

An Introduction to the diveMove Package

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Contents

1	Introduction
2	Features
3	Preliminary Procedures
4	How to Represent TDR Data?
5	Identification of Activities at Various Scales
6	How to Represent Calibrated TDR Data?
7	Dive Summaries
8	Calibrating Speed Sensor Readings
9	Bout Detection
10	Summary

1 Introduction

Remarkable developments in technology for electronic data collection and archival have increased researchers' ability to study the behaviour of aquatic animals while reducing the effort involved and impact on study animals. For example, interest in the study of diving behaviour led to the development of minute time-depth recorders (TDRs) that can collect more than 15 MB of data on depth, velocity, light levels, and other parameters as animals

move through their habitat. Consequently, extracting useful information from TDRs has become a time-consuming and tedious task. Therefore, there is an increasing need for efficient software to automate these tasks, without compromising the freedom to control critical aspects of the procedure.

There are currently several programs available for analyzing TDR data to study diving behaviour. The large volume of peer-reviewed literature based on results from these programs attests to their usefulness. However, none of them are in the free software domain, to the best of my knowledge, with all the disadvantages it entails. Therefore, the main motivation for writing `diveMove` was to provide an R package for diving behaviour analysis allowing for more flexibility and access to intermediate calculations. The advantage of this approach is that researchers have all the elements they need at their disposal to take the analyses beyond the standard information returned by the program.

The purpose of this article is to outline the functionality of `diveMove`, demonstrating its most useful features through an example of a typical diving behaviour analysis session. Further information can be obtained by reading the vignette that is included in the package (`vignette("diveMove")`) which is currently under development, but already shows basic usage of its main functions. `diveMove` is available from CRAN, so it can easily be installed using `install.packages()`.

2 Features

`diveMove` offers functions to perform the following tasks:

*An earlier version of this introduction to `diveMove` has been published in R News (Luque 2007)

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- Identification of wet vs. dry periods, defined by consecutive readings with or without depth measurements, respectively, lasting more than a user-defined threshold. Depending on the sampling protocol programmed in the instrument, these correspond to wet vs. dry periods, respectively. Each period is individually identified for later retrieval.
- Calibration of depth readings, which is needed to correct for shifts in the pressure transducer. This can be done using a `tcltk` graphical user interface (GUI) for chosen periods in the record, or by providing a value determined a priori for shifting all depth readings.
- Identification of individual dives, with their different phases (descent, bottom, and ascent), using various criteria provided by the user. Again, each individual dive and dive phase is uniquely identified for future retrieval.
- Calibration of speed readings using the method described by [Blackwell et al. \(1999\)](#), providing a unique calibration for each animal and deployment. Arguments are provided to control the calibration based on given criteria. Diagnostic plots can be produced to assess the quality of the calibration.
- Summary of time budgets for wet vs. dry periods.
- Dive statistics for each dive, including maximum depth, dive duration, bottom time, post-dive duration, and summaries for each dive phases, among other standard dive statistics.
- `tcltk` plots to conveniently visualize the entire dive record, allowing for zooming and panning across the record. Methods are provided to include the information obtained in the points above, allowing the user to quickly identify what part of the record is being displayed (period, dive, dive phase).

Additional features are included to aid in analysis of movement and location data, which are often collected concurrently with *TDR* data. They include calculation of distance and speed between successive locations, and filtering of erroneous locations using various methods. However, `diveMove` is primarily a diving behaviour analysis package, and other packages are available which provide more extensive animal movement analysis features (e.g. `trip`).

The tasks described above are possible thanks to the implementation of three formal S4 classes to represent TDR data. Classes *TDR* and *TDRspeed* are used to represent data from TDRs with and without speed sensor readings, respectively. The latter class inherits from the former, and other concurrent data can be included with either of these objects. A third formal class (*TDRcalibrate*) is used to represent data obtained during the various intermediate steps described above. This structure greatly facilitates the retrieval of useful information during analyses.

3 Preliminary Procedures

As with other packages in R, to use the package we load it with the function `library`:

```
> library(diveMove)
```

This makes the objects in the package available in the current R session. A short overview of the most important functions can be seen by running the examples in the package's help page:

```
> example(diveMove)
```

Data Preparation

TDR data are essentially a time-series of depth readings, possibly with other concurrent parameters, typically taken regularly at a user-defined interval. Depending on the instrument and manufacturer, however, the files obtained may contain various errors, such as repeated lines, missing sampling intervals, and invalid data. These errors are better dealt with using tools other than R, such as `awk` and its variants, because such stream editors use much less memory than R for this type of problems, especially with the typically large files obtained from TDRs. Therefore, `diveMove` currently makes no attempt to fix these errors. Validity checks for the TDR classes, however, do test for time series being in increasing order.

Most TDR manufacturers provide tools for downloading the data from their TDRs, but often in a proprietary format. Fortunately, some of these manufacturers also offer software to convert the files from their proprietary format into a portable format, such as comma-separated-values (csv). At least one

of these formats can easily be understood by R, using standard functions, such as `read.table()` or `read.csv()`. `diveMove` provides constructors for its two main formal classes to read data from files in one of these formats, or from simple data frames.

4 How to Represent TDR Data?

TDR is the simplest class of objects used to represent TDR data in `diveMove`. This class, and its *TDRspeed* subclass, stores information on the source file for the data, the sampling interval, the time and depth readings, and an optional data frame containing additional parameters measured concurrently. The only difference between *TDR* and *TDRspeed* objects is that the latter ensures the presence of a speed vector in the data frame with concurrent measurements. These classes have the following slots:

file: character,
mtime: numeric,
time: POSIXct,
depth: numeric,
concurrentData: data.frame

Once the TDR data files are free of errors and in a portable format, they can be read into a data frame, using e.g.:

```
> ff <- system.file(file.path("data",
+ "dives.csv"), package = "diveMove")
> tdrXcsv <- read.csv(ff)
```

and then put into one of the *TDR* classes using the function `createTDR()`. Note, however, that this approach requires knowledge of the sampling interval and making sure that the data for each slot are valid:

```
> library(diveMove)
> ddt.str <- paste(tdrXcsv$date,
+ tdrXcsv$time)
> ddt <- strptime(ddt.str,
+ format = "%d/%m/%Y %H:%M:%S")
> time.posixct <- as.POSIXct(ddt,
+ tz = "GMT")
> tdrX <- createTDR(time = time.posixct,
+ depth = tdrXcsv$depth,
+ concurrentData = tdrXcsv[,
+ -c(1:3)], dtmte = 5,
+ file = ff)
> tdrX <- createTDR(time = time.posixct,
+ depth = tdrXcsv$depth,
+ concurrentData = tdrXcsv[,
```

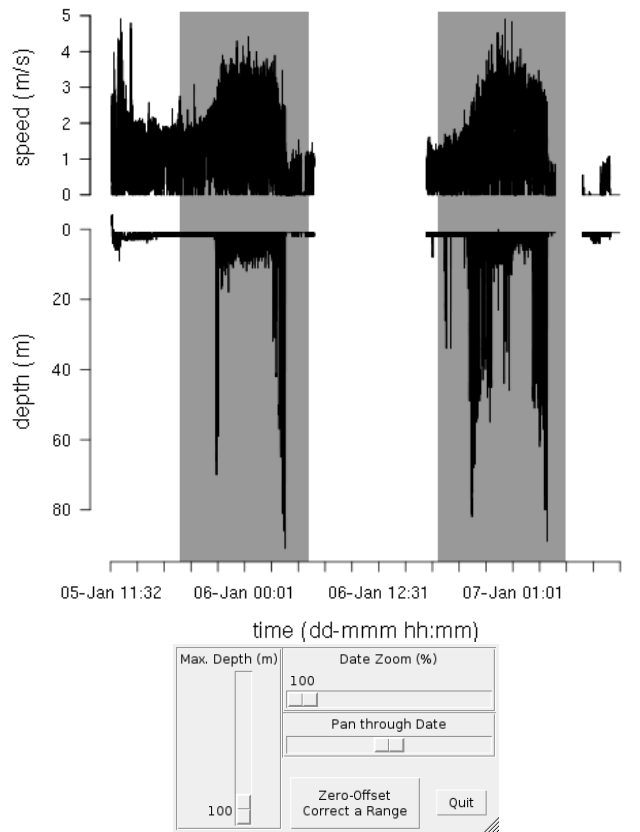


Figure 1. The `plotTDR()` method for *TDR* objects produces an interactive plot of the data, allowing for zooming and panning.

```
+ -c(1:3)], dtmte = 5,
+ file = ff, speed = TRUE)
```

If the files are in *.csv format, these steps can be automated using the `readTDR()` function to create an object of one of the formal classes representing TDR data (*TDRspeed* in this case), and immediately begin using the methods provided:

```
> tdrX <- readTDR(ff, speed = TRUE)
> plotTDR(tdrX)
```

Several arguments for `readTDR()` allow mapping of data from the source file to the different slots in `diveMove`'s classes, the time format in the input and the time zone attribute to use for the time readings.

Various methods are available for displaying TDR objects, including `show()`, which provides an informative summary of the data in the object, extractors and replacement methods for all the slots. There is a `plotTDR()` method (Figure 1) for both *TDR* and *TDRspeed* objects. The *interact* argument allows for suppression of the `tcltk` inter-

face. Information on these methods is available from *methods?TDR*.

TDR objects can easily be coerced to data frame (`as.data.frame()` method), without losing information from any of the slots. *TDR* objects can additionally be coerced to *TDRspeed*, whenever it makes sense to do so, using an *as.TDRspeed()* method.

5 Identification of Activities at Various Scales

One the first steps of dive analysis involves correcting depth for shifts in the pressure transducer, so that surface readings correspond to zero. Such shifts are usually constant for an entire deployment period, but there are cases where the shifts vary within a particular deployment, so shifts remain difficult to detect and dives are often missed. Therefore, a visual examination of the data is often the only way to detect the location and magnitude of the shifts. Visual adjustment for shifts in depth readings is tedious, but has many advantages which may save time during later stages of analysis. These advantages include increased understanding of the data, and early detection of obvious problems in the records, such as instrument malfunction during certain intervals, which should be excluded from analysis.

Zero-offset correction (ZOC) is done using the function `zoc()`. However, a more efficient method of doing this is with function `calibrateDepth()`, which takes a *TDR* object to perform three basic tasks. The first is to ZOC the data, optionally using the `tcltk` package to be able to do it interactively:

```
> dcalib <- calibrateDepth(tdrX)
```

This command brings up a plot with `tcltk` controls allowing to zoom in and out, as well as pan across the data, and adjust the `depth` scale. Thus, an appropriate time window with a unique surface depth value can be displayed. This allows the user to select a `depth` scale that is small enough to resolve the surface value using the mouse. Clicking on the ZOC button waits for two clicks: i) the coordinates of the first click define the starting time for the window to be ZOC'ed, and the depth corresponding to the surface, ii) the second click defines the end time for the window (i.e. only the x coordinate has any

meaning). This procedure can be repeated as many times as needed. If there is any overlap between time windows, then the last one prevails. However, if the offset is known a priori, there is no need to go through all this procedure, and the value can be provided as the argument *offset* to `calibrateDepth()`. For example, preliminary inspection of object `tdrX` would have revealed a 3 m offset, and we could have simply called (without plotting):

```
> dcalib <- calibrateDepth(tdrX,
+   offset = 3)
```

Once depth has been ZOC'ed, the second step `calibrateDepth()` will perform is identify dry and wet periods in the record. Wet periods are those with depth readings, dry periods are those without them. However, records may have aberrant missing depth that should not define dry periods, as they are usually of very short duration¹. Likewise, there may be periods of wet activity that are too short to be compared with other wet periods, and need to be excluded from further analyses. These aspects can be controlled by setting the arguments *dry.thr* and *wet.thr* to appropriate values.

Finally, `calibrateDepth()` identifies all dives in the record, according to a minimum depth criterion given as its *dive.thr* argument. The value for this criterion is typically determined by the resolution of the instrument and the level of noise close to the surface. Thus, dives are defined as departures from the surface to maximal depths below *dive.thr* and the subsequent return to the surface. Each dive may subsequently be referred to by an integer number indicating its position in the time series.

Dive phases are also identified at this last stage. Detection of dive phases is controlled by three arguments: a critical quantile for rates of vertical descent (*descent.crit.q*), a critical quantile for rates of ascent (*ascent.crit.q*), and a proportion of maximum depth (*wiggle.tol*). The first two arguments are used to define the rate of descent below which the descent phase is deemed to have ended, and the rate of ascent above which the ascent phases is deemed to have started, respectively. The rates are obtained from all successive rates of vertical movement from the surface to the first (descent) and last (ascent) maximum dive depth. Only positive rates are con-

¹They may result from animals resting at the surface of the water long enough to dry the sensors.

sidered for the descent, and only negative rates are considered for the ascent. The purpose of this restriction is to avoid having any reversals of direction or hysteresis events resulting in phases determined exclusively by those events. The *wiggle.tol* argument determines the proportion of maximum dive depth above which wiggles are not allowed to terminate descent, or below which they should be considered as part of the bottom phase.

A more refined call to `calibrateDepth()` for object `tdrX` may be:

```
> dcalib <- calibrateDepth(tdrX,
+   offset = 3, wet.thr = 70,
+   dry.thr = 3610, dive.thr = 4,
+   descent.crit.q = 0.1,
+   ascent.crit.q = 0.1, wiggle.tol = 0.8)
```

The result (value) of this function is an object of class *TDRcalibrate*, where all the information obtained during the tasks described above are stored.

6 How to Represent Calibrated TDR Data?

Objects of class *TDRcalibrate* contain the following slots, which store information during the major procedures performed by `calibrateDepth()`:

tdr: *TDR*. The object which was calibrated.

gross.activity: *list*. This list contains four components with details on wet/dry activities detected, such as start and end times, durations, and identifiers and labels for each activity period. Five activity categories are used for labelling each reading, indicating dry (L), wet (W), underwater (U), diving (D), and brief wet (Z) periods. However, underwater and diving periods are collapsed into wet activity at this stage (see below).

dive.activity: *data.frame*. This data frame contains three components with details on the diving activities detected, such as numeric vectors identifying to which dive and post-dive interval each reading belongs to, and a factor labelling the activity each reading represents. Compared to the **gross.activity** slot, the underwater and diving periods are discerned here.

dive.phases: *factor*. This identifies each reading

with a particular dive phase. Thus, each reading belongs to one of descent, descent/bottom, bottom, bottom/ascent, and ascent phases. The descent/bottom and bottom/ascent levels are useful for readings which could not unambiguously be assigned to one of the other levels.

dry.thr: *numeric*.

wet.thr: *numeric*.

dive.thr: *numeric*. These last three slots store information given as arguments to `calibrateDepth()`, documenting criteria used during calibration.

speed.calib.coefs: *numeric*. If the object calibrated was of class *TDRspeed*, then this is a vector of length 2, with the intercept and the slope of the speed calibration line (see below).

All the information contained in each of these slots is easily accessible through extractor methods for objects of this class (see `class?TDRcalibrate`). An appropriate *show()* method is available to display a short summary of such objects, including the number of dry and wet periods identified, and the number of dives detected.

The *TDRcalibrate* `plotTDR()` method for these objects allows visualizing the major wet/dry activities throughout the record (Figure 2):

```
> plotTDR(dcalib, concurVars = "light",
+   concurVarTitles = c("speed (m/s)",
+   "light"), surface = TRUE)
```

The `dcalib` object contains a *TDRspeed* object in its `tdr` slot, and speed is plotted by default in this case. Additional measurements obtained concurrently can also be plotted using the *concurVars* argument. Titles for the depth axis and the concurrent parameters use separate arguments; the former uses *ylab.depth*, while the latter uses *concurVarTitles*. Convenient default values for these are provided. The *surface* argument controls whether post-dive readings should be plotted; it is `FALSE` by default, causing only dive readings to be plotted which saves time plotting and re-plotting the data. All plot methods use the underlying `plotTD()` function, which has other useful arguments that can be passed from these methods.

A more detailed view of the record can be obtained by using a combination of the *diveNo* and the *labels* arguments to this `plotTDR()` method. This is useful

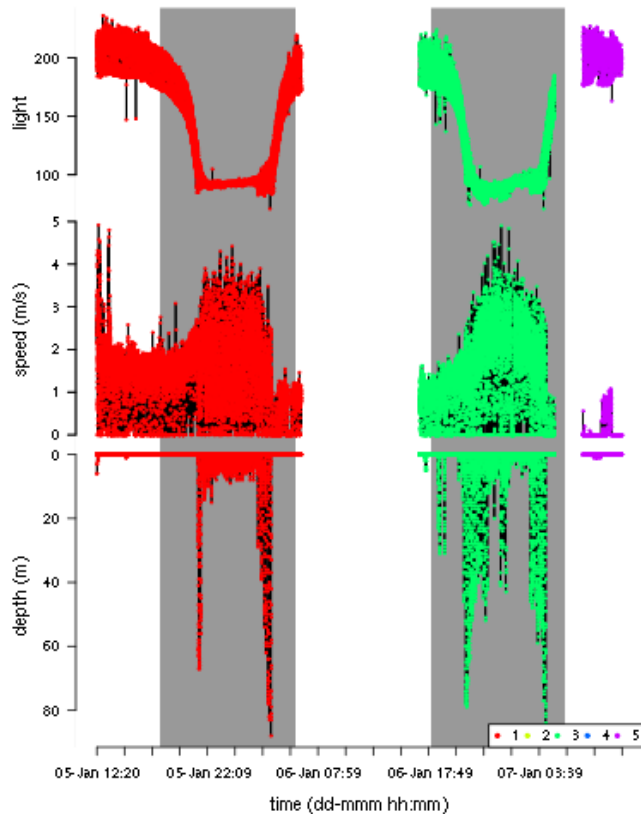


Figure 2. The `plotTDR()` method for *TDRcalibrate* objects displays information on the major activities identified throughout the record (wet/dry periods here).

if, for instance, closer inspection of certain dives is needed. The following call displays a plot of dives 2 through 8 (Figure 3):

```
> plotTDR(dcalib, diveNo = 2:8,
+ labels = "dive.phase")
```

The `labels` argument allows the visualization of the identified dive phases for all dives selected. The same information can also be obtained with the `extractDive()` method for *TDRcalibrate* objects:

```
> extractDive(dcalib, diveNo = 2:8)
```

Other useful extractors include: `getGAct()` and `getDAct()`. These methods extract the whole `gross.activity` and `dive.activity`, respectively, if given only the *TDRcalibrate* object, or a particular component of these slots, if supplied a string with the name of the component. For example: `getGAct(dcalib, "trip.act")` would retrieve the factor identifying each reading with a wet/dry activity and `getDAct(dcalib, "dive.activity")` would retrieve a more detailed factor with informa-

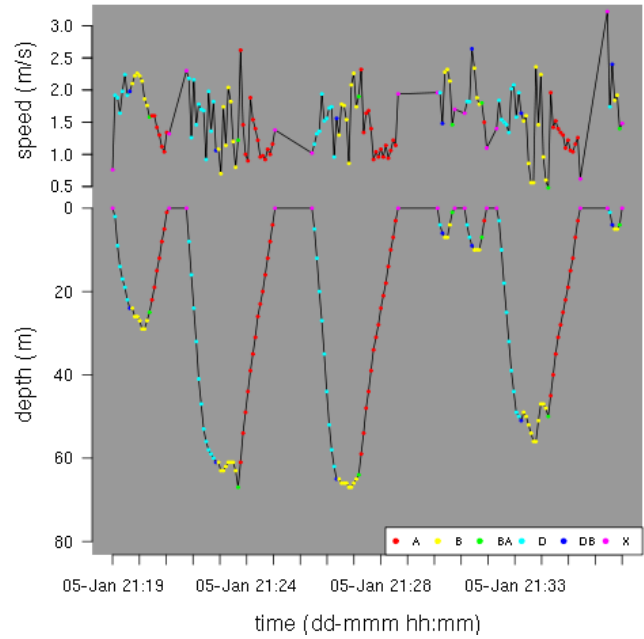


Figure 3. The `plotTDR()` method for *TDRcalibrate* objects can also display information on the different activities during each dive record (descent=D, descent/bottom=DB, bottom=B, bottom/ascent=BA, ascent=A, X=surface).

tion on whether the reading belongs to a dive or a brief aquatic period. Below is a demonstration of these methods.

`getTDR()`: This method simply takes the *TDRcalibrate* object as its single argument and extracts the *TDR* object²:

```
> getTDR(dcalib)
```

```
Time-Depth Recorder data -- Class TDRspeed object
Source File       : dives.csv
Sampling Interval (s): 5
Number of Samples  : 34199
Sampling Begins    : 2002-01-05 11:32:00
Sampling Ends      : 2002-01-07 11:01:50
Total Duration (d) : 1.979
Measured depth range : [ 0 , 88 ]
Other variables    : light temperature speed
```

`getGAct()`: There are two methods for this generic, allowing access to a list with details about all wet/dry periods found. One of these extracts the entire *list* (output omitted for brevity):

```
> getGAct(dcalib)
```

²In fact, a *TDRspeed* object in this example

The other provides access to particular elements of the *list*, by their name. For example, if we are interested in extracting only the vector that tells us to which period number every row in the record belongs to, we would issue the command:

```
> getGAct(dcalib, "phase.id")
```

Other elements that can be extracted are named “activity”, “begin”, and “end”, and can be extracted in a similar fashion. These elements correspond to the activity performed for each reading (see `?detPhase` for a description of the labels for each activity), the beginning and ending time for each period, respectively.

`getDAct()`: This generic also has two methods; one to extract an entire data frame with details about all dive and postdive periods found (output omitted):

```
> getDAct(dcalib)
```

The other method provides access to the columns of this data frame, which are named “dive.id”, “dive.activity”, and “postdive.id”. Thus, providing any one of these strings to `getDAct`, as a second argument will extract the corresponding column.

`getDPhaseLab()`: This generic function extracts a factor identifying each row of the record to a particular dive phase (see `?detDive` for a description of the labels of the factor identifying each dive phase). Two methods are available; one to extract the entire factor, and the other to select particular dive(s), by its (their) index number, respectively (output omitted):

```
> getDPhaseLab(dcalib)
> getDPhaseLab(dcalib, 20)

> dphases <- getDPhaseLab(dcalib,
+   c(100:300))
```

The latter method is useful for visually inspecting the assignment of points to particular dive phases. Before doing that though, this is a good time to introduce another generic function that allows the subsetting of the original *TDR* object to a single a dive or group of dives’ data:

```
> sealX <- extractDive(dcalib,
+   diveNo = c(100:300))
> sealX
```

```
Time-Depth Recorder data -- Class TDRspeed object
Source File      : dives.csv
Sampling Interval (s): 5
```

```
Number of Samples      : 2410
Sampling Begins        : 2002-01-06 00:45:15
Sampling Ends          : 2002-01-07 03:27:10
Total Duration (d)     : 1.112
Measured depth range   : [ 0 , 88 ]
Other variables        : light temperature speed
```

As can be seen, the function `extractDive` takes a *TDRcalibrate* object and a vector indicating the dive numbers to extract, and returns a *TDR* object containing the subsetting data. Once a subset of data has been selected, it is possible to plot them and pass the factor labelling dive phases as the argument *phaseCol* to the `plotTDR` method³:

```
> plotTDR(sealX, phaseCol = dphases)
```

With the information obtained during this calibration procedure, it is possible to calculate dive statistics for each dive in the record.

7 Dive Summaries

A table providing summary statistics for each dive can be obtained with the function `diveStats()` (Figure 4).

`diveStats()` returns a data frame with the final summaries for each dive (Figure 4), providing the following information:

- The time of start of the dive, the end of descent, and the time when ascent began.
- The total duration of the dive, and that of the descent, bottom, and ascent phases.
- The vertical distance covered during the descent, the bottom (a measure of the level of “wiggling”, i.e. up and down movement performed during the bottom phase), and the vertical distance covered during the ascent.
- The maximum depth attained.
- The duration of the post-dive interval.

A summary of time budgets of wet vs. dry periods can be obtained with `timeBudget()`, which returns a data frame with the beginning and ending times for each consecutive period (Figure 4).

³The function that the method uses is actually `plotTD`, so all the possible arguments can be studied by reading the help page for `plotTD`

```

> tdrXSumm1 <- diveStats(dcalib)
> names(tdrXSumm1)

[1] "begdesc"          "enddesc"          "begasc"           "desctim"
[5] "botttim"          "asctim"           "descdist"         "bottdist"
[9] "ascdist"          "desc.tdist"       "desc.mean.speed"  "desc.angle"
[13] "bott.tdist"       "bott.mean.speed"  "asc.tdist"        "asc.mean.speed"
[17] "asc.angle"        "divetim"          "maxdep"           "postdive.dur"
[21] "postdive.tdist"   "postdive.mean.speed"

> tbudget <- timeBudget(dcalib, ignoreZ = TRUE)
> head(tbudget, 4)

  phaseno activity          beg          end
1      1      W 2002-01-05 11:32:00 2002-01-06 06:30:00
2      2      L 2002-01-06 06:30:05 2002-01-06 17:01:10
3      3      W 2002-01-06 17:01:15 2002-01-07 05:00:30
4      4      L 2002-01-07 05:00:35 2002-01-07 07:34:00

> trip.labs <- stampDive(dcalib, ignoreZ = TRUE)
> tdrXSumm2 <- data.frame(trip.labs, tdrXSumm1)
> names(tdrXSumm2)

[1] "trip.no"          "trip.type"        "beg"              "end"
[5] "begdesc"          "enddesc"          "begasc"           "desctim"
[9] "botttim"          "asctim"           "descdist"         "bottdist"
[13] "ascdist"          "desc.tdist"       "desc.mean.speed"  "desc.angle"
[17] "bott.tdist"       "bott.mean.speed"  "asc.tdist"        "asc.mean.speed"
[21] "asc.angle"        "divetim"          "maxdep"           "postdive.dur"
[25] "postdive.tdist"   "postdive.mean.speed"

```

Figure 4. Per-dive summaries can be obtained with functions `diveStats()`, and a summary of time budgets with `timeBudget()`. `diveStats()` takes a *TDRcalibrate* object as a single argument (object `dcalib` above, see text for how it was created).

It takes a *TDRcalibrate* object and another argument (*ignoreZ*) controlling whether aquatic periods that were briefer than the user-specified threshold⁴ should be collapsed within the enclosing period of dry activity.

These summaries are the primary goal of `diveMove`, but they form the basis from which more elaborate and customized analyses are possible, depending on the particular research problem. These include investigation of descent/ascent rates based on the depth profiles, and bout structure analysis. Some of these will be implemented in the future.

In the particular case of *TDRspeed* objects, however, it may be necessary to calibrate the speed readings before calculating these statistics.

8 Calibrating Speed Sensor Readings

Calibration of speed sensor readings is performed using the procedure described by [Blackwell et al.](#)

⁴This corresponds to the value given as the *wet.thr* argument to `calibrateDepth()`.

(1999). Briefly the method rests on the principle that for any given rate of depth change, the lowest measured speeds correspond to the steepest descent angles, i.e. vertical descent/ascent. In this case, measured speed and rate of depth change are expected to be equal. Therefore, a line drawn through the bottom edge of the distribution of observations in a plot of measured speed vs. rate of depth change would provide a calibration line. The calibrated speeds, therefore, can be calculated by reverse estimation of rate of depth change from the regression line.

`diveMove` implements this procedure with function `calibrateSpeed()`. This function performs the following tasks:

1. Subset the necessary data from the record. By default only data corresponding to depth changes > 0 are included in the analysis, but higher constraints can be imposed using the *z* argument. A further argument limiting the data to be used for calibration is *bad*, which is a vector with the minimum *rate* of depth change and minimum speed readings to include in the

calibration. By default, values > 0 for both parameters are used.

2. Calculate the binned bivariate kernel density and extract the desired contour. Once the proper data were obtained, a bivariate normal kernel density grid is calculated from the relationship between measured speed and rate of depth change (using the `KernSmooth` package). The choice of bandwidths for the binned kernel density is made using `bw.nrd`. The `contour.level` argument to `calibrateSpeed()` controls which particular contour should be extracted from the density grid. Since the interest is in defining a regression line passing through the lower densities of the grid, this value should be relatively low (it is set to 0.1 by default).
3. Define the regression line passing through the lower edge of the chosen contour. A quantile regression through a chosen quantile is used for this purpose. The quantile can be specified using the `tau` argument, which is passed to the `rq()` function in package `quantreg`. `tau` is set to 0.1 by default.
4. Finally, the speed readings in the `TDR` object are calibrated.

As recognized by [Blackwell et al. \(1999\)](#), the advantage of this method is that it calibrates the instrument based on the particular deployment conditions (i.e. controls for effects of position of the instrument on the animal, and size and shape of the instrument, relative to the animal's morphometry, among others). However, it is possible to supply the coefficients of this regression if they were estimated separately; for instance, from an experiment. The argument `coefs` can be used for this purpose, which is then assumed to contain the intercept and the slope of the line. `calibrateSpeed()` returns a `TDRcalibrate` object, with calibrated speed readings included in its `tdr` slot, and the coefficients used for calibration.

For instance, to calibrate speed readings using the 0.1 quantile regression of measured speed vs. rate of depth change, based on the 0.1 contour of the bivariate kernel densities, and including only changes in depth > 1 , measured speeds and rates of depth change > 0 :

```
> vcalib <- calibrateSpeed(dcalib,
+   tau = 0.1, contour.level = 0.1,
+   z = 1, bad = c(0, 0),
```

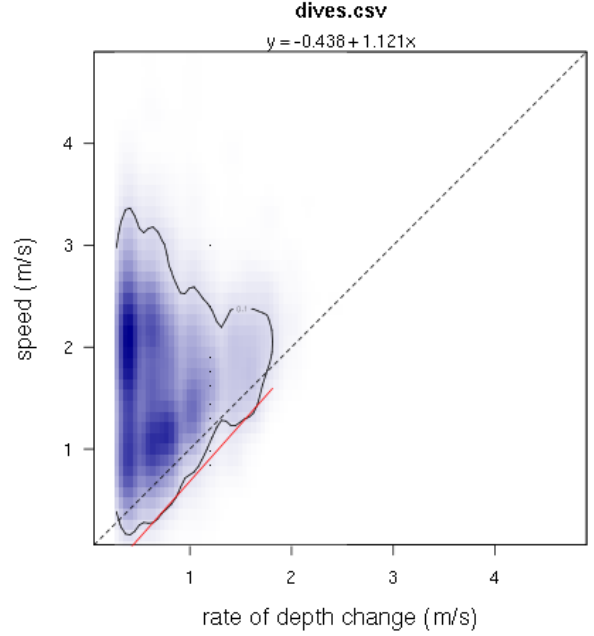


Figure 5. The relationship between measured speed and rate of depth change can be used to calibrate speed readings. The line defining the calibration for speed measurements passes through the bottom edge of a chosen contour, extracted from a bivariate kernel density grid.

```
+   cex.pts = 0.2)
```

This call produces the plot shown in Figure 5, which can be suppressed by the use of the logical argument `plot`. Calibrating speed readings allows for the meaningful interpretation of further parameters calculated by `diveStats()`, whenever a `TDRspeed` object was found in the `TDRcalibrate` object:

- The total distance travelled, mean speed, and diving angle during the descent and ascent phases of the dive.
- The total distance travelled and mean speed during the bottom phase of the dive, and the post-dive interval.

9 Bout Detection

Diving behaviour often occurs in bouts for several species, so `diveMove` implements procedures for defining bout ending criteria ([Langton et al. 1995](#); [Luque and Guinet 2007](#)). Please see `?bouts2.mle` and `?bouts2.nls` for examples.

10 Summary

The `diveMove` package provides tools for analyzing diving behaviour, including convenient methods for the visualization of the typically large amounts of data collected by TDRs. The package's main strengths are its ability to:

1. identify wet vs. dry periods,
2. calibrate depth readings,
3. identify individual dives and their phases,
4. summarize time budgets,
5. calibrate speed sensor readings,
6. provide basic summaries for each dive identified in TDR records, and
7. provide tools for identification of dive bout end criteria.

Formal `S4` classes are supplied to efficiently store TDR data and results from intermediate analysis, making the retrieval of intermediate results readily available for customized analysis. Development of the package is ongoing, and feedback, bug reports, or other comments from users are very welcome.

Acknowledgements

Many of the ideas implemented in this package developed over fruitful discussions with my mentors John P.Y. Arnould, Christophe Guinet, and Edward H. Miller. I would like to thank Laurent Dubroca who wrote draft code for some of `diveMove`'s functions. I am also greatly indebted to the regular contributors to the R-help newsgroup who helped me solve many problems during development.

References

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S. P. Luque. Diving behaviour analysis in R. *R News*, 7:8–14, 2007.

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diveMove

November 3, 2008

R topics documented:

austFilter	2
bout-methods	4
bout-misc	6
bouts2MLE	8
bouts2NLS	11
calibrateDepth	12
calibrateSpeed	14
detDive-internal	15
detPhase-internal	16
distSpeed	17
diveMove-internal	18
diveMove-package	20
dives	21
diveStats	22
extractDive-methods	24
labDive-internal	25
plotTDR-methods	26
readLocs	27
readTDR	28
rqPlot	30
sealLocs	31
TDR-accessors	32
TDRcalibrate-accessors	33
TDRcalibrate-class	35
TDR-class	36
timeBudget-methods	37
zoc	38
Index	41

austFilter

Filter satellite locations

Description

Apply a three stage algorithm to eliminate erroneous locations, based on the procedure outlined in Austin et al. (2003).

Usage

```
austFilter(time, lon, lat, id=gl(1, 1, length(time)),
           speed.thr, dist.thr, window=5)
grpSpeedFilter(x, speed.thr, window=5)
rmsDistFilter(x, speed.thr, window=5, dist.thr)
```

Arguments

time	POSIXct object with dates and times for each point.
lon	Numeric vectors of longitudes, in decimal degrees.
lat	Numeric vector of latitudes, in decimal degrees.
id	A factor grouping points in different categories (e.g. individuals).
speed.thr	Speed threshold (m/s) above which filter tests should fail any given point.
dist.thr	Distance threshold (km) above which the last filter test should fail any given point.
window	Integer indicating the size of the moving window over which tests should be carried out.
x	3-column matrix with column 1: POSIXct vector; column 2: numeric longitude vector; column 3: numeric latitude vector.

Details

These functions implement the location filtering procedure outlined in Austin et al. (2003). `grpSpeedFilter` and `rmsDistFilter` can be used to perform only the first stage or the second and third stages of the algorithm on their own, respectively. Alternatively, the three filters can be run in a single call using `austFilter`.

The first stage of the filter is an iterative process which tests every point, except the first and last $(w/2) - 1$ (where w is the window size) points, for travel velocity relative to the preceeding/following $(w/2) - 1$ points. If all $w - 1$ speeds are greater than the specified threshold, the point is marked as failing the first stage. In this case, the next point is tested, removing the failing point from the set of test points.

The second stage runs McConnell et al. (1992) algorithm, which tests all the points that passed the first stage, in the same manner as above. The root mean square of all $w - 1$ speeds is calculated, and if it is greater than the specified threshold, the point is marked as failing the second stage (see Warning section below).

The third stage is run simultaneously with the second stage, but if the mean distance of all $w - 1$ pairs of points is greater than the specified threshold, then the point is marked as failing the third stage.

The speed and distance threshold should be obtained separately (see [distSpeed](#)).

Value

`grpSpeedFilter` returns a logical vector indicating those lines that passed the test.

`rmsDistFilter` and `austFilter` return a matrix with 2 or 3 columns, respectively, of logical vectors with values TRUE for points that passed each stage. For the latter, positions that fail the first stage fail the other stages too. The second and third columns returned by `austFilter`, as well as those returned by `rmsDistFilter` are independent of one another; i.e. positions that fail stage 2 do not necessarily fail stage 3.

Warning

This function applies McConnell et al.'s filter as described in Freitas et al. (2008). According to the original description of the algorithm in McConnell et al. (1992), the filter makes a single pass through all locations. Austin et al. (2003) and other authors may have used the filter this way. However, as Freitas et al. (2008) noted, this causes locations adjacent to those flagged as failing to fail also, thereby rejecting too many locations. In `diveMove`, the algorithm was modified to reject only the "peaks" in each series of consecutive locations having root mean square speed higher than threshold.

Author(s)

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References

- McConnell BJ, Chambers C, Fedak MA. 1992. Foraging ecology of southern elephant seals in relation to bathymetry and productivity of the Southern Ocean. *Antarctic Science* 4:393-398.
- Austin D, McMillan JI, Bowen D. 2003. A three-stage algorithm for filtering erroneous Argos satellite locations. *Marine Mammal Science* 19: 371-383.
- Freitas C, Lydersen, C, Fedak MA, Kovacs KM. 2008. A simple new algorithm to filter marine mammal ARGOS locations. *Marine Mammal Science* DOI: 10.1111/j.1748-7692.2007.00180.x

See Also

[distSpeed](#)

Examples

```
locs <- readLocs(system.file(file.path("data", "sealLocs.csv"),
                             package="diveMove"), idCol=1, dateCol=2,
                dtformat="%Y-%m-%d %H:%M:%S", classCol=3, lonCol=4,
                latCol=5)
ringy <- subset(locs, id == "ringy" & !is.na(lon) & !is.na(lat))
```



```

## Austin et al.'s group filter alone
grp <- grpSpeedFilter(ringy[, 3:5], speed.thr=1.1)

## McConnell et al.'s filter (root mean square test), and distance test alone
rms <- rmsDistFilter(ringy[, 3:5], speed.thr=1.1, dist.thr=300)

## Show resulting tracks
n <- nrow(ringy)
plot.nofilter <- function(main) {
  plot(lat ~ lon, ringy, type="n", main=main)
  with(ringy, segments(lon[-n], lat[-n], lon[-1], lat[-1]))
}
layout(matrix(1:4, ncol=2, byrow=TRUE))
plot.nofilter(main="Unfiltered Track")
plot.nofilter(main="Group Filter")
n1 <- length(which(grp))
with(ringy[grp, ], segments(lon[-n1], lat[-n1], lon[-1], lat[-1],
  col="blue"))
plot.nofilter(main="Root Mean Square Filter")
n2 <- length(which(rms[, 1]))
with(ringy[rms[, 1], ], segments(lon[-n2], lat[-n2], lon[-1], lat[-1],
  col="red"))
plot.nofilter(main="Distance Filter")
n3 <- length(which(rms[, 2]))
with(ringy[rms[, 2], ], segments(lon[-n3], lat[-n3], lon[-1], lat[-1],
  col="green"))

## All three tests (Austin et al. procedure)
austin <- with(ringy, austFilter(time, lon, lat, speed.thr=1.1,
  dist.thr=300))
layout(matrix(1:4, ncol=2, byrow=TRUE))
plot.nofilter(main="Unfiltered Track")
plot.nofilter(main="Stage 1")
n1 <- length(which(austin[, 1]))
with(ringy[austin[, 1], ], segments(lon[-n1], lat[-n1], lon[-1], lat[-1],
  col="blue"))
plot.nofilter(main="Stage 2")
n2 <- length(which(austin[, 2]))
with(ringy[austin[, 2], ], segments(lon[-n2], lat[-n2], lon[-1], lat[-1],
  col="red"))
plot.nofilter(main="Stage 3")
n3 <- length(which(austin[, 3]))
with(ringy[austin[, 3], ], segments(lon[-n3], lat[-n3], lon[-1], lat[-1],
  col="green"))

```

Description

Plot results from fitted mixture of 2-process Poisson models, and calculate the bout ending criterion.

Usage

```
## S4 method for signature 'nls':
plotBouts(fit, ...)
## S4 method for signature 'mle':
plotBouts(fit, x, ...)
## S4 method for signature 'nls':
bec2(fit)
## S4 method for signature 'mle':
bec2(fit)
```

Arguments

<code>fit</code>	<code>nls</code> or <code>mle</code> object.
<code>x</code>	Numeric object with variable modelled.
<code>...</code>	Arguments passed to the underlying <code>plotBouts2.nls</code> and <code>plotBouts2.mle</code> .

General Methods

plotBouts signature (fit="nls"): Plot fitted 2-process model of log frequency vs the interval mid points, including observed data.

plotBouts signature (x="mle"): As the `nls` method, but models fitted through maximum likelihood method. This plots the fitted model and a density plot of observed data.

bec2 signature (fit="nls"): Extract the estimated bout ending criterion from a fitted 2-process model.

bec2 signature (fit="mle"): As the `nls` method, but extracts the value from a maximum likelihood model.

Author(s)

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- Langton, S.; Collett, D. and Sibly, R. (1995) Splitting behaviour into bouts; a maximum likelihood approach. *Behaviour* **132**, 9-10.
- Luque, S. P. and Guinet, C. (2007) A maximum likelihood approach for identifying dive bouts improves accuracy, precision, and objectivity. *Behaviour* **144**, 1315-1332.
- Mori, Y.; Yoda, K. and Sato, K. (2001) Defining dive bouts using a sequential differences analysis. *Behaviour* **138**, 1451-1466.
- Sibly, R.; Nott, H. and Fletcher, D. (1990) Splitting behaviour into bouts. *Animal Behaviour* **39**, 63-69.

See Also

`bouts.mle`, `bouts2.nls` for examples.

bout-misc

Fit a Broken Stick Model on Log Frequency Data for identification of bouts of behaviour

Description

Application of methods described by Sibly et al. (1990) and Mori et al. (2001) for the identification of bouts of behaviour, based on sequential differences of a variable.

Usage

```
boutfreqs(x, bw, method=c("standard", "seq.diff"), plot=TRUE)
boutinit(lnfreq, x.break, plot=TRUE)
labelBouts(x, bec, bec.method=c("standard", "seq.diff"))
logit(p)
unLogit(logit)
```

Arguments

<code>x</code>	numeric vector on which bouts will be identified based on “method”. For <code>labelBouts</code> it can also be a matrix with different variables for which bouts should be identified.
<code>bw</code>	bin width for the histogram.
<code>method</code> , <code>bec.method</code>	method used for calculating the frequencies: “standard” simply uses <code>x</code> , while “seq.diff” uses the sequential differences method.
<code>plot</code>	logical, whether to plot results or not.
<code>lnfreq</code>	data frame with components <i>lnfreq</i> (log frequencies) and corresponding <code>x</code> (mid points of histogram bins).
<code>x.break</code>	<code>x</code> value defining the break point for broken stick model, such that <code>x < xlim</code> is 1st process, and <code>x >= xlim</code> is 2nd one.
<code>bec</code>	numeric vector or matrix with values for the bout ending criterion which should be compared against the values in <code>x</code> for identifying the bouts.
<code>p</code>	vector of proportions (0-1) to transform to the logit scale.
<code>logit</code>	Logit value to transform back to original scale.

Details

This follows the procedure described in Mori et al. (2001), which is based on Sibly et al. 1990. Currently, only a two process model is supported.

`boutfreqs` creates a histogram with the log transformed frequencies of x with a chosen bin width and upper limit. Bins following empty ones have their frequencies averaged over the number of previous empty bins plus one.

`boutinit` fits a "broken stick" model to the log frequencies modelled as a function of x (well, the midpoints of the binned data), using a chosen value to separate the two processes.

`labelBouts` labels each element (or row, if a matrix) of x with a sequential number, identifying which bout the reading belongs to.

`logit` and `unLogit` are useful for reparameterizing the negative maximum likelihood function, if using Langton et al. (1995).

Value

`boutfreqs` returns a data frame with components *Infreq* containing the log frequencies and x , containing the corresponding mid points of the histogram. Empty bins are excluded. A plot is produced as a side effect if argument `plot` is TRUE. See the Details section.

`boutinit` returns a list with components `a1`, `lambda1`, `a2`, and `lambda2`, which are starting values derived from broken stick model. A plot is produced as a side effect if argument `plot` is TRUE.

`labelBouts` returns a numeric vector sequentially labelling each row or element of x , which associates it with a particular bout.

`unLogit` and `logit` return a numeric vector with the (un)transformed arguments.

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References

- Langton, S.; Collett, D. and Sibly, R. (1995) Splitting behaviour into bouts; a maximum likelihood approach. *Behaviour* **132**, 9-10.
- Luque, S.P. and Guinet, C. (2007) A maximum likelihood approach for identifying dive bouts improves accuracy, precision, and objectivity. *Behaviour*, **144**, 1315-1332.
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- Sibly, R.; Nott, H. and Fletcher, D. (1990) Splitting behaviour into bouts. *Animal Behaviour* **39**, 63-69.

See Also

[bouts2.nls](#), [bouts.mle](#).

Examples

```
data(divesSummary)
postdives <- divesSummary$postdive.dur[divesSummary$strip.no == 2]
## Remove isolated dives
postdives <- postdives[postdives < 2000]
lnfreq <- boutfreqs(postdives, bw=0.1, method="seq.diff", plot=FALSE)
boutinit(lnfreq, 50)
```

bouts2MLE

Maximum Likelihood Model of mixture of 2 Poisson Processes

Description

Functions to model a mixture of 2 random Poisson processes to identify bouts of behaviour. This follows Langton et al. (1995).

Usage

```
bouts2.mleFUN(x, p, lambda1, lambda2)
bouts2.ll(x)
bouts2.LL(x)
bouts.mle(ll.fun, start, x, ...)
bouts2.mleBEC(fit)
plotBouts2.mle(fit, x, xlab="x", ylab="Log Frequency", bec.lty=2, ...)
plotBouts2.cdf(fit, x, draw.bec=FALSE, bec.lty=2, ...)
```

Arguments

<code>x</code>	Numeric vector with values to model.
<code>p, lambda1, lambda2</code>	Parameters of the mixture of Poisson processes.
<code>ll.fun</code>	function returning the negative of the maximum likelihood function that should be maximized. This should be a valid <code>minuslogl</code> argument to <code>mle</code> .
<code>start, ...</code>	Arguments passed to <code>mle</code> . For <code>plotBouts2.cdf</code> , arguments passed to <code>plot.ecdf</code> . For <code>plotBouts2.mle</code> , arguments passed to <code>curve</code> .
<code>fit</code>	<code>mle</code> object.
<code>xlab, ylab</code>	Titles for the x and y axes.
<code>bec.lty</code>	Line type specification for drawing the BEC reference line.
<code>draw.bec</code>	Logical; do we draw the BEC?

Details

For now only a mixture of 2 Poisson processes is supported. Even in this relatively simple case, it is very important to provide good starting values for the parameters.

One useful strategy to get good starting parameter values is to proceed in 4 steps. First, fit a broken stick model to the log frequencies of binned data (see `boutinit`), to obtain estimates of 4 parameters corresponding to a 2-process model (Sibly et al. 1990). Second, calculate parameter p from the 2 alpha parameters obtained from the broken stick model, to get 3 tentative initial values for the 2-process model from Langton et al. (1995). Third, obtain MLE estimates for these 3 parameters, but using a reparameterized version of the -log L2 function. Lastly, obtain the final MLE estimates for the 3 parameters by using the estimates from step 3, un-transformed back to their original scales, maximizing the original parameterization of the -log L2 function.

`boutinit` can be used to perform step 1. Calculation of the mixing parameter p in step 2 is trivial from these estimates. Function `bouts2.LL` is a reparameterized version of the -log L2 function given by Langton et al. (1995), so can be used for step 3. This uses a logit (see `logit`) transformation of the mixing parameter p , and log transformations for both density parameters `lambda1` and `lambda2`. Function `bouts2.ll` is the -log L2 function corresponding to the un-transformed model, hence can be used for step 4.

`bouts.mle` is the function performing the main job of maximizing the -log L2 functions, and is essentially a wrapper around `mle`. It only takes the -log L2 function, a list of starting values, and the variable to be modelled, all of which are passed to `mle` for optimization. Additionally, any other arguments are also passed to `mle`, hence great control is provided for fitting any of the -log L2 functions.

In practice, step 3 does not pose major problems using the reparameterized -log L2 function, but it might be useful to use method “L-BFGS-B” with appropriate lower and upper bounds. Step 4 can be a bit more problematic, because the parameters are usually on very different scales. Therefore, it is almost always the rule to use method “L-BFGS-B”, again bounding the parameter search, as well as passing a `control` list with proper `parscale` for controlling the optimization. See `Note` below for useful constraints which can be tried.

Value

`bouts.mle` returns an object of class `mle`.
`bouts2.mleBEC` and `bouts2.mleFUN` return a numeric vector.
`bouts2.LL` and `bouts2.ll` return a function.
`plotBouts2.mle` and `plotBouts2.cdf` return nothing, but produce a plot as side effect.

Note

In the case of a mixture of 2 Poisson processes, useful values for lower bounds for the `bouts.LL` reparameterization are `c(-2, -5, -10)`. For `bouts2.ll`, useful lower bounds are `rep(1e-08, 3)`. A useful `parscale` argument for the latter is `c(1, 0.1, 0.01)`. However, I have only tested this for cases of diving behaviour in pinnipeds, so these suggested values may not be useful in other cases.

Author(s)

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References

- Langton, S.; Collett, D. and Sibly, R. (1995) Splitting behaviour into bouts; a maximum likelihood approach. *Behaviour* **132**, 9-10.
- Luque, S.P. and Guinet, C. (2007) A maximum likelihood approach for identifying dive bouts improves accuracy, precision, and objectivity. *Behaviour*, **144**, 1315-1332.
- Sibly, R.; Nott, H. and Fletcher, D. (1990) Splitting behaviour into bouts. *Animal Behaviour* **39**, 63-69.

See Also

[mle](#), [optim](#), [logit](#), [unLogit](#) for transforming and fitting a reparameterized model.

Examples

```
data(divesSummary)
postdives <- divesSummary$postdive.dur[divesSummary$strip.no == 2]
postdives.diff <- abs(diff(postdives))

## Remove isolated dives
postdives.diff <- postdives.diff[postdives.diff < 2000]
lnfreq <- boutfreqs(postdives.diff, bw=0.1, plot=FALSE)
startval <- boutinit(lnfreq, 50)
p <- startval$a1 / (startval$a1 + startval$a2)

## Fit the reparameterized (transformed parameters) model
init.parms <- list(p=logit(p), lambda1=log(startval$lambda1),
                  lambda2=log(startval$lambda2))
bout.fit1 <- bouts.mle(bouts2.LL, start=init.parms, x=postdives.diff,
                      method="L-BFGS-B", lower=c(-2, -5, -10))
coefs <- as.vector(coef(bout.fit1))

## Un-transform and fit the original parameterization
init.parms <- list(p=unLogit(coefs[1]), lambda1=exp(coefs[2]),
                  lambda2=exp(coefs[3]))
bout.fit2 <- bouts.mle(bouts2.ll, x=postdives.diff, start=init.parms,
                      method="L-BFGS-B", lower=rep(1e-08, 3),
                      control=list(parscale=c(1, 0.1, 0.01)))
plotBouts(bout.fit2, postdives.diff)

## Plot cumulative frequency distribution
plotBouts2.cdf(bout.fit2, postdives.diff)

## Estimated BEC
bec2(bout.fit2)
```

bouts2NLS

Fit mixture of 2 Poisson Processes to Log Frequency data

Description

Functions to model a mixture of 2 random Poisson processes to histogram-like data of log frequency vs interval mid points. This follows Sibly et al. (1990) method.

Usage

```
bouts2.nlsFUN(x, a1, lambda1, a2, lambda2)
bouts2.nls(lnfreq, start, maxiter)
bouts2.nlsBEC(fit)
plotBouts2.nls(fit, lnfreq, bec.lty, ...)
```

Arguments

<code>x</code>	Numeric vector with values to model.
<code>a1, lambda1, a2, lambda2</code>	Parameters from the mixture of Poisson processes.
<code>lnfreq</code>	data frame with named components <i>lnfreq</i> (log frequencies) and corresponding <i>x</i> (mid points of histogram bins).
<code>start, maxiter</code>	Arguments passed to <code>nls</code> .
<code>fit</code>	<code>nls</code> object.
<code>bec.lty</code>	Line type specification for drawing the BEC reference line.
<code>...</code>	Arguments passed to <code>plot.default</code> .

Details

`bouts2.nlsFUN` is the function object defining the nonlinear least-squares relationship in the model. It is not meant to be used directly, but is used internally by `bouts2.nls`.

`bouts2.nls` fits the nonlinear least-squares model itself.

`bouts2.nlsBEC` calculates the BEC from a list object, as the one that is returned by `nls`, representing a fit of the model. `plotBouts2.nls` plots such an object.

Value

`bouts2.nlsFUN` returns a numeric vector evaluating the mixture of 2 Poisson process.

`bouts2.nls` returns an `nls` object resulting from fitting this model to data.

`bouts2.nlsBEC` returns a number corresponding to the bout ending criterion derived from the model.

`plotBouts2.nls` plots the fitted model with the corresponding data.

Author(s)

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References

Sibly, R.; Nott, H. and Fletcher, D. (1990) Splitting behaviour into bouts Animal Behaviour **39**, 63-69.

See Also

[bouts.mle](#) for a better approach.

Examples

```
data(divesSummary)
## Postdive durations
postdives <- divesSummary$postdive.dur[divesSummary$strip.no == 2]
postdives.diff <- abs(diff(postdives))
## Remove isolated dives
postdives.diff <- postdives.diff[postdives.diff < 2000]

## Construct histogram
lnfreq <- boutfreqs(postdives.diff, bw=0.1, plot=FALSE)
startval <- boutinit(lnfreq, 50)

## Fit the 2 process model
bout.fit1 <- bouts2.nls(lnfreq, start=startval, maxiter=500)
summary(bout.fit1)
plotBouts(bout.fit1)

## Estimated BEC
bec2(bout.fit1)
```

calibrateDepth

Calibrate Depth and Generate a "TDRcalibrate" object

Description

Detect periods of major activities in a TDR record, calibrate depth readings, and generate a [TDRcalibrate](#) object essential for subsequent summaries of diving behaviour.

Usage

```
calibrateDepth(x, dry.thr=70, wet.thr=3610, dive.thr=4, offset,
               descent.crit.q=0.1, ascent.crit.q=0.1, wiggle.tol=0.8)
```

Arguments

<code>x</code>	An object of class <code>TDR</code> for <code>calibrateDepth</code> or an object of class <code>TDRcalibrate</code> for <code>calibrateSpeed</code> .
<code>dry.thr</code>	Dry error threshold in seconds. Dry phases shorter than this threshold will be considered as wet.
<code>wet.thr</code>	Wet threshold in seconds. At-sea phases shorter than this threshold will be considered as trivial wet.
<code>dive.thr</code>	Threshold depth below which an underwater phase should be considered a dive.
<code>offset</code>	Argument to <code>zoc</code> . If not provided, the offset is obtained using an interactive plot of the data.
<code>descent.crit.q</code>	Critical quantile of rates of descent below which descent is deemed to have ended.
<code>ascent.crit.q</code>	Critical quantile of rates of ascent above which ascent is deemed to have started.
<code>wiggle.tol</code>	Proportion of maximum depth above which wiggles should not be allowed to define the end of descent. It's also the proportion of maximum depth below which wiggles should be considered part of bottom phase.

Details

This function is really a wrapper around `.detPhase` and `.detDive`, which perform the work on simplified objects. It performs zero-offset correction of depth, wet/dry phase detection, and detection of dives, as well as proper labelling of the latter.

The procedure starts by first creating a factor with value "L" (dry) for rows with NAs for `depth` and value "W" (wet) otherwise. It subsequently calculates the duration of each of these phases of activity. If the duration of an dry phase ("L") is less than `dry.thr`, then the values in the factor for that phase are changed to "W" (wet). The duration of phases is then recalculated, and if the duration of a phase of wet activity is less than `wet.thr`, then the corresponding value for the factor is changed to "Z" (trivial wet). The durations of all phases are recalculated a third time to provide final phase durations.

The next step is to detect dives whenever the zero-offset corrected depth in an underwater phase is below the supplied dive threshold. A new factor with finer levels of activity is thus generated, including "U" (underwater), and "D" (diving) in addition to the ones described above.

Once dives have been detected and assigned to a period of wet activity, phases within dives are detected using the descent, ascent and wiggle criteria. This procedure generates a factor with levels "D", "DB", "B", "BA", "A", "DA", and "X", breaking the input into descent, descent/bottom, bottom, bottom/ascent, ascent, and non-dive, respectively.

Value

An object of class `TDRcalibrate`.

Author(s)

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See Also

[TDRcalibrate](#), [zoc](#)

Examples

```
data(divesTDR)
divesTDR

## Consider a 3 m offset, and a dive threshold of 3 m
dcalib <- calibrateDepth(divesTDR, dive.thr=3, offset=3)
if (dev.interactive (orNone=TRUE)) {
  plotTDR(dcalib, labels="dive.phase", surface=TRUE)
}
```

calibrateSpeed

Calibrate and build a "TDRcalibrate" object

Description

These functions create a [TDRcalibrate](#) object which is necessary to obtain dive summary statistics.

Usage

```
calibrateSpeed(x, tau=0.1, contour.level=0.1, z=0, bad=c(0, 0),
  main=slot(getTDR(x), "file"), coefs, plot=TRUE,
  postscript=FALSE, ...)
```

Arguments

<code>x</code>	An object of class TDR for calibrateDepth or an object of class TDRcalibrate for calibrateSpeed .
<code>tau</code>	Quantile on which to regress speed on rate of depth change; passed to rq .
<code>contour.level</code>	The mesh obtained from the bivariate kernel density estimation corresponding to this contour will be used for the quantile regression to define the calibration line.
<code>z</code>	Only changes in depth larger than this value will be used for calibration.
<code>bad</code>	Length 2 numeric vector indicating that only rates of depth change and speed greater than the given value should be used for calibration, respectively.
<code>coefs</code>	Known speed calibration coefficients from quantile regression as a vector of length 2 (intercept, slope). If provided, these coefficients are used for calibrating speed, ignoring all other arguments, except <code>x</code> .
<code>main, ...</code>	Arguments passed to rqPlot .
<code>plot</code>	Logical indicating whether to plot the results.
<code>postscript</code>	Logical indicating whether to produce postscript file output.

Details

This calibrates speed readings following the procedure outlined in Blackwell et al. (1999).

Value

An object of class `TDRcalibrate`.

Author(s)

Sebastian P. Luque (spluque@gmail.com)

References

Blackwell S, Haverl C, Le Boeuf B, Costa D (1999). A method for calibrating swim-speed recorders. *Marine Mammal Science* 15(3):894-905.

See Also

`TDRcalibrate`

Examples

```
data(divesTDRcalibrate)
divesTDRcalibrate

## Calibrate speed using only changes in depth > 2 m
vcalib <- calibrateSpeed(divesTDRcalibrate, z=2)
vcalib
```

detDive-internal	<i>Detect dives from depth readings</i>
------------------	---

Description

Identify dives in TDR records based on a dive threshold.

Usage

```
.detDive(zdepth, act, dive.thr=4, ...)
```

Arguments

<code>zdepth</code>	Vector of zero-offset corrected depths.
<code>act</code>	Factor as long as <code>depth</code> coding activity, with levels specified as in <code>.detPhase</code> .
<code>dive.thr</code>	Threshold depth below which an underwater phase should be considered a dive.
<code>...</code>	The sampling interval in seconds.

Value

A data frame with the following elements for `.detDive`

<code>dive.id</code>	Numeric vector numbering each dive in the record.
<code>dive.activity</code>	Factor with levels “L”, “W”, “U”, “D”, and “Z”, see <code>.detPhase</code> . All levels may be represented.
<code>postdive.id</code>	Numeric vector numbering each postdive interval with the same value as the preceding dive.

Author(s)

Sebastian P. Luque (spluque@gmail.com)

See Also

[.detPhase](#), [zoc](#)

`detPhase-internal` *Detect phases of activity from depth readings*

Description

Functions to identify sections of a TDR record displaying one of three possible activities: dry, wet, and trivial wet.

Usage

```
.detPhase(time, depth, dry.thr, wet.thr, ...)
```

Arguments

<code>time</code>	POSIXct object with date and time for all depths.
<code>depth</code>	Numeric vector with depth readings.
<code>dry.thr</code> , <code>wet.thr</code>	Passed from calibrateDepth .
<code>...</code>	Passed from calibrateDepth ; sampling interval in seconds.

Details

`.detPhase` first creates a factor with value “L” (dry) for rows with NAs for depth and value “W” (wet) otherwise. It subsequently calculates the duration of each of these phases of activity. If the duration of an dry phase (“L”) is less than `dry.thr`, then the values in the factor for that phase are changed to “W” (wet). The duration of phases is then recalculated, and if the duration of a phase of wet activity is less than `wet.thr`, then the corresponding value for the factor is changed to “Z” (trivial wet). The durations of all phases are recalculated a third time to provide final phase durations.

Value

A list with components:

<code>phase.id</code>	Numeric vector identifying each activity phase, starting from 1 for every input record.
<code>activity</code>	Factor with levels “L” indicating dry, “W” indicating wet, “U” for underwater (above dive criterion), “D” for diving, “Z” for trivial wet animal activities. Only “L”, “W”, and “Z” are actually represented.
<code>begin</code>	A <code>POSIXct</code> object as long as the number of unique activity phases identified, indicating the start times for each activity phase.
<code>end</code>	A <code>POSIXct</code> object as long as the number of unique activity phases identified, indicating the end times for each activity phase.

Author(s)

Sebastian P. Luque (spluque@gmail.com) and Andy Liaw.

See Also

`.detDive`

<code>distSpeed</code>	<i>Calculate distance and speed between locations</i>
------------------------	---

Description

Calculate distance, time difference, and speed between pairs of points defined by latitude and longitude, given the time at which all points were measured.

Usage

```
distSpeed(pt1, pt2)
```

Arguments

<code>pt1</code>	A matrix or data frame with three columns; the first a <code>POSIXct</code> object with dates and times for all points, the second and third numeric vectors of longitude and latitude for all points, respectively, in decimal degrees.
<code>pt2</code>	A matrix with the same size and structure as <code>pt1</code> .

Value

A matrix with three columns: distance (km), time difference (s), and speed (m/s).

Author(s)

Sebastian P. Luque (spluque@gmail.com)

Examples

```
locs <- readLocs(system.file(file.path("data", "sealLocs.csv"),
                             package="diveMove"), idCol=1, dateCol=2,
                 dtformat="%Y-%m-%d %H:%M:%S", classCol=3, lonCol=4,
                 latCol=5)

## Travel summary between successive standard locations
locs.std <- subset(locs, subset=class == "0" | class == "1" |
                  class == "2" | class == "3" &
                  !is.na(lon) & !is.na(lat))
locs.std.tr <- by(locs.std, locs.std$id, function(x) {
  distSpeed(x[-nrow(x), 3:5], x[-1, 3:5])
})
lapply(locs.std.tr, head)

## Particular quantiles from travel summaries
lapply(locs.std.tr, function(x) {
  quantile(x[, 3], seq(0.90, 0.99, 0.01), na.rm=TRUE) # speed
})
lapply(locs.std.tr, function(x) {
  quantile(x[, 1], seq(0.90, 0.99, 0.01), na.rm=TRUE) # distance
})

## Travel summary between arbitrary two sets of points
distSpeed(locs[c(1, 5, 10), 3:5], locs[c(25, 30, 35), 3:5])
```

diveMove-internal *Internal diveMove Functions*

Description

Functions used for very particular tasks within larger functions in diveMove

Usage

```
.diveIndices(diveID, diveNo)
.getInterval(time)
.speedStats(x, vdist)
.night(time, sunrise.time, sunset.time)
.rleActivity(time, act, interval)
.speedCol(x)
```

Arguments

diveID	Numeric vector of all dive and non dive IDs.
diveNo	Numeric vector of unique dive indices to extract from diveID.

<code>time</code>	POSIXct object representing time.
<code>x</code>	For <code>.speedStats</code> , a matrix with a dive's section data (time, speed). A single dive's data, a 3-col matrix with time, depth, and speed. For <code>.speedCol</code> , a data frame where names are searched for strings matching <code>.speedNames</code> (see Details).
<code>vdist</code>	Vertical distance travelled during this time. If <code>vdist</code> is missing, then it's all horizontal movements (no angles).
<code>sunrise.time, sunset.time</code>	Passed from <code>plotTD</code> .
<code>act</code>	A numeric vector indicating the activity for every element of <code>time</code> .
<code>interval</code>	Sampling interval in seconds.

Details

These functions are not meant to be called directly by the user, as he/she could not care less (right?). This may change in the future.

`.speedNames` is a character vector with possible names for a speed vector.

`.rleActivity` takes a factor indicating different activity phases, their associated time, and the sampling interval to return a factor uniquely identifying each phase of activity, i.e. labelling them. In addition, it returns the duration of each phase, and their beginning and end times.

Value

`.diveIndices` returns a numeric vector with the indices of dives (and their beginning/end indices) in `diveID`.

`.getInterval` returns a scalar, the mode of intervals between time readings.

`.speedStats` returns a 3-column matrix with total distance, mean speed, and angle for a section of a dive.

`.night` returns a list with sunrise and sunset times for dates in `time`.

`.speedCol` returns column number where speed is located in `x`.

`.rleActivity` returns a list with components:

`time.br` A factor dividing `act` into different periods of activity.

`time.peract` The duration of each period of activity.

`beg.time, end.time` POSIXct objects indicating the beginning and ending times of each period of activity.

Author(s)

Sebastian P. Luque (spluque@gmail.com)

Description

This package is a collection of functions for visualizing, and analyzing depth and speed data from time-depth recorders TDRs. These can be used to zero-offset correct depth, calibrate speed, and divide the record into different phases, or time budget. Functions are provided for calculating summary dive statistics for the whole record, or at smaller scales within dives.

Author(s)

Sebastian P. Luque (spluque@gmail.com)

See Also

A vignette with a guide to this package is available by doing `'vignette("diveMove")'`. [TDR-class](#), [calibrateDepth](#), [calibrateSpeed](#), [timeBudget](#), [stampDive](#).

Examples

```
## read in data and create a TDR object
(sealX <- readTDR(system.file(file.path("data", "dives.csv"),
                                package="diveMove"), speed=TRUE))

if (dev.interactive(orElse=TRUE)) plotTDR(sealX) # interactively pan and zoom

## detect periods of activity, and calibrate depth, creating
## a 'TDRcalibrate' object
if (dev.interactive(orElse=TRUE)) dcalib <- calibrateDepth(sealX)
(dcalib <- calibrateDepth(sealX, offset=3)) # zero-offset correct at 3 m

if (dev.interactive(orElse=TRUE)) {
  ## plot all readings and label them with the phase of the record
  ## they belong to, excluding surface readings
  plotTDR(dcalib, labels="phase.id", surface=FALSE)
  ## plot the first 300 dives, showing dive phases and surface readings
  plotTDR(dcalib, diveNo=seq(300), labels="dive.phase", surface=TRUE)
}

## calibrate speed (using changes in depth > 1 m and default remaining arguments)
(vcalib <- calibrateSpeed(dcalib, z=1))

## Obtain dive statistics for all dives detected
dives <- diveStats(vcalib)
head(dives)

## Attendance table
att <- timeBudget(vcalib, FALSE) # taking trivial aquatic activities into account
att <- timeBudget(vcalib, TRUE)  # ignoring them
```

```
## Add trip stamps to each dive
stamps <- stampDive(vcalib)
sumtab <- data.frame(stamps, dives)
head(sumtab)
```

dives

Sample of TDR data from a fur seal

Description

This data set is meant to show a typical organization of a TDR *.csv file, suitable as input for [readTDR](#), or to construct a [TDR](#) object. `divesTDR` and `divesTDRcalibrate` are example [TDR](#) and [TDRcalibrate](#) objects.

Format

A comma separated value (csv) file with 69560 TDR readings with the following columns:

`date` Date

`time` Time

`depth` Depth in m

`light` Light level

`temperature` Temperature in C

`speed` Speed in m/s

The data are also provided as a [TDR](#) object (*.RData format) for convenience.

Details

The data are a subset of an entire TDR record, so they are not meant to make valid inferences from this particular individual/deployment.

`divesTDR` is a [TDR](#) object representation of the data in `dives`.

`divesTDRcalibrate` is a [TDRcalibrate](#) object representing the data in `dives`, calibrated at default criteria (see [calibrateDepth](#)), and 3 m offset.

`divesSummary` is a data frame containing a summary of all dives in this dataset (see [diveStats](#) and [stampDive](#) for the information contained in this object).

Source

Sebastian P. Luque, Christophe Guinet, John P.Y. Arnould

See Also

[readTDR](#), [diveStats](#).

Examples

```
dives <- read.csv(system.file(file.path("data", "dives.csv"),
                                     package="diveMove"))
str(dives)
```

diveStats	<i>Per-dive statistics</i>
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Description

Calculate dive statistics in TDR records.

Usage

```
diveStats(x)
oneDiveStats(x, interval, speed=FALSE)
stampDive(x, ignoreZ=TRUE)
```

Arguments

x	A TDRcalibrate-class object for diveStats and stampDive, and a data frame containing a single dive's data (a factor identifying the dive phases, a POSIXct object with the time for each reading, a numeric depth vector, and a numeric speed vector) for oneDiveStats.
interval	Sampling interval for interpreting x.
speed	Logical; should speed statistics be calculated?
ignoreZ	Logical indicating whether trips should be numbered considering all aquatic activities ("W" and "Z") or ignoring "Z" activities.

Details

diveStats calculates various dive statistics based on time and depth for an entire TDR record. oneDiveStats obtains these statistics from a single dive, and stampDive stamps each dive with associated trip information.

Value

A [data.frame](#) with one row per dive detected (durations are in s, and linear variables in m):

begdesc	A POSIXct object, specifying the start time of each dive.
enddesc	A POSIXct object, as begdesc indicating descent's end time.
begasc	A POSIXct object, as begdesc indicating the time ascent began.
desctim	Descent duration of each dive.
botttim	Bottom duration of each dive.

<code>asctim</code>	Ascent duration of each dive.
<code>descdist</code>	Numeric vector with descent depth.
<code>botttdist</code>	Numeric vector with the sum of absolute depth differences while at the bottom of each dive; measure of amount of “wiggling” while at bottom.
<code>ascdist</code>	Numeric vector with ascent depth.
<code>desc.tdist</code>	Numeric vector with descent total distance, estimated from speed.
<code>desc.mean.speed</code>	Numeric vector with descent mean speed.
<code>desc.angle</code>	Numeric vector with descent angle, from the surface plane.
<code>bott.tdist</code>	Numeric vector with bottom total distance, estimated from speed.
<code>bott.mean.speed</code>	Numeric vector with bottom mean speed.
<code>asc.tdist</code>	Numeric vector with ascent total distance, estimated from speed.
<code>asc.mean.speed</code>	Numeric vector with ascent mean speed.
<code>asc.angle</code>	Numeric vector with ascent angle, from the bottom plane.
<code>divetim</code>	Dive duration.
<code>maxdep</code>	Numeric vector with maximum depth.
<code>postdive.dur</code>	Postdive duration.
<code>postdive.tdist</code>	Numeric vector with postdive total distance, estimated from speed.
<code>postdive.mean.speed</code>	Numeric vector with postdive mean speed.

The number of columns depends on the value of speed.

`stampDive` returns a data.frame with trip number, trip type, and start and end times for each dive.

Author(s)

Sebastian P. Luque (spluque@gmail.com)

See Also

`.detPhase`, `zoc`, `TDRcalibrate-class`

Examples

```
data(divesTDRcalibrate)
divesTDRcalibrate

tdrX <- diveStats(divesTDRcalibrate)
stamps <- stampDive(divesTDRcalibrate, ignoreZ=TRUE)
tdrX.tab <- data.frame(stamps, tdrX)
summary(tdrX.tab)
```

`extractDive-methods`*Extract Dives from "TDR" or "TDRcalibrate" Objects*

Description

Extract data corresponding to a particular dive(s), referred to by number.

Usage

```
## S4 method for signature 'TDR, numeric, numeric':  
extractDive(obj, diveNo, id)  
## S4 method for signature 'TDRcalibrate, numeric,  
##      missing':  
extractDive(obj, diveNo)
```

Arguments

<code>obj</code>	TDR object.
<code>diveNo</code>	Numeric vector or scalar with dive numbers to extract.
<code>id</code>	Numeric vector of dive numbers from where <code>diveNo</code> should be chosen.

Value

An object of class [TDR](#) or [TDRspeed](#).

Author(s)

Sebastian P. Luque (spluque@gmail.com)

Examples

```
data(divesTDR)  
divesTDR  
data(divesTDRcalibrate)  
divesTDRcalibrate  
  
diveX <- extractDive(divesTDR, 9, getDAct(divesTDRcalibrate, "dive.id"))  
plotTDR(diveX, interact=FALSE)  
  
diveX <- extractDive(divesTDRcalibrate, 5:10)  
plotTDR(diveX, interact=FALSE)
```

labDive-internal *Internal Functions used for Detection of Dives*

Description

These functions provide information for particular dives,

Usage

```
.cutDive(x, descent.crit.q, ascent.crit.q, wiggle.tol)
.labDive(act, string, interval)
.labDivePhase(x, diveID, descent.crit.q, ascent.crit.q, wiggle.tol)
```

Arguments

x	For .labDivePhase, a class TDR object. For .cutDive, a 3-col matrix with subscript in original TDR object, non NA depths, and numeric vector representing POSIXct times.
descent.crit.q, ascent.crit.q, wiggle.tol	Passed from calibrateDepth.
act	Factor with values to label.
string	A character belonging to a level of act to search for and label sequentially.
interval	The sampling interval in seconds.
diveID	Numeric vector indexing each dive (non-dives should be 0)

Details

These functions are for internal use and are not meant to be called by the user.

Value

.labDive returns a matrix with as many rows as its first two arguments with two columns: dive.id, and postdive.id, each one sequentially numbering each dive and postdive period.

.labDivePhase returns a factor with levels “D”, “DB”, “B”, “BA”, “A”, “DA”, and “X”, breaking the input into descent, descent/bottom, bottom, bottom/ascent, ascent, and non-dive, respectively. If x contains no dives, only level “X” is present for all readings.

.cutDive generates a character vector that breaks a dive into descent, descent/bottom, bottom, bottom/ascent, ascent, and/or descent/ascent given a proportion of maximum depth for bottom time. It return a character matrix with orig ID and corresponding label.

Author(s)

Sebastian P. Luque (spluque@gmail.com)

plotTDR-methods	<i>Methods for plotting objects of class "TDR", "TDRspeed", and "TDRcalibrate"</i>
-----------------	--

Description

Main plotting method for objects of these classes.

Usage

```
## S4 method for signature 'TDR':
plotTDR(x, ...)
## S4 method for signature 'TDRspeed':
plotTDR(x, concurVars, concurVarTitles, ...)
## S4 method for signature 'TDRcalibrate':
plotTDR(x, diveNo=seq(max(getDAct(x, "dive.id"))),
        labels="phase.id", concurVars, surface=FALSE, ...)
```

Arguments

<code>x</code>	<code>TDR</code> , <code>TDRspeed</code> , or <code>TDRcalibrate</code> object.
<code>concurVars</code> , <code>concurVarTitles</code> , ...	Arguments passed to <code>plotTD</code> . For the <code>TDRspeed</code> method, <code>concurVars</code> is a matrix with variables to plot, in addition to speed, if any. <code>concurVarTitles</code> in this case is a character vector with axis labels for speed and the additional variables supplied in <code>concurVars</code> . For the <code>TDRcalibrate</code> method, <code>concurVars</code> is a character vector indicating which additional components from the concurrent data frame should also be plotted, if any.
<code>diveNo</code>	Numeric vector with dive numbers to plot.
<code>labels</code>	One of “phase.id” or “dive.phase”, specifying whether to label observations based on the gross phase ID of the <code>TDR</code> object, or based on each dive phase, respectively.
<code>surface</code>	Logical indicating whether to plot surface readings.

Value

If called with the `interact` argument set to `TRUE`, returns coordinates from the ZOC procedure (see `zoc`).

Methods

plotTDR signature (`x`="TDR"): interactive graphical display of the data, with zooming and panning capabilities.

plotTDR signature (`x`="TDRspeed"): As the `TDR` method, but also plots the concurrent speed readings.

plotTDR signature (`x`="TDRcalibrate"): plot the `TDR` object, labelling identified sections of it (see `Usage`).

Author(s)

Sebastian P. Luque (spluque@gmail.com)

See Also

[zoc](#)

Examples

```
data(divesTDR)
divesTDR

plotTDR(divesTDR, interact=FALSE)

data(divesTDRcalibrate)
divesTDRcalibrate

plotTDR(divesTDRcalibrate, interact=FALSE)
plotTDR(divesTDRcalibrate, diveNo=19:25, interact=FALSE)
plotTDR(divesTDRcalibrate, labels="dive.phase", interact=FALSE)
```

readLocs	<i>Read comma-delimited file with location data</i>
----------	---

Description

Read a comma delimited (*.csv) file with (at least) time, latitude, longitude readings.

Usage

```
readLocs(file, loc.idCol, idCol, dateCol, timeCol=NULL,
         dtformat="%m/%d/%Y %H:%M:%S", tz="GMT",
         classCol, lonCol, latCol, alt.lonCol=NULL, alt.latCol=NULL, ...)
```

Arguments

file	A string indicating the name of the file to read. Provide the entire path if the file is not on the current directory.
loc.idCol	Column number containing location ID. If missing, a loc.id column is generated with sequential integers as long as the input.
idCol	Column number containing an identifier for locations belonging to different groups. If missing, an id column is generated with number one repeated as many times as the input.
dateCol	Column number containing dates, and, optionally, times.
timeCol	Column number containing times.

<code>dtformat</code>	A string, specifying the format in which the date and time columns, when pasted together, should be interpreted (see <code>strptime</code>) in <code>file</code> .
<code>tz</code>	A string indicating the time zone for the date and time readings.
<code>lonCol</code>	Column number containing longitude readings.
<code>latCol</code>	Column number containing latitude readings.
<code>classCol</code>	Column number containing the ARGOS rating for each location.
<code>alt.lonCol</code>	Column number containing alternative longitude readings.
<code>alt.latCol</code>	Column number containing alternative latitude readings.
<code>...</code>	Passed to <code>read.csv</code>

Details

The file must have a header row identifying each field, and all rows must be complete (i.e. have the same number of fields). Field names need not follow any convention.

Value

A data frame.

Author(s)

Sebastian P. Luque (spluque@gmail.com)

Examples

```
locs <- readLocs(system.file(file.path("data", "sealLocs.csv"),
                             package="diveMove"), idCol=1, dateCol=2,
                 dtformat="%Y-%m-%d %H:%M:%S",
                 classCol=3, lonCol=4, latCol=5)

summary(locs)
```

`readTDR`

Read comma-delimited file with "TDR" data

Description

Read a comma delimited (*.csv) file containing time-depth recorder (*TDR*) data from various TDR models. Return a TDR or TDRspeed object. `createTDR` creates an object of one of these classes from other objects.

Usage

```
readTDR(file, dateCol=1, timeCol=2, depthCol=3, speed=FALSE,
        subsamp=5, concurrentCols=4:6,
        dtformat="%d/%m/%Y %H:%M:%S", tz="GMT")
createTDR(time, depth, concurrentData=data.frame(), speed=FALSE, dtime, file)
```

Arguments

<code>file</code>	A string indicating the path to the file to read.
<code>dateCol</code>	Column number containing dates, and optionally, times.
<code>timeCol</code>	Column number with times.
<code>depthCol</code>	Column number containing depth readings.
<code>speed</code>	For <code>readTDR</code> : Logical indicating whether speed is included in one of the columns of <code>concurrentCols</code> .
<code>subsamp</code>	Subsample rows in <code>file</code> with <code>subsamp</code> interval, in s.
<code>concurrentCols</code>	Column numbers to include as concurrent data collected.
<code>dtformat</code>	A string, specifying the format in which the date and time columns, when pasted together, should be interpreted (see <code>strptime</code>).
<code>tz</code>	A string indicating the time zone assumed for the date and time readings.
<code>time</code>	A <code>POSIXct</code> object with date and time readings for each reading.
<code>depth</code>	Numeric vector with depth readings.
<code>concurrentData</code>	Data frame with additional, concurrent data collected.
<code>dtime</code>	Sampling interval used in seconds. If missing, it is calculated from the <code>time</code> argument.

Details

The input file is assumed to have a header row identifying each field, and all rows must be complete (i.e. have the same number of fields). Field names need not follow any convention. However, depth and speed are assumed to be in m, and $m \cdot s^{-1}$, respectively, for further analyses.

If `speed` is `TRUE` and `concurrentCols` contains a column named `speed` or `velocity`, then an object of class `TDRspeed` is created, where `speed` is considered to be the column matching this name.

Value

An object of class `TDR` or `TDRspeed`.

Note

Although `TDR` and `TDRspeed` classes check that time stamps are in increasing order, the integrity of the input must be thoroughly verified for common errors present in text output from TDR devices such as duplicate records, missing time stamps and non-numeric characters in numeric fields. These errors are much more efficiently dealt with outside of GNU R using tools like GNU `awk` or GNU `sed`, so `diveMove` does not currently attempt to fix these errors.

Author(s)

Sebastian P. Luque (spluque@gmail.com)

Examples

```
readTDR(system.file(file.path("data", "dives.csv"),
                      package="diveMove"), speed=TRUE)

## Or more pedestrian
tdrX <- read.csv(system.file(file.path("data", "dives.csv"),
                                package="diveMove"), na.strings="", as.is=TRUE)
date.time <- paste(tdrX$date, tdrX$time)
tdr.time <- as.POSIXct(strptime(date.time, format="%d/%m/%Y %H:%M:%S"),
                      tz="GMT")
createTDR(tdr.time, tdrX$depth, concurrentData=data.frame(speed=tdrX$speed),
          file="dives.csv", speed=TRUE)
```

rqPlot

Plot of quantile regression for speed calibrations

Description

Plot of quantile regression for assessing quality of speed calibrations

Usage

```
rqPlot(rddepth, speed, z, contours, rqFit, main="qtRegression",
       xlab="rate of depth change (m/s)", ylab="speed (m/s)",
       colramp=colorRampPalette(c("white", "darkblue")),
       col.line="red", cex.pts=1)
```

Arguments

speed	Speed in m/s.
rddepth	Numeric vector with rate of depth change.
z	A list with the bivariate kernel density estimates (1st component the x points of the mesh, 2nd the y points, and 3rd the matrix of densities).
contours	List with components: <code>pts</code> which should be a matrix with columns named <code>x</code> and <code>y</code> , <code>level</code> a number indicating the contour level the points in <code>pts</code> correspond to.
rqFit	Object of class "rq" representing a quantile regression fit of rate of depth change on mean speed.
main	String; title prefix to include in ouput plot.
xlab, ylab	axis labels.
colramp	Function taking an integer <code>n</code> as an argument and returning <code>n</code> colors.
col.line	Color to use for the regression line.
cex.pts	A numerical value specifying the amount by which to enlarge the size of points.

Description

Basic methods for manipulating objects of class [TDR](#).

Show Methods

show signature(object="TDR"): print an informative summary of the data.

Coerce Methods

as.data.frame signature(x="TDR"): Coerce object to data.frame. This method returns a data frame, with attributes "file" and "dtime" indicating the source file and the interval between samples.

as.data.frame signature(x="TDRspeed"): Coerce object to data.frame. Returns an object as for [TDR](#) objects.

as.TDRspeed signature(x="TDR"): Coerce object to [TDRspeed](#) class.

Extractor Methods

[signature(x="TDR"): Subset a TDR object; these objects can be subsetted on a single index *i*. Selects given rows from object.

getDepth signature(x = "TDR"): depth slot accessor.

getCCData signature(x="TDR", y="missing"): concurrentData slot accessor.

getCCData signature(x="TDR", y="character"): access component named y in x.

getTime signature(x = "TDR"): sampling interval accessor.

getFileName signature(x="TDR"): source file name accessor.

getTime signature(x = "TDR"): time slot accessor.

getSpeed signature(x = "TDRspeed"): speed accessor for TDRspeed objects.

Replacement Methods

depth<- signature(x="TDR"): depth replacement.

speed<- signature(x="TDR"): speed replacement.

ccData<- signature(x="TDR"): concurrent data frame replacement.

Author(s)

Sebastian P. Luque (spluque@gmail.com)

See Also

[extractDive](#), [plotTD](#).

Examples

```
data(divesTDR)

## Retrieve the name of the source file
getFileName(divesTDR)
## Retrieve concurrent temperature measurements
temp <- getCCData(divesTDR, "temperature")

## Coerce to a data frame
dives.df <- as.data.frame(divesTDR)
head(dives.df)

## Replace speed measurements
newspeed <- getSpeed(divesTDR) + 2
speed(divesTDR) <- newspeed
```

TDRcalibrate-accessors

*Methods to Show and Extract Basic Information from "TDRcalibrate"
Objects*

Description

Plot, print summaries and extract information from [TDRcalibrate](#) objects.

Usage

```
## S4 method for signature 'TDRcalibrate, missing':
getDAct(x)
## S4 method for signature 'TDRcalibrate, character':
getDAct(x, y)
## S4 method for signature 'TDRcalibrate, missing':
getDPhaseLab(x)
## S4 method for signature 'TDRcalibrate, numeric':
getDPhaseLab(x, diveNo)
## S4 method for signature 'TDRcalibrate, missing':
getGAct(x)
## S4 method for signature 'TDRcalibrate, character':
getGAct(x, y)
```

Arguments

<code>x</code>	TDRcalibrate object.
<code>diveNo</code>	numeric vector with dive numbers to plot.
<code>y</code>	string; “dive.id”, “dive.activity”, or “postdive.id” in the case of <code>getDAct</code> , to extract the numeric dive ID, the factor identifying dive phases in each dive, or the numeric postdive ID, respectively. In the case of <code>getGAct</code> it should be

one of "phase.id", "activity", "begin", or "end", to extract the numeric phase ID for each observation, a factor indicating what major activity the observation corresponds to, or the beginning and end times of each phase in the record, respectively.

Value

The extractor methods return an object of the same class as elements of the slot they extracted.

Show Methods

`show` signature (object="TDRcalibrate"): prints an informative summary of the data.

Extractor Methods

getDAct signature (x="TDRcalibrate", y="missing"): this accesses the `dive.activity` slot of [TDRcalibrate](#) objects. Thus, it extracts a data frame with vectors identifying all readings to a particular dive and postdive number, and a factor identifying all readings to a particular activity.

getDAct signature (x="TDRcalibrate", y = "character"): as the method for missing y, but selects a particular vector to extract. See [TDRcalibrate](#) for possible strings.

getDPhaseLab signature (x="TDRcalibrate", diveNo = "missing"): extracts a factor identifying all readings to a particular dive phase. This accesses the `dive.phases` slot of [TDRcalibrate](#) objects, which is a factor.

getDPhaseLab signature (x="TDRcalibrate", diveNo = "numeric"): as the method for missing y, but selects data from a particular dive number to extract.

getGAct signature (x="TDRcalibrate", y="missing"): this accesses the `gross.activity` slot of [TDRcalibrate](#) objects, which is a named list. It extracts elements that divide the data into major wet and dry activities.

getGAct signature (x="TDRcalibrate", y="character"): as the method for missing y, but extracts particular elements.

getTDR signature (x="TDRcalibrate"): this accesses the `tdr` slot of [TDRcalibrate](#) objects, which is a [TDR](#) object.

getSpeedCoef signature (x="TDRcalibrate"): this accesses the `speed.calib.coefs` slot of [TDRcalibrate](#) objects; the speed calibration coefficients.

Author(s)

Sebastian P. Luque (spluque@gmail.com)

Examples

```
data(divesTDRcalibrate)

divesTDRcalibrate          # show

## Beginning times of each successive phase in record
```

```

getGAct(divesTDRcalibrate, "begin")

## Factor of dive IDs
dids <- getDAct(divesTDRcalibrate, "dive.id")
table(dids[dids > 0])           # samples per dive

## Factor of dive phases for given dive
getDPhaseLab(divesTDRcalibrate, 19)

```

TDRcalibrate-class *Class "TDRcalibrate" for dive analysis*

Description

This class holds information produced at various stages of dive analysis. Methods are provided for extracting data from each slot.

Details

This is perhaps the most important class in `diveMove`, as it holds all the information necessary for calculating requested summaries for a TDR.

Objects from the Class

Objects can be created by calls of the form `new("TDRcalibrate", ...)`. The objects of this class contain information necessary to divide the record into sections (e.g. dry/water), dive/surface, and different sections within dives. They also contain the parameters used to calibrate speed and criteria to divide the record into phases.

Slots

tdr: Object of class `TDR`.

This slot contains the time, zero-offset corrected depth, and possibly a data frame. If the object is also of class `"TDRspeed"`, then the data frame might contain calibrated or uncalibrated speed. See `readTDR` and the accessor function `getTDR` for this slot.

gross.activity: Object of class `'list'`.

This slot holds a list of the form returned by `.detPhase`, composed of 4 elements. It contains a vector (named `phase.id`) numbering each major activity phase found in the record, a factor (named `activity`) labelling each row as being dry, wet, or trivial wet activity. These two elements are as long as there are rows in `tdr`. This list also contains two more vectors, named `begin` and `end`: one with the beginning time of each phase, and another with the ending time; both represented as `POSIXct` objects. See `.detPhase`.

dive.activity: Object of class `'data.frame'`.

This slot contains a data.frame of the form returned by `.detDive`, with as many rows as those in `tdr`, consisting of three vectors named: `dive.id`, which is an integer vector, sequentially numbering each dive (rows that are not part of a dive are labelled 0), `dive.activity` is

a factor which completes that in `activity` above, further identifying rows in the record belonging to a dive. The third vector in `dive.activity` is an integer vector sequentially numbering each postdive interval (all rows that belong to a dive are labelled 0). See `.detDive`, and `getDAct` to access all or any one of these vectors.

dive.phases: Object of class 'factor'. must be the same as value returned by `.labDivePhase`.

This slot is a factor that labels each row in the record as belonging to a particular phase of a dive. It has the same form as objects returned by `.labDivePhase`.

dry.thr: Object of class 'numeric' the temporal criteria used for detecting dry periods that should be considered as wet.

wet.thr: Object of class 'numeric' the temporal criteria used for detecting periods wet that should not be considered as foraging time.

dive.thr: Object of class 'numeric' the criteria used for defining a dive.

speed.calib.coefs: Object of class 'numeric' the intercept and slope derived from the speed calibration procedure. Defaults to `c(0, 1)` meaning uncalibrated speeds.

Author(s)

Sebastian P. Luque (spluque@gmail.com)

See Also

[TDR](#) for links to other classes in the package. [TDRcalibrate-methods](#) for the various methods available.

TDR-class

Classes "TDR" and "TDRspeed" for representing TDR information

Description

These classes store information gathered by time-depth recorders.

Details

Since the data to store in objects of these classes usually come from a file, the easiest way to construct such objects is with the function `readTDR` to retrieve all the necessary information. The methods listed above can thus be used to access all slots.

Objects from the Class

Objects can be created by calls of the form `new("TDR", ...)` and `new("TDRspeed", ...)`.

'TDR' objects contain concurrent time and depth readings, as well as a string indicating the file the data originates from, and a number indicating the sampling interval for these data. 'TDRspeed' extends 'TDR' objects containing additional concurrent speed readings.

Slots

In class *TDR*:

file: Object of class 'character', string indicating the file where the data comes from.

dtime: Object of class 'numeric', sampling interval in seconds.

time: Object of class *POSIXct*, time stamp for every reading.

depth: Object of class 'numeric', depth (m) readings.

concurrentData: Object of class *data.frame*, optional data collected concurrently.

Class 'TDRspeed' must also satisfy the condition that a component of the concurrentData slot is named speed or velocity, containing the measured speed, a vector of class 'numeric' containing speed measurements in (m/s) readings.

Author(s)

Sebastian P. Luque (spluque@gmail.com)

See Also

[readTDR](#), [TDRcalibrate](#).

timeBudget-methods *Describe the Time Budget of Major Activities from "TDRcalibrate" object.*

Description

Summarize the major activities recognized into a time budget.

Usage

```
## S4 method for signature 'TDRcalibrate, logical':
timeBudget(obj, ignoreZ)
```

Arguments

obj [TDRcalibrate](#) object.

ignoreZ Logical indicating whether to ignore trivial aquatic periods.

Details

Ignored trivial aquatic periods are collapsed into the enclosing dry period.

Value

A data frame with components:

<code>phaseno</code>	A numeric vector numbering each period of activity.
<code>activity</code>	A factor labelling the period with the corresponding activity.
<code>beg, end</code>	<code>POSIXct</code> objects indicating the beginning and end of each period.

Author(s)

Sebastian P. Luque (spluque@gmail.com)

See Also

`calibrateDepth`

Examples

```
data(divesTDRcalibrate)

timeBudget(divesTDRcalibrate, TRUE)
```

`zoc`

Interactive zero-offset correction of "TDR" data

Description

Correct zero-offset in TDR records, with the aid of a graphical user interface (GUI), allowing for dynamic selection of offset and multiple time windows to perform the adjustment.

Usage

```
zoc(time, depth, offset)
plotTD(time, depth, concurVars=NULL, xlim=NULL, depth.lim=NULL,
        xlab="time (dd-mmm hh:mm)", ylab.depth="depth (m)",
        concurVarTitles=deparse(substitute(concurVars)),
        xlab.format="%d-%b %H:%M", sunrise.time="06:00:00",
        sunset.time="18:00:00", night.col="gray60",
        phaseCol=NULL, interact=TRUE, key=TRUE, cex.pts=0.4, ...)
```

Arguments

<code>time</code>	POSIXct object with date and time.
<code>depth</code>	Numeric vector with depth in m.
<code>offset</code>	Known amount of meters to subtract for zero-offset correcting depth throughout the entire TDR record.
<code>concurVars</code>	Matrix with additional variables in each column to plot concurrently with depth.
<code>xlim</code>	Vector of length 2, with lower and upper limits of time to be plotted.
<code>depth.lim</code>	Numeric vector of length 2, with the lower and upper limits of depth to be plotted.
<code>xlab, ylab.depth</code>	Strings to label the corresponding y-axes.
<code>concurVarTitles</code>	Character vector of titles to label each new variable given in <code>concurVars</code> .
<code>xlab.format</code>	Format string for formatting the x axis; see strptime .
<code>sunrise.time, sunset.time</code>	Character string with time of sunrise and sunset, respectively, in 24 hr format. This is used for shading night time.
<code>night.col</code>	Color for shading night time.
<code>phaseCol</code>	Factor dividing rows into sections.
<code>interact</code>	Logical; whether to provide interactive tcltk controls and access to the associated ZOC functionality.
<code>key</code>	Logical indicating whether to draw a key.
<code>cex.pts</code>	Passed to points to set the relative size of points to plot (if any).
<code>...</code>	Arguments passed to par ; useful defaults <code>las=1</code> , <code>bty="n"</code> , and <code>mar</code> (the latter depending on whether additional concurrent data will be plotted) are provided, but they can be overridden.

Details

These functions are used primarily to correct, visually, drifts in the pressure transducer of TDR records. `zoc` calls `plotDive`, which plots depth and, optionally, speed vs. time with the possibility zooming in and out on time, changing maximum depths displayed, and panning through time. The option to zero-offset correct sections of the record gathers x and y coordinates for two points, obtained by clicking on the plot region. The first point clicked indicates the offset and beginning time of section to correct, and the second one indicates the ending time of the section to correct. Multiple sections of the record can be corrected in this manner, by panning through the time and repeating the procedure. In case there's overlap between zero offset corrected windows, the last one prevails.

Once the whole record has been zero-offset corrected, remaining points with depth values lower than zero, are turned into zeroes, as these are assumed to be values at the surface.

Value

`zoc` returns a numeric vector, as long as `depth` of zero-offset corrected depths.

`plotTD` returns (invisibly) a list with as many components as sections of the record that were zero-offset corrected, each consisting of two further lists with the same components as those returned by `locator`.

Author(s)

Sebastian P. Luque (spluque@gmail.com), with many ideas from CRAN package `sfsmisc`.

See Also

`calibrateDepth`, and `plotTDR`.

Examples

```
data(divesTDR)

## Use interact=TRUE (default) to set the offset interactively
depth.zoc <- zoc(getTime(divesTDR), getDepth(divesTDR), offset=3)
plotTD(getTime(divesTDR), depth.zoc, interact=FALSE)
```

Index

- *Topic **arith**
 - diveStats, 21
 - rqPlot, 29
- *Topic **classes**
 - TDR-class, 35
 - TDRcalibrate-class, 34
- *Topic **datasets**
 - dives, 20
 - sealLocs, 30
- *Topic **hplot**
 - rqPlot, 29
- *Topic **internal**
 - detDive-internal, 14
 - detPhase-internal, 15
 - diveMove-internal, 17
 - labDive-internal, 24
- *Topic **iplot**
 - zoc, 37
- *Topic **iteration**
 - austFilter, 1
- *Topic **manip**
 - austFilter, 1
 - bout-misc, 5
 - bouts2MLE, 7
 - bouts2NLS, 10
 - calibrateDepth, 11
 - calibrateSpeed, 13
 - distSpeed, 16
 - readLocs, 26
 - readTDR, 27
 - rqPlot, 29
- *Topic **math**
 - calibrateDepth, 11
 - calibrateSpeed, 13
 - distSpeed, 16
 - diveStats, 21
- *Topic **methods**
 - bout-methods, 4
 - extractDive-methods, 23
 - plotTDR-methods, 25
 - TDR-accessors, 31
 - TDRcalibrate-accessors, 32
 - timeBudget-methods, 36
- *Topic **misc**
 - bout-misc, 5
- *Topic **models**
 - bouts2MLE, 7
 - bouts2NLS, 10
- *Topic **package**
 - diveMove-package, 19
 - .cutDive (*labDive-internal*), 24
 - .detDive, 16, 34, 35
 - .detDive (*detDive-internal*), 14
 - .detPhase, 14, 15, 22, 34
 - .detPhase (*detPhase-internal*), 15
 - .diveIndices (*diveMove-internal*), 17
 - .getInterval (*diveMove-internal*), 17
 - .labDive (*labDive-internal*), 24
 - .labDivePhase, 35
 - .labDivePhase (*labDive-internal*), 24
 - .night (*diveMove-internal*), 17
 - .rleActivity (*diveMove-internal*), 17
 - .speedCol (*diveMove-internal*), 17
 - .speedNames (*diveMove-internal*), 17
 - .speedStats (*diveMove-internal*), 17
 - [, TDR-method (*TDR-accessors*), 31
 - as.data.frame, TDR-method (*TDR-accessors*), 31
 - as.TDRspeed (*TDR-accessors*), 31
 - as.TDRspeed, TDR-method (*TDR-accessors*), 31
 - austFilter, 1

bec2 (*bout-methods*), 4
 bec2, mle-method (*bout-methods*), 4
 bec2, nls-method (*bout-methods*), 4
 bout-methods, 4
 bout-misc, 5
 boutfreqs (*bout-misc*), 5
 boutinit, 8
 boutinit (*bout-misc*), 5
 bouts.mle, 5, 7, 11
 bouts.mle (*bouts2MLE*), 7
 bouts2.LL, 8
 bouts2.LL (*bouts2MLE*), 7
 bouts2.ll, 8
 bouts2.ll (*bouts2MLE*), 7
 bouts2.mleBEC (*bouts2MLE*), 7
 bouts2.mleFUN (*bouts2MLE*), 7
 bouts2.nls, 5, 7
 bouts2.nls (*bouts2NLS*), 10
 bouts2.nlsBEC (*bouts2NLS*), 10
 bouts2.nlsFUN (*bouts2NLS*), 10
 bouts2MLE, 7
 bouts2NLS, 10

 calibrateDepth, 11, 12, 13, 15, 19, 20, 37, 39
 calibrateSpeed, 12, 13, 13, 19
 ccData<- (*TDR-accessors*), 31
 ccData<-, TDR, data.frame-method (*TDR-accessors*), 31
 coerce, TDR, data.frame-method (*TDR-accessors*), 31
 coerce, TDR, TDRspeed-method (*TDR-accessors*), 31
 createTDR (*readTDR*), 27
 curve, 7

 data.frame, 21, 36
 depth<- (*TDR-accessors*), 31
 depth<-, TDR, numeric-method (*TDR-accessors*), 31
 detDive-internal, 14
 detPhase-internal, 15
 distSpeed, 2, 3, 16, 30
 diveMove, 28
 diveMove (*diveMove-package*), 19
 diveMove-internal, 17
 diveMove-package, 19
 dives, 20
 divesSummary (*dives*), 20

 diveStats, 20, 21, 30
 divesTDR (*dives*), 20
 divesTDRcalibrate (*dives*), 20

 extractDive, 31
 extractDive
 (*extractDive-methods*), 23
 extractDive, TDR, numeric, numeric-method (*extractDive-methods*), 23
 extractDive, TDRcalibrate, numeric, missing-method (*extractDive-methods*), 23
 extractDive-methods, 23

 getCCData (*TDR-accessors*), 31
 getCCData, TDR, character-method (*TDR-accessors*), 31
 getCCData, TDR, missing-method (*TDR-accessors*), 31
 getDAct, 35
 getDAct (*TDRcalibrate-accessors*), 32
 getDAct, TDRcalibrate, character-method (*TDRcalibrate-accessors*), 32
 getDAct, TDRcalibrate, missing-method (*TDRcalibrate-accessors*), 32
 getDepth (*TDR-accessors*), 31
 getDepth, TDR-method (*TDR-accessors*), 31
 getDPhaseLab
 (*TDRcalibrate-accessors*), 32
 getDPhaseLab, TDRcalibrate, missing-method (*TDRcalibrate-accessors*), 32
 getDPhaseLab, TDRcalibrate, numeric-method (*TDRcalibrate-accessors*), 32
 getDtime (*TDR-accessors*), 31
 getDtime, TDR-method (*TDR-accessors*), 31
 getFileName (*TDR-accessors*), 31
 getFileName, TDR-method (*TDR-accessors*), 31
 getGAct (*TDRcalibrate-accessors*), 32
 getGAct, TDRcalibrate, character-method (*TDRcalibrate-accessors*),

- 32
- getGAct, TDRcalibrate, missing-method
(TDRcalibrate-accessors),
32
- getSpeed (TDR-accessors), 31
- getSpeed, TDRspeed-method
(TDR-accessors), 31
- getSpeedCoef
(TDRcalibrate-accessors),
32
- getSpeedCoef, TDRcalibrate-method
(TDRcalibrate-accessors),
32
- getTDR, 34
- getTDR (TDRcalibrate-accessors),
32
- getTDR, TDRcalibrate-method
(TDRcalibrate-accessors),
32
- getTime (TDR-accessors), 31
- getTime, TDR-method
(TDR-accessors), 31
- grpSpeedFilter (austFilter), 1
- labDive-internal, 24
- labelBouts (bout-misc), 5
- locator, 39
- logit, 8, 9
- logit (bout-misc), 5
- mle, 4, 7–9
- nls, 4, 10
- oneDiveStats (diveStats), 21
- optim, 9
- par, 38
- plot.default, 10
- plot.ecdf, 7
- plotBouts (bout-methods), 4
- plotBouts, mle-method
(bout-methods), 4
- plotBouts, nls-method
(bout-methods), 4
- plotBouts2.cdf (bouts2MLE), 7
- plotBouts2.mle, 4
- plotBouts2.mle (bouts2MLE), 7
- plotBouts2.nls, 4
- plotBouts2.nls (bouts2NLS), 10
- plotTD, 25, 31
- plotTD (zoc), 37
- plotTDR, 39
- plotTDR (plotTDR-methods), 25
- plotTDR, TDR-method
(plotTDR-methods), 25
- plotTDR, TDRcalibrate-method
(plotTDR-methods), 25
- plotTDR, TDRspeed-method
(plotTDR-methods), 25
- plotTDR-methods, 25
- points, 38
- POSIXct, 16, 24, 34, 36, 37
- read.csv, 27
- readLocs, 26, 30
- readTDR, 20, 27, 34–36
- rmsDistFilter (austFilter), 1
- rq, 13
- rqPlot, 13, 29
- sealLocs, 30
- show, TDR-method (TDR-accessors),
31
- show, TDRcalibrate-method
(TDRcalibrate-accessors),
32
- speed<- (TDR-accessors), 31
- speed<-, TDRspeed, numeric-method
(TDR-accessors), 31
- stampDive, 19, 20
- stampDive (diveStats), 21
- strptime, 27, 28, 38
- TDR, 12, 13, 20, 23–25, 28, 31, 33–35
- TDR (TDR-class), 35
- TDR-class, 19
- TDR-accessors, 31
- TDR-class, 35
- TDR-methods (TDR-accessors), 31
- TDRcalibrate, 11–14, 20, 25, 32, 33, 36
- TDRcalibrate
(TDRcalibrate-class), 34
- TDRcalibrate-class, 21, 22
- TDRcalibrate-methods, 35
- TDRcalibrate-accessors, 32
- TDRcalibrate-class, 34

TDRcalibrate-methods
 (*TDRcalibrate-accessors*),
 32
TDRspeed, 23, 25, 28, 31
TDRspeed (*TDR-class*), 35
TDRspeed-class (*TDR-class*), 35
timeBudget, 19
timeBudget (*timeBudget-methods*),
 36
timeBudget, TDRcalibrate, logical-method
 (*timeBudget-methods*), 36
timeBudget-methods, 36

unLogit, 9
unLogit (*bout-misc*), 5

zoc, 12, 13, 15, 22, 25, 26, 37