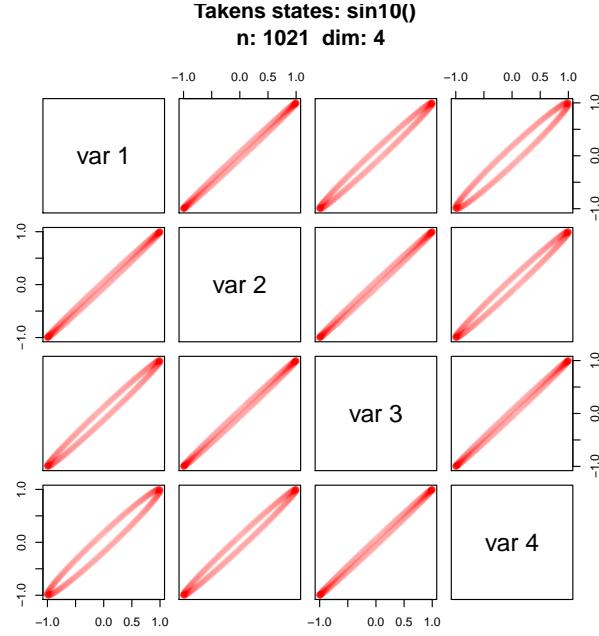


FIGURE 7. Takens states. Test case: sinus. Note that $2 - dim$ marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.835 sec.

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 8 on the next page.

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

See Figure 9 on the following page.

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

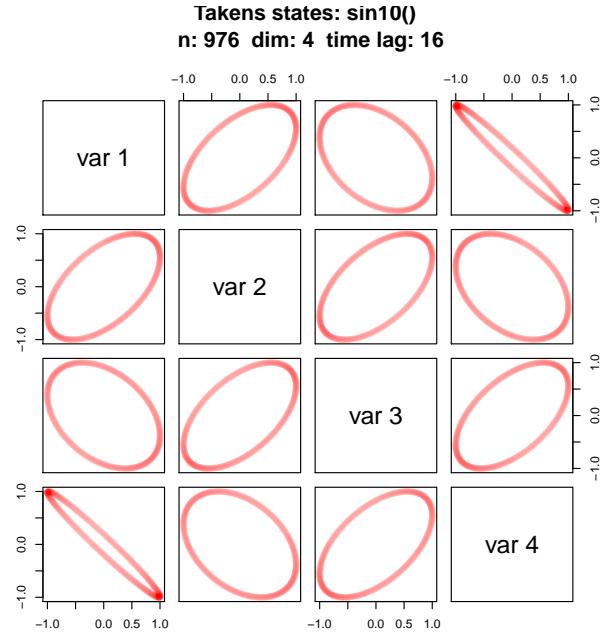


FIGURE 8. Takens states. Test case: sinus at time lag 16. Note that 2–dim marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.664 sec.

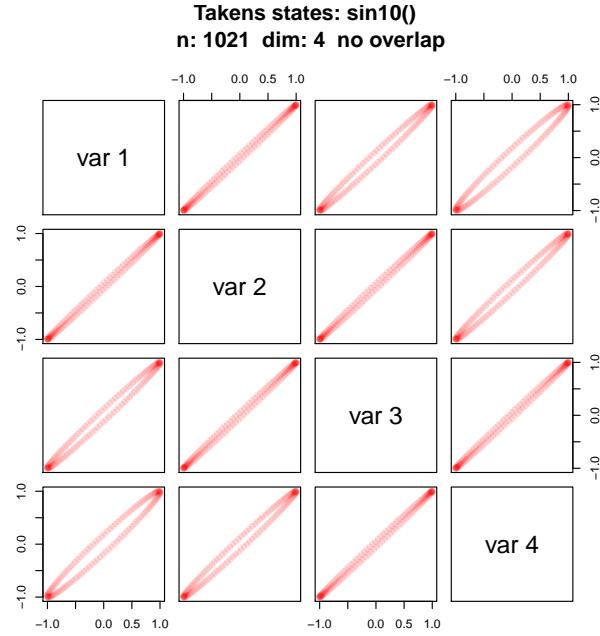


FIGURE 9. Takens states. Test case: sinus, no overlap. Note that 2–dim marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.833 sec.

See Figure 10.

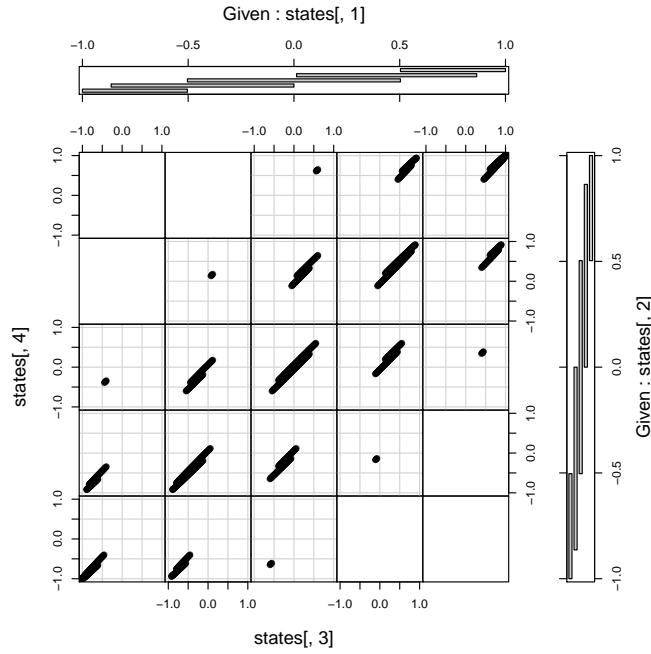


FIGURE 10. State coplot. Test case: sinus. Note that $2 - \text{dim}$ marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.238 sec.

Input

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

See Figure 11 on the following page.

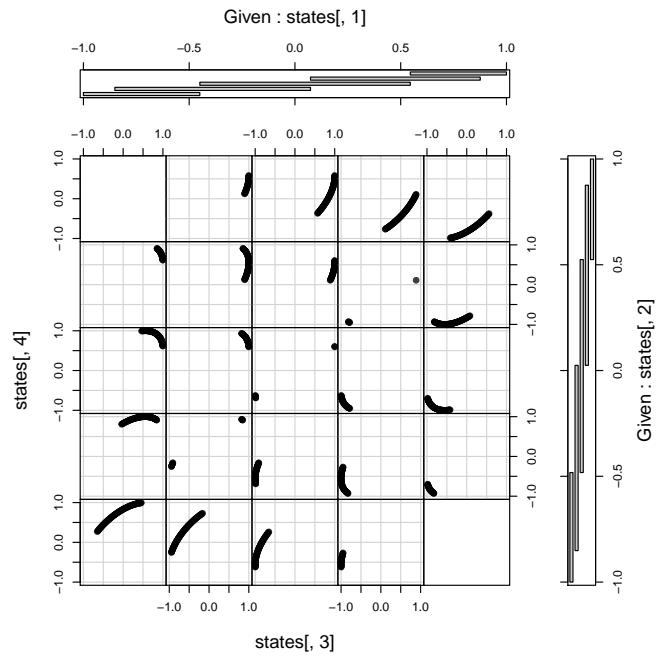


FIGURE 11. State coplot. Test case: sinus, time lag 16. Note that 2-dim marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.236 sec.

Input

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

See Figure 12.

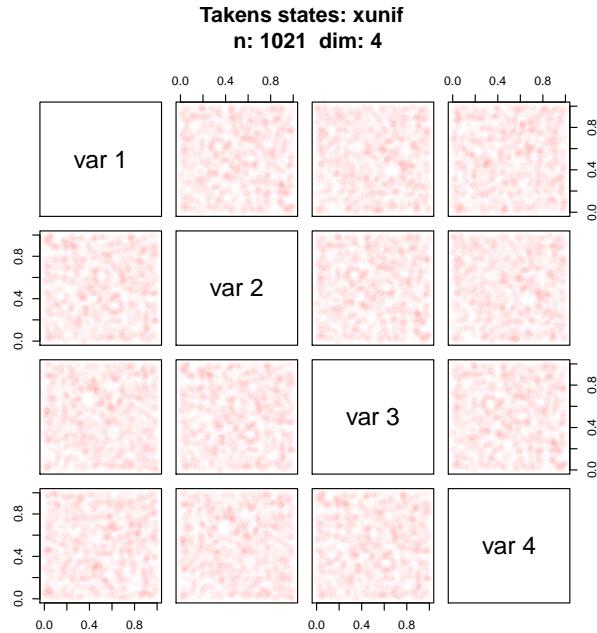


FIGURE 12. Takens states. Test case: uniform random numbers. Time used: 0.718 sec.

Input

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

See Figure 13 on the following page.

Input

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

See Figure 14 on the next page.

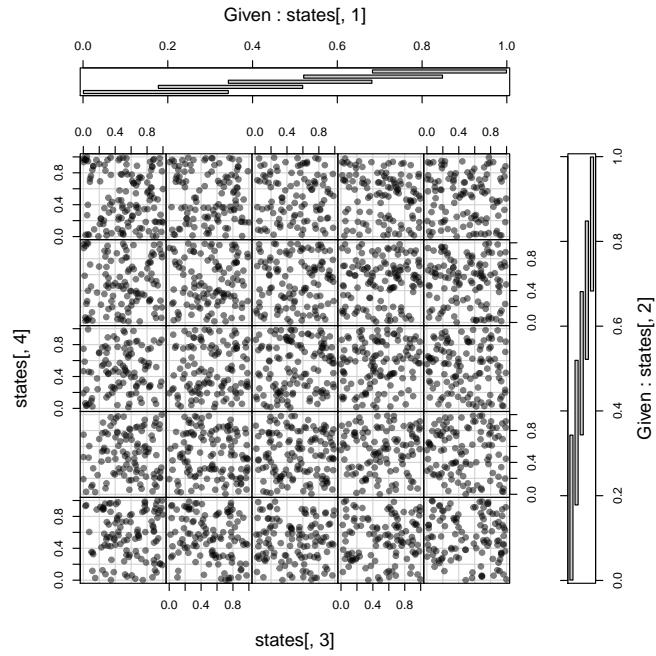


FIGURE 13. State coplot. Test case: uniform random numbers. Time used: 0.976 sec.

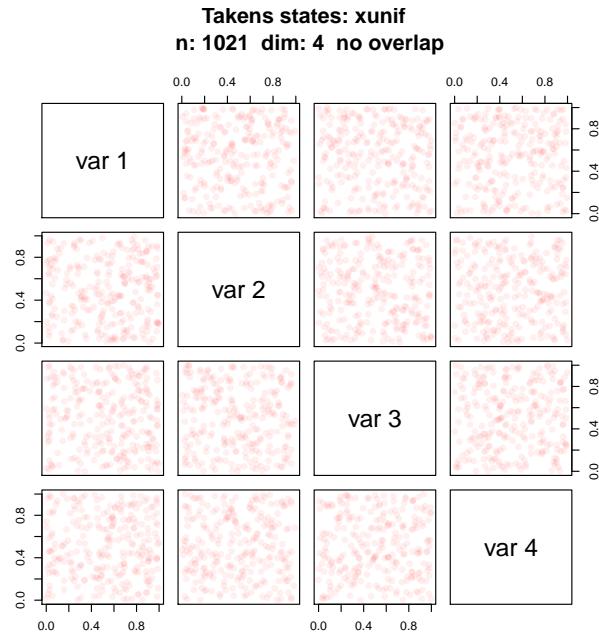


FIGURE 14. Takens states. Test case: uniform random numbers. Time used: 1.246 sec.

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

See Figure 15.

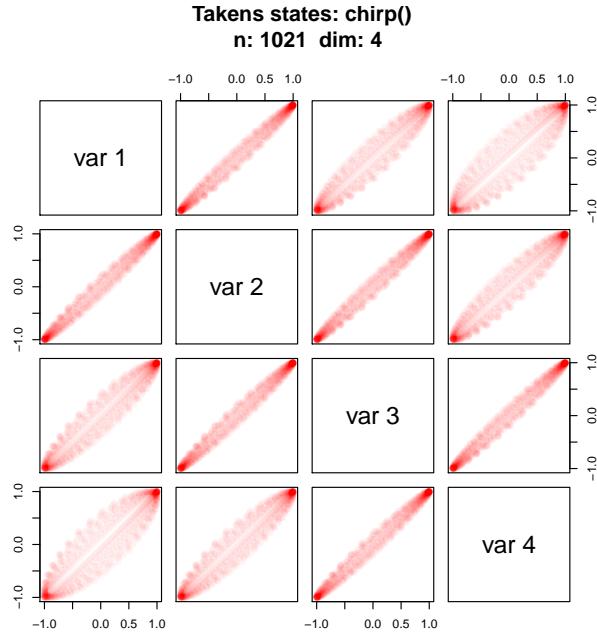


FIGURE 15. Takens states. Test case: chirp signal. Time used: 0.758 sec.

```
Input
statecplot(chirptakens) #dim=4
```

See Figure 16 on the next page.

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

See Figure 17 on the following page.

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

See Figure 18 on page 37.

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.

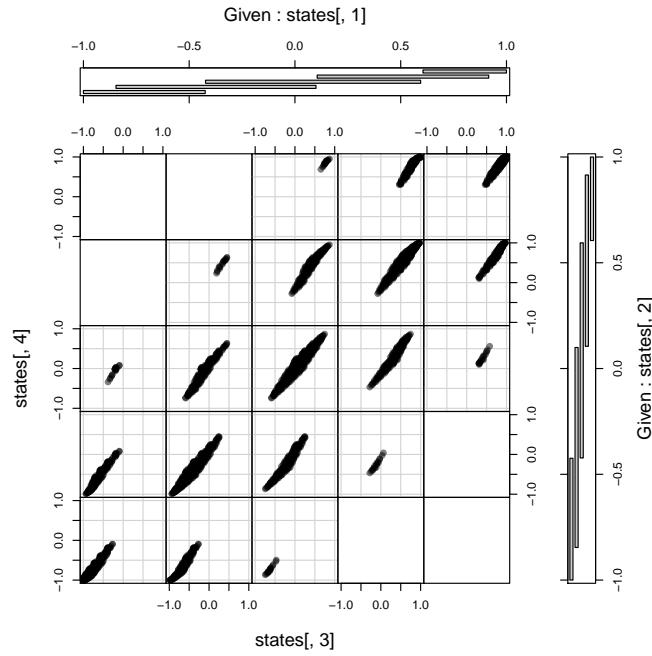


FIGURE 16. State coplot. Test case: chirp signal. Time used: 1.016 sec.

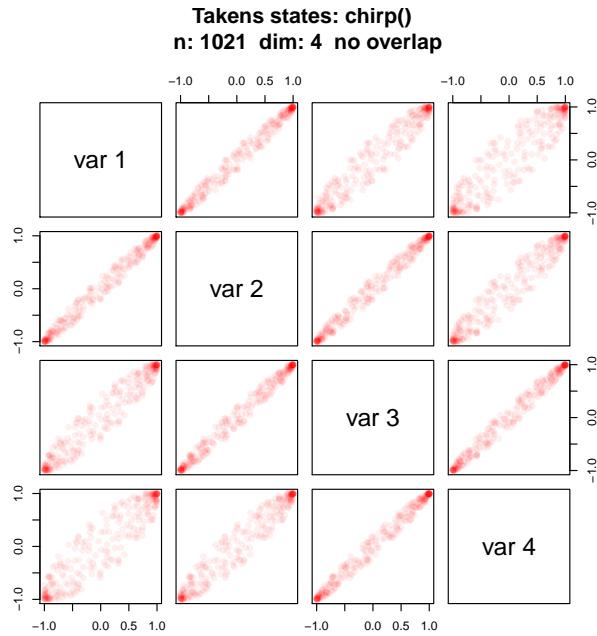


FIGURE 17. Takens states. Test case: chirp signal. Time used: 1.312 sec-

```

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

```

See Figure 19 on the facing page.

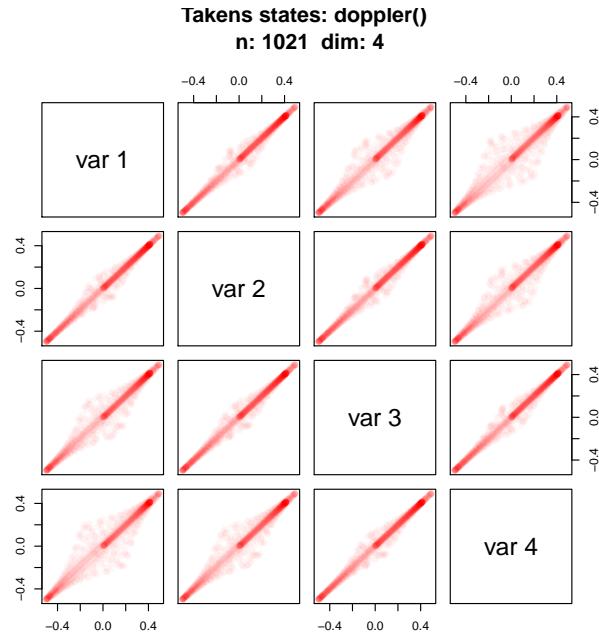


FIGURE 18. Takens states. Test case: Doppler. Note that $2 - \dim$ marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.728 sec.

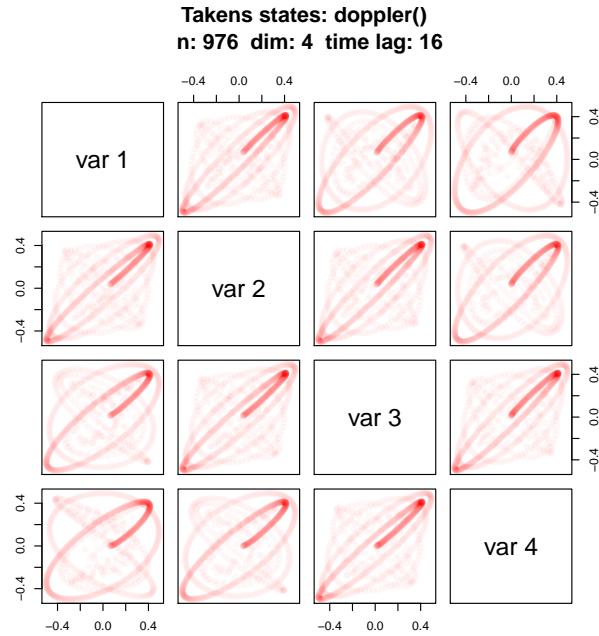


FIGURE 19. Takens states. Test case: doppler at time lag 16. Note that $2 - \dim$ marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.749 sec.

Input

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

See Figure 20.

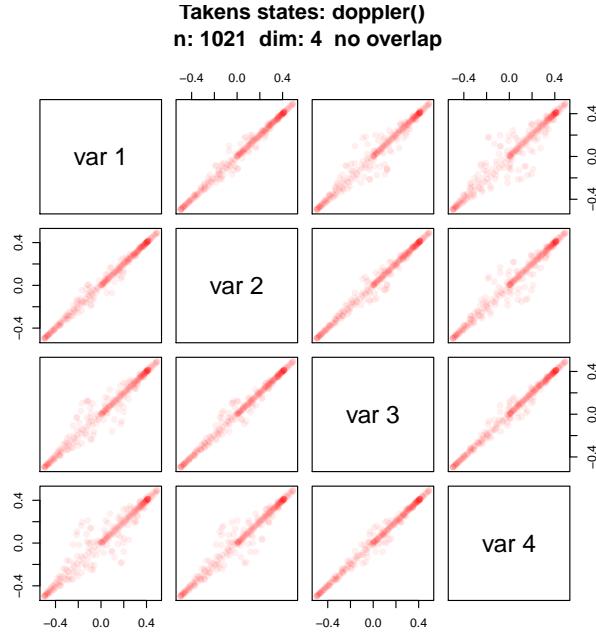


FIGURE 20. Takens states. Test case: doppler, no overlap. Note that 2-dim marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.969 sec.

Input

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

See Figure 21 on the facing page.

Input

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

See Figure 22 on the next page.

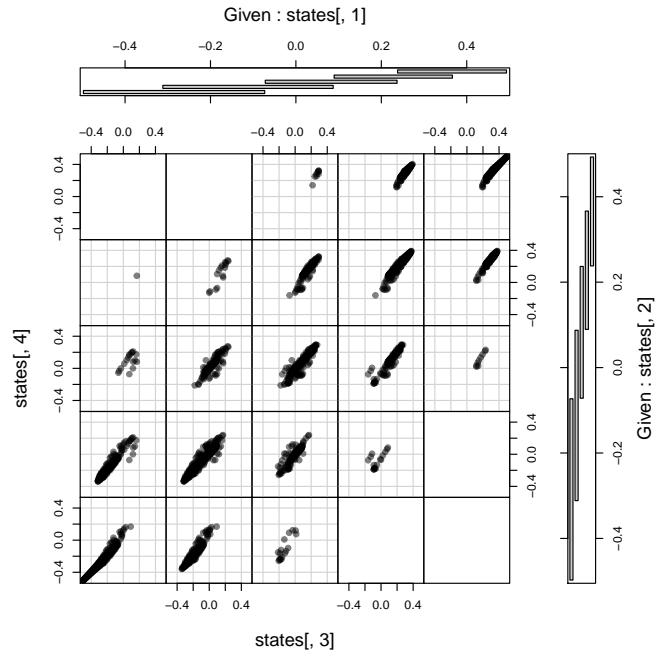


FIGURE 21. State coplot. Test case: Doppler. Note that 2-dim marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.313 sec.

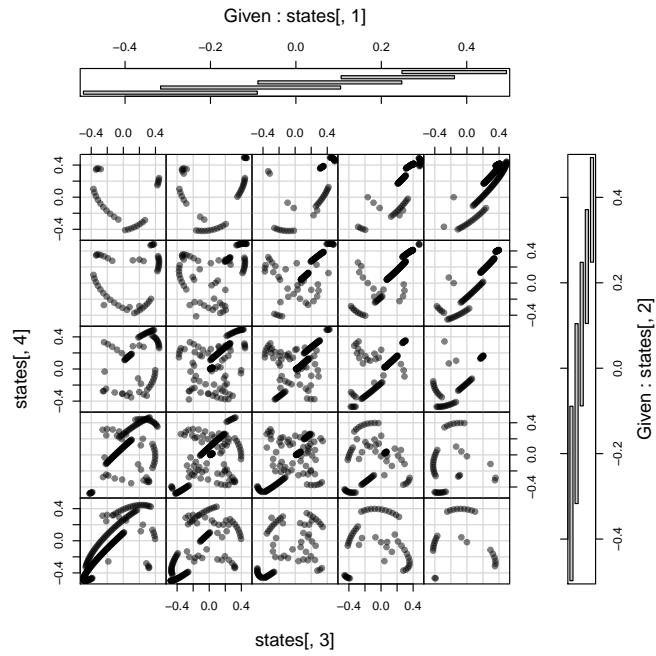


FIGURE 22. State coplot. Test case: Doppler, time lag 16. Note that 2-dim marginal views of 1-dimensional circles in d space generally appear as ellipses. Time used: 0.25 sec.

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 23.

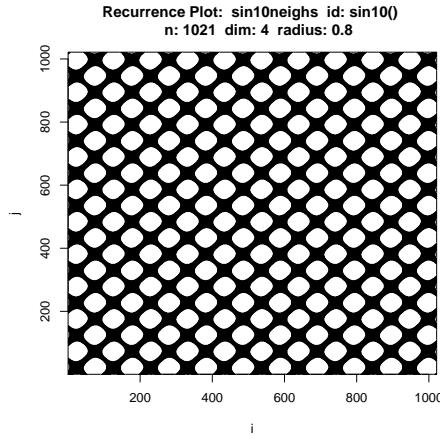


FIGURE 23. Recurrence plot. Test case: sinus. Time used: 1.665 sec.

```

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
Ratio 2.016253 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
```

RQA Test case: sinus. Radius=0.8.. Time used: 2.482 sec. For graphical ouput, see Figure 24 on the next page.

```

Input
sin10lag16neighs <- local.findAllNeighbours(sintakenslag16, radius=0.2)
save(sin10lag16neighs, file="sin10lag16neighs.Rdata")
# load(file="sin10lag16neighs.RData")
local.recurrencePlotAux(sin10lag16neighs, dim=4, radius=0.2)
```

See Figure 25 on the facing page.

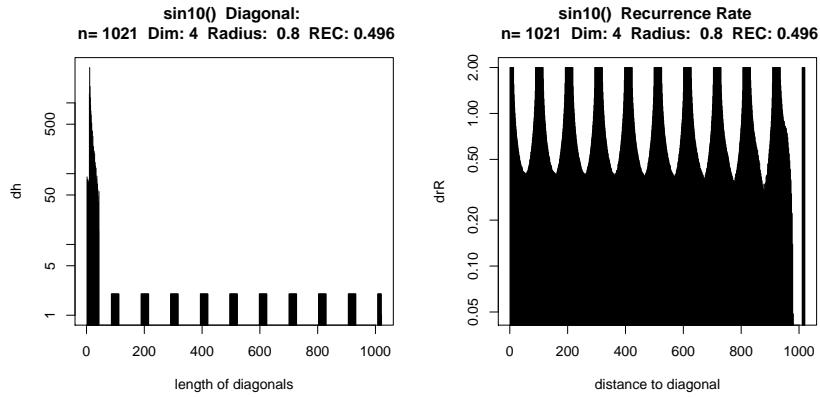


FIGURE 24. RQA. Test case: sinus. Radius=0.8., 0.82

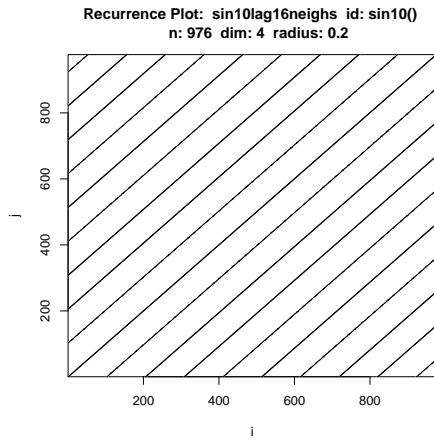


FIGURE 25. Recurrence plot. Test case: sinus curve, time lag 16. Time used: 3.115 sec.

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
Ratio 15.00875 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`

RQA Test case: sinus curve, time lag 16. Time used: 3.385 sec. For graphical output, see Figure 26 on the next page.

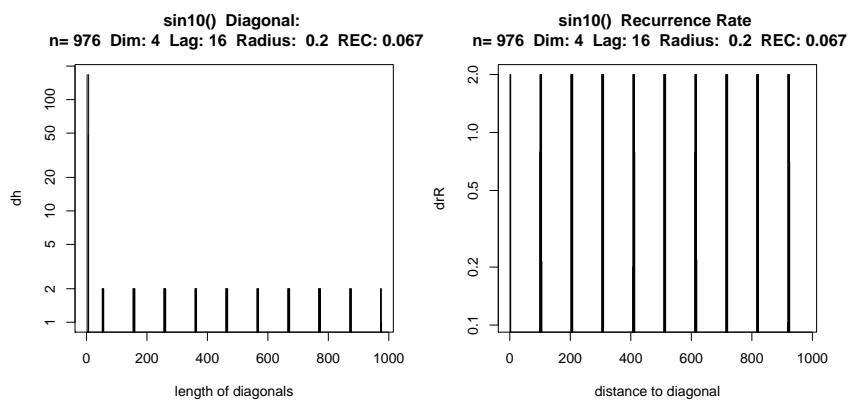


FIGURE 26. RQA. Test case: sinus curve, time lag 16, 0.82

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 27.

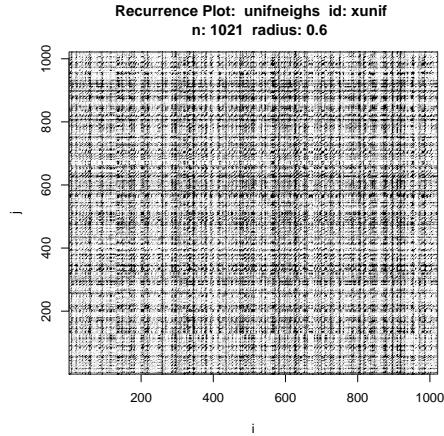


FIGURE 27. Recurrence plot. Test case: uniform random numbers. Time used: 2 sec.

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
Ratio 1.981289 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
```

RQA Test case: uniform random numbers, radius=0.6. Time used: 2.743 sec. For graphical output, see Figure 28 on the next page.

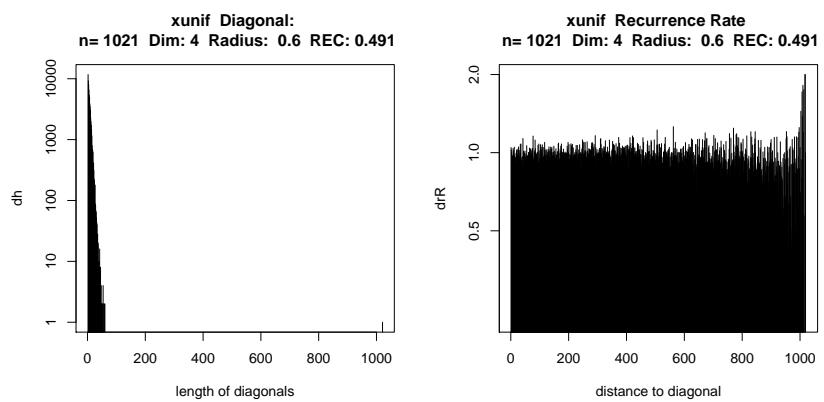


FIGURE 28. RQA. Test case: uniform random numbers, radius=0.6, 0.82

6.0.3. Chirp Signal Recurrence Plots.

Input

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

See Figure 29.

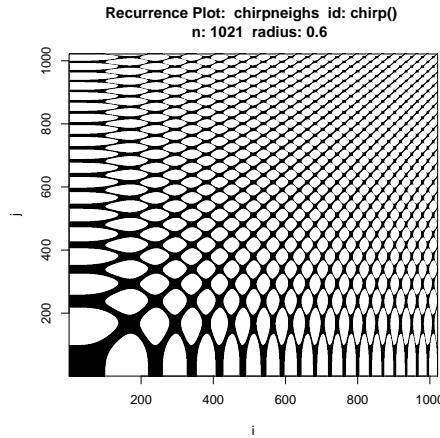


FIGURE 29. Recurrence plot. Test case: chirp signal. Time used: 1.294 sec.

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
Ratio 2.899648 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
```

RQA Test case: chirp signal. Time used: 1.752 sec. For graphical output, see Figure 30 on the next page.

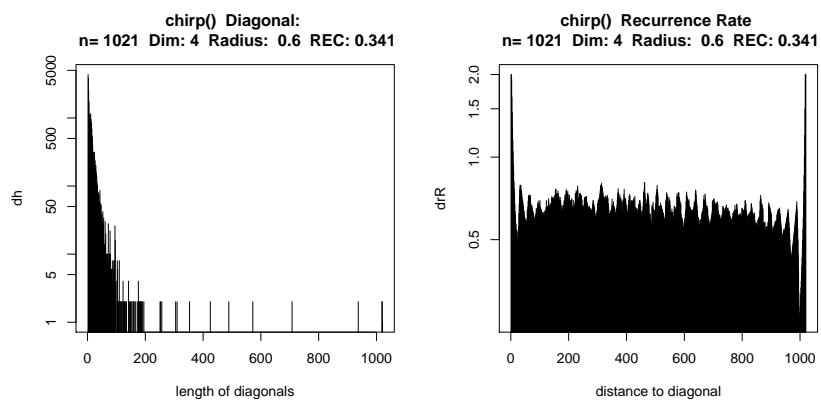


FIGURE 30. RQA. Test case: chirp signal, 0.82

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 31.

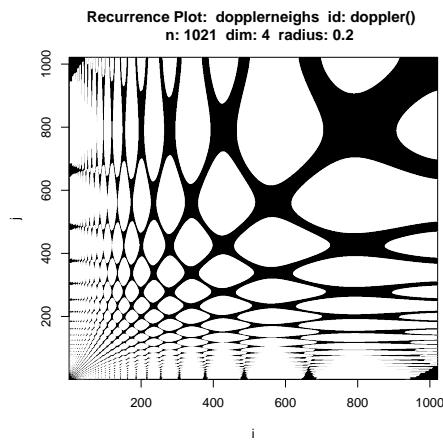


FIGURE 31. Recurrence plot. Test case: Doppler. Time used: 0.901 sec.

```
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
Ratio 3.314572 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
```

RQA Test case: Doppler. Time used: 0.464 sec. For graphical output, see Figure 32 on the next page.

```
Input
dopplerlag16neighs <- local.findAllNeighbours(dopplertakenslag16, radius=0.2)
save(dopplerlag16neighs, file="dopplerlag16neighs.Rdata")
# load(file="dopplerlag16neighs.RData")
local.recurrencePlotAux(dopplerlag16neighs, dim=4, radius=0.2)
```

See Figure 33 on the following page.

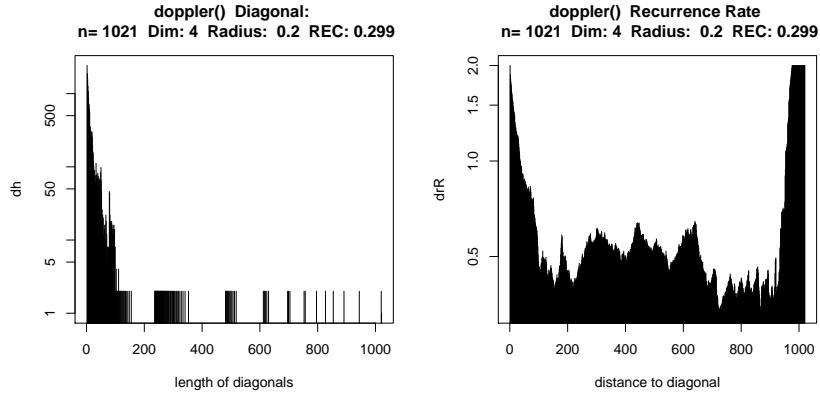


FIGURE 32. RQA. Test case: Doppler, 0.82

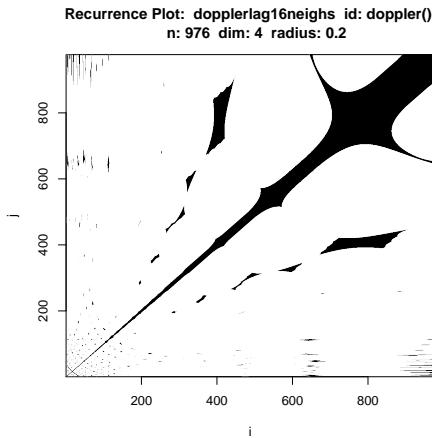


FIGURE 33. Recurrence plot. Test case: Doppler. Time used: 0.639 sec.

Input	
<code>showrqa(dopplertakenslag16, radius=0.2)</code>	
Output	
<code>doppler() n: 976 Dim: 4</code>	
<code>Radius: 0.2 Recurrence coverage REC: 0.098 log(REC)/log(R): 1.443</code>	
<code>Ratio 9.984234 Determinism: 0.98 Laminarity: 0.989</code>	
<code>DIV: 0.001</code>	
<code>Trend: 0 Entropy: 2.815</code>	
<code>Diagonal lines max: 975 Mean: 28.978 Mean off main: 28.678</code>	
<code>Vertical lines max: 256 Mean: 31.539</code>	

RQA Test case: Doppler. Time used: 0.856 sec. For graphical output, see Figure 34 on the next page.

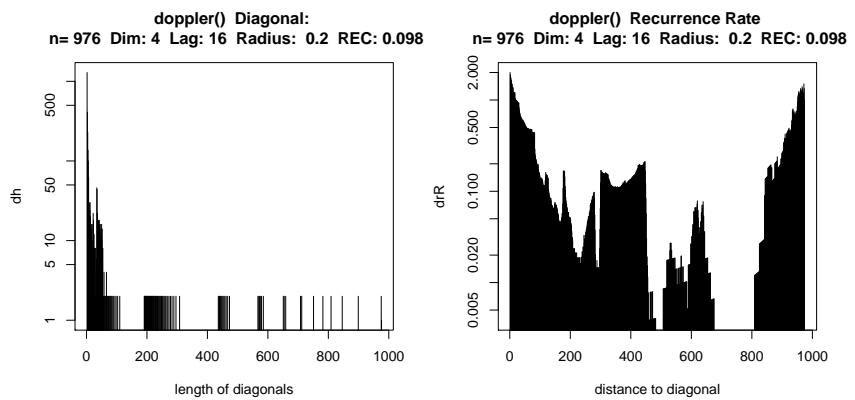


FIGURE 34. RQA. Test case: Doppler, 0.82

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

7. CASE STUDY: GEYSER EXAMPLE AND BIVARIATE RECURRENCE PLOTS

7.1. Paired sequences. This is a classical data set with a two dimensional structure. Components are *duration* and *waiting*.

More specific the Geyser 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-modal structures - a peculiarity of this data set. The main application problem is to predict waiting, based on the available information from the past.

Note for data analysis: The time to predict is the waiting time for the next eruption; so for prediction use a shifted sequence *waiting*[−1].

Note for data analysis: Some data are not recorded, but replaced by codes such as short, long. Handling of partially encoded data is required.

After 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)
attach(geyser)
```

To remove scale effects when comparing two sequences, we standardize both.

Input

```
duration <- duration - median(duration, na.rm=TRUE)
iqr_duration <- quantile(duration, probs = c(0.25, 0.75), na.rm = TRUE)
duration <- duration / (iqr_duration[2]-iqr_duration[1])
waiting <- waiting - median(waiting, na.rm=TRUE)
iqr_waiting <- quantile(waiting, probs = c(0.25, 0.75), na.rm = TRUE)
waiting <- waiting / (iqr_waiting[2]-iqr_waiting[1])
```

Input

```
plotsignal(duration)
```

Input

```
plotsignal(waiting)
```

Time used: 0.24 sec. Signal components and linear interpolation. See Figure 35 on the facing page.

Input

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

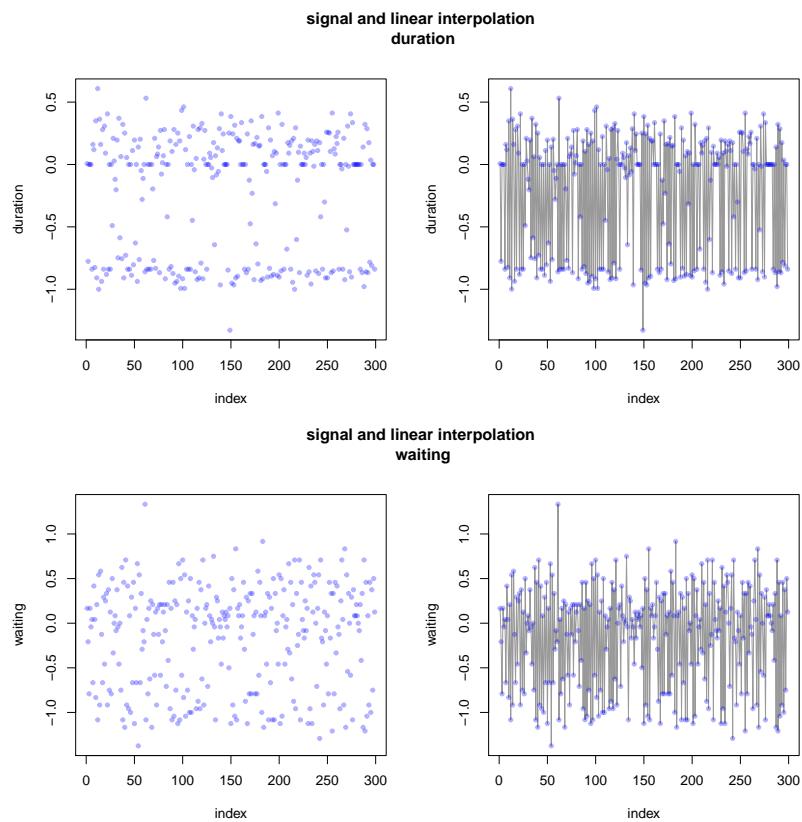


FIGURE 35. Example case: Old Faithful Geyser eruption durations and waiting time. Signals and linear interpolation. Time used: 0.24 sec.

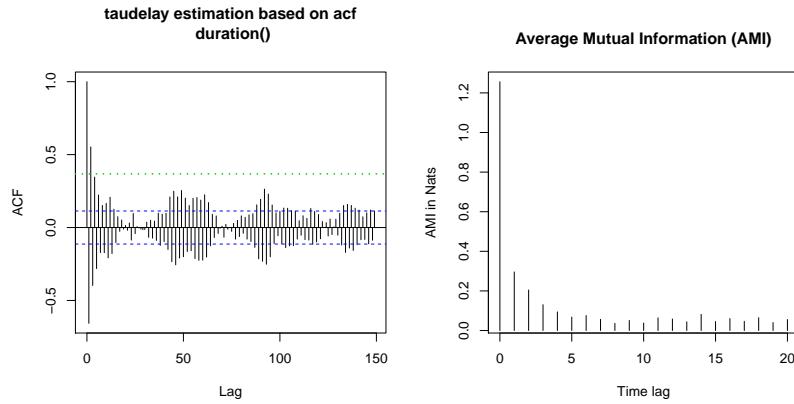
```
# tau delay estimation based on the mutual information function
tau.ami=NA
#try(tau.ami <- timeLag(duration, technique = "ami", do.plot = T,
#main=paste("tau delay estimation based on ami\n","duration")) )
try(tau.ami <- timeLag(duration, technique = "ami",
do.plot = T, selection.method="first.minimum",
main=paste("tau delay estimation based on ami\n","sin()")) )
cat("duration tau.acf:",tau.acf," tau.ami:",tau.ami)
```

Output

duration tau.acf: 1 tau.ami: 5

Input

par(oldpar)



Input

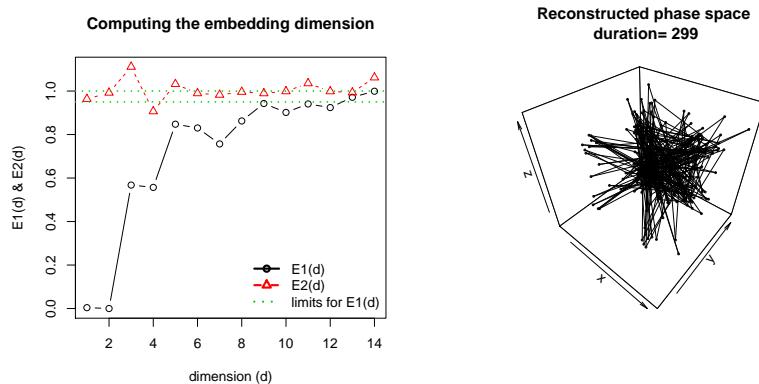
```
oldpar <- par(mfrow=c(1,2))
if (is.numeric(tau.ami)) {
  emb.dim = estimateEmbeddingDim(duration, time.lag = tau.ami,
  max.embedding.dim = 15)
  cat("duration Lag tau.ami", tau.ami,"Estimated embedding dim:", emb.dim)
} else {
  emb.dim = estimateEmbeddingDim(duration, time.lag = tau.acf,
  max.embedding.dim = 15)
  cat("duration Lag tau.acf", tau.acf,"Estimated embedding dim:", emb.dim)
}
```

Output

```
duration Lag tau.ami 5 Estimated embedding dim: 13
```

Input

```
#%<<takfsinN, fig=TRUE>>
takduration = buildTakens(duration, embedding.dim = emb.dim, time.lag = tau.ami)
scatter3D(takduration[,1], takduration[,2], takduration[,3],
  main = paste("Reconstructed phase space\n duration=", length(duration)),
  col = 1, type="o",cex = 0.3)
par(oldpar)
```



Input

```
oldpar <- par(mfrow=c(1,2))
# taudelay estimation based on the autocorrelation function
```

```

tau.acf = timeLag(waiting, technique = "acf", do.plot = T,
main=paste("taudelay estimation based on acf\n","waiting()"))
# taudelay estimation based on the mutual information function
tau.ami=NA
#try(tau.ami <- timeLag(waiting, technique = "ami", do.plot = T,
#main=paste("taudelay estimation based on ami\n","waiting()"))
try(tau.ami <- timeLag(waiting, technique = "ami",
do.plot = T, selection.method="first.minimum",
main=paste("taudelay estimation based on ami\n","waiting()"))
cat("waiting tau.acf:",tau.acf," tau.ami:",tau.ami)

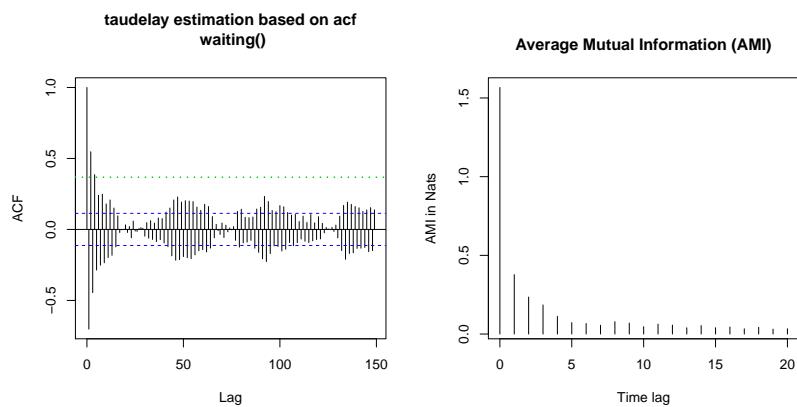
```

Output

```
waiting tau.acf: 1  tau.ami: 7
```

Input

```
par(oldpar)
```



Input

```

oldpar <- par(mfrow=c(1,2))
if (is.numeric(tau.ami)) {
emb.dim = estimateEmbeddingDim(waiting, time.lag = tau.ami,
max.embedding.dim = 15)
cat("waiting Lag tau.ami", tau.ami,"Estimated embedding dim:", emb.dim)
} else {
emb.dim = estimateEmbeddingDim(waiting, time.lag = tau.acf,
max.embedding.dim = 15)
cat("waiting Lag tau.acf", tau.acf,"Estimated embedding dim:", emb.dim)
}

```

Output

```
waiting Lag tau.ami 7 Estimated embedding dim: 10
```

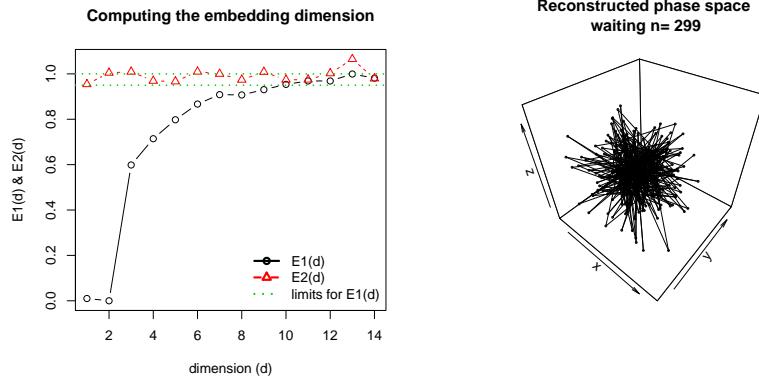
Input

```

#@%
#%%
#%<<takfwaiting, fig=TRUE>>=
takwaiting = buildTakens(waiting, embedding.dim = emb.dim, time.lag = tau.ami)
scatter3D(takwaiting[,1], takwaiting[,2], takwaiting[,3],
#%main = paste("Reconstructed phase space\n",deparse(substitute(time.series))), 
main = paste("Reconstructed phase space\n waiting n=",length(waiting)),

```

```
col = 1, type="o", cex = 0.3)
par(oldpar)
```



Input

```
takens.duration4 <- buildTakens( time.series=duration, embedding.dim=4, time.lag=1)
takens.waiting4 <- buildTakens( time.series=waiting, embedding.dim=4, time.lag=1)
```

Time used: 5.653 sec.

Input

```
duration4rqa <- showrqa(takens.duration4, radius=0.5, log=TRUE)
```

Output

```
duration n: 296 Dim: 4
Radius: 0.5 Recurrence coverage REC: 0.168 log(REC)/log(R): 2.577
Ratio 5.628595 Determinism: 0.943 Laminarity: 0.07
DIV: 0.036
Trend: 0 Entropy: 1.937
Diagonal lines max: 28 Mean: 4.359 Mean off main: 4.267
Vertical lines max: 5 Mean: 3.065
```

RQA Geyser duration. Radius=0.5.. Time used: 5.727 sec. For graphical ouput, see Figure 36.

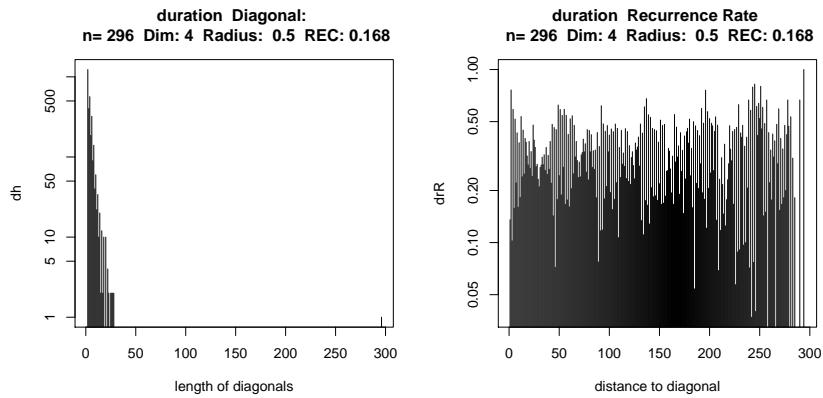


FIGURE 36. RQA. Geyser duration. Radius=0.5., 0.82

Input

```
waiting4rqa <- showrqa(takens.waiting4, radius=0.5, log=TRUE)
```

Output

```
waiting n: 296 Dim: 4
Radius: 0.5 Recurrence coverage REC: 0.112 log(REC)/log(R): 3.154
Ratio 8.004975 Determinism: 0.899 Laminarity: 0.088
DIV: 0.05
Trend: 0 Entropy: 1.8
Diagonal lines max: 20 Mean: 3.904 Mean off main: 3.775
Vertical lines max: 7 Mean: 3.024
```

RQA Geyser waiting. Radius=0.5.. Time used: 5.804 sec. For graphical ouput, see Figure 37.

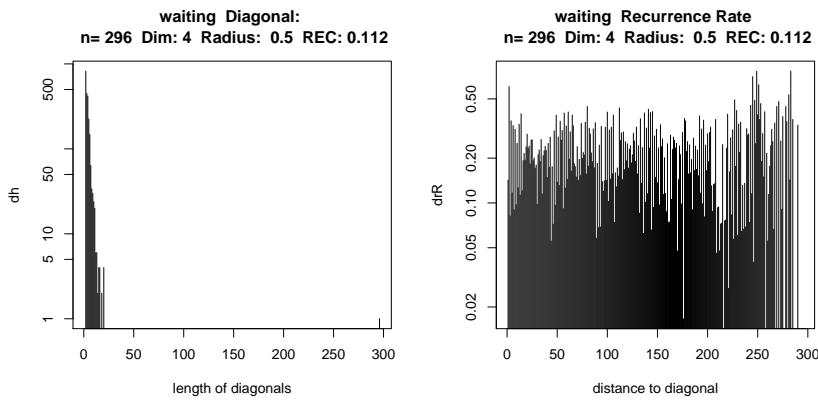


FIGURE 37. RQA. Geyser waiting. Radius=0.5., 0.82

Input

```
statepairs(takens.duration4) #dim=4
```

Input

```
statepairs(takens.waiting4) #dim=4
```

Example case: Old Faithful Geyser eruption data. Time used: 6.325 sec. See Figure 39 on the next page.

To Do: use nooverlap ?

Input

```
statecoplot(takens.duration4) #dim=4
```

See Figure 38 on the following page.

Input

```
durationneighs4<- findAllNeighbours(takens.duration4, radius=0.5)
waitingneighs4<-findAllNeighbours(takens.waiting4, radius=0.5)
```

Input

```
local.recurrencePlotAux(durationneighs4)
```

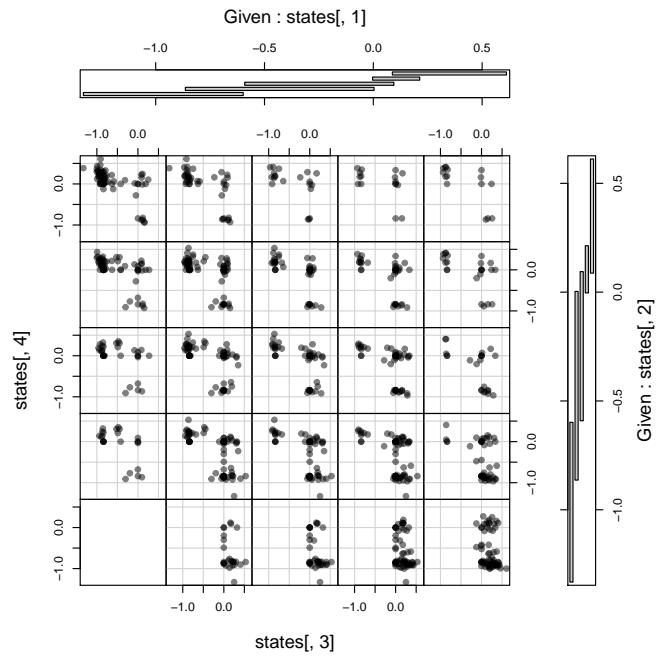


FIGURE 38. State coplot. Example case: Old Faithful Geyser eruption durations. Time used: 6.458 sec.

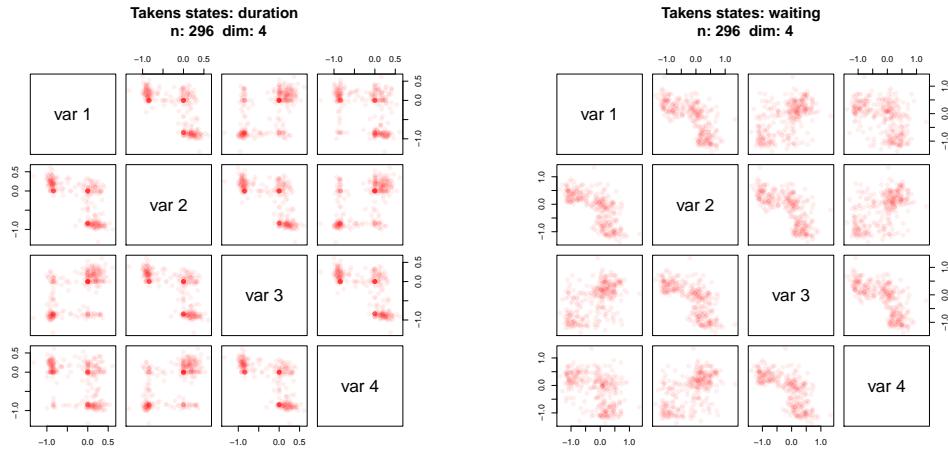


FIGURE 39. Old Faithful Geyser eruption durations and waiting time. Takens states, dim=4. Time used: 6.458 sec.

Input

```
local.recurrencePlotAux(waitingneighs4)
```

See Figure 40 on the next page.

Assuming that labels etc. are propagated as attributes, we can use a modified version of `recurrencePlot()`

Input

```
# univariate variant, assuming attributes
local.recurrencePlot1=function(neighs){
```

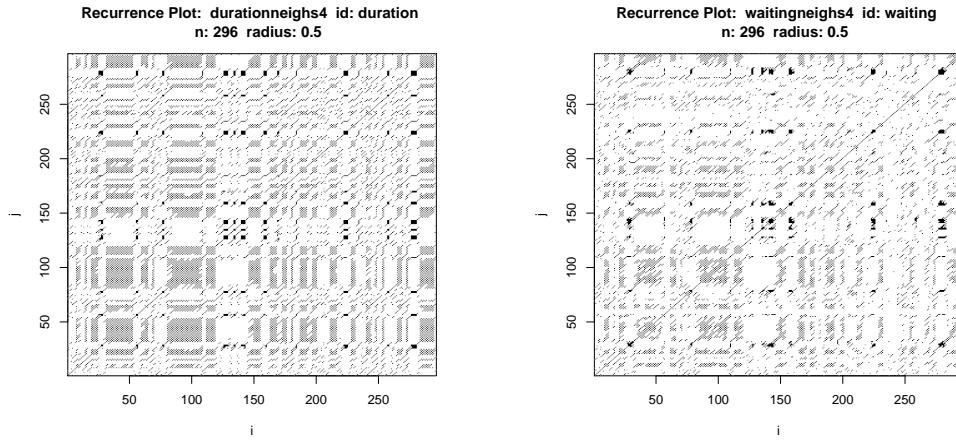


FIGURE 40. Old Faithful Geyser eruption durations and waiting time.
Time used: 6.654 sec.

```

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)

```

Input

```

showrqa(takens.duration4, radius=0.5)

```

Output

```

duration n: 296 Dim: 4
Radius: 0.5 Recurrence coverage REC: 0.168 log(REC)/log(R): 2.577
Ratio 5.628595 Determinism: 0.943 Laminarity: 0.07
DIV: 0.036
Trend: 0 Entropy: 1.937
Diagonal lines max: 28 Mean: 4.359 Mean off main: 4.267
Vertical lines max: 5 Mean: 3.065

```

RQA Example case: Old Faithful Geyser eruption durations. Radius=2.4 Dim=4. Time used: 7.011 sec. For graphical ouput, see Figure 41.

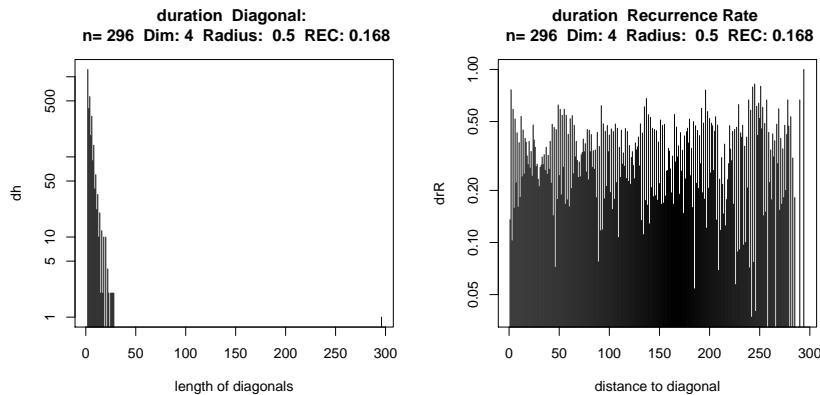


FIGURE 41. RQA. Example case: Old Faithful Geyser eruption durations. Radius=2.4 Dim=4, 0.82

Input

```
showrqa(takens.waiting4, radius=0.5)
```

Output

```
waiting n: 296 Dim: 4
Radius: 0.5 Recurrence coverage REC: 0.112 log(REC)/log(R): 3.154
Ratio 8.004975 Determinism: 0.899 Laminarity: 0.088
DIV: 0.05
Trend: 0 Entropy: 1.8
Diagonal lines max: 20 Mean: 3.904 Mean off main: 3.775
Vertical lines max: 7 Mean: 3.024
```

RQA Example case: Old Faithful Geyser eruption waiting. Radius=0.5 Dim=4. Time used: 7.086 sec. For graphical output, see Figure 42.

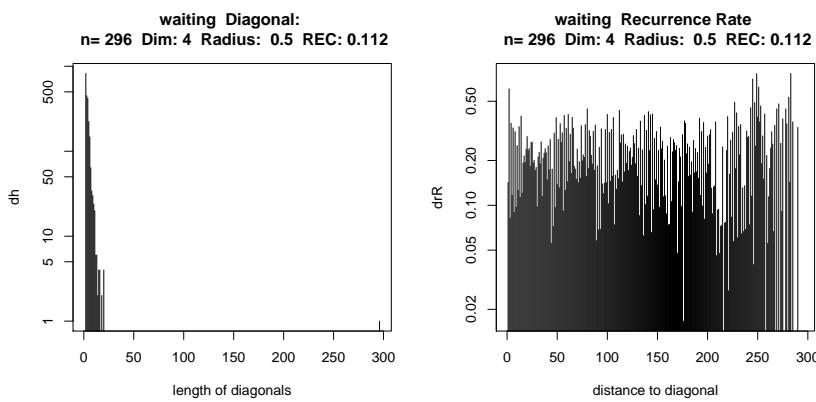


FIGURE 42. RQA. Example case: Old Faithful Geyser eruption waiting.
Radius=0.5 Dim=4, 0.82

Each plot shows a symmetric matrix. Since dimensions match, we can use the upper and lower 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)

```

See Figure 43.

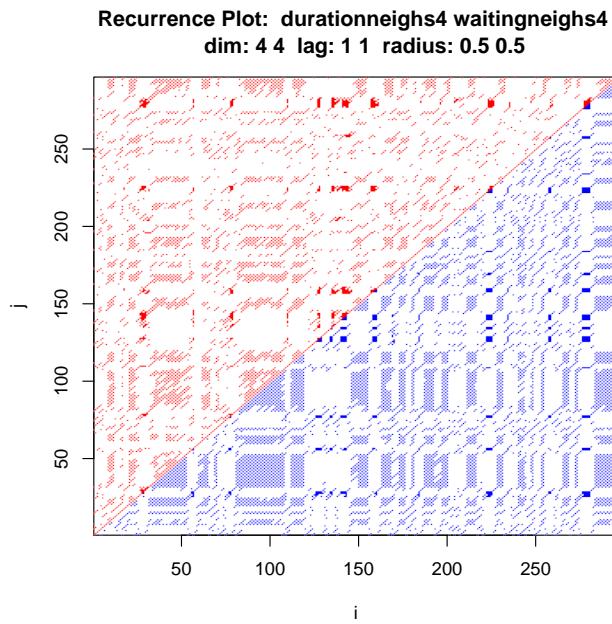


FIGURE 43. Recurrence plot: Lower triangle: duration. Upper triangle: waiting.

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. See Marwan and Kurths [2002], Marwan *et al.* [2002].

Marwan uses a “covariance”

$$CR[i,j] = \Theta(\epsilon - |xv[i] - yv[j]|)$$

with a maximum distance as $|\cdot|$, where xv, yv are imbeddings. Other distances may be used. Signed distances for example may be used for experiments.

We use two examples:

Input

```

maxdist <- function (x){ max(abs(x), na.rm=TRUE) } # works on delta
cordist <- function (x, y){ suppressWarnings(cor(x,y)) }

```

ToDo: Epsilon/radius and Heaviside not use here - thresholding is handled in image rendering.

ToDo: propagate names from Takens

Here is a brute force implementation.

```
Input
```

```
CR0 <- function (xtakens, ytakens, sdist= maxdist) {
  # returns a cross distance matrix usin sdist
  # using signed. Warnings for zero #
  # variances are suppressed

  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)
}
```

ToDo: this needs optimisation on triangle

Variant *CR2* allows a distance that is not factored via $x - y$.

```
Input
```

```
CR2 <- function (xtakens, ytakens, cdist= cordist) {
  # returns a cross distance matrix usin cdist
  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)
}
```

```
Input
```

```
## for experiments only. do not copy large matrices
crossrecurrencePlotFromMatrix <- function(neighs.matrix,
                                             zlim= range(neighs.matrix, na.rm=TRUE),
                                             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. This is done in this section for the Geyser data (see above).

Input

```
cr4 <- CR0(takens.duration4,takens.waiting4) # maxdist by default
cr4C <- CR2(takens.duration4,takens.waiting4) # cordist by default
```

Input

```
oldpar <- par(mfrow=c(1,2))
image(cr4, main="CR0")
image(cr4C, main="CR2")
# neighs.matrix <- cr4;range(cr4) # 70.5500 107.1667
par(oldpar)
cat("Range cr4:", range(cr4), "Range cr4C:", range(cr4C, na.rm=TRUE, finite=TRUE))
```

Output

```
Range cr4: 0.03350814 2.662005 Range cr4C: -1 1
```

See Figure 44.

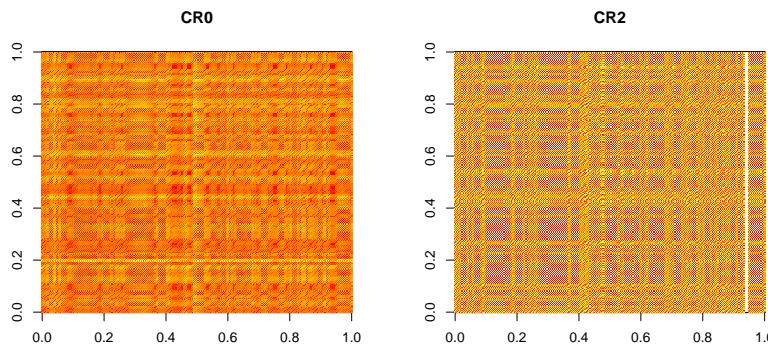


FIGURE 44. Recurrence plot. Cross recurrence. Left:using maxdist distance. Right:cor. Time used: 16.232 sec.

A max distance.

Input

```
oldpar <- par(mfrow=c(1,2))
crossrecurrencePlotFromMatrix(cr4,
  main="Cross Recurrence plot\n max",
  xlab="duration4 index", ylab="waiting4 index") # ugly heat matrix
```

Output

```
NULL
NULL
```

Input

```
#@
#\insertrecurrence{CRPFromMatrix}{Cross recurrence ??using max distance}{\Sexpr{laptimel()}}
#
```

```
#<<crossrecurrencePlot, fig=TRUE, include=FALSE>>=
crossrecurrencePlotFromMatrix(cr4, col=grey((1:10)/10),
main="Cross Recurrence plot\nnmax",
xlab="duration4 index", ylab="waiting4 index")
```

Output
NULL
NULL

Input
near conventional bw,
introducing radius/cut by zlim
par(oldpar)

See Figure 45.

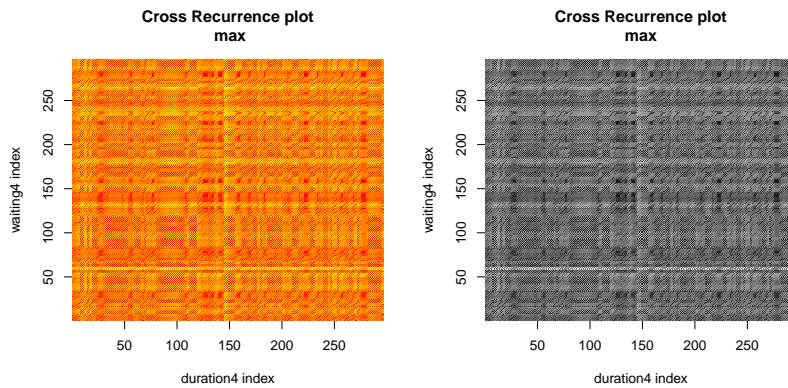


FIGURE 45. Recurrence plot. Cross recurrence using max distance. Time used: 18.455 sec.

Input
oldpar <- par(mfrow=c(1,2))
a correlation distance
crossrecurrencePlotFromMatrix(cr4C,
main="Cross Recurrence plot\nn cor",
xlab="duration4 index", ylab="waiting4 index") # ugly heat matrix

Output
NULL
NULL

Input
#@
#\insertrecurrence{corrdist}{Cross recurrence ??using cor distance, heat colours}{\Sexpr{laptimes()}}
#<<CRPFromMatrixC, fig=TRUE, include=FALSE>>=
quantile(cr4C, na.rm=TRUE)

Output
0% 25% 50% 75% 100%
-1.00000000 -0.68688423 -0.03466478 0.72172812 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
par(oldpar)
```

See Figure 46.

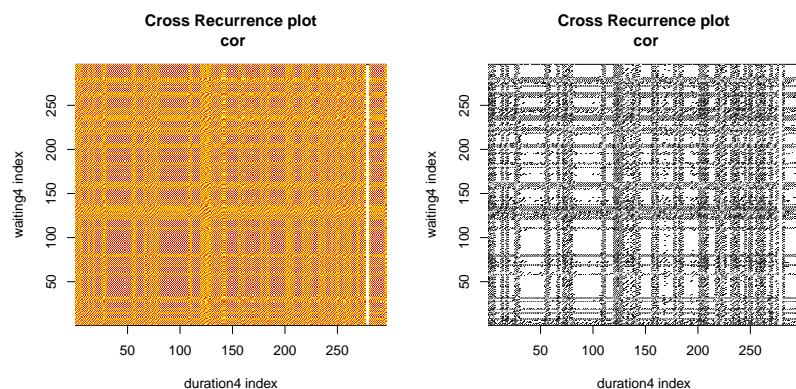


FIGURE 46. Recurrence plot. Cross recurrence using cor distance. Time used: 20.324 sec.

8. CASE STUDY: GEYSER DATA –DEFUNCT

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

This section is using original data (not rescaled).

8.1. Geyser Eruption Durations.

ToDo: remove this section

8.1.1. Geyser eruption durations. Dim=2.

Input

```
eruptionstakens2 <-  
  local.buildTakens(time.series=geyser$duration,  
                    embedding.dim=2, time.lag=1)  
statepairs(eruptionstakens2) #dim=2
```

See Figure 47.

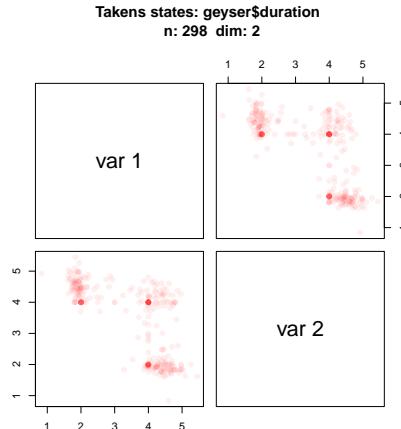


FIGURE 47. Recurrence plot. Old Faithful Geyser eruption durations.
Dim=2. Time used: 0.094 sec.

Input

```
statepairs(eruptionstakens2, nooverlap=TRUE) #dim=2
```

See Figure 48 on the next page

Input

```
eruptionsneighs2 <- local.findAllNeighbours(eruptionstakens2,  
                                               radius=0.8)  
save(eruptionsneighs2, file="eruptionsneighs2.RData")  
# load(file="eruptionsneighs2.RData")  
local.recurrencePlotAux(eruptionsneighs2)
```

See Figure 49 on the facing page.

Input

```
showrqa(eruptionstakens2, radius=0.8)
```

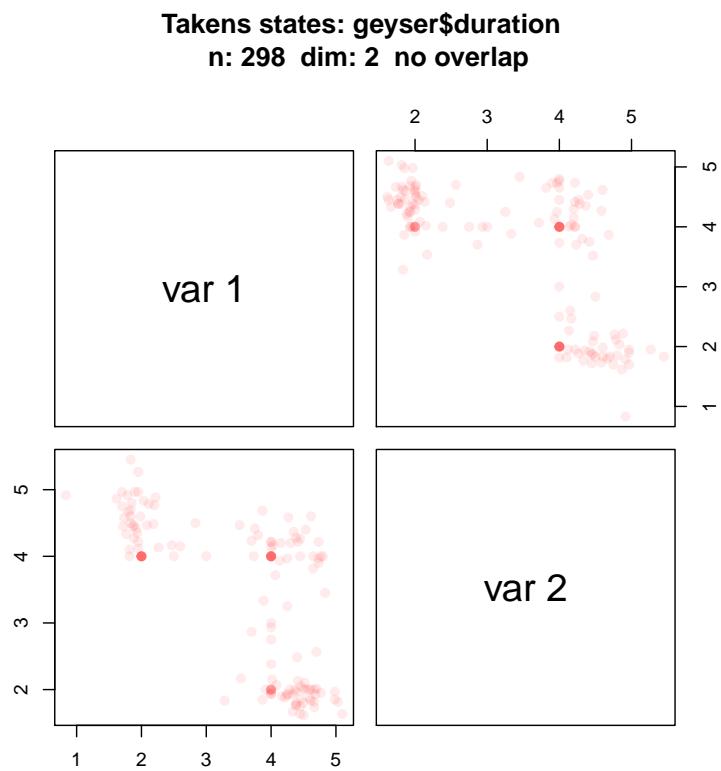


FIGURE 48. Example case: Old Faithful Geyser eruption durations.
Dim=2. Time used: 0.148 sec.

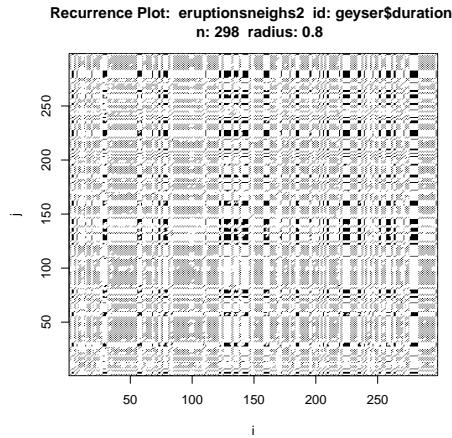


FIGURE 49. Recurrence plot. Old Faithful Geyser eruption durations.
Dim=2. Time used: 0.156 sec.

Output

```

geyser$duration n: 298 Dim: 2
Radius: 0.8 Recurrence coverage REC: 0.274 log(REC)/log(R): 5.806
Ratio 3.259348 Determinism: 0.892 Laminarity: 0.205
DIV: 0.045
Trend: 0 Entropy: 1.691

```

```
Diagonal lines max: 22 Mean: 3.644 Mean off main: 3.595
Vertical lines max: 7 Mean: 3.457
```

RQA Example case: Old Faithful Geyser eruption durations. Dim=2. Time used: 0.243 sec. For graphical output, see Figure 50.

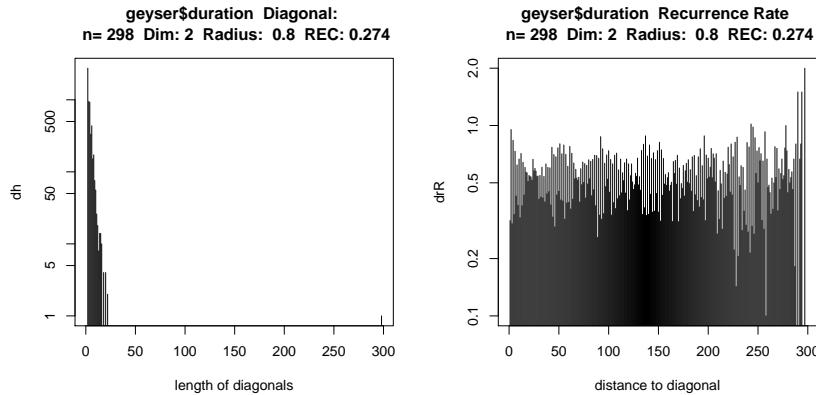


FIGURE 50. RQA. Example case: Old Faithful Geyser eruption durations. Dim=2, 0.82

8.1.2. Geyser eruptions. Dim=4.

Input

```
eruptionsneighs4 <- local.findAllNeighbours(takens.duration4,
                                              radius=0.8)
save(eruptionsneighs4, file="eruptionsneighs4.RData")
```

Input

```
load(file="eruptionsneighs4.RData")
local.recurrencePlotAux(eruptionsneighs4)
```

See Figure 51 on the facing page.

Input

```
showrqa(takens.duration4, radius=0.8)
```

Output

```
duration n: 296 Dim: 4
Radius: 0.8 Recurrence coverage REC: 0.257 log(REC)/log(R): 6.09
Ratio 3.735308 Determinism: 0.96 Laminarity: 0.137
DIV: 0.02
Trend: 0 Entropy: 2.316
Diagonal lines max: 49 Mean: 5.415 Mean off main: 5.343
Vertical lines max: 13 Mean: 3.133
```

See Figure 52 on the next page.

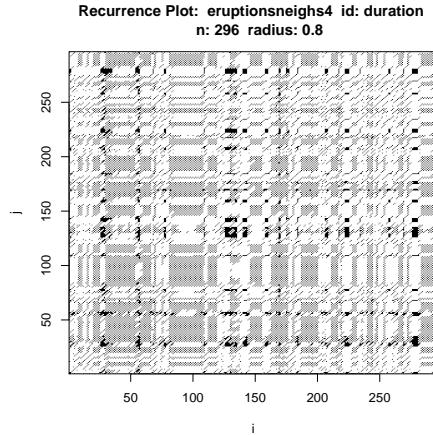


FIGURE 51. Recurrence plot. Example case: Old Faithful Geyser eruption durations. Dim=4. Time used: 0.139 sec.

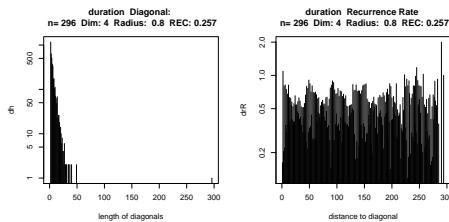


FIGURE 52. Recurrence plot. Old Faithful Geyser eruption durations. Dim=4. Time used: 0.234 sec.

8.1.3. Geyser eruption durations. Dim=8.

Input

```
eruptionstakens8 <- local.buildTakens( time.series=geyser$duration,
                                         embedding.dim=8,time.lag=1)
statepairs(eruptionstakens8) #dim=8
```

See Figure 53 on the following page.

Input

```
statepairs(eruptionstakens8, nooverlap=TRUE) #dim=8
```

See Figure 54 on the next page.

Input

```
eruptionsneighs8 <- local.findAllNeighbours(eruptionstakens8,
                                                radius=2.6)
save(eruptionsneighs8, file="eruptionsneighs8.RData")
#load(file="eruptionsneighs8.RData")
local.recurrencePlotAux(eruptionsneighs8)
```

See Figure 55 on page 71.

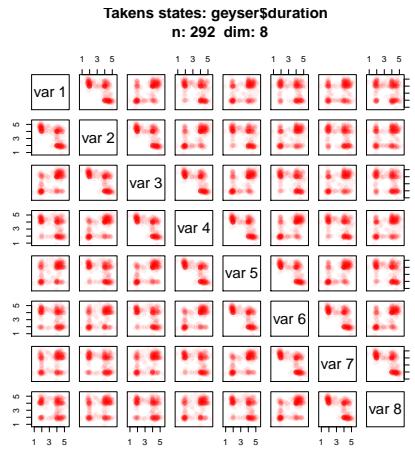


FIGURE 53. Recurrence plot. Old Faithful Geyser eruption durations.
Dim=8. Time used: 1.07 sec.

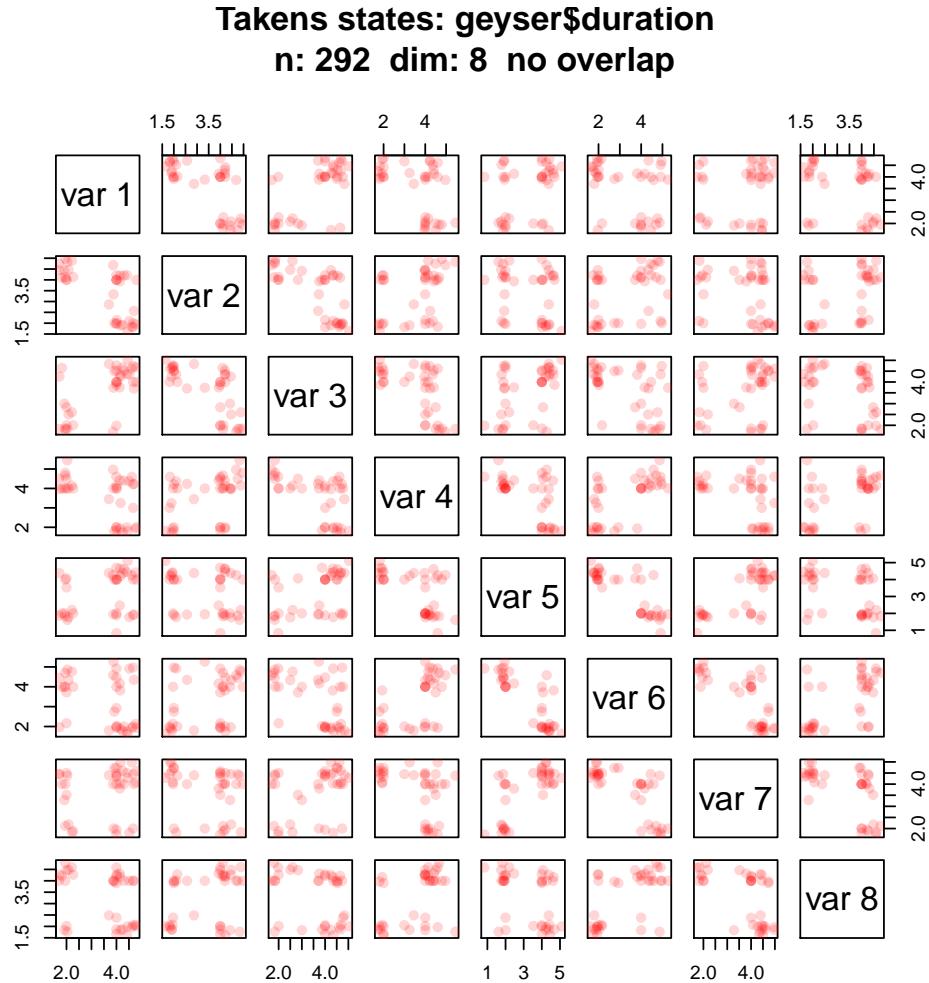


FIGURE 54. Example case: Old Faithful Geyser eruption durations.
Dim=8. Time used: 1.393 sec.

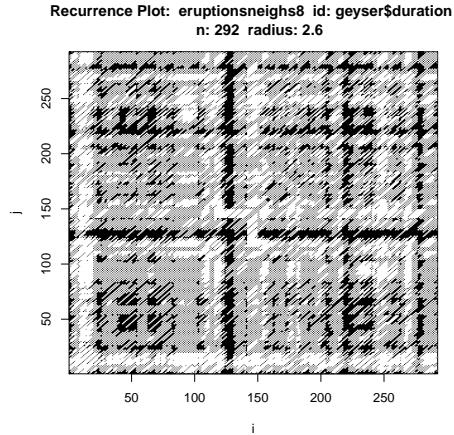


FIGURE 55. Recurrence plot. Example case: Old Faithful Geyser eruption durations. Dim=8. Time used: 0.207 sec.

<pre>showrqa(eruptionstakens8, radius=2.6)</pre>	<i>Input</i>
<hr/>	
<pre>geyser\$duration n: 292 Dim: 8 Radius: 2.6 Recurrence coverage REC: 0.494 log(REC)/log(R): -0.738 Ratio 2.006807 Determinism: 0.991 Laminarity: 0.5 DIV: 0.011 Trend: 0 Entropy: 3.338 Diagonal lines max: 93 Mean: 12.635 Mean off main: 12.55 Vertical lines max: 36 Mean: 4.073</pre>	<i>Output</i>
<hr/>	

RQA Example case: Old Faithful Geyser eruption durations. Dim=8. Time used: 0.329 sec. For graphical ouput, see Figure 56.

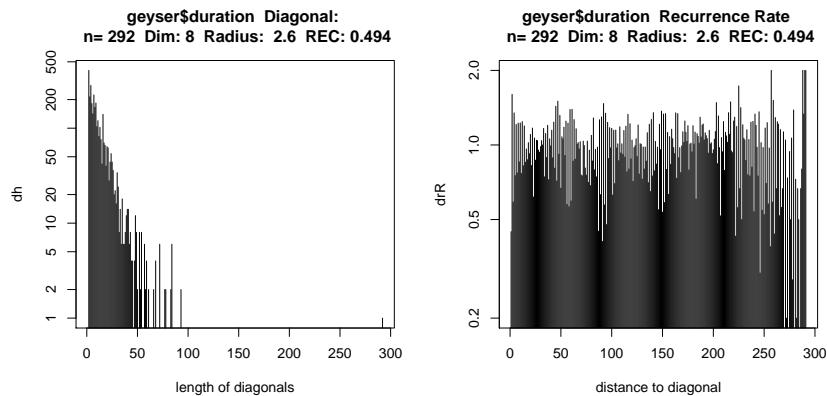


FIGURE 56. RQA. Example case: Old Faithful Geyser eruption durations. Dim=8, 0.82

8.1.4. *Geyser eruption durations: Comparison by Dimension.* For comparison, recurrence plots for the Geyser data with varying dimension are in Figure 57

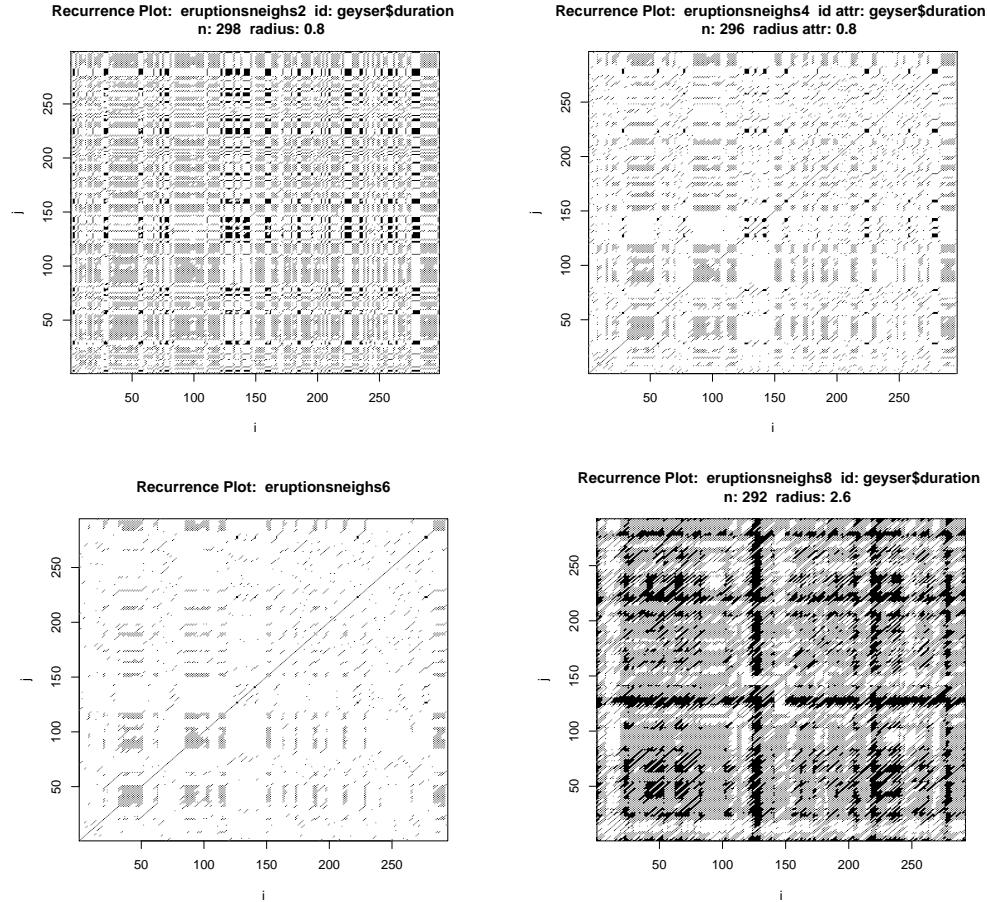


FIGURE 57. Recurrence Plot. Example case: Old Faithful Geyser eruptions. Dim=2, 4, 6, 8.

8.2. **Geyser Waiting, lag=4.** Note: is this of any use? Any good example for use of lag?

Input

```
waitingtakens <-
  local.buildTakens( time.series=geyser$waiting,
                     embedding.dim=4, time.lag=4)
statepairs(waitingtakens) #dim=4
```

See Figure 58 on the next page.

Input

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

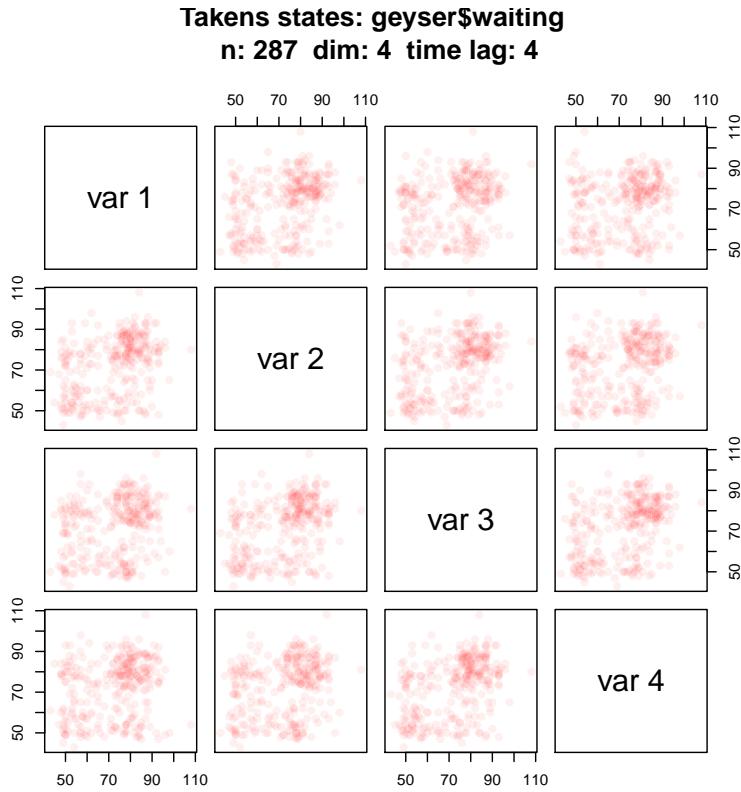


FIGURE 58. Example case: Old Faithful Geyser waiting. lag 4. Time used: 0.696 sec.

Input

```
showrqa(waitingtakens, radius=16)
```

Output

```
geyser$waiting n: 287 Dim: 4
Radius: 16 Recurrence coverage REC: 0.137 log(REC)/log(R): -0.718
Ratio 2.799047 Determinism: 0.382 Laminarity: 0.053
DIV: 0.053
Trend: 0 Entropy: 1.002
Diagonal lines max: 19 Mean: 2.878 Mean off main: 2.688
Vertical lines max: 3 Mean: 2.315
```

RQA Example case: Old Faithful Geyser waiting. Time used: 0.095 sec. For graphical output, see Figure 59 on the following page.

Input

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

See Figure 60 on the next page.

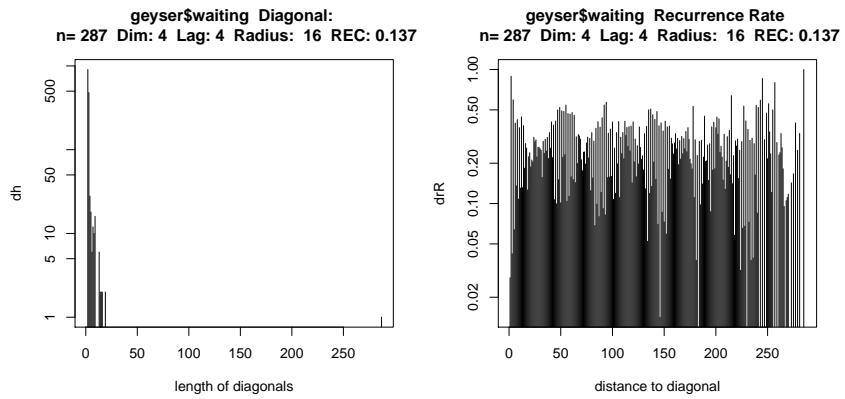


FIGURE 59. RQA. Example case: Old Faithful Geyser waiting, 0.82

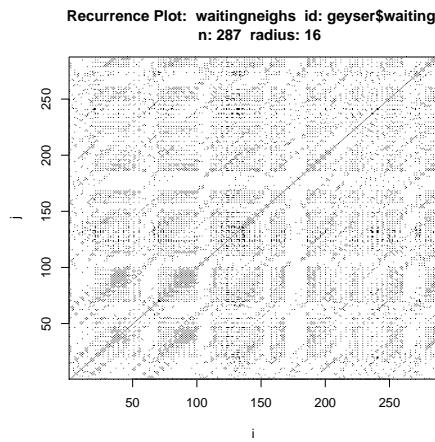


FIGURE 60. Recurrence plot. Example case: Old Faithful Geyser waiting. Time used: 0.19 sec.

9. CASE STUDY: TENSION DATA

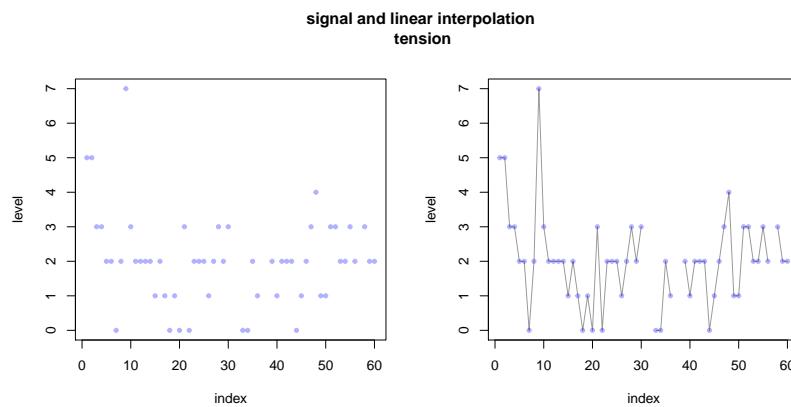
9.1. Raw data.

Note for data analysis: a logistic transform is used in 9.2

The tension data set (from [Ebner-Priemer *et al.*, 2007], [W.Ebner-Priemer and Sawitzki, 2007]) is one sample case of recordings of psychological tension data, recorded in regular interval on a subjective tension level ranked 0 ... 10. The data are ranked data, and may contain missing data. Missing data are just removed here.

Input

```
tension <- scan("../media/tension.dat")
plotsignal(tension, "tension", "level")
tension<-tension[!is.na(tension)]
```



ToDo: fix segfault
in `mutualInformation()` if NA is included

Input

```
oldpar <- par(mfrow=c(1,2))
# tau delay estimation based on the autocorrelation function
tau.acf = timeLag(tension, technique = "acf", do.plot = T,
main=paste("$\tau_{delay}$ estimation based on acf\n", "tension()"))
# tau delay estimation based on the mutual information function
tau.ami=NA
try(tau.ami <- timeLag(tension, technique = "ami",
do.plot = T, selection.method="first.minimum",
main=paste("$\tau_{delay}$ estimation based on ami\n", "tension()")))
par(oldpar)
cat("tension tau.acf:", tau.acf, " tau.ami:", tau.ami)
```

Output

```
tension tau.acf: 1  tau.ami: 1
```

See Figure 61 on the following page.

Input

```
oldpar <- par(mfrow=c(1,2))
if (is.numeric(tau.ami)) {
emb.dim = estimateEmbeddingDim(tension, time.lag = tau.ami,
max.embedding.dim = 15)
cat("tension() Lag tau.ami", tau.ami, "Estimated embedding dim:", emb.dim)
```

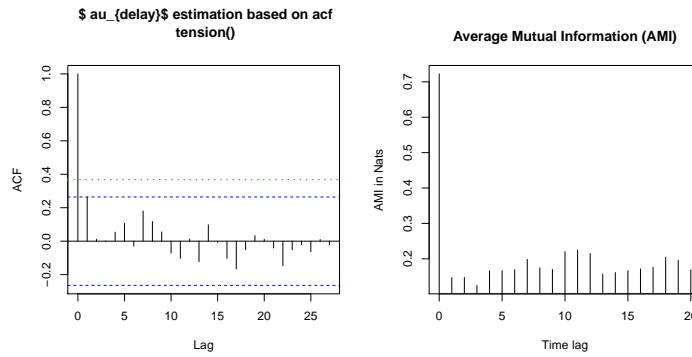


FIGURE 61. τ_{delay} estimation. "Tension" Left: based on the autocorrelation function ACF. Right: AMI

```

} else {
    emb.dim = estimateEmbeddingDim(tension, time.lag = tau.acf,
                                    max.embedding.dim = 15)
cat("tension() Lag tau.acf", tau.acf,"Estimated embedding dim:", emb.dim)
}

```

Output

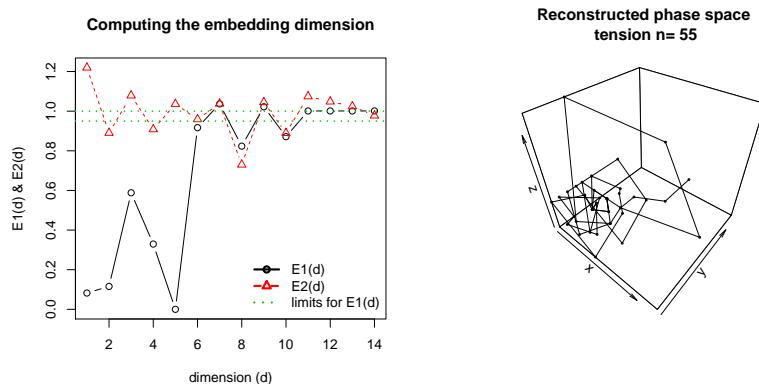
```
tension() Lag tau.ami 1 Estimated embedding dim: 9
```

Input

```

#@
#%%
#%<<takfsinN, fig=TRUE>>=
# taktension = buildTakens(tension, embedding.dim = 6, time.lag = 1)
takf = buildTakens(tension, embedding.dim = emb.dim, time.lag = tau.ami)
scatter3D(takf[,1], takf[,2], takf[,3],
#%main = paste("Reconstructed phase space\n",deparse(substitute(time.series))),
main = paste("Reconstructed phase space\n tension n=",length(tension)),
col = 1, type="o",cex = 0.3)
par(oldpar)

```



Input

```

tensionneighs <- local.findAllNeighbours(takf, radius=2.0)
save(tensionneighs, file="tensionneighs.Rdata")

```

```
# load(file="tensionneighs.Rdata")
local.recurrencePlotAux(tensionneighs, dim=dim(taktension)[2], radius=2.0)
```

See Figure 62.

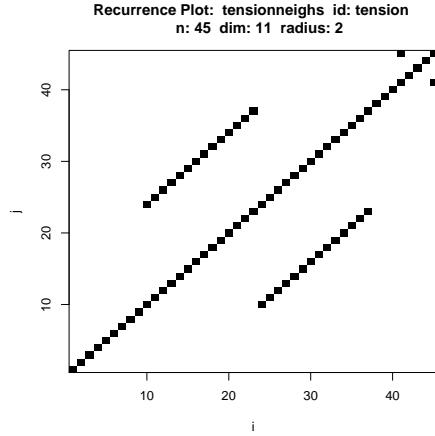


FIGURE 62. Recurrence plot. Test case: tension. Time used: 1.227 sec.

Input

```
tensionrqa <- showrqa(taktension, radius=2.0, log=TRUE)
```

Output

```
tension n: 45 Dim: 11
Radius: 2 Recurrence coverage REC: 0.037 log(REC)/log(R): -4.755
Ratio 26.28 Determinism: 0.973 Laminarity: 0
DIV: 0.071
Trend: -0.001 Entropy: 0.637
Diagonal lines max: 14 Mean: 24.333 Mean off main: 14
Vertical lines max: 0 Mean: 0
```

RQA Test case: tension. Radius=2.0. Time used: 1.286 sec. For graphical output, see Figure 63.

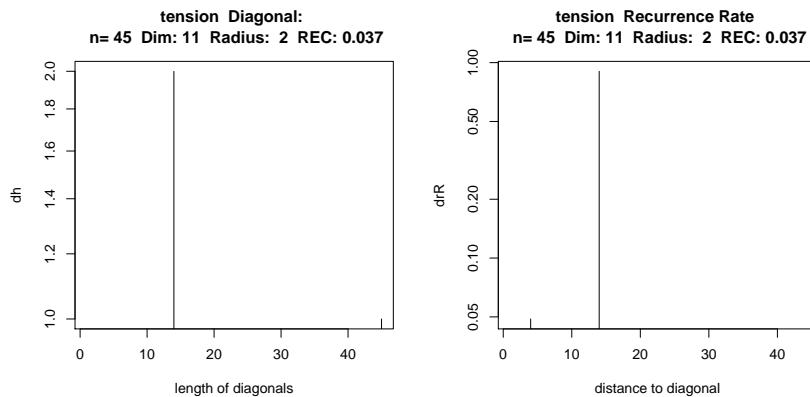


FIGURE 63. RQA. Test case: tension. Radius=2.0, 0.82

9.2. **Tension: transformed scale.** Try rescaled logits:

Input

```

k=11 # levels 0..11
#
tension1 <- (tension+1)/(k+2)
tension1 <- log(tension1/(1-tension1))

```

Input

```

oldpar <- par(mfrow=c(1,2))
# tau delay estimation based on the autocorrelation function
tau.acf = timeLag(tension1, technique = "acf", do.plot = T,
main=paste("$\tau_{delay}$ estimation based on acf\n", "tension1()"))
# tau delay estimation based on the mutual information function
tau.ami=NA
try(tau.ami <- timeLag(tension1, technique = "ami",
do.plot = T, selection.method="first.minimum",
main=paste("$\tau_{delay}$ estimation based on ami\n", "tension1()")))
par(oldpar)
cat("tension rescaled. tau.acf:",tau.acf," tau.ami:",tau.ami)

```

Output

```
tension rescaled. tau.acf: 1 tau.ami: 1
```

See Figure 64.

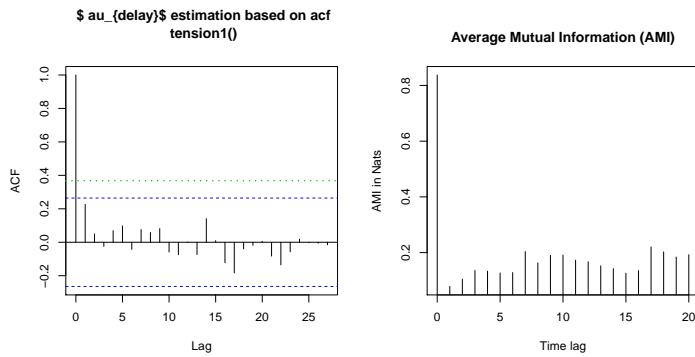


FIGURE 64. τ_{delay} estimation. "tension1" Left: based on the autocorrelation function ACF. Right: AMI

Input

```

oldpar <- par(mfrow=c(1,2))
if (is.numeric(tau.ami)) {
emb.dim = estimateEmbeddingDim(tension1, time.lag = tau.ami,
max.embedding.dim = 15)
cat("tension1() Lag tau.ami", tau.ami, "Estimated embedding dim:", emb.dim)
} else {
emb.dim = estimateEmbeddingDim(tension1, time.lag = tau.acf,
max.embedding.dim = 15)
cat("tension1() Lag tau.acf", tau.acf, "Estimated embedding dim:", emb.dim)
}

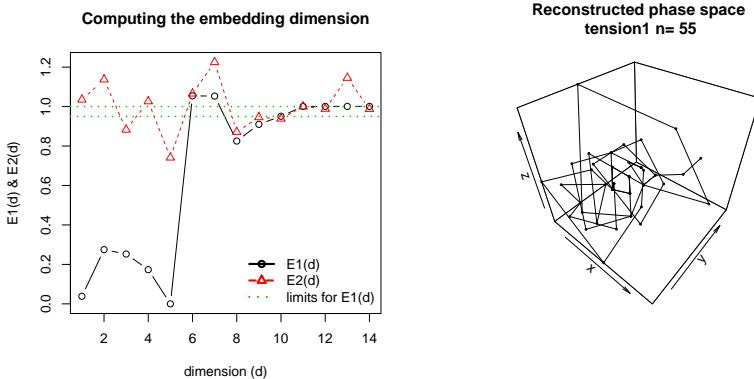
```

Output

```
tension1() Lag tau.ami 1 Estimated embedding dim: 9
```

Input

```
#%<<takfsinN, fig=TRUE>>
taktension1 = buildTakens(tension1, embedding.dim = emb.dim, time.lag = tau.ami)
scatter3D(taktension1[,1], taktension1[,2], taktension1[,3],
          main = paste("Reconstructed phase space\n tension1 n=",length(tension1)),
          col = 1, type="o",cex = 0.3)
par(oldpar)
```



Input

```
tension1neighs <- local.findAllNeighbours(taktension1, radius=1.4)
save(tension1neighs, file="tension1neighs.Rdata")
# load(file="tension1neighs.Rdata")
local.recurrencePlotAux(tension1neighs, dim=dim(taktension1)[2], radius=1.4)
```

See Figure 65.

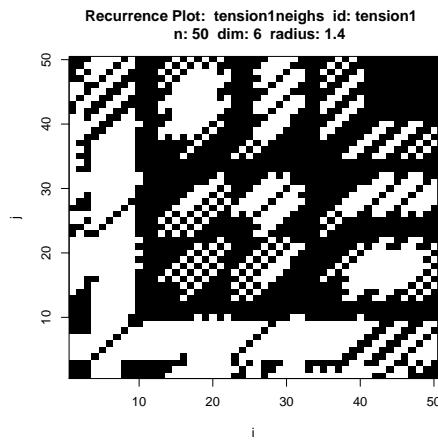


FIGURE 65. Recurrence plot. Test case: tension1. Time used: 2.265 sec.

Input

```
tension1rqa <- showrqa(taktension1, radius=2, log=TRUE)
```

Output

```
tension1 n: 50 Dim: 6
Radius: 2 Recurrence coverage REC: 0.877 log(REC)/log(R): -0.19
Ratio 1.137389 Determinism: 0.997 Laminarity: 0.971
```

```
DIV: 0.02
Trend: 0.001 Entropy: 3.137
Diagonal lines max: 49 Mean: 15.956 Mean off main: 15.706
Vertical lines max: 50 Mean: 11.628
```

RQA Test case: tension1. Radius=1.4.. Time used: 2.329 sec. For graphical output, see Figure 66.

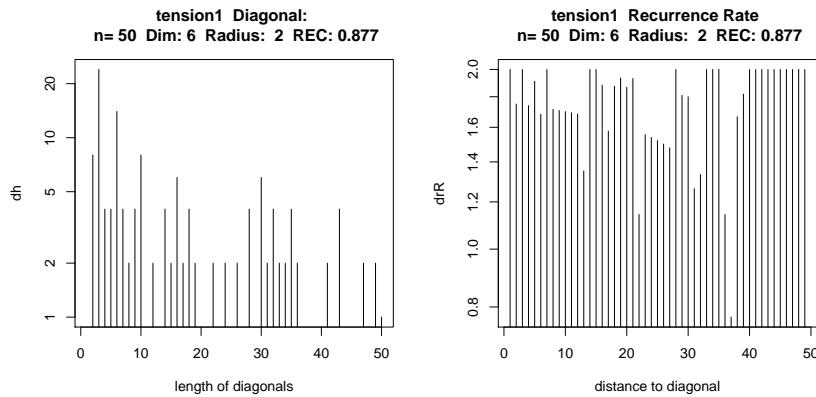


FIGURE 66. RQA. Test case: tension1. Radius=1.4., 0.82

10. CASE STUDY: HRV DATA EXAMPLE.BEATS

Note for data analysis: The data include missing beats, or spurious artefacts. These need to be handled. Graphical display is heavily affected by the scales implied by outliers.

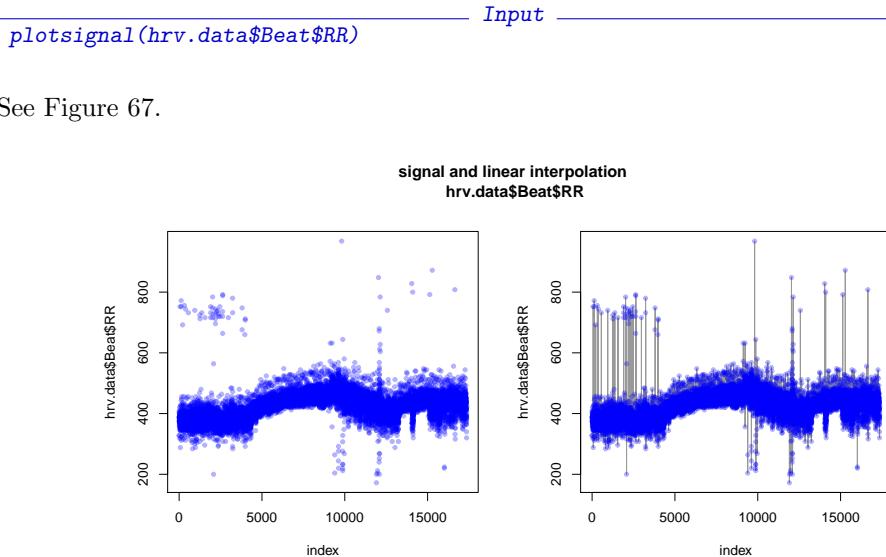
Only 1024 data points used in recurrence plots in this section

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)
```



See Figure 67.

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

FIGURE 67. 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 68.

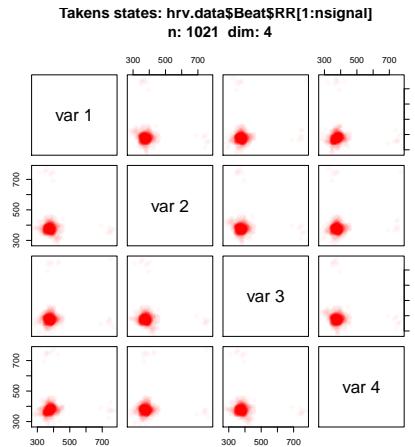


FIGURE 68. Recurrence plot. RHRV tutorial example.beats.. Time used: 0.665 sec.

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

See Figure 69 on the facing page.

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

See Figure 70 on the next page.

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

See Figure 71 on page 84.

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

Time used: 0.715 sec.

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

See Figure 72 on page 84.

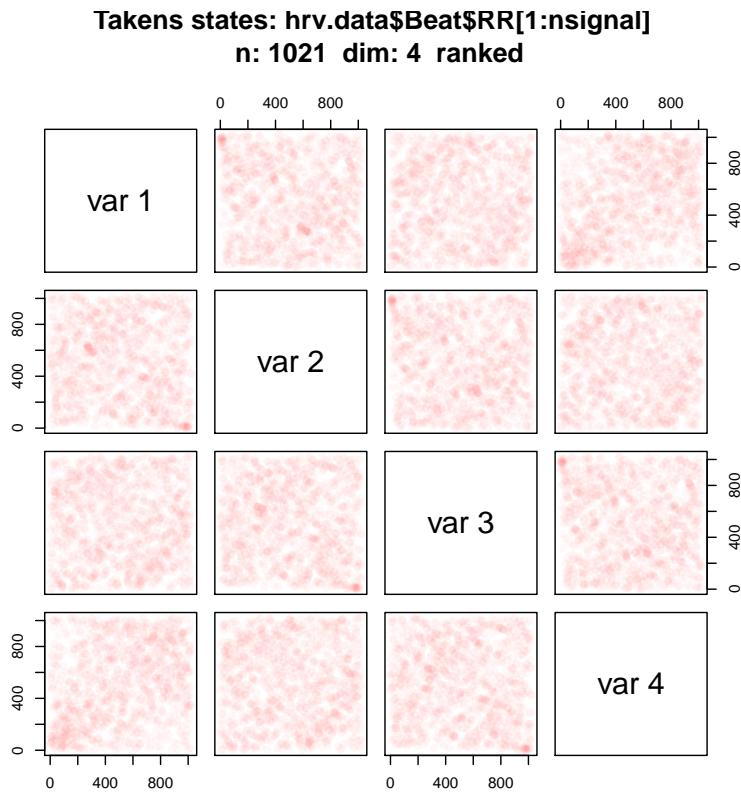


FIGURE 69. RHRV tutorial example.beats. Ranked data. Time used: 1.418 sec.

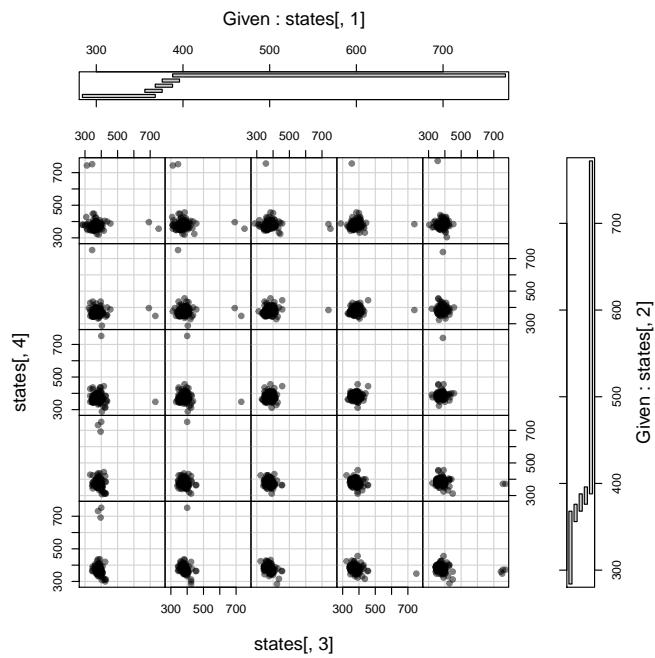


FIGURE 70. State coplot. RHRV tutorial example.beats. Time used: 0.229 sec.

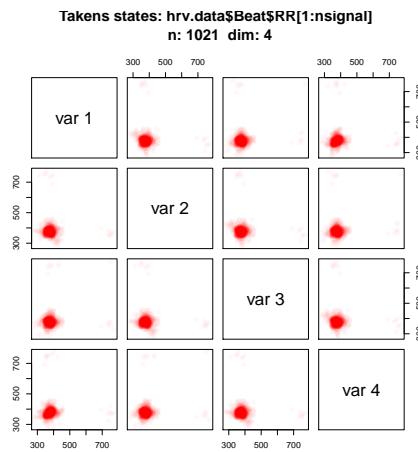


FIGURE 71. Recurrence plot. RHRV tutorial example.beats. Time used: 0.605 sec.

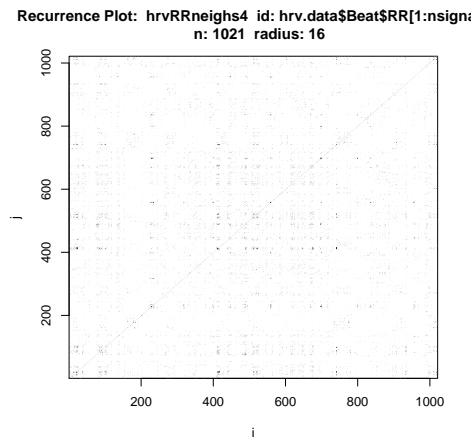


FIGURE 72. Recurrence plot. Example: RHRV tutorial example.beats. Dim=4.. Time used: 0.537 sec.

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

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

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
Ratio 3.945784 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 73.

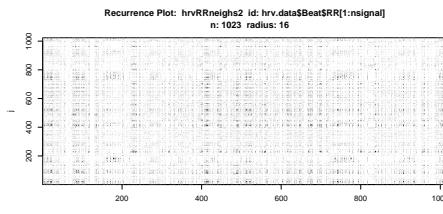


FIGURE 73. Recurrence plot. Dim=2.. Time used: 1.37 sec.

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: 0.672 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: 0.84 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: 1.917 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: 0.937 sec.

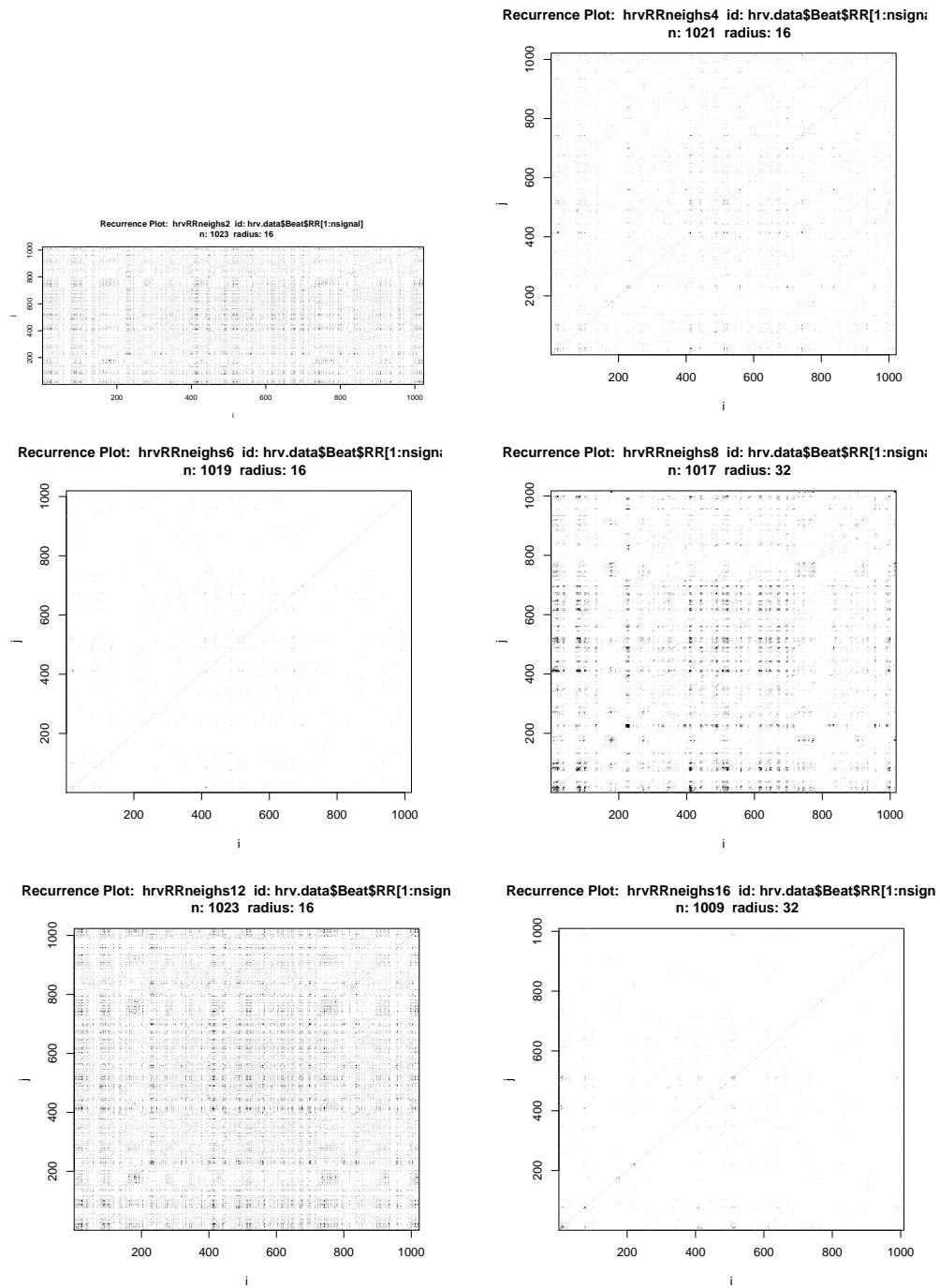


FIGURE 74. Recurrence Plot. Example case: RHRV tutorial example.beats. Dim=2, 4, 6, 8, 12, 16. Time used: 0.937 sec.

ToDo: This is an experimental proposal

10.1. **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.

```
# source('/users/gs/projects/rforge/rhrv/pkg/R/BuildNIHR2.R', chdir = TRUE) _____ Input _____
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 75,

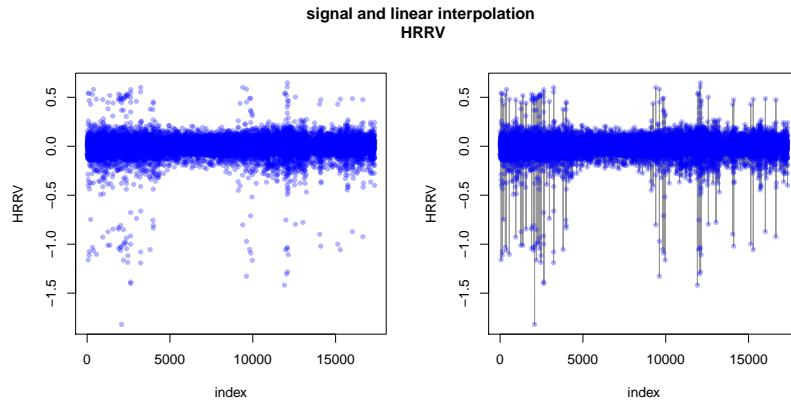


FIGURE 75. RHRV tutorial example.beats. HRRV Signal and linear interpolation.

Only 1024 data points used in this section

Input

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

See Figure 76 on the following page

Input

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

See Figure 77 on page 91

ToDo: findAllNeighbours does not handle NAs

Input

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

Time used: 0.235 sec.

Input

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

ToDo: check. There seem to be strange artefacts.

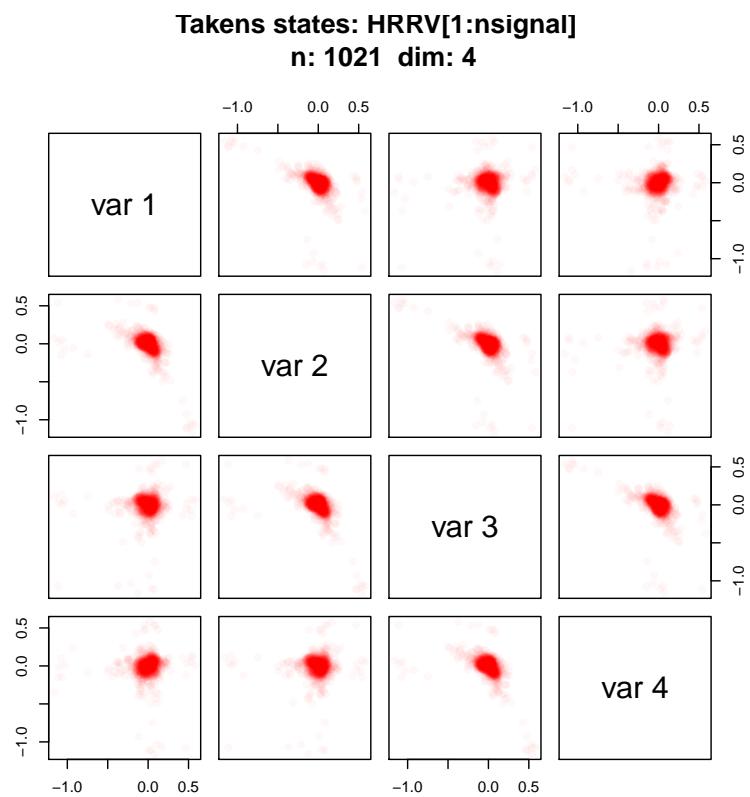


FIGURE 76. RHRV tutorial example.beats. HRRV Time used: 0.711 sec.

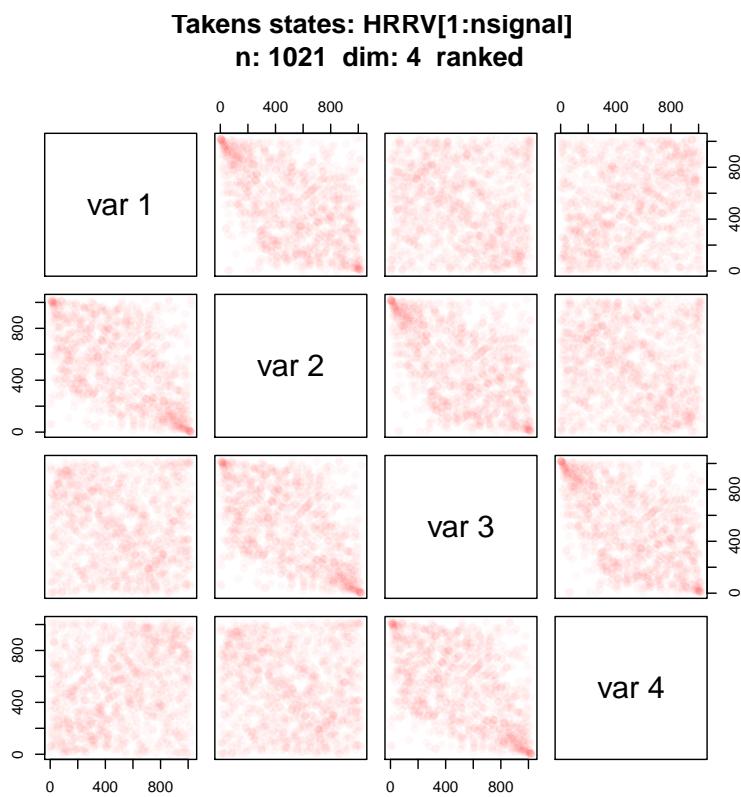


FIGURE 77. RHRV tutorial example.beats. Ranked HRRV data. Time used: 1.422 sec.

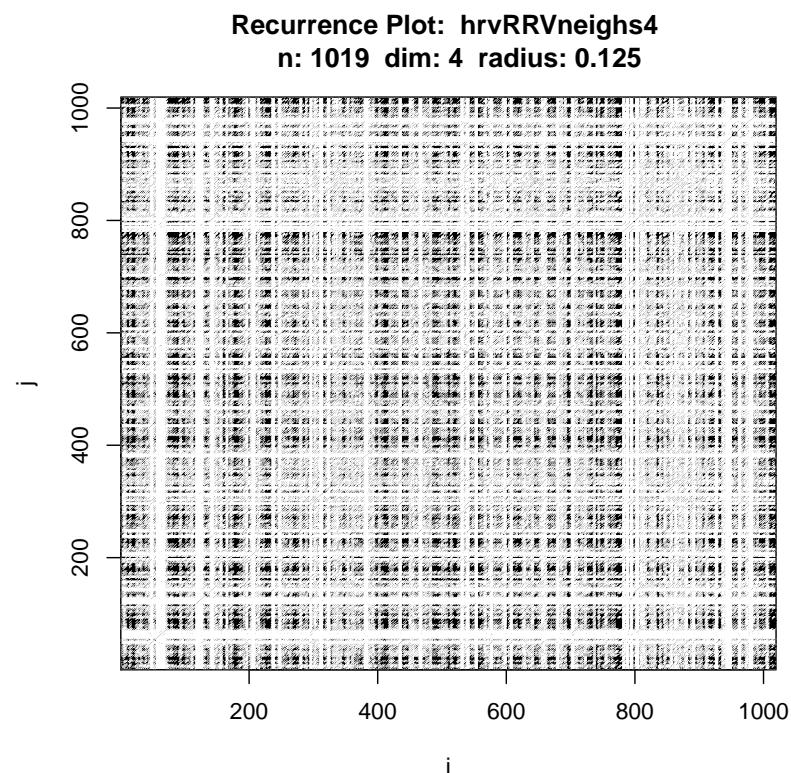


FIGURE 78. Recurrence Plot. Example case: RHRV tutorial example.beats. HRRV Dim=4. Time used: 1.288 sec.

10.1.1. *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
Ratio 1.824474 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: 2.546 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
Ratio 5.261147 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: 1.496 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)
```

We should expect the breathing rhythm, so a time lag in the order of 10 is to be expected. **To Do:** fix default setting for radius. Eckmann uses nearest neighbours with NN=10

```

hrvRRVtakens8[-(1:2), ] n: 1015 Dim: 8
Radius: 0.125 Recurrence coverage REC: 0.105 log(REC)/log(R): 1.084
Ratio 8.977958 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: 1.536 sec.

Input

```

hrvRRVtakens12 <-
  local.buildTakens( time.series=HRRV[1:nseries],
                     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
Ratio 4.202561 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: 2.015 sec.

Input

```

hrvRRVtakens16 <- local.buildTakens( time.series=HRRV[1:nseries],
                                         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
Ratio 6.715081 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: 1.628 sec.

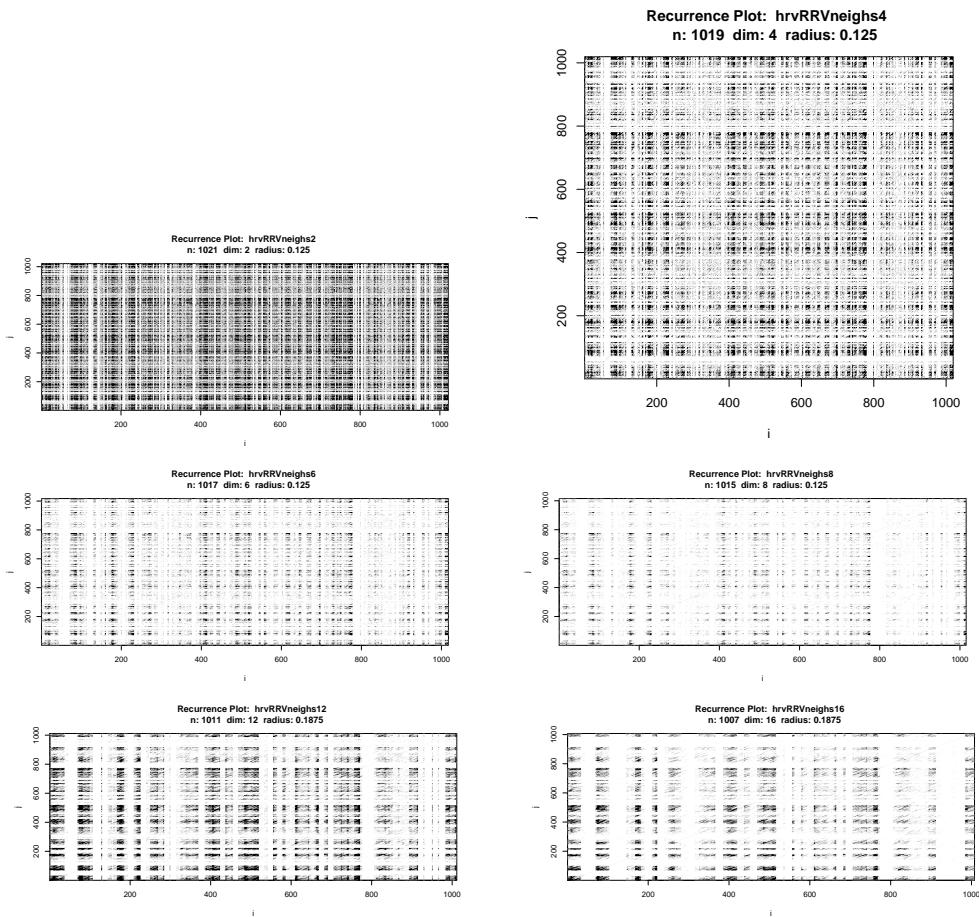


FIGURE 79. Recurrence Plot. Example case: RHRV tutorial example.beats variation. Dim=2, 4, 6, 8, 12, 16. Time used: 1.629 sec.

10.1.2. *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
Ratio 1.726809 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: 2.402 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
Ratio 1.726809 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: 1.969 sec.

Input

```
statepairs(hrvRRVtakens4Lag08)
```

Input

```
statecplot(hrvRRVtakens4Lag08)
```

Output

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

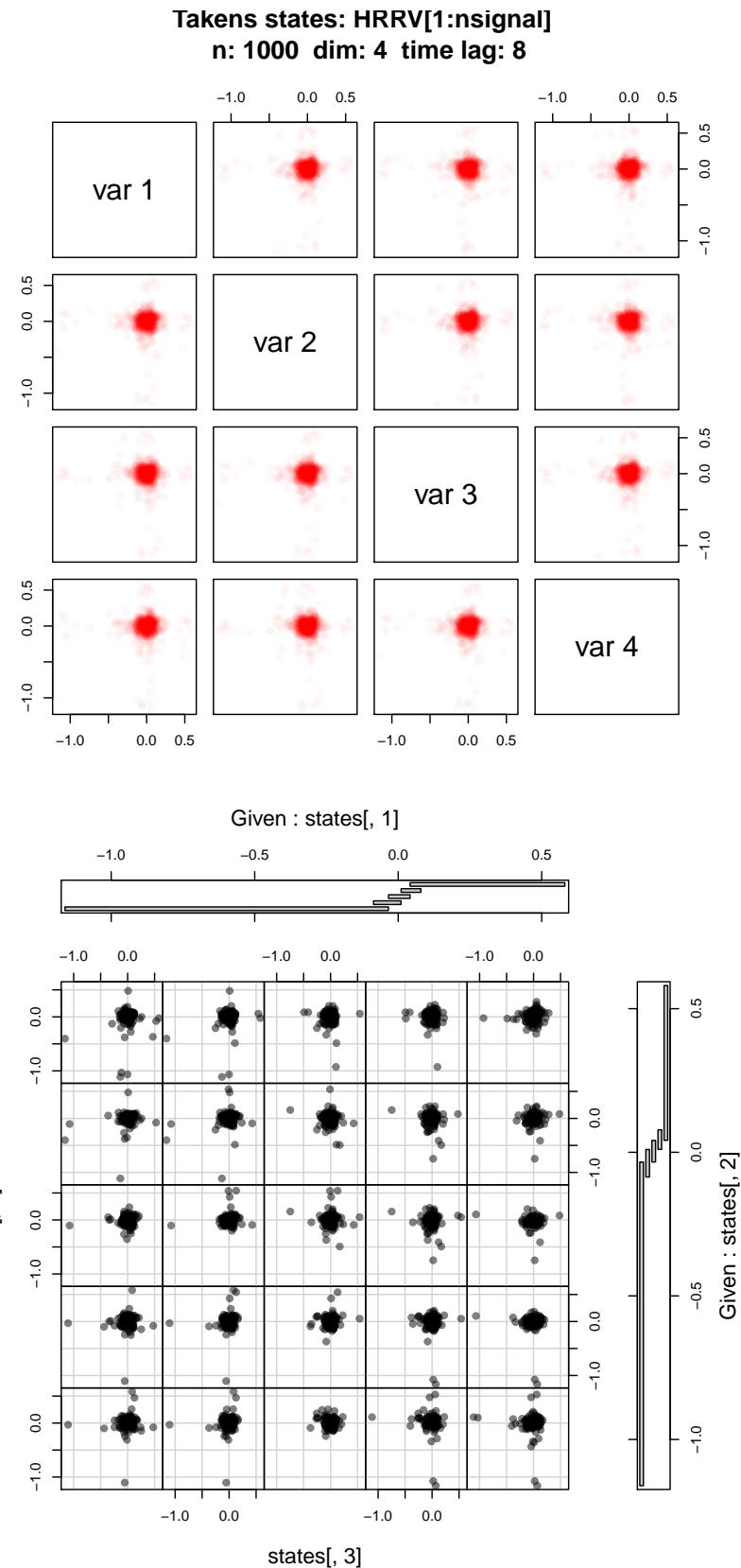


FIGURE 80. Takens states. Example case: RHRV tutorial example.beats variation. Dim=4, time.lag=8. Time used: 2.93 sec.

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:nseries],
                                           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
Ratio 3.566204 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: 5.283 sec.

Input

```
hrvRRVtakens8Lag08 <- local.buildTakens( time.series=HRRV[1:nseries],
                                           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
Ratio 4.917975 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: 1.343 sec.

Input

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

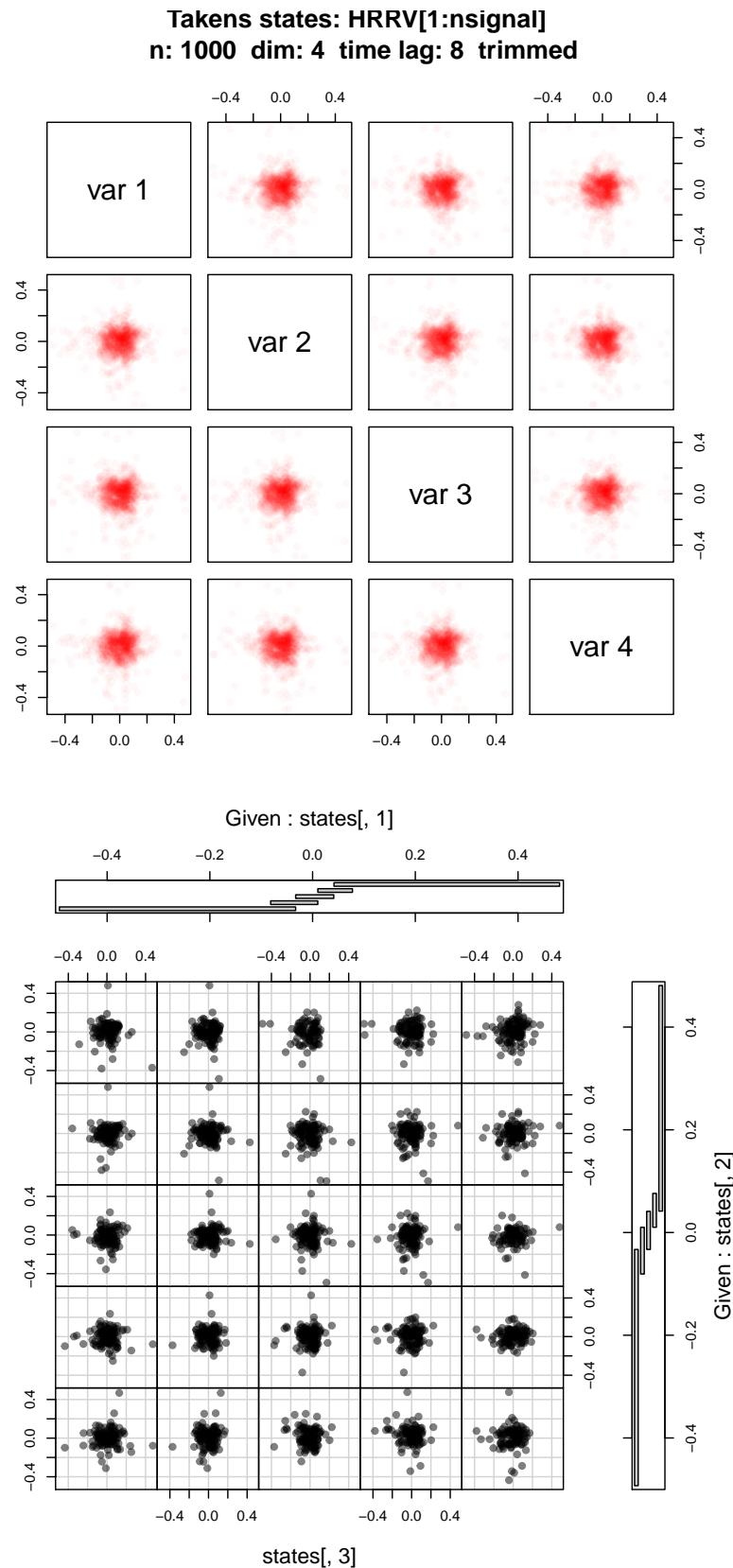


FIGURE 81. Takens states. Example case: RHRV tutorial example.beats variation, trimmed. Dim=4, time.lag=8. Time used: 3.956 sec.

```

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)

```

Input _____ Output _____

```

hrvRRVtakens12Lag08[-(1:2), ] n: 934 Dim: 12
Radius: 0.1875 Recurrence coverage REC: 0.133 log(REC)/log(R): 1.207
Ratio 3.562863 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: 1.436 sec.

Input _____ Output _____

```

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)

```

Input _____ Output _____

```

hrvRRVtakens16Lag08[-(1:2), ] n: 902 Dim: 16
Radius: 0.1875 Recurrence coverage REC: 0.071 log(REC)/log(R): 1.581
Ratio 4.776416 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: 1.257 sec.

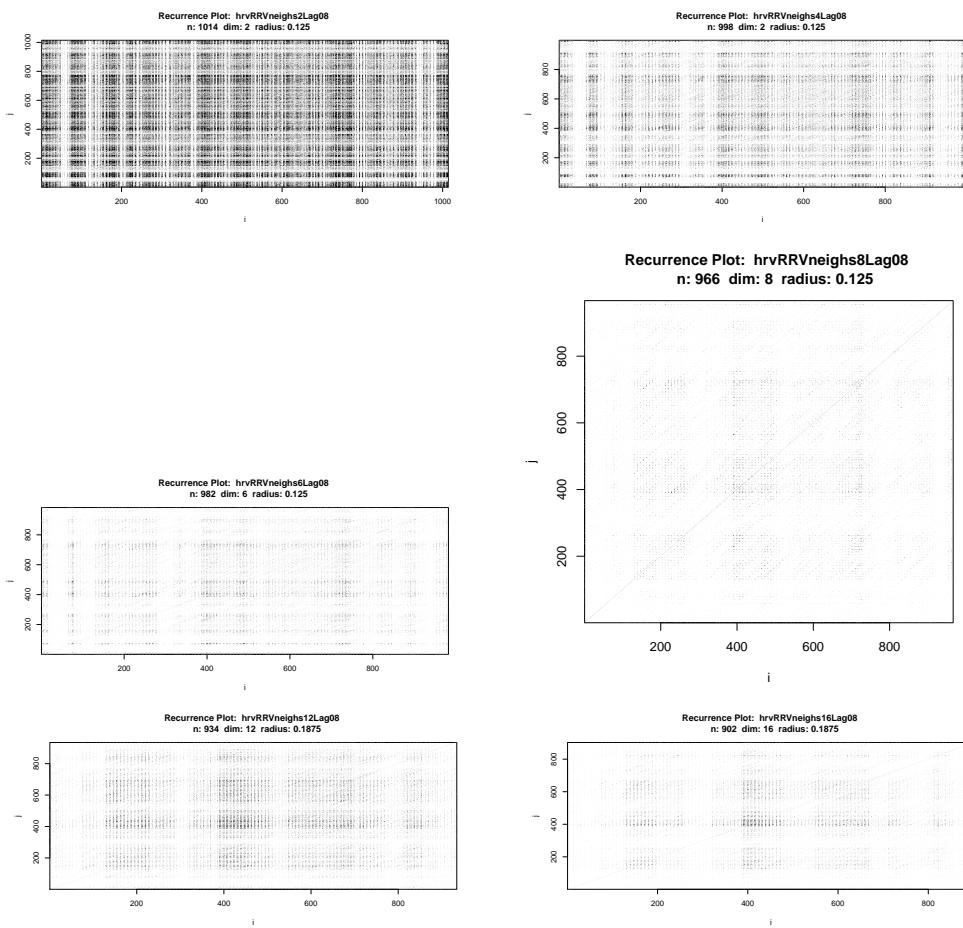


FIGURE 82. Recurrence Plot. Example case: RHRV tutorial example.beats variation. Dim=2, 4, 6, 8, 12, 16. Time.lag=8. Time used: 1.258 sec.

11. 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)

```

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

See Figure 83.

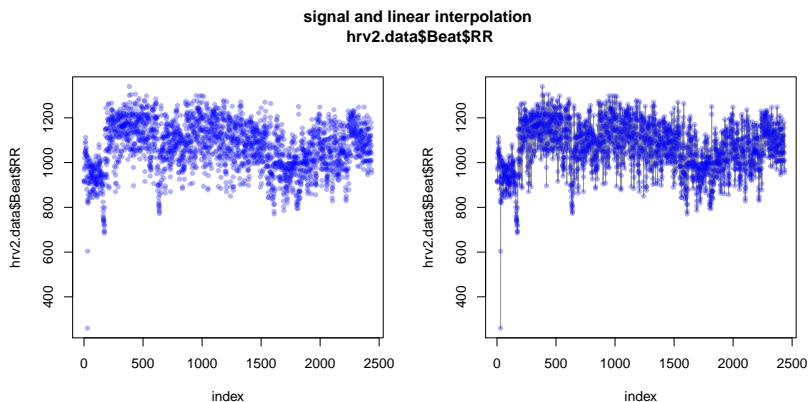


FIGURE 83. RHRV tutorial example2.beats. Signal and linear interpolation.

Input

```

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

```

Only 1024 data points used in this plot

See Figure 84 on the next page.

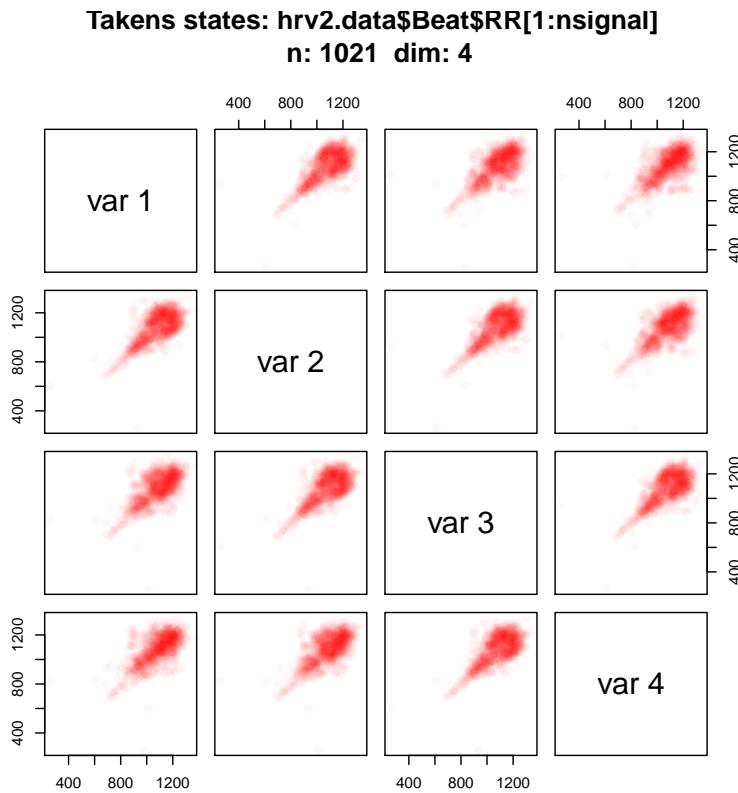


FIGURE 84. RHRV tutorial example2.beats. Time used: 0.769 sec.

Input
`statepairs(hrv2RRTakens4, rank=TRUE) #dim=4`

See Figure 85 on the following page.

Input
`statecplot(hrv2RRTakens4) #dim=4`

See Figure 86 on the next page.

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
Ratio 1.993144 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`

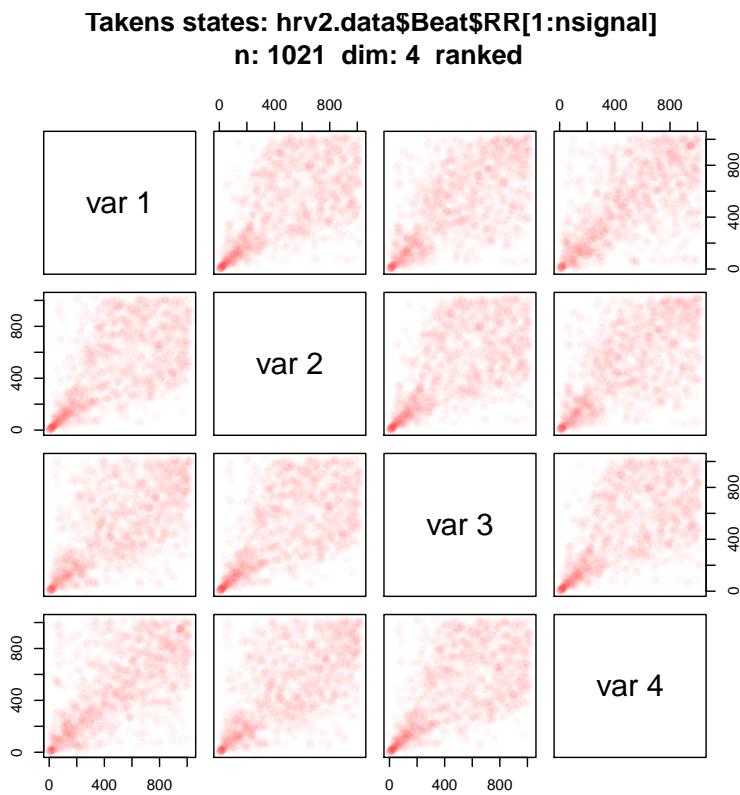


FIGURE 85. RHRV tutorial example2.beats. Ranked data. Time used: 1.514 sec.

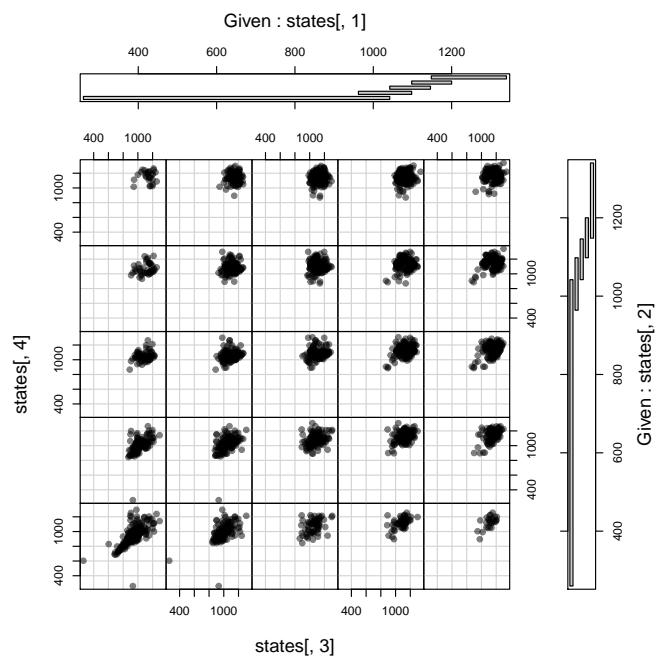


FIGURE 86. State coplot. RHRV tutorial example2.beats. Time used: 0.253 sec.

Dim=4. Time used: 2.924 sec.

See Figure 87.

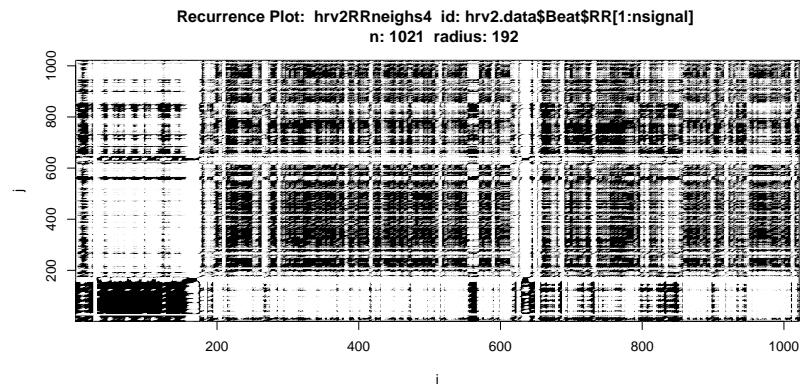


FIGURE 87. Recurrence Plot. Example case: RHRV tutorial example2.beats. Dim=4. Time used: 2.925 sec.

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

11.0.1. 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
Ratio 1.824356 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: 2.466 sec.

See Figure 88 on page 108.

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
Ratio 1.882666 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: 2.781 sec.

See Figure 88 on page 108.

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)
```

<pre>hrv2RRtakens8[-(1:2),] n: 1015 Dim: 8 Radius: 256 Recurrence coverage REC: 0.584 log(REC)/log(R): -0.097 Ratio 1.706571 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</pre>	Output
---	---------------

Dim=8. Time used: 2.953 sec.

See Figure 88 on the next page.

<pre>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)</pre>	Input
---	--------------

<pre>hrv2RRtakens12[-(1:2),] n: 1011 Dim: 12 Radius: 256 Recurrence coverage REC: 0.488 log(REC)/log(R): -0.129 Ratio 2.043437 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</pre>	Output
--	---------------

Dim=12. Time used: 2.937 sec.

<pre>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)</pre>	Input
--	--------------

<pre>hrv2RRtakens16[-(1:2),] n: 1007 Dim: 16 Radius: 288 Recurrence coverage REC: 0.544 log(REC)/log(R): -0.107 Ratio 1.83565 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</pre>	Output
---	---------------

Dim=16. Time used: 3.061 sec.

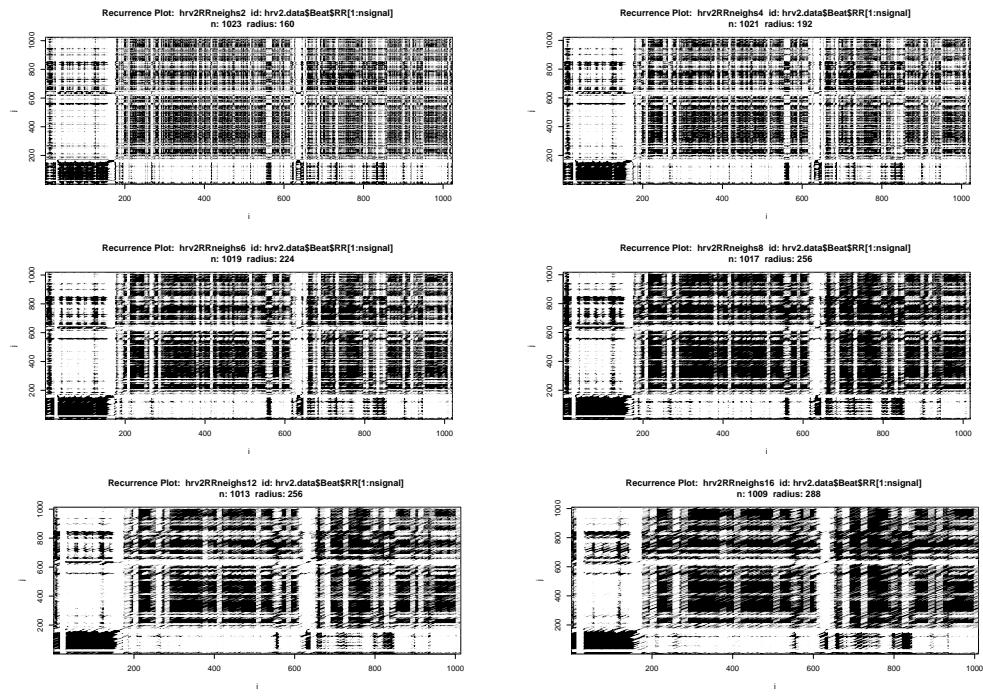


FIGURE 88. Recurrence Plot. Example case: RHRV tutorial example2.beats. Dim=2, 4, 6, 8, 12, 16. Time used: 3.062 sec.

11.1. 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.

ToDo: Consider using differences
differences for HRV

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 89,

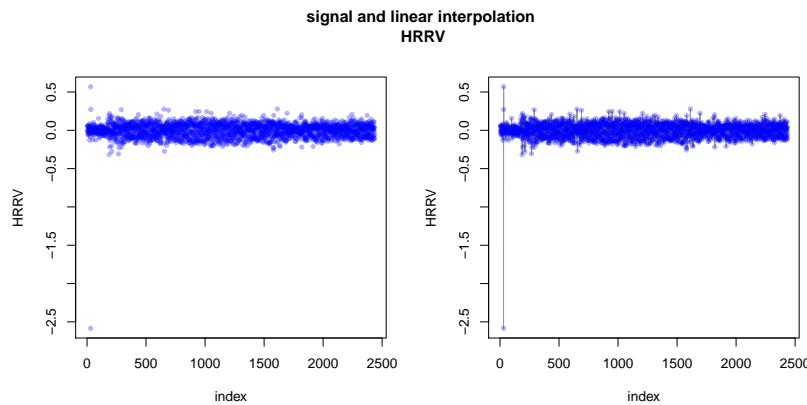


FIGURE 89. RHRV tutorial example2.beats. HRRV Signal and linear interpolation.

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 90 on the next page.

Input

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

Output

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

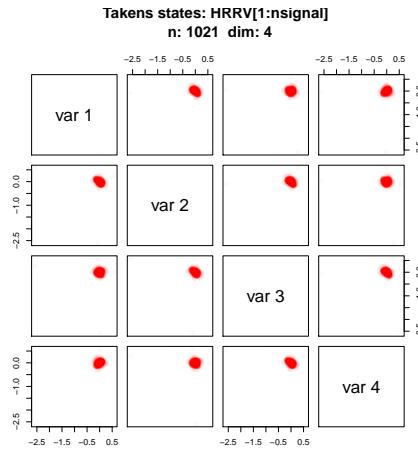


FIGURE 90. Recurrence plot. RHRV tutorial example2.beats. HRRV.
Time used: 0.888 sec.

See Figure 91.

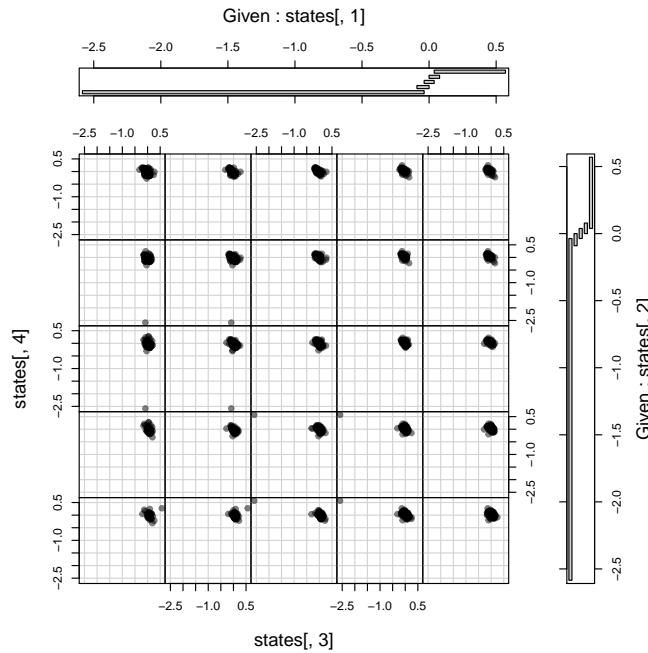


FIGURE 91. State coplot. RHRV tutorial example2.beats. HRRV. Time
used: 1.127 sec.

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

See Figure 92 on the next page

Input
`hrv2RRVtakens41 <- hrv2RRVtakens4
hrv2RRVtakens41[hrv2RRVtakens41 < -1.5] <- NA`

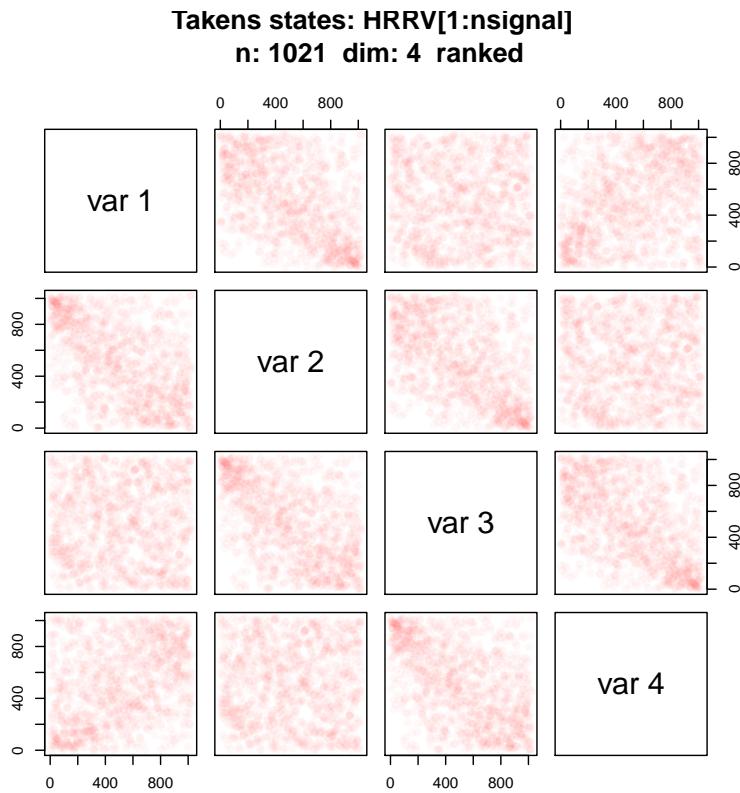


FIGURE 92. RHRV tutorial example2.beats. Ranked HRRV data. Time used: 2.097 sec.

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

See Figure 93.

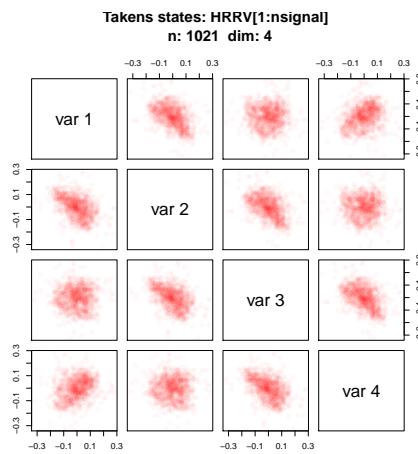


FIGURE 93. Recurrence plot. RHRV tutorial example2.beats. HRRV. Time used: 2.827 sec.

Input
statecoplot(hrv2RRVtakens41) #dim=4

Missing rows: 1, 2, 27, 28, 29, 30, 31 *Output*

See Figure 94.

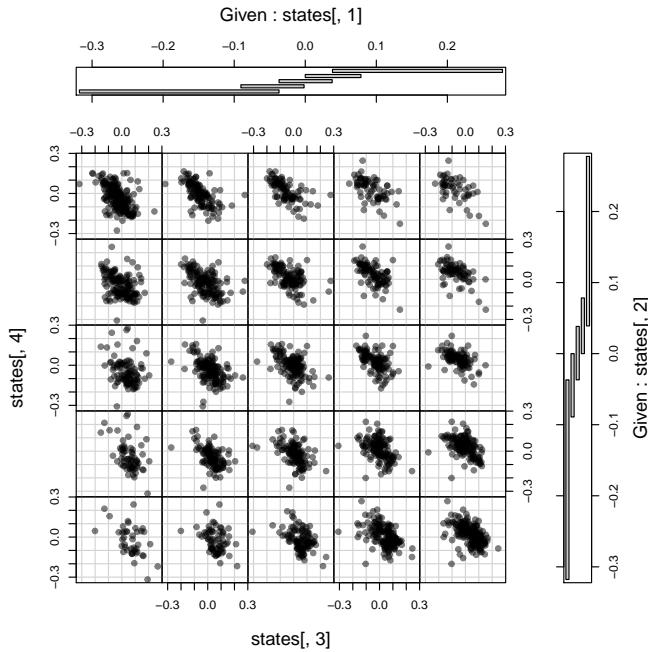


FIGURE 94. State coplot. RHRV tutorial example2.beats. HRRV. Time used: 3.065 sec.

ToDo: findAll-
Neighbours 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")

Time used: 0.161 sec.

ToDo: check. There
seem to be strange
artefacts.

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

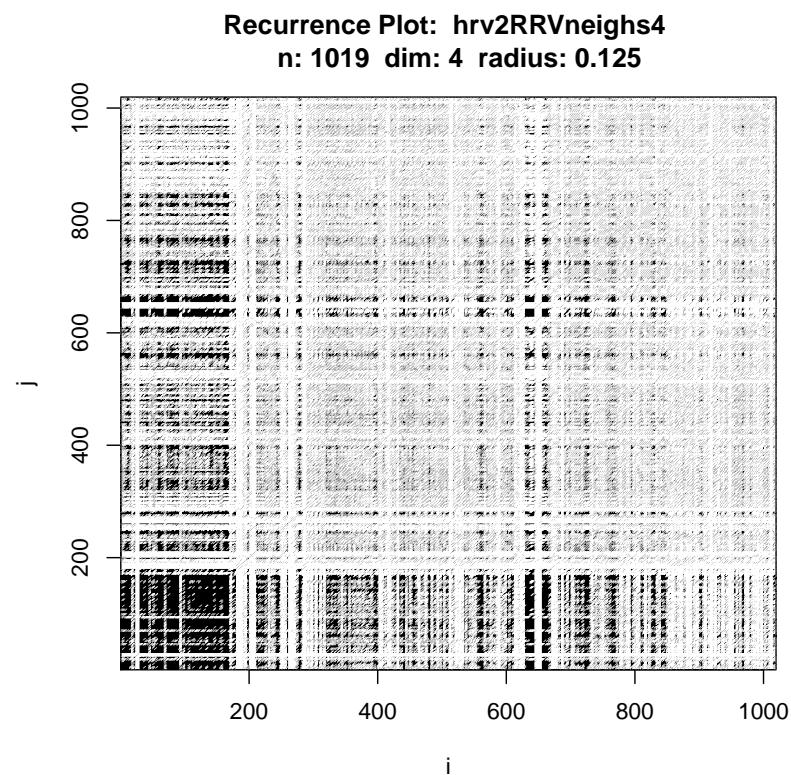


FIGURE 95. Recurrence Plot. Example case: RHRV tutorial example2.beats. HRRV Dim=4. Time used: 1.131 sec.

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

11.1.1. 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
Ratio 1.797625 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: 2.598 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
Ratio 1.921114 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: 3.118 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
Ratio 2.296476 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: 2.481 sec.

Input

```

hrv2RRVtakens12 <-
  local.buildTakens( time.series=HRRV[1:nseries],
                     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
Ratio 2.081523 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: 3.865 sec.

Input

```

hrv2RRVtakens16 <- local.buildTakens( time.series=HRRV[1:nseries],
                                         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
Ratio 1.758873 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: 3.197 sec.

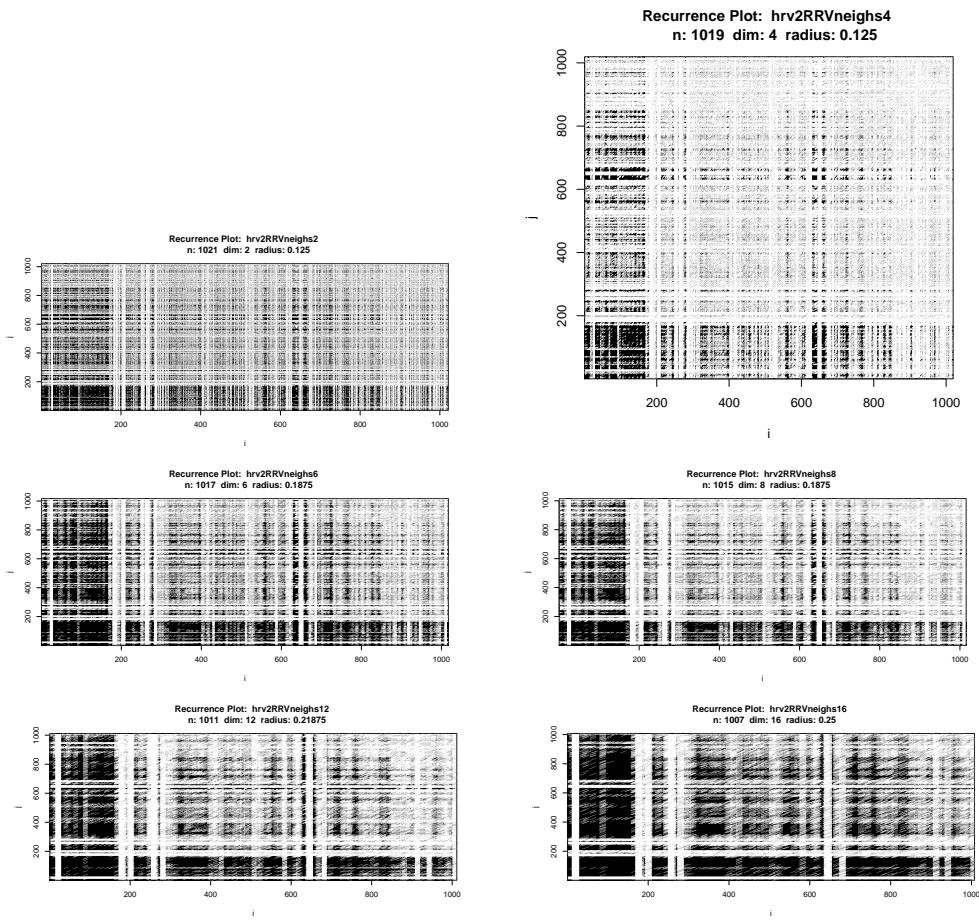


FIGURE 96. Recurrence Plot. Example case: RHRV tutorial example2.beats. Dim=2, 4, 6, 8, 12, 16. Time used: 3.198 sec.

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.. /sda

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R session info:

Total Sweave time used: 165.059 sec. at Thu Jun 22 19:31:50 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, tkplot 0.0-23, TSA 1.01, tsries 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

L^AT_EX information:

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textheight: 9.21922in
```

Bibliography style: jss

CVS/Svn repository information:

```
$Source: /u/math/j40/cvsroot/lectures/src/dataanalysis/Rnw/recurrence.Rnw,v $
copied to r-forge
$HeadURL: svn+ssh://gsawitzki@scm.r-forge.r-project.org/svnroot/rhrv/gs/Rnw/recurrence.Rnw $
$Revision: 257 $
$Date: 2017-06-19 17:26:34 +0200 (Mon, 19 Jun 2017) $
$Name:  $
$Author: gsawitzki $
```

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