

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

Bernhard Pfaff

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## 1 Introduction

The topic of this article is to elucidate the creation of the R package **hiker** by means of literate programming (henceforth: LP). LP has been introduced by [Knuth \(1984\)](#). Its constituent characteristic is that the source code of a program as well as the documentation thereof resides in the same file. To stay in the example of the **hiker** package: within the file you are currently reading, *i.e.*, **hiker.Rnw**, the whole R source code of the package as well as an explanation of it, is provided.<sup>1</sup> This file can then be processed by the facilities offered in the R package **Rnoweb** (see [Ihaka, 2013](#)). **Rnoweb** is a reimplementaion of the **noweb** software (see [Ramsey, 1994](#)) written entirely in R. Creating the whole R package **hiker** by mere processing (tangling of the R code) of this file, is however not entirely true. Given that R packages must meet certain requirements with respect to the directory structure and the documentation of the provided functions, methods and classes, some additional tools become necessary. With respect to setting up the package structure and saving the produced R source files into the package's sub-directory `/R`, a **Makefile** is employed (the content of this file is provided in the appendix of this article, see section 4.5). The generation of the **man**-pages is accomplished by utilizing the facilities provided in the **roxygen2** and **devtools** packages (see [Wickham et al., 2015](#); [Wickham and Chang, 2016](#), respectively).

What is the package **hiker** (pronounce as 'hike—R') about? Within **hiker** the routines for detecting local peaks/troughs of a time series as proposed by [Palshikar \(2009\)](#) have been implemented. The knowledge of these points and the time spans in between these local maxima/minima can be utilized for analyzing the behavior of predictor variables in up-/down markets of a financial time series, *e.g.*, a stock price, for instance. Surely, these phases could in principal be detected by mere eyeball-econometrics, but this approach becomes burdensome if local peaks/troughs of many time series must be determined. The package itself is purely written in R and S4-classes and methods are employed.

In the remainder of this article, the proposed algorithms are presented in the subsequent section. The package structure, the defined S4-classes with the available methods are discussed in Section 3. In the Appendix of this paper the documentation of the package in the **roxygen**-format is provided. This

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<sup>1</sup>This file and the requirements for generating the R package **hiker** are made available on github as project [lp4rp](#).

organization has the advantage that the focus is shifted on the R code snippets only and is not interspersed with the documentation of the classes and methods and functions provided by the package.

## 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.<sup>2</sup> If this score value surpasses a user-provided threshold value  $\theta$ , 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 centered window of size  $2*k+1$  around  $y_i$  is considered. That is, for a positive integer  $k$  the  $k$  right neighbors  $N^+(i, k, T) = \{y_{i+1}, \dots, y_{i+k}\}$  and the  $k$  left neighbors  $N^-(i, k, T) = \{y_{i-k}, \dots, y_{i-1}\}$  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 center 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 neighbors. The function is defined as:

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

For a span of a time series  $\mathbf{y}$  of length  $2k+1$ , denoted by  $\mathbf{x}$ , the equation (1) can be casted in R as:

```
2  <score-maxdiff 2>≡
    scmaxdiff <- function(x, k){
      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 [5–7](#).

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<sup>2</sup>It suffices to provide a score function for peaks only. Trough points can be detected by using the negative values of the series  $\mathbf{y}$ .

Instead of using the maximum differences of  $y_i$  with its  $k$  left and right neighbors 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:

```
3a  <score-diffmean 3a>≡
    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 5–7.

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 neighbors, 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:

```
3b  <score-avgdiff 3b>≡
    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 5–7.

The fourth proposed score function differs from the previous three in the sense that it does take the differences between  $y_i$  and its neighbors 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()`.

4 `<score-entropy 4>≡`  
`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 5–7.

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 `scttype()` below:

```
5a  <score-ttype 5a>≡
    scttype <- 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:

`scttype`, used in chunks 5–7.

Incidentally, an ensemble forecast of these five algorithms can be utilized for local peak/trough classification. 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.

```
5b  <score-hybrid 5b>≡
    schybrid <- function(x, k, tval, ...){
      s <- c(sign(scmxdiff(x, k)),
             sign(scmvgdiff(x, k)),
             sign(scdiffmean(x, k)),
             sign(scentropy(x, k, ...)),
             sign(scttype(x, k, tval)))
      val <- unique(s)
      if ( length(val) < 2 ){
        return(s[1])
      } else {
        return(0)
      }
    }
```

Defines:

`schybrid`, used in chunk 7.

Uses `scavgdiff` 3b, `scdiffmean` 3a, `scentropy` 4, `scmxdiff` 2, and `scttype` 5a.

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.

```
6  <score-vote 6>≡
    scvote <- function(x, k, tval, confby = 3, ...){
      s <- c(sign(scmxdiff(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 7.

Uses `scavgdifff` 3b, `scdiffmean` 3a, `scentropy` 4, `scmxdiff` 2, and `scttype` 5a.

## 2.3 Combining score methods

What has been accomplished so far, are the function definitions of the five proposed heuristics and combinations thereof with respect to a sub-sample a time series of length  $2k + 1$ . These functions are now combined into a single `score()` function as shown in the subsequent R code chunk. The selection of the kind of score computation is conducted by calling the `switch()` function.

```
7  <score-wrapper 7>≡
    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 = scavgdifff(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 8b.

Uses `scavgdifff` 3b, `scdiffmean` 3a, `scentropy` 4, `schybrid` 5b, `scmaxdiff` 2, `scttype` 5a, and `scvote` 6.

The functions for computing scores are grouped together in the R file `score.R` as shown in the next chunk. The function definitions are interspersed with the roxygen tags, which will be parsed to the Rd-file `score.Rd`. Incidentally, only code chunk with names ending in `.R` are treated as files that should be tangled and saved under the given code chunk's name.

```
8a <score.R 8a>≡
  <man-func-score 25>
  <score-wrapper 7>
  #' @rdname score
  <score-maxdiff 2>
  #' @rdname score
  <score-diffmean 3a>
  #' @rdname score
  <score-avgdiff 3b>
  #' @rdname score
  <score-entropy 4>
  #' @rdname score
  <score-ttype 5a>
  #' @rdname score
  <score-hybrid 5b>
  #' @rdname score
  <score-vote 6>
```

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

@

So far the wrapper 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 then be applied to each data point and its left/right neighbors. This task is accomplished with the function `hiker()` as defined next.

```
8b <hiker-func 8b>≡
  hiker <- function(y, k,
                    scoreby = c("vote", "avg", "diff", "max", "ent",
                                "ttype", "hybrid"),
                    tval = 1.0, confby = 3, ...){
    <hiker-check 9>
    ## rolling centered window for peak scores
    s <- rollapply(y, width = ms, FUN = score,
                  k = k, scoreby = scoreby, tval = tval, ...)
    <hiker-output 10a>
  }
```

Uses `score 7`.



@

The arguments of the function are `y` for the time series object, `k` for the count of left/right neighbors, 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` (see [Zeileis and Grothendieck, 2005](#)). Finally, the returned object is created.

```
9  <hiker-check 9>≡
    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 neighbors 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.

In the final part of the function body of `hiker()`, the returned object is created as depicted in the subsequent R code chunk.

```
10a  <hiker-output 10a>≡
      ## 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)
```

@

First, the time series object `y` is merged with the series of the computed scores and assigned to `ans`. Next the type of scoring method is stored as character string to `des`. Finally, an object of S4-class `HikeR` is created and returned. The definition of this formal class is provided in section 3.2.

Given that `hiker()` is the core function of the package, it will be stored in its own `hiker.R` file, as commanded by the next chunk.

```
10b  <hiker.R 10b>≡
      <man-func-hiker 26a>
      <hiker-func 8b>
```

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

@

## 3 Package structure

### 3.1 Preliminaries

R packages must contain a DESCRIPTION and a NAMESPACE file. Both reside in the package's root directory. As mentioned earlier, only chunks with names ending in '.R' are saved to disk by the tangling function of **Rnoweb**. Therefore, the content of the description file is first, casted in the DESCRIPTION.R file as shown below and is then moved by a directive in the Makefile to the root directory of the package **hiker** without the file's suffix.

```
11a <DESCRIPTION.R 11a>≡
    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.

@

With respect to the creation of the NAMESPACE file, matters are a bit different. The import/export directives contained in this file can be written as **roxygen** tags and the assembly of the tags and the saving of the file under the package's root directory is conducted by the **document()** function of **devtools**. Hence, it suffices to include the tags in a named chunk with suffix '.R'. In the case **hiker** the import directives are included in the R-file **Allclasses.R**. As is indicated by the file name, the definitions of the S4-classes will also reside in this file. The skeleton of this this file is provided in the subsequent chunk.

```
11b <Allclasses.R 11b>≡
    <NAMESPACE 12a>
    <HikerClass 12b>
    <PtbbClass 12c>
```

This code is written to file Allclasses.R.

@

The import directives for the required packages and functions are then given as:

```
12a <NAMESPACE 12a>≡
    #' @import methods
    NULL
    #' @import zoo
    NULL
    #' @importFrom graphics plot
    NULL
    #' @importFrom stats density sd na.omit start end smooth
    NULL
    #' @importFrom utils head tail
    NULL

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

@

## 3.2 S4-classes and generics

Two S4-classes are defined. The first, `HikeR`, has been mentioned briefly in the discussion of the core function `hiker()`. The class consists of four slots, as shown in the subsequent code chunk. Objects of the slot `ys` are of class `zoo` and contain the time series and the score value. The slot `k` is of type `integer` and holds the count of left/right neighbors. The character slot `scoreby` provides a literal description of the employed scoring algorithm and the slot `yname` is a character string of the time series name.

```
12b <HikerClass 12b>≡
    <man-class-HikeR 26b>
    setClass("HikeR", slots = list(ys = "zoo",
                                   k = "integer",
                                   scoreby = "character",
                                   yname = "character"))
```

@

The `HikeR`-class does not contain explicitly the information whether a certain data point is classified as a peak or trough, or does belong to a certain phase of the time series progression. This lack of explicit information is filled by the S4-class `PTBB`; it is a short-hand for ‘PeaksTroughsBurstBust’. Its slot `pt` is of informal class `zoo` and is a logical whether a data point does belong to one the above mentioned points/phases. The slot `type` is a literal description thereof and the employed threshold value for making this classification is available in the slot `h`. The class definition is provided in the subsequent code chunk.

```
12c <PtbbClass 12c>≡
    <man-class-PTBB 27a>
    setClass("PTBB", slots = list(pt = "zoo",
                                   type = "character",
                                   h = "numeric"))
```

@

Next, the following generic functions are defined in the file `Allgenerics.R`.  
The methods of these generics are discussed in the section 3.3.

```
13  <Allgenerics.R 13>≡
    # generic for extracting peaks
    setGeneric("peaks", function(object, ...) standardGeneric("peaks"))
    # generic for extracting troughs
    setGeneric("troughs", function(object, ...) standardGeneric("troughs"))
    # generic for extracting bursts
    setGeneric("bursts", function(object, ...) standardGeneric("bursts"))
    # generic for extracting busts
    setGeneric("busts", function(object, ...) standardGeneric("busts"))
    # generic for computing ridges
    setGeneric("ridges", function(object, ...) standardGeneric("ridges"))
    # generic for computing phases
    setGeneric("phases", function(object, ...) standardGeneric("phases"))
    # generic for extracting topeaks
    setGeneric("topeaks", function(object, ...) standardGeneric("topeaks"))
    # generic for extracting totroughs
    setGeneric("totroughs", function(object, ...) standardGeneric("totroughs"))
    # generic for computing runs
    setGeneric("runs", function(x) standardGeneric("runs"))
```

This code is written to file `Allgenerics.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.

```
14a <HikerMethods.R 14a>≡
    <HikeR-show 14b>
    <HikeR-summary 15a>
    <HikeR-peaks 15b>
    <HikeR-troughs 15c>
    <HikeR-bursts 16a>
    <HikeR-busts 16b>
    <HikeR-ridges 17a>
    <HikeR-phases 17b>
    <HikeR-topeaks 18>
    <HikeR-totroughs 19>
    <HikeR-plot 20>
```

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

@

#### 3.3.1 show-method

The `show`-method provides a brief overview of `HikeR`-objects. Its definition is given in the following chunk. The `roxygen` documentation is deferred to the chunk labeled `man-HikeR-show` and provided in the appendix 4.3.

```
14b <HikeR-show 14b>≡
    <man-HikeR-show 27b>
    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))
              })
    )
```

@

First, the employed scoring-method and the count of left/right neighbors is printed *via* the `cat()` and `paste()` functions. Second, the `summary`-method is called, which provides descriptive statistics of the scores and is formally defined in the next section.

### 3.3.2 summary-method

The `summary`-method for numerics is applied to the second column of the slot `ys`, *i.e.*, the computed score values. These numbers are extracted from the `zoo` object by utilizing the `coredata()` function. Akin, to the `show`-method, the within-package documentation is deferred to the appendix.

```
15a <HikeR-summary 15a>≡  
    <man-HikeR-summary 27c>  
    setMethod("summary",  
              signature(object = "HikeR"),  
              function (object, ...){  
                summary(na.omit(coredata(object@ys[, 2])))  
              }  
    )  
@
```

### 3.3.3 peaks-method

```
15b <HikeR-peaks 15b>≡  
    <man-HikeR-peaks 27d>  
    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

```
15c <HikeR-troughs 15c>≡  
    <man-HikeR-troughs 27e>  
    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

```
16a <HikeR-bursts 16a>≡  
<man-HikeR-bursts 27f>  
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

```
16b <HikeR-busts 16b>≡  
<man-HikeR-busts 28a>  
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

```
17a <HikeR-ridges 17a>≡  
    <man-HikeR-ridges 28b>  
    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

```
17b <HikeR-phases 17b>≡  
    <man-HikeR-phases 28c>  
    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

```
18  <HikeR-topeaks 18>≡
    <man-HikeR-topeaks 28d>
    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)
        troupe <- troughs(object, h)@pt
        tidx <- which(troupe == 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)
      })
```

@

### 3.3.10 totroughs-method

```
19   $\langle \text{HikeR-totroughs } 19 \rangle \equiv$   
     $\langle \text{man-HikeR-totroughs } 28e \rangle$   
    setMethod("totroughs",  
              signature(object = "HikeR"),  
              function (object, h = 0) {  
                ans <- topeaks(object, h)  
                ans@pt <- !ans@pt  
                ans@type <- "tottrough"  
                ans  
              })
```

@

### 3.3.11 plot-method

```
20  <HikeR-plot 20>≡
    <man-HikeR-plot 28f>
    setMethod("plot",
      signature(x = "HikeR", y = "missing"),
      function (x, type = c("series", "score", "both", "zoo"),
        h = 0, b = x@k, phase = c("none", "pt", "bb"),
        main = NULL, sub = NULL,
        pt.peak = list(col = "darkgreen", pch = 19, cex = 0.8),
        pt.trough = list(col = "darkred", pch = 19, cex = 0.8),
        area.se = list(col = "lightgray"),
        area.pb = list(col = "seagreen", density = 20),
        area.tb = list(col = "red2", density = 20),
        ...){
        type <- match.arg(type)
        phase <- match.arg(phase)
        N <- nrow(x@ys)
        xidx <- 1:N
        if ( is.null(sub) ){
          sub <- paste("Score method: ", x@scoreby,
            ", k = ", x@k, sep = "")
        }
        if ( type == "score" ){
          srange <- range(na.omit(x@ys[, 2]))
          if ( is.null(main) ){
            main <- paste("Scores of time series:", x@yname)
          }
          plot(c(1, N), srange, axes = FALSE,
            main = main,
            sub = sub,
            xlab = "Time", ylab = "Score", type = "n")
          do.call(graphics::rect, c(list(xleft = 1,
            ybottom = srange[1],
            xright = x@k,
            ytop = srange[2]),
            area.se))
          do.call(graphics::rect, c(list(xleft = N - x@k + 1,
            ybottom = srange[1],
            xright = N,
            ytop = srange[2]),
            area.se))
          graphics::lines(coredata(x@ys[, 2]), type = "h", ...)
          graphics::abline(h = 0)
          graphics::abline(h = c(h, -h), col = "red")
          graphics::box()
          graphics::axis(1, at = xidx, labels = index(x@ys), tick = FALSE)
          idx <- pretty(srange)
```

```

    graphics::axis(2, at = idx, labels = idx)
}
if ( type == "series" ){
  yrange <- range(na.omit(x@ys[, 1]))
  if ( is.null(main) ){
    if ( phase == "none" ){
      main <- paste("Peaks and Troughs of:", x@yname)
    } else if ( phase == "pt" ){
      main <- paste("To-Peak and To-Trough Phases of:", x@yname)
    }
    else if ( phase == "bb" ) {
      main <- paste("Burst and Bust Phases of:", x@yname)
    }
  }
  plot(c(1, N), yrange, axes = FALSE,
       main = main, sub = sub,
       xlab = "Time", ylab = "", type = "n")
  do.call(graphics::rect, c(list(xleft = 1,
                                ybottom = yrange[1],
                                xright = x@k,
                                ytop = yrange[2]),
                            area.se))
  do.call(graphics::rect, c(list(xleft = N - x@k + 1,
                                ybottom = yrange[1],
                                xright = N,
                                ytop = yrange[2]),
                            area.se))
  graphics::lines(coredata(x@ys[, 1]), ...)
  peakidx <- which(peaks(x, h = h)@pt == TRUE)
  ynum <- coredata(x@ys[index(x@ys)[peakidx], 1])
  do.call(graphics::points, c(list(y = ynum, x = peakidx),
                              pt.peak))
  troughidx <- which(troughs(x, h = h)@pt == TRUE)
  ynum <- coredata(x@ys[index(x@ys)[troughidx], 1])
  do.call(graphics::points, c(list(y = ynum, x = troughidx),
                              pt.trough))
  if ( phase == "bb" ){
    p <- phases(x, h = h, b = b)
    pchar <- as.character(coredata(p@pt))
    burstz <- new("PTBB",
                  pt = zoo(pchar == "burst",
                           order.by = index(p@pt)),
                  type = "burst",
                  h = p@h)
    burstr <- runs(burstz)
    if ( !is.null(burstr) ) {
      xleft <- which(as.character(index(burstz@pt)) %in%
                    as.character(burstr[, "From"]))
      xright <- which(as.character(index(burstz@pt)) %in%
                     as.character(burstr[, "To"]))
    }
  }
}

```

```

        for (i in 1:length(xleft)) {
            do.call(graphics::rect, c(list(xleft = xleft[i],
                                           ybottom = yrange[1],
                                           xright = xright[i],
                                           ytop = yrange[2]),
                                           area.pb))
        }
    }
    bustz <- new("PTBB",
                pt = zoo(pchar == "bust",
                        order.by = index(p@pt)),
                type = "bust",
                h = p@h)
    bustr <- runs(bustz)
    if ( !is.null(bustr) ) {
        xleft <- which(as.character(index(bustz@pt)) %in%
                      as.character(bustr[, "From"]))
        xright <- which(as.character(index(bustz@pt)) %in%
                      as.character(bustr[, "To"]))
        for (i in 1:length(xleft)) {
            do.call(graphics::rect, c(list(xleft = xleft[i],
                                           ybottom = yrange[1],
                                           xright = xright[i],
                                           ytop = yrange[2]),
                                           area.tb))
        }
    }
}

if ( phase == "pt" ){
    top <- topeaks(x, h)
    topr <- runs(top)
    tot <- totroughs(x, h)
    totr <- runs(tot)
    if ( !is.null(topr) ) {
        xleft <- which(as.character(index(top@pt)) %in%
                      as.character(topr[, "From"]))
        xright <- which(as.character(index(top@pt)) %in%
                      as.character(topr[, "To"]))
        for (i in 1:length(xleft)) {
            do.call(graphics::rect, c(list(xleft = xleft[i],
                                           ybottom = yrange[1],
                                           xright = xright[i],
                                           ytop = yrange[2]),
                                           area.pb))
        }
    }
    if ( !is.null(totr) ) {
        xleft <- which(as.character(index(tot@pt)) %in%
                      as.character(totr[, "From"]))
        xright <- which(as.character(index(tot@pt)) %in%

```

```

                                as.character(totr[, "To"]))
    for (i in 1:length(xleft)) {
        do.call(graphics::rect, c(list(xleft = xleft[i],
                                       ybottom = yrange[1],
                                       xright = xright[i],
                                       ytop = yrange[2]),
                                   area.tb))
    }
}
graphics::box()
graphics::axis(1, at = xidx, labels = index(x@ys),
               tick = FALSE)
idx <- pretty(yrange)
graphics::axis(2, at = idx, labels = idx)
}
if ( type == "both" ){
    op <- graphics::par(no.readonly = TRUE)
    graphics::par(mfrow = c(2, 1))
    plot(x, type = "series", h = h, ...)
    plot(x, type = "score", h = h, ...)
    graphics::par(op)
}
if ( type == "zoo" ){
    plot(x@ys, ...)
}
}
)

```

@

### 3.4 runs-method for S4-class 'PTBB'

```
24 <PtbbMethods.R 24>≡  
  <man-PTBB-runs 29a>  
  setMethod("runs",  
    signature(x = "PTBB"), function(x){  
    if ( any(na.omit(x@pt)) ){  
      p <- as.numeric(coredata(x@pt))  
      run <- rle(p)  
      peakruns <- which(run$values == 1)  
      cumidx <- cumsum(run$lengths)  
      n <- length(cumidx)  
      xidxright <- cumidx  
      xidxleft <- c(1, cumidx + 1)[-c(n + 1)]  
      xidx <- cbind(xidxleft, xidxright)  
      peakidx <- xidx[peakruns, ]  
      runscout <- nrow(xidx)  
      runsidx <- 1:runscout  
      ans <- sapply(runsidx, function(i)  
        x@pt[xidx[i, 1]:xidx[i, 2]])  
      pidx <- which(unlist(lapply(ans, function(r)  
        is.element(TRUE, r[1]))))  
      anstrue <- ans[pidx]  
      per <- lapply(anstrue, function(i)  
        data.frame(start(i), end(i)))  
      ans <- data.frame(do.call("rbind", per))  
      ans[, "Type"] <- x@type  
      colnames(ans) <- c("From", "To", "Type")  
      return(ans)  
    } else {  
      return(NULL)  
    }  
  }  
)
```

This code is written to file PtbbMethods.R.



@

## 4 Appendix

### 4.1 Documentation of functions

```
25 <man-func-score 25>≡
    #' 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
```

@

```
26a <man-func-hiker 26a>≡
#' 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

```
26b <man-class-HikeR 26b>≡
#' 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
```

```

27a  @
      <man-class-PTBB 27a>≡
      #' 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

```

27b  <man-HikeR-show 27b>≡
      #' @rdname HikeR-class
      #' @param object An object of S4 class \code{HikeR}.
      #' @export

```

@

```

27c  <man-HikeR-summary 27c>≡
      #' @rdname HikeR-class
      #' @aliases summary
      #' @param ... Ellipsis argument.
      #' @export

```

@

```

27d  <man-HikeR-peaks 27d>≡
      #' @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

```

@

```

27e  <man-HikeR-troughs 27e>≡
      #' @rdname HikeR-class
      #' @aliases troughs
      #' @export

```

@

```

27f  <man-HikeR-bursts 27f>≡
      #' @rdname HikeR-class
      #' @aliases bursts
      #' @param b \code{integer}, intermittent count of points between peaks.
      #' @export

```

```

@
28a  <man-HikeR-busts 28a>≡
      #' @rdname HikeR-class
      #' @aliases busts
      #' @export

@
28b  <man-HikeR-ridges 28b>≡
      #' @rdname HikeR-class
      #' @aliases ridges
      #' @export

@
28c  <man-HikeR-phases 28c>≡
      #' @rdname HikeR-class
      #' @aliases phases
      #' @export

@
28d  <man-HikeR-topeaks 28d>≡
      #' @rdname HikeR-class
      #' @aliases topeaks
      #' @export

@
28e  <man-HikeR-totroughs 28e>≡
      #' @rdname HikeR-class
      #' @aliases totroughs
      #' @export

@
28f  <man-HikeR-plot 28f>≡
      #' @rdname HikeR-class
      #' @aliases plot
      #' @param x An object of S4 class \code{HikeR}.
      #' @param type \code{character}, whether series, scores or both should be plotted.
      #' @param phase \code{character}, whether burst/bust or topeak/totrough phases
      #' should be drawn in series plot.
      #' @param pt.peak \code{list}, named elements are passed to \code{graphics::points()}.
      #' @param main \code{character}, main title of plot.
      #' @param sub \code{character}, sub title of plot
      #' @param pt.trough \code{list}, named elements are passed to \code{graphics::points()}.
      #' @param area.se \code{list}, named elements are passed to \code{graphics::rect()}
      #' for areas of pre- and post sample points.
      #' @param area.pb \code{list}, named elements are passed to \code{graphics::rect()}
      #' for 'to-peak' or 'burst' phases.
      #' @param area.tb \code{list}, named elements are passed to \code{graphics::rect()}
      #' for 'to-trough' or 'bust' phases.
      #' @export

```

```

29a  @
      <man-PTBB-runs 29a>≡
      #' @rdname PTBB-class
      #' @aliases runs
      #' @param x An object of S4 class \code{PTBB}.
      #' @export

```

```
@
```

#### 4.4 Documentation of data set

```

29b  <data.R 29b>≡
      #' 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

---

```
# Makefile for creating the R package hiker

PKGNAME := hiker
PKGVERS = $(shell sed -n "s/Version: *\([^\ ]*\)/\1/p" ./${PKGNAME}/DESCRIPTION)
PKGTAR = ${PKGNAME}_${PKGVERS}.tar.gz
TEXCMD := pdflatex
RFILES := Allclasses.R Allgenerics.R score.R hiker.R data.R HikerMethods.R PtbbMethods.R
DFILES := SP500.rda

all: deps tex pdf pkg check
tex: ${PKGNAME}.tex
pdf: ${PKGNAME}.pdf

deps:
    Rscript -e 'if (!require("devtools")) install.packages("devtools")'
    Rscript -e 'if (!require("Rnoweb")) install.packages("Rnoweb_1.1.tar.gz", repos = NULL, type="source")'

${PKGNAME}.tex: ${PKGNAME}.Rnw
    Rscript -e 'library(Rnoweb); noweb("${PKGNAME}.Rnw", tangle = FALSE)'

${PKGNAME}.pdf: ${PKGNAME}.tex
    ${TEXCMD} $<
    ${TEXCMD} $<
    bibtex ${PKGNAME}.aux
    ${TEXCMD} $<
    ${TEXCMD} $<

pkg: ${PKGNAME}.Rnw
    Rscript -e 'library(Rnoweb); noweb("${PKGNAME}.Rnw", weave = FALSE)'
# creating package skeleton
if [ ! -d "${PKGNAME}" ]; then mkdir ${PKGNAME}; fi
if [ ! -d "${PKGNAME}/R" ]; then mkdir ${PKGNAME}/R; fi
if [ ! -d "${PKGNAME}/data" ]; then mkdir ${PKGNAME}/data; fi
# handling R files
find ./${PKGNAME}/R/ -type f -delete
mv DESCRIPTION.R ${PKGNAME}/DESCRIPTION
mv ${RFILES} ${PKGNAME}/R/
cp ${DFILES} ${PKGNAME}/data/
# handling man files
if [ ! -d "${PKGNAME}/man" ]; then mkdir ${PKGNAME}/man; fi
find ./${PKGNAME}/man/ -type f -delete
Rscript -e 'library(devtools); devtools::document(pkg = "${PKGNAME}")'
# building the source tarball
R CMD build ${PKGNAME}

check: pkg
    R CMD check ${PKGTAR}

clean:
    $(RM) -r ${PKGNAME}.Rcheck/
    $(RM) ${PKGNAME}.aux ${PKGNAME}.log ${PKGNAME}.out ${PKGNAME}.bbl ${PKGNAME}.blg
```

---

## 5 Chunk Index

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