

R Package Development by Means of Literate Programming (**noweb**)

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1 Introduction

2 Detecting Peaks/Troughs

2.1 Notation

A uniformly sampled time series $\mathbf{y} = \{y_1, \dots, y_i, \dots, y_T\}$ with T data points is considered. The detection of peak/trough points is achieved by a function $S(i, y_i, T)$ that returns for data point y_i a score value.¹ If this score value surpasses a user-provided threshold value θ , /i.e./, $S(i, y_i, T) \geq \theta$ then the point is considered as a local peak/trough.

Furthermore, in case local peak/trough points appear closely together with respect to time (clustered), then these points can be classified as a burst or bust, respectively.

2.2 Algorithms

In [Palshikar \(2009\)](#) five different score functions S have been suggested. All have in common, that a centred window of size $2*k+1$ around y_i is considered. That is, for a positive integer k the k right neighbours $N^+(i, k, T) = \{y_{i+1}, \dots, y_{i+k}\}$ and the k left neighbours $N^-(i, k, T) = \{y_{i-k}, \dots, y_{i-1}\}$ are employed for assessing y_i as a local peak/trough. The union of $N^-(i, k, T)$ and $N^+(i, k, T)$ is defined as $N(i, k, T) = N^-(i, k, T) \cup N^+(i, k, T)$ and if the centre point is included as $N'(i, k, T) = N^-(i, k, T) \cup y_i \cup N^+(i, k, T)$.

The first function, S_1 , computes the score value as the average of the maximum differences between y_i with its left and right neighbours. The function is defined as:

$$S_1 = \frac{\max(y_i - y_{i-1}, \dots, y_i - y_{i-k}) + \max(y_i - y_{i+1}, \dots, y_i - y_{i+k})}{2} \quad (1)$$

The equation (1) can be casted in R as:

```
1 <score-maxdiff 1>≡  
  scmaxdiff <- function(x, k){
```

¹It suffices to provide a score function for peaks only. Trough points can be detected by using the negative values of the series \mathbf{y} .

```

    cp <- k + 1L
    lmax <- max(x[cp] - head(x, k))
    rmax <- max(x[cp] - tail(x, k))
    (lmax + rmax) / 2.0
}

```

Defines:

`scmaxdiff`, used in chunks 4–6.

Instead of using the maximum differences of y_i with its k left and right neighbours as in (1), an alternative is to compute the mean differences and evaluate the average thereof:

$$S_2 = \frac{\frac{(y_i - y_{i-1}, \dots, y_i - y_{i-k})}{k} + \frac{(y_i - y_{i+1}, \dots, y_i - y_{i+k})}{k}}{2} \quad (2)$$

This equation can be casted in R as:

```

2a  <score-diffmean 2a>≡
    scdiffmean <- function(x, k){
      cp <- k + 1L
      ldmean <- x[cp] - mean(head(x, k))
      rdmean <- x[cp] - mean(tail(x, k))
      (ldmean + rdmean) / 2.0
    }

```

Defines:

`scdiffmean`, used in chunks 4–6.

Another variation of score computation that has been proposed by [Palshikar \(2009\)](#) is to consider the differences to the mean of the k left and right neighbours, that is:

$$S_3 = \frac{(y_i - \frac{(y_{i-1}, \dots, y_{i-k})}{k}) + (y_i - \frac{(y_{i+1}, \dots, y_{i+k})}{k})}{2} \quad (3)$$

The equation (3) can be casted as R function `scavgdiff` for instance as follows:

```

2b  <score-avgdiff 2b>≡
    scavgdiff <- function(x, k){
      cp <- k + 1L
      lmean <- mean(x[cp] - head(x, k))
      rmean <- mean(x[cp] - tail(x, k))
      (lmean + rmean) / 2.0
    }

```

Defines:

`scavgdiff`, used in chunks 4–6.

The fourth proposed score function differs from the previous three in the sense that it does take explicitly the differences between y_i and its neighbours explicitly into account, but tries to capture its information content by means of relative entropy. The entropy of a vector A with elements $A = \{a_1, \dots, a_m\}$ is given as:

$$H_w(A) = \sum_{i=1}^M (-p_w(a_i) \log(p_w(a_i))) \quad (4)$$

where $p_w(a_i)$ is an estimate of the density value at a_i . The score function is now based on computing the entropies of $H(N((k, i, T)))$ and $H(N'(k, i, T))$. Hereby, the densities can be determined by means of a kernel density estimator. The score function is then defined as the difference of the entropies:

$$S_4 = H(N((k, i, T))) - H(N'((k, i, T))) \quad (5)$$

This concept is implemented in the function `scentropy()`. The empirical density is computed by calling `density()`. The ellipsis argument of `scentropy()` is passed down to this function and hereby allowing the user to employ other than the default arguments of `density()`.

3 *<score-entropy 3>*≡
`scentropy <- function(x, k, ...){`
`cp <- k + 1L`
`dfull <- density(x, ...)$y`
`hfull <- sum(-dfull * log(dfull))`
`dexct <- density(x[-cp], ...)$y`
`hexct <- sum(-dexct * log(dexct))`
`hfull - hexct`
`}`

Defines:

`scentropy`, used in chunks 4–6.

Finally, a moment-based score function has been put forward in the article by Palshikar. Hereby, the first and second moment of $N((k, i, T))$ are computed and a t-type statistic can be computed as $(y_i - m)/s$. If this statistic surpasses a provided threshold h , then the data point is considered as a local peak/trough.

$$S_5 = \begin{cases} 1 & (y_i - m)/s \geq h \\ 0 & \text{else} \end{cases} \quad (6)$$

This type of scoring algorithm is implemented as function `sctttype()` below:

```
4a  <score-tttype 4a>≡
    sctttype <- function(x, k, tval){
      cp <- k + 1L
      m <- mean(x[-cp])
      s <- sd(x[-cp])
      tstat <- (x[cp] - m) / s
      if ( abs(tstat) < tval ){
        tstat <- 0
      }
      tstat
    }
```

Defines:

`sctttype`, used in chunks 4-6.

Incidentally, an ensemble forecast of these five algorithms can be utilized for local peak/trough classification can be employed. Hereby, one could either use a hybrid approach, whereby only those data points are considered as peak/trough points, if all five methods coincide. This concept is casted in the function `schybrid()`. Hereby, the signs of all five scoring algorithm are tested for equality.

```
4b  <score-hybrid 4b>≡
    schybrid <- function(x, k, tval, ...){
      s <- c(sign(scmxdiff(x, k)),
             sign(scvdiff(x, k)),
             sign(scdiffmean(x, k)),
             sign(scentropy(x, k, ...)),
             sign(sctttype(x, k, tval)))
      val <- unique(s)
      if ( length(val) < 2 ){
        return(s[1])
      } else {
        return(0)
      }
    }
```

Defines:

`schybrid`, used in chunk 6a.

Uses `scvdiff` 2b, `scdiffmean` 2a, `scentropy` 3, `scmxdiff` 1, and `sctttype` 4a.

It is also conceivable to base the classification on a majority vote. For instance, if three out of the five algorithm classify a data point as a local peak/trough, then this is taken as sufficient evidence. This approach is defined in the function `scvote()` below. The count of same 'votes' is set by the argument `confby`. Its default value is 3, *i.e.* a simple majority. For `confby = 5` the function would return the same classification as `schybrid()` does.

```
5  <score-vote 5>≡
    scvote <- function(x, k, tval, confby = 3, ...){
      s <- c(sign(scmaydiff(x, k)),
             sign(scavgdifff(x, k)),
             sign(scdiffmean(x, k)),
             sign(scentropy(x, k, ...)),
             sign(scttype(x, k, tval)))
      pos <- rep(1, 5)
      zer <- rep(0, 5)
      neg <- rep(-1, 5)
      spos <- sum(s == pos)
      szer <- sum(s == zer)
      sneg <- sum(s == neg)
      v <- c(spos, szer, sneg)
      idx <- which(v >= confby)
      vals <- c(1, 0, -1)
      if ( length(idx) > 0 ){
        return(vals[idx])
      } else {
        return(0)
      }
    }
}
```

Defines:

`scvote`, used in chunk 6a.

Uses `scavgdifff` 2b, `scdiffmean` 2a, `scentropy` 3, `scmaydiff` 1, and `scttype` 4a.

2.3 Combining score methods

```
6a  <score-wrapper 6a>≡
    score <- function(x, k,
                      scoreby = c("vote", "avg", "diff", "max", "ent",
                                   "ttype", "hybrid"),
                      tval = 1.0, confby = 3, ...){
      scoreby <- match.arg(scoreby)
      ans <- switch(scoreby,
                    vote = scvote(x, k, tval, confby, ...),
                    avg = scavgdiff(x, k),
                    diff = scdiffmean(x, k),
                    max = scmaxdiff(x, k),
                    ent = scentropy(x, k, ...),
                    ttype = scttype(x, k, tval),
                    hybrid = schybrid(x, k, tval, ...)
                    )
      ans
    }
```

Defines:

`score`, used in chunk 7.

Uses `scavgdiff` 2b, `scdiffmean` 2a, `scentropy` 3, `schybrid` 4b, `scmaxdiff` 1, `scttype` 4a, and `scvote` 5.

The content/structure of the file `score.R` is given as:

```
6b  <score.R 6b>≡
    <man-func-score 16>
    <score-wrapper 6a>
    #' @rdname score
    <score-maxdiff 1>
    #' @rdname score
    <score-diffmean 2a>
    #' @rdname score
    <score-avgdiff 2b>
    #' @rdname score
    <score-entropy 3>
    #' @rdname score
    <score-ttype 4a>
    #' @rdname score
    <score-hybrid 4b>
    #' @rdname score
    <score-vote 5>
```

This code is written to file `score.R`.

@

Within this file, all score-related methods and the wrapper-function `score()` is included. The function definitions are interspersed with the roxygen tags, which will be parsed to the Rd-file `score.Rd`.

So far the function `score()` has been created, by which a single point is assessed for being a local maximum or minimum. For analyzing a whole time series for its local extrema, this routine can be applied to each data point and its left/right neighbours. This task is accomplished with the function `hiker()` as defined next.

```
7 <hiker-func 7>≡
  hiker <- function(y, k,
                    scoreby = c("vote", "avg", "diff", "max", "ent",
                                "ttype", "hybrid"),
                    tval = 1.0, confby = 3, ...){
  <hiker-check 8>
    ## rolling centered window for peak scores
    s <- rollapply(y, width = ms, FUN = score,
                  k = k, scoreby = scoreby, tval = tval, ...)
  <hiker-output 9a>
  }

```

Uses `score 6a`.

@

The arguments of the function are `y` for the time series object, `k` for the count of left/right neighbours, and `scoreby` for the selection of the scoring method. The arguments `tval` and `confby` belong the scoring concepts 'ttype' and 'hybrid', respectively, and the ellipsis argument is passed down to the call of `scentropy()` for `scoreby = 'ent'`.

The function body consists of three parts. First, the provided arguments are checked for their validity (as shown in the following code chunk). The computation of the scores is accomplished with the `rollapply()` function of the package **zoo**. Finally, the returned object is created.

```
8  <hiker-check 8>≡
    y <- as.zoo(y)
    ## checking arguments
    k <- as.integer(abs(k))
    ms <- 2 * k + 1L
    if ( is.null(dim(y)) ){
      yname <- "series"
      n <- length(y)
      if ( n < ms ) {
        stop(paste("Sample size of 'y' is ", n,
                    " and k = ", k, ".\n", sep = ""))
      }
    } else {
      n <- nrow(y)
      yname <- colnames(y)[1]
      if ( n < ms ) {
        stop(paste("Sample size of 'y' is ", n,
                    " and k = ", k, ".\n", sep = ""))
      }
      if ( ncol(y) > 1 ) {
        stop("Provide univariate time series of S3-class 'zoo'.\n")
      }
    }
    if ( (confby < 3) || (confby > 5) ){
      stop("\nArgument 'confby' must be integer and in set {3, 4, 5}.\n")
    }
    scoreby <- match.arg(scoreby)
```


@

Within the check section of the function body, the object `y` is first coerced to a `zoo` object and the count of neighbours is coerced to a positive integer. Next, the size of the sub-sample for computing the scores is assigned to the object `ms`. The remaining part consists of checks whether the series is univariate and its length is at least $2 \times k + 1$. Finally, the scoring method is determined from the argument `scoreby` by means of the `match.arg` function.

```
9a  <hiker-output 9a>≡
    ## merging time series and scores
    ans <- merge(y, s)
    colnames(ans) <- c("Series", "Scores")
    des <- switch(scoreby,
                  vote = "majority vote",
                  avg = "average of averaged differences",
                  diff = "average of mean differences",
                  max = "average of maximum differences",
                  ent = "difference of entropies",
                  ttype = "t-type statistic",
                  hybrid = "hybrid")
    new("HikeR", ys = ans, k = k, scoreby = des, yname = yname)
```

@

```
9b  <hiker.R 9b>≡
    <man-func-hiker 17a>
    <hiker-func 7>
```

This code is written to file `hiker.R`.

@

3 Package structure

3.1 Preliminaries

First, a skeleton of the package

```
9c  <DESCRIPTION.R 9c>≡
    Package: hiker
    Title: Local Peak and Trough of a Time Series
    Version: 0.0.0.9000
    Authors@R: person("Bernhard", "Pfaff", email = "bernhard@pfaffikus.de",
                      role = c("aut", "cre"))
    Description: Methods for detecting local peaks and troughs of a time series.
    Depends: R (>= 3.3.1), zoo, methods
    License: GPL-3
    Encoding: UTF-8
    LazyData: true
```

This code is written to file `DESCRIPTION.R`.

@

3.2 Import directives and S4-classes

```
10 <Allclasses.R 10>≡
    #' @import methods
    NULL
    #' @import zoo
    NULL
    #' @importFrom stats density sd na.omit start end smooth
    NULL
    #' @importFrom utils head tail
    NULL

    # Setting old (aka S3) classes
    setOldClass("zoo")

    <man-class-HikeR 17b>
    setClass("HikeR", slots = list(ys = "zoo",
                                   k = "integer",
                                   scoreby = "character",
                                   yname = "character"))

    <man-class-PTBB 18a>
    setClass("PTBB", slots = list(pt = "zoo",
                                   type = "character",
                                   h = "numeric"))
```

This code is written to file `Allclasses.R`.

@

3.3 Methods for S4-class 'HikeR'

In this section the S4-methods for objects of class `HikeR` are discussed. The provided methods are for showing `show()`, summarizing `summary()`, retrieval of peaks `peaks()` and troughs `troughs()` for this type of objects. Furthermore, the concept of bursts phases (close occurrence of peaks with respect to time) and busts (close occurrence of troughs with respect to time) are defined as methods `bursts()` and `busts()`, respectively. Additional methods for characterising the progression of a time series, such as 'ridges', 'phases', 'to-peaks' and 'to-troughs' are provided, too. Finally, a `plot()`-method is available whereby the user can highlight/shade the local optima and the phases in between them. All of these methods are contained in the file `hiker-methods.R`. The skeleton of this file is provided next.

```
11a  <HikerMethods.R 11a>≡
      <HikeR-show 11b>
      <HikeR-summary 12a>
      <HikeR-peaks 12b>
      <HikeR-troughs 12c>
      <HikeR-bursts 13a>
      <HikeR-busts 13b>
      <HikeR-ridges 14a>
      <HikeR-phases 14b>
      <HikeR-topeaks 15>
```

This code is written to file `HikerMethods.R`.

@

3.3.1 show-method

```
11b  <HikeR-show 11b>≡
      <man-HikeR-show 18b>
      setMethod("show",
                 signature(object = "HikeR"), function(object){
                   cat(paste("Peak/trough score computed as: ",
                             object@scoreby, ".\n", sep = ""))
                   cat(paste("Count of left/right neighbours: ", object@k,
                             ".\n", sep = ""))
                   cat("\nSummary statistics of scores:\n")
                   print(summary(object))
                 })
      )
```

@

3.3.2 summary-method

```
12a <HikeR-summary 12a>≡  
  <man-HikeR-summary 18c>  
  setMethod("summary",  
            signature(object = "HikeR"),  
            function (object, ...){  
              summary(na.omit(coredata(object@ys[, 2])))  
            })  
  )
```

@

3.3.3 peaks-method

```
12b <HikeR-peaks 12b>≡  
  # generic for extracting peaks  
  setGeneric("peaks", function(object, ...) standardGeneric("peaks"))  
  <man-HikeR-peaks 18d>  
  setMethod("peaks",  
            signature(object = "HikeR"),  
            function (object, h = 0) {  
              ans <- object@ys[, 2] > h  
              new("PTBB", pt = ans, type = "peak", h = h)  
            })  
  )
```

@

3.3.4 troughs-method

```
12c <HikeR-troughs 12c>≡  
  # generic for extracting troughs  
  setGeneric("troughs", function(object, ...) standardGeneric("troughs"))  
  <man-HikeR-troughs 18e>  
  setMethod("troughs",  
            signature(object = "HikeR"),  
            function (object, h = 0) {  
              ans <- object@ys[, 2] < -h  
              new("PTBB", pt = ans, type = "trough", h = h)  
            })  
  )
```

@

3.3.5 bursts-method

```
13a <HikeR-bursts 13a>≡
# generic for extracting bursts
setGeneric("bursts", function(object, ...) standardGeneric("bursts"))
<man-HikeR-bursts 18f>
setMethod("bursts",
  signature(object = "HikeR"),
  function (object, h = 0, b = object@k) {
    lpts <- object@ys[, 2] > h
    lidx <- which(lpts == TRUE)
    nidx <- length(lidx)
    if ( nidx > 1 ){
      for ( i in 2:nidx ){
        didx <- lidx[i] - lidx[i - 1]
        if ( didx <= b ){
          lpts[(lidx[i]):(lidx[i - 1])] <- TRUE
        }
      }
    }
    ans <- zoo(lpts, order.by = index(object@ys))
    new("PTBB", pt = ans, type = "burst", h = h)
  })
```

@

3.3.6 busts-method

```
13b <HikeR-busts 13b>≡
# generic for extracting busts
setGeneric("busts", function(object, ...) standardGeneric("busts"))
<man-HikeR-busts 19a>
setMethod("busts",
  signature(object = "HikeR"),
  function (object, h = 0, b = object@k) {
    lpts <- object@ys[, 2] < h
    lidx <- which(lpts == TRUE)
    nidx <- length(lidx)
    if ( nidx > 1 ){
      for ( i in 2:nidx ){
        didx <- lidx[i] - lidx[i - 1]
        if ( didx <= b ){
          lpts[(lidx[i]):(lidx[i - 1])] <- TRUE
        }
      }
    }
    ans <- zoo(lpts, order.by = index(object@ys))
    new("PTBB", pt = ans, type = "bust", h = h)
  })
```

@

3.3.7 ridges-method

```
14a <HikeR-ridges 14a>≡  
# generic for computing ridges  
setGeneric("ridges", function(object, ...) standardGeneric("ridges"))  
<man-HikeR-ridges 19b>  
setMethod("ridges",  
  signature(object = "HikeR"),  
  function (object, h = 0, b = object@k) {  
    N <- nrow(object@ys)  
    k <- object@k  
    bustp <- busts(object, h = h, b = b)@pt  
    burstp <- bursts(object, h = h, b = b)@pt  
    bbp <- cbind(bustp, burstp)  
    ans <- zoo(FALSE, order.by = index(bustp))  
    ridx <- which ( (rowSums(bbp) > 1) | (rowSums(bbp) < 1) )  
    ans[ridx] <- TRUE  
    ans[1:object@k] <- NA  
    ans[(N - k + 1):N] <- NA  
    new("PTBB", pt = ans, type = "ridge", h = h)  
  })
```

@

3.3.8 phases-method

```
14b <HikeR-phases 14b>≡  
# generic for computing phases  
setGeneric("phases", function(object, ...) standardGeneric("phases"))  
<man-HikeR-phases 19c>  
setMethod("phases",  
  signature(object = "HikeR"),  
  function (object, h = 0, b = object@k) {  
    N <- nrow(object@ys)  
    ans <- rep(NA, N)  
    bustp <- busts(object, h = h, b = b)@pt  
    ans[which(bustp == TRUE)] <- "bust"  
    burstp <- bursts(object, h = h, b = b)@pt  
    burstp  
    ans[which(burstp == TRUE)] <- "burst"  
    ridgep <- ridges(object, h = h, b = b)@pt  
    ans[which(ridgep == TRUE)] <- "ridge"  
    ans <- factor(ans)  
    ans <- zoo(ans, order.by = index(object@ys))  
    new("PTBB", pt = ans, type = "phase", h = h)  
  })
```

@

3.3.9 topeaks-method

```
15  <HikeR-topeaks 15>≡
    # generic for extracting topeaks
    setGeneric("topeaks", function(object, ...) standardGeneric("topeaks"))
    <man-HikeR-topeaks 19d>
    setMethod("topeaks",
      signature(object = "HikeR"),
      function (object, h = 0) {
        N <- nrow(object@ys)
        k <- object@k
        ans <- zoo(rep(TRUE, N), order.by = index(object@ys))
        ans[1:k] <- NA
        ans[(N - k + 1):N] <- NA
        peakp <- peaks(object, h)@pt
        pidx <- which(peakp == TRUE)
        npidx <- length(pidx)
        troupp <- troughs(object, h)@pt
        tidx <- which(troupp == TRUE)
        ntidx <- length(tidx)
        if ( npidx == 0 ){
          warning("\nNo local peak points.\n")
          return(NULL)
        }
        if ( ntidx == 0 ){
          warning("\nNo local trough points.\n")
          return(NULL)
        }
        ## if trough comes first, set prior points to FALSE
        if ( tidx[1] < pidx[1] ){
          ans[(k + 1):tidx[1]] <- FALSE
        }
        for ( i in 1:ntidx ) {
          previouspeaks <- which(pidx < tidx[i])
          countpreviouspeaks <- length(previouspeaks)
          if ( countpreviouspeaks > 0 ){
            maxpos <- which.max(object@ys[pidx[previouspeaks], 1])
            ans[(pidx[maxpos] + 1):tidx[i]] <- FALSE
            pidx <- pidx[-c(1:countpreviouspeaks)]
          }
        }
        new("PTBB", pt = ans, type = "topeak", h = h)
      })
```

@

4 Appendix

4.1 Documentation of functions

```
16 <man-func-score 16>≡
    #' Basic scoring methods for local minima and maxima
    #'
    #' These are basic functions for evaluating the centre
    #' point of a time series as local minimum or maximum.
    #' Hereby, a score value is computed according to various methods.
    #' If the score is positive, the centre point is tentatively
    #' classified as a local peak.
    #' Incidentally, negative scores indicate a local minima.
    #'
    #' @param x \code{numeric}, vector of length \code{2 * k + 1}.
    #' @param k \code{integer}, the count of left/right neighbours.
    #' @param scoreby \code{character}, the scoring method to be used.
    #' @param tval \code{numeric}, factor for standard deviation band
    #' if \code{scoreby = 'ttype'}.
    #' @param confby \code{integer}, count of minimum vote,
    #' values in the set \code{3:5}.
    #' @param ... ellipsis argument.
    #'
    #' @name score
    #' @family scores
    #' @return \code{numeric}, the score value.
    NULL

    #' @rdname score
    #' @export
```


@

```
17a <man-func-hiker 17a>≡  
  #' Peak/trough scores of time series points  
  #'  
  #' This function computes the score value for each  
  #' data point of a time series. The first and last  
  #' \code{k} observations are set to \code{NA}.  
  #'  
  #' @inheritParams score  
  #' @param y \code{zoo}, univariate time series.  
  #' @return An object of S4-class \code{HikeR}.  
  #' @family scores  
  #'  
  #' @references Girish K. Palshikar. Simple Algorithms for  
  #' Peak Detection in Time-Series. In \emph{Proc. 1st Int. Conf.  
  #' Advanced Data Analysis,  
  #' Business Analytics and Intelligence}, 2009.  
  #'  
  #' @examples  
  #' TEX <- SP500[, "TEX"]  
  #' ans <- hiker(TEX, k = 8, scoreby = "hybrid", tval = 0.1)  
  #' #ans  
  #' #plot(ans)  
  #'  
  #' @export
```

@

4.2 Documentation of S4-classes

```
17b <man-class-HikeR 17b>≡  
  #' S4 class \code{HikeR}  
  #'  
  #' Formal class for classifying local minima and maxima  
  #' of a time series.  
  #'  
  #' @slot ys \code{zoo}, time series with associated scores.  
  #' @slot k \code{integer}, count of left/right neighbours around centre point.  
  #' @slot scoreby \code{character}, scoring method.  
  #' @slot yname \code{character}, name of the series.  
  #' @exportClass HikeR
```

```

@
18a  <man-class-PTBB 18a>≡
      #' S4 class \code{PTBB}
      #'
      #' Formal class for peaks, troughs, burst, busts and
      #' intermittent phase of a time series.
      #'
      #' @slot pt \code{zoo}, logical: indicating peak/trough points.
      #' @slot type \code{character}, type of point/phase.
      #' @slot h \code{numeric}, the threshold for score evaluation.
      #' @exportClass PTBB

```

@

4.3 Documentation of S4-methods

```

18b  <man-HikeR-show 18b>≡
      #' @rdname HikeR-class
      #' @param object An object of S4 class \code{HikeR}.
      #' @export

```

@

```

18c  <man-HikeR-summary 18c>≡
      #' @rdname HikeR-class
      #' @aliases summary
      #' @param ... Ellipsis argument.
      #' @export

```

@

```

18d  <man-HikeR-peaks 18d>≡
      #' @rdname HikeR-class
      #' @aliases peaks
      #' @param h \code{numeric}, the threshold value for scores
      #' to be considered as peaks/troughs.
      #' @return Object of S4-class \code{PTBB}.
      #' @export

```

@

```

18e  <man-HikeR-troughs 18e>≡
      #' @rdname HikeR-class
      #' @aliases troughs
      #' @export

```

@

```

18f  <man-HikeR-bursts 18f>≡
      #' @rdname HikeR-class
      #' @aliases bursts
      #' @param b \code{integer}, intermittent count of points between peaks.
      #' @export

```

```

@
19a  <man-HikeR-busts 19a>≡
      #' @rdname HikeR-class
      #' @aliases busts
      #' @export

```

```

@
19b  <man-HikeR-ridges 19b>≡
      #' @rdname HikeR-class
      #' @aliases ridges
      #' @export

```

```

@
19c  <man-HikeR-phases 19c>≡
      #' @rdname HikeR-class
      #' @aliases phases
      #' @export

```

```

@
19d  <man-HikeR-topeaks 19d>≡
      #' @rdname HikeR-class
      #' @aliases topeaks
      #' @export

```

```

@

```

4.4 Documentation of data set

```

19e  <data.R 19e>≡
      #' Weekly price data of 476 S&P 500 constituents.
      #'
      #' The data set was used in the reference below. The authors adjusted
      #' the price data for dividends and have removed stocks if two or
      #' more consecutive missing values were found. In the remaining cases
      #' the NA entries have been replaced by interpolated values.
      #'
      #'
      #' @format A S3-class \code{zoo} object with 265 weekly observations
      #' of 476 members of the S&P 500 index. The sample starts at 2003-03-03
      #' and ends in 2008-03-24.
      #'
      #' @references Cesarone, F. and Scozzari, A. and Tardella, F.: Portfolio
      #' selection problems in practice: a comparison between linear and
      #' quadratic optimization models, Working Paper, Universita degli
      #' Studi Roma Tre, Universita Telematica delle Scienze Umane and
      #' Universita di Roma, July 2010.
      #' \url{http://arxiv.org/ftp/arxiv/papers/1105/1105.3594.pdf}
      #'
      #' @source \url{http://w3.uniroma1.it/Tardella/datasets.html},\cr
      #' \url{http://finance.yahoo.com/}
      "SP500"

```

This code is written to file `data.R`.

@

4.5 Makefile

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References

- Palshikar, G. (2009). Simple algorithms for peak detection in time-series. In *First Int. Conf. Advanced Data Analysis, Business Analytics and Intelligence*, Ahmedabad, India.