

# Package ‘hab’

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**Title** Habitat and movement functions

**Description** A set of functions related to habitat selection and movement analyses. Also includes a few patches for functions from the adehabitatXY package family.

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**Depends** R (>= 3.1.0),adehabitatLT,adehabitatHR

**Suggests** survival,tkrplot

**License** GPL (>= 3)

**URL** <http://ase-research.org/basille/hab>

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acf.test	<i>Test of autocorrelation in SSFs</i>
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**Description**

Test of autocorrelation and partial autocorrelation in SSF models, based on the estimation of autocorrelation functions (ACF).

**Usage**

```
acf.test(residuals, id, type = c("correlation", "covariance", "partial"),
ci = 0.95)
```

**Arguments**

residuals	A vector of residuals on which to compute the ACF. The residuals must be sorted chronologically.
id	A vector of corresponding animal IDs.
type	A character string giving the type of ACF to be computed. Allowed values are correlation (default), covariance or partial.
ci	A numeric giving the confidence interval to be used to test the ACF.

**Value**

- A list, with the following parameters:
- acfk: a list with the individual autocorrelation functions
  - threshold: a vector with individual thresholds
  - lag: a vector with the resulting individual lags

**Author(s)**

Mathieu Basille <basille@ase-research.org>

**See Also**

See [acf](#) for further details on the ACF.

**Description**

Faster version of [as.ltraj](#), which can be up to 5-10 times faster.

**Usage**

```
as.ltraj(xy, date = NULL, id, burst = id, typeII = TRUE,
         slsp = c("remove", "missing"), infolocs = data.frame(pkey = paste(id,
         date, sep = ".")))
```

**Author(s)**

Modified by Mathieu Basille <basille@ase-research.org>

**See Also**

See [ld](#) for further details on the function and all available arguments.

**Examples**

```
data(puechabonsp)
locs <- puechabonsp$relocs
xy <- coordinates(locs)
df <- as.data.frame(locs)
id <- df[,1]
da <- as.POSIXct(strptime(as.character(df$Date), "%y%m%d"))
ltr1 <- adehabitatLT::as.ltraj(xy, da, id = id)
ltr2 <- as.ltraj(xy, da, id = id)
all.equal(ltr1, ltr2)
```

**Description**

Faster versions of [ld](#) and [dl](#).

**Usage**

```
dl(x, strict = TRUE)

ld(ltraj, strict = TRUE)
```

## Arguments

`strict` Logical. Whether to use the regular `ld` or `dl` functions, which enforce more verifications.

## Details

In `ld`, `strict = FALSE` can be up to 10 times faster, but assumes that the `ltraj` is well structured (i.e. not modified by the user). In `dl`, `strict = FALSE` can be up to 20 times faster, but assumes that the trajectory parameters in the data frame (x/y increments, angles, etc.) are still valid (e.g. no locations have been removed).

## Author(s)

Modified by Mathieu Basille <basille@ase-research.org>

## See Also

See `ld` for further details on the function and all available arguments.

## Examples

```
data(puechcirc)
puechcirc ## class ltraj

## ld
df1 <- adehabitatLT::ld(puechcirc)
df2 <- ld(puechcirc, strict = FALSE)
all.equal(df1, df2)
## Note a difference in row names:
attr(df1, "row.names")
attr(df2, "row.names")

## dl
all.equal(dl(df2), adehabitatLT::dl(df2))
dl(df2, strict = FALSE)
## Comparison regarding 'strict'
all.equal(dl(df2), dl(df2, strict = FALSE))
## Differences in row.names (numeric in regular 'dl', characters using
## 'strict = FALSE') + NAs in R2n (for a reason, 'puechcirc[[2]]'
## starts by a sequence of missing values, but has several 'R2n'
## values. As a result, 'strict = FALSE' keeps the 'R2n' values)
```

## Description

A set of functions related to habitat selection and movement analyses. Also includes a few patches for functions from the `adehabitatXY` package family. For a list of documented functions, use `library(help = "hab")`

## Author(s)

Mathieu Basille <basille@ase-research.org>

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infolocs

*Infolocs of an Object of Class ltraj*

---

## Description

Modified version of [infolocs](#) that returns NULL if infolocs exists, but which is not a colum of it.

## Usage

```
infolocs(ltraj, which, perani = FALSE, simplify = FALSE)
```

## Arguments

perani	Logical. Should the function return one element per burst (FALSE, default) or per animal (TRUE).
simplify	Logical. If a single variable is requested, should the function return 1-column data frames (FALSE, default) or vector (TRUE).

## Author(s)

Modified by Mathieu Basille <basille@ase-research.org>

## See Also

See [infolocs](#) for further details on the function and all available arguments.

## Examples

```
## Load puechcirc data, and add some random infolocs:
data(puechcirc)
info <- list(data.frame(A = rnorm(80), B = runif(80), C = rpois(80,
  1)), data.frame(A = rnorm(69, 10), B = runif(69, 10, 11),
  C = rpois(69, 10)), data.frame(A = rnorm(66, -10), B = runif(66,
  -10, -9), C = rpois(66, 100)))
## Watch the row names:
info <- mapply(function(x, y) {
  row.names(x) <- row.names(y)
  return(x)
}, info, puechcirc, SIMPLIFY = FALSE)
infolocs(puechcirc) <- info

## Try to retrieve the column `toto`:
infolocs(puechcirc, "toto")
```

kerneloverlap

*Spatial Interaction between Animals Monitored Using Radio-Tracking***Description**

Modified version of [kerneloverlap](#), which now allows to select several methods at once, and works on `SpatialPointsDataFrame` or `estUDm` in the same function.

**Usage**

```
kerneloverlap(x, method = c("HR", "PHR", "VI", "BA", "UDOI", "HD"),
  percent = 95, conditional = FALSE, ...)

summary.kerneloverlap(object, ...)
```

**Arguments**

<code>x</code>	an object of class <code>SpatialPointsDataFrame</code> containing only one column (which is a factor indicating the identity associated to the relocations) or an object of class <code>estUDm</code> containing several home-ranges for which the overlap is to be calculated
<code>method</code>	the desired method(s) for the estimation of overlap (several methods can be chosen, defaults to all at once)
<code>object</code>	An array or matrix of class <code>kerneloverlap</code>

**Value**

An array of class `kerneloverlap` with as many matrices as chosen methods (if only one method is chosen, a matrix of class `kerneloverlap`); each matrix gives the value of indices of overlap for all pairs of animals.

**Author(s)**

Modified by Mathieu Basille <basille@ase-research.org>

**See Also**

See [kerneloverlap](#) for further details on the function and all available arguments.

**Examples**

```
## Prepare the data:
data(puechabonsp)
loc <- puechabonsp$relocs
elev <- puechabonsp$map

## Kernel overlap using various approaches:
kerneloverlap(puechabonsp$relocs[,1], grid = 200, meth = "HR", conditional = TRUE)
```

```
kerneloverlap(puechabonsp$relocs[,1], grid = elev, meth = c("HR", "VI"), conditional = TRUE)
kerneloverlap(puechabonsp$relocs[,1], grid = 200, conditional = TRUE)

## Summarizing the results:
summary(kerneloverlap(puechabonsp$relocs[,1], grid = 200))
summary(kerneloverlap(puechabonsp$relocs[,1], grid = 200, percent = 50))
```

---

kernelUD

*Estimation of Kernel Home-Range*

---

## Description

Modified version of [kernelUD](#), which silences the use of same4all when working on a SpatialPixels as a grid.

## Usage

```
kernelUD(xy, h = "href", grid = 60, same4all = FALSE, hlim = c(0.1,
  1.5), kern = c("bivnorm", "epa"), extent = 0.5, boundary = NULL)
```

## Author(s)

Modified by Mathieu Basille <basille@ase-research.org>

## See Also

See [kernelUD](#) for further details on the function and all available arguments.

## Examples

```
## Prepare the data:
data(puechabonsp)
loc <- puechabonsp$relocs
elev <- puechabonsp$map

## Compute the kernel estimation
ker1 <- kernelUD(puechabonsp$relocs[,1], grid = elev, same4all = TRUE)

## Summarizing the overlaps
summary(kerneloverlap(ker1, conditional = TRUE))
```

---

`kfold`*kfold*

---

**Description**

Cross-validation for regression models.

**Usage**

```
kfold(mod, k = 5, nrepet = 100, jitter = FALSE, reproducible = TRUE,  
      details = FALSE)
```

**Arguments**

<code>mod</code>	A fitted model for which there exists a <code>kfold</code> method (currently <code>coxph</code> and <code>clogit</code> models).
<code>k</code>	The number of equal size subsamples of the partition.
<code>nrepet</code>	The number of repetitions.
<code>jitter</code>	Logical, whether to add some random noise to the predictions (useful when the model is fitted on categorical variables, which can produces error in the ranking process).
<code>reproducible</code>	Logical, whether to use a fixed seed for each repetition.
<code>details</code>	Logical, whether to return details of each repetition (useful for debugging).

**Details**

Note: needs complete names in the `coxph/clogit` call, and not `'cos(var)'` or `'I(var*10)'`, except for `'strata()'` and `'cluster()'`.

Also needs complete case in the model (e.g. it fails if there is at least one NA in the observed steps for any variable of the model). Returns an error if some stratas have no case.

**Value**

A data frame with the correlations (`cor`) and the type of value (`type`).

**Author(s)**

Mathieu Basille <basille@ase-research.org>, with the help of Terry Therneau and Guillaume Bastille-Rousseau



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lincircor	<i>Linear-circular correlation</i>
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---

**Description**

Compute Linear-circular correlation, and test it.

**Usage**

```
lincircor(xl, theta)
```

```
lincircor.test(xl, theta)
```

**Arguments**

x1	A numeric, providing the linear variable.
theta	A numeric, providing the circular variable, in radians ( $\text{rad} = \text{deg} * \pi / 180$ ).

**Value**

lincircor returns a numeric providing the linear-circular correlation. lincircor.test returns a list with class "htest" containing the following components:

- statistic: the value of the test statistic
- parameter: the degrees of freedom of the test statistic, which follows a F distribution if x, and theta are independent and x is normally distributed
- p.value: the p-value of the test
- estimate: the estimated measure of linear-circular correlation
- null.value: the value of the correlation measure under the null hypothesis, always 0
- alternative: a character string describing the alternative hypothesis
- method: a character string indicating how the correlation was measured
- data.name: a character string giving the names of the data

**Author(s)**

Mathieu Basille <basille@ase-research.org>

**References**

Mardia, K. V. & Jupp, P. E. (2000) Directional statistics. Wiley, 429 pp.

## Examples

```
## From Mardia & Jupp (2000), p.246
xl <- c(28, 85.2, 80.5, 4.7, 45.9, 12.7, 72.5, 56.6, 31.5, 112,
       20, 72.5, 16, 45.9, 32.6, 56.6, 52.6, 91.8, 55.2)
theta <- c(327, 91, 88, 305, 344, 270, 67, 21, 281, 8, 204, 86,
          333, 18, 57, 6, 11, 27, 84)
## 'xl' is not in radians (but the test is computed anyway)
lincircor(xl, theta)
## Conversion to radians
lincircor(xl, theta*pi/180)
## Test
lincircor.test(xl, theta*pi/180)
```

---

ltraj2sldf

---

*Conversion of the class ltraj to the package sp*


---

## Description

ltraj2spdf: Add a proj4string parameter, and keeps id and burst. ltraj2sldf: Add a proj4string parameter, and by is now a character, which accepts "id", "burst" (default) and "step". Warning: the conversion to SLDF using by = "step" is significantly longer, of a factor of ~50, than the other two (it takes about 10 sec for each 10,000 steps on a relatively recent computer).

## Usage

```
ltraj2sldf(ltr, by = c("burst", "id", "step"), strict = TRUE,
          proj4string = CRS(as.character(NA)))

ltraj2spdf(ltr, strict = TRUE, proj4string = CRS(as.character(NA)))
```

## Arguments

by	Sets the level of aggregation: if id, one object of class Lines corresponds to one animal; if burst (default), it corresponds to one burst; if step, it corresponds to one step.
strict	Logical (TRUE by default). See ld. For ltraj2sldf, only applies to by = "step".
proj4string	A valid proj4 string (see <a href="#">proj4string</a> for more details).

## Author(s)

Modified by Mathieu Basille <basille@ase-research.org>

## See Also

See [ltraj2spdf](#) for further details on the function and all available arguments.

## Examples

```
## Load puechcirc data, and add some random infolocs:
data(puechcirc)
info <- list(data.frame(A = rnorm(80), B = runif(80), C = rpois(80,
  1)), data.frame(A = rnorm(69, 10), B = runif(69, 10, 11),
  C = rpois(69, 10)), data.frame(A = rnorm(66, -10), B = runif(66,
  -10, -9), C = rpois(66, 100)))
## Watch the row names:
info <- mapply(function(x, y) {
  row.names(x) <- row.names(y)
  return(x)
}, info, puechcirc, SIMPLIFY = FALSE)
infolocs(puechcirc) <- info

## Conversion to SPDF:
summary(adehabitatLT::ltraj2spdf(puechcirc))
summary(ltraj2spdf(puechcirc, strict = FALSE))
summary(ltraj2spdf(puechcirc, strict = FALSE, proj4string = CRS("+init=epsg:27572")))

## Conversion to SLDF:
summary(adehabitatLT::ltraj2sldf(puechcirc, byid = TRUE))
summary(ltraj2sldf(puechcirc, by = "id"))
summary(ltraj2sldf(puechcirc, proj4string = CRS("+init=epsg:27572")))
summary(ltraj2sldf(puechcirc, strict = FALSE, by = "step",
  proj4string = CRS("+init=epsg:27572")))
```

---

makeCluster

---

*Create independent clusters*


---

## Description

Create independant clusters from a sequence of (observed + random) steps.

## Usage

```
makeCluster(seq, strata, case, ndrop, nclust = NULL, nstep = NULL)
```

## Arguments

seq	A numeric, indicating the continuous sequences of steps. See Details.
strata	A numeric, indicating the strata of each observed and random steps.
case	A numeric, with 1 for observed steps and 0 for random steps.
ndrop	The number of steps to drop between each cluster. They will be NAs in the resulting vector.
nclust	The ideal number of clusters to obtain. See Details.
nstep	The number of steps consisting in a single cluster. See Details.

**Details**

There must be one and only one case per strata. In addition, the sequences must be ordered in ascending order (there is no check on this), and the case and strata should correspond to that order.

It is only necessary to provide nclust to get at least that many clusters (if possible). The argument nloc can be set instead, if one wants exactly a number of successive steps in a cluster.

**Value**

A vector of the same length as seq, strata and case, with the cluster number for each step, and three attributes giving the number of clusters (nclust), the number of successive steps kept per cluster (nstep) and the number of successive steps dropped between each cluster (ndrop).

**Author(s)**

Mathieu Basille <basille@ase-research.org>

**Examples**

```
## case (1 observed + 9 random)
case <- rep(rep(1:0, c(1, 9)), 100)
## 100 stratas of 10 steps (1 observed + 9 random)
strata <- rep(1:100, each = 10)
## 5 sequences of 20*10 steps
seq <- rep(1:5, each = 200)
head(data.frame(case, strata, seq), 22)
## Make at least 15 clusters by dropping 2 steps between each of them
makeCluster(seq, strata, case, ndrop = 2, nclust = 15)
## Same result with 'nstep = 7' directly
makeCluster(seq, strata, case, ndrop = 2, nstep = 7)
```

---

modWeights

---

*Model weights using Information Theory*


---

**Description**

Compute model weights using Information Theory criteria.

**Usage**

```
modWeights(..., criterion = QIC, names = TRUE)
```

**Arguments**

...	All fitted model objects.
criterion	The function to be used as the Information Theory criterion. Only tested with QIC (default).
names	Logical, whether to assign names to the result.

**Value**

A numeric vector with the corresponding weights.

**Author(s)**

Mathieu Basille <basille@ase-research.org>

---

`na.omit.ltraj`*Handle Missing Values in Objects of Class 'ltraj'*

---

**Description**

`na.omit` removes missing locations from a `ltraj` object.

**Usage**

```
## S3 method for class 'ltraj'  
na.omit(object, rec = TRUE, ...)
```

**Arguments**

<code>object</code>	An object of class <code>ltraj</code> .
<code>rec</code>	Logical, whether to recompute descriptive parameters of the trajectory (in particular <code>dx</code> , <code>dy</code> , and angles). Use <code>FALSE</code> with care.
<code>...</code>	Further arguments not used.

**Value**

A `ltraj` object, without missing locations.

**Author(s)**

Mathieu Basille <basille@ase-research.org>

**Examples**

```
data(puechcirc)  
puechcirc  
na.omit(puechcirc)
```

plot.ltraj

*Graphical Display of an Object of Class "ltraj"***Description**

New arguments to allow a better control by the user, plus a computation of xlim/ylim that ensures that the bounding box of the maps are the same for each burst (see parameter center). Also enables the plot of a SpatialPoints(DataFrame) in the background.

**Usage**

```
plot.ltraj(x, id = unique(adehabitatLT::id(x)),
  burst = adehabitatLT::burst(x), na.rm = TRUE, spixdf = NULL,
  spolddf = NULL, spotdf = NULL, xlim = NULL, ylim = NULL,
  center = FALSE, addpoints = TRUE, addlines = TRUE, perani = FALSE,
  final = TRUE, mfrow, ppar = list(pch = 21, col = "black", bg = "white"),
  lpar = list(), spixdfpar = list(col = gray((240:1)/256)),
  spolddfpar = list(col = "green"), spotdfpar = list(pch = 3, col =
    "darkgreen"), ...)
```

**Arguments**

na.rm	Logical, whether to remove missing locations.
spotdf	An object of class SpatialPoints.
center	Logical, whether to center each plot around the current burst (default = FALSE).
mfrow	A vector of the form c(nr, nc), which allows the user to define the numbers of rows (nr) and columns (nc) in the device (the default uses n2mfrow(length(id)) if length(id) <= 12, and mfrow = c(3, 4) otherwise).
ppar	A list of arguments that allows the user to modify point display, using any argument available to points. Default is list(pch = 21, col = "black", bg = "white"). See Details.
lpar	A list of arguments that allows the user to modify line display, using any argument available to lines. Default is list(), i.e. an empty list. See Details.
spixdfpar	A list of arguments that allows the user to modify SpatialPixelsDataFrame display, using any argument available to image. Default is list(col = gray((240:1)/256)).
spolddfpar	A list of arguments that allows the user to modify SpatialPolygons display, using any argument available to plot. Default is list(col = "green").
spotdfpar	A list of arguments that allows the user to modify SpatialPoints display, using any argument available to plot. Default is list(pch = 3, col = "darkgreen").

**Details**

It is possible to use point and line parameters globally for every trajectory displayed. In this case, ppar and lpar need just be a list of graphical parameters, such as list(pch = 21, col = "black", bg = "white"). It is also possible to use parameters for single steps, using as graphical parameter a list of vectors of length equal to each trajectory. Such information can be based on infolocs, see Example.

**Author(s)**

Modified by Mathieu Basille <basille@ase-research.org>

**See Also**

See [plot.ltraj](#) for further details on the function and all available arguments.

**Examples**

```
data(puechcirc)
##'
## Point and line parameters
plot(puechcirc)
plot(puechcirc, ppar = list(pch = 2, cex = .5), lpar = list(lty = 2,
  col = grey(.5)))
##'
## id/perani and mfrow
plot(puechcirc, perani = FALSE)
## Not run:
plot(puechcirc, perani = FALSE, mfrow = c(1, 2))
## End(Not run)
plot(puechcirc, id = "JE93", perani = FALSE)
##'
## Using parameters for single steps
info <- list(data.frame(col = sample(c("red",
  "grey"), 80, rep = TRUE), stringsAsFactors = FALSE),
  data.frame(col = sample(c("blue", "darkred"),
    69, rep = TRUE), stringsAsFactors = FALSE),
  data.frame(col = sample(c("darkgreen", "purple"),
    66, rep = TRUE), stringsAsFactors = FALSE))
info <- mapply(function(x, y) {
  row.names(x) <- row.names(y)
  return(x)
}, info, puechcirc, SIMPLIFY = FALSE)
infolocs(puechcirc) <- info
##'
## Per burst (default)
plot(puechcirc, ppar = list(pch = 19, col = infolocs(puechcirc,
  "col", simplify = TRUE)), lpar = list(col = infolocs(puechcirc,
  "col", simplify = TRUE)), na.rm = FALSE)
##'
## Per animal
plot(puechcirc, ppar = list(pch = 19, col = infolocs(puechcirc,
  "col", simplify = TRUE, perani = TRUE)), lpar = list(col = infolocs(puechcirc,
  "col", simplify = TRUE, perani = TRUE)), na.rm = FALSE, perani = TRUE)
##'
## Using a SpatialPixelsDataFrame
data(puechabonsp)
##'
plot(puechcirc, perani = FALSE, spixdf = puechabonsp$map[,1])
plot(puechcirc, perani = FALSE, spixdf = puechabonsp$map[,1],
  ppar = list(pch = 2, cex = .5), lpar = list(lty = 2, col = "white"),
```

```

    spixdfpar = list(col = gray((1:240)/256)))
##'
## Using a SpatialPolygonsDataFrame
cont <- getcontour(puechabonsp$map[,1])
plot(puechcirc, spoldf = cont)
plot(puechcirc, spoldf = cont, ppar = list(pch = 2, cex = .5),
      lpar = list(lty = 2, col = grey(.5)), spoldfpar = list(col = "cornsilk",
      border = grey(.5)))

```

---

plotltr

---

*Changes in Traject Parameters Over Time*


---

## Description

Four new arguments to allow a better control by the user (note that arguments pch and cex have been removed and are now used in ppar).

## Usage

```

plotltr(x, which = "dist", perani = FALSE, addlines = TRUE, mfrow,
        ppar = list(pch = 16, cex = 0.7), lpar = list(), ...)

```

## Arguments

perani	logical. If FALSE (default), one plot is drawn for each value of burst. If TRUE, one plot is drawn for each value of id, and the several bursts are superposed on the same plot for a given animal.
mfrow	A vector of the form c(nr, nc), which allows the user to define the numbers of rows (nr) and columns (nc) in the device (the default uses n2mfrow(length(id)) if length(id) <= 12, and mfrow = c(3, 4) otherwise).
ppar	A list of arguments that allows the user to modify point display, using any argument available to points. Default is list(pch = 21, col = "black", bg = "white").
lpar	A list of arguments that allows the user to modify line display, using any argument available to lines. Default is list(), i.e. an empty list.

## Details

Also corrects a bug if the burst contains infolocs, in which case other attributes (notably burst and id) were lost.

## Author(s)

Modified by Mathieu Basille <basille@ase-research.org>

Modified by Mathieu Basille <basille@ase-research.org>



**See Also**

See [plotltr](#) for further details on the function and all available arguments.

**Examples**

```
data(puehcirc)

adehabitatLT::plotltr(puehcirc, "cos(rel.angle)")
plotltr(puehcirc, "cos(rel.angle)")
## Not run:
plotltr(puehcirc, "cos(rel.angle)", ppar = list(pch = 2, cex = 2),
        lpar = list(lty = 2, lwd = 2), mfrow = c(2, 1))
## End(Not run)

adehabitatLT::plotltr(puehcirc, "dist")
plotltr(puehcirc, "dist")
plotltr(puehcirc, "dist", ppar = list(pch = 3, col = "blue"),
        lpar = list(lty = 3, col = "red"), perani = TRUE)

adehabitatLT::plotltr(puehcirc, "dx")
plotltr(puehcirc, "dx")
plotltr(puehcirc, "dx", ppar = list(col = rep(1:8, each = 6)),
        addlines = FALSE)
```

---

plotNALtraj

*Highlighting the Patterns in Missing Values in Trajects*


---

**Description**

Five new arguments to allow a better control by the user.

**Usage**

```
plotNALtraj(x, perani = FALSE, addlines = TRUE, mfrow, ppar = list(pch =
  16, cex = 0.3), lpar = list(), ...)
```

**Arguments**

perani	logical. If FALSE (default), one plot is drawn for each value of burst. If TRUE, one plot is drawn for each value of id, and the several bursts are superposed on the same plot for a given animal.
addlines	Logical. Indicates whether lines should be added to the plot.
mfrow	A vector of the form <code>c(nr, nc)</code> , which allows the user to define the numbers of rows ( <code>nr</code> ) and columns ( <code>nc</code> ) in the device (the default uses <code>n2mfrow(length(id))</code> if <code>length(id) &lt;= 12</code> , and <code>mfrow = c(3, 4)</code> otherwise).
ppar	A list of arguments that allows the user to modify point display, using any argument available to points. Default is <code>list(pch = 21, col = "black", bg = "white")</code> .

`lpar` A list of arguments that allows the user to modify line display, using any argument available to `lines`. Default is `list()`, i.e. an empty list.

### Author(s)

Modified by Mathieu Basille <basille@ase-research.org>

### See Also

See [plotNALtraj](#) for further details on the function and all available arguments.

### Examples

```
data(puechcirc)
adehabitatLT::plotNALtraj(puechcirc)
plotNALtraj(puechcirc, perani = TRUE, addlines = FALSE, mfrow = c(1,
  2), ppar = list(pch = 15, cex = 0.5))
```

---

QIC

*QIC: Quasi-likelihood under Independence Criterion*

---

### Description

QIC: Quasi-likelihood under Independence Criterion

### Usage

```
QIC(mod, ..., details = FALSE)
```

### Arguments

<code>mod</code>	A <code>coxph</code> or <code>clogit</code> model.
<code>...</code>	Optionally more fitted model objects.
<code>details</code>	Logical, whether to provide detailed outputs (turned automatically to <code>TRUE</code> when several models are fitted).

### Value

If `details = FALSE`, simply returns the QIC. If `details = TRUE`, returns a data frame presenting the QIC, the quasi-likelihood, the number of observations, the number of events, the number of parameters and the trace. If several models are provided, two additional columns present the delta QIC and the model weights.

### Author(s)

Mathieu Basille <basille@ase-research.org> and Thierry Duchesne

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rec	<i>Recalculates the descriptive parameters of a lttraj</i>
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---

**Description**

Modified version of [rec](#) that keeps the original row.names. Also throws an error if the row.names are different between the lttraj and its infolocs.

**Usage**

```
rec(x, slsp = c("remove", "missing"))
```

**Author(s)**

Modified by Mathieu Basille <basille@ase-research.org>

**See Also**

See [rec](#) for further details on the function and all available arguments.

**Examples**

```
data(puechcirc)
(bla <- rec(puechcirc))
head(puechcirc[[2]])
head(bla[[2]])
```

---

setNA	<i>Place Missing Values in Objects of Class lttraj</i>
-------	--------------------------------------------------------

---

**Description**

The function does not allow a numeric for date.ref anymore. In addition, a warning is issued if the length of date.ref is not 1 or the length of the lttraj object. See [setNA](#) for further details on the function and all available arguments.

**Usage**

```
setNA(lttraj, date.ref, dt, tol = dt/10, units = c("sec", "min", "hour",
"day"), ...)
```

**Author(s)**

Modified by Mathieu Basille <basille@ase-research.org>

**See Also**

See [setNA](#) for further details on the function and all available arguments.

subset.ltraj

*Subsetting a ltraj***Description**

Return subsets of a ltraj which meet conditions (over the descriptive parameters of the ltraj or is infolocs).

**Usage**

```
## S3 method for class 'ltraj'
subset(x, subset, rec = FALSE, ...)
```

**Arguments**

x	A ltraj object.
subset	Logical expression indicating elements or rows to keep: missing values are taken as false.
rec	Logical, whether to recompute the ltraj parameters or not (default = FALSE).

**Value**

A ltraj object.

**Author(s)**

Mathieu Basille <basille@ase-research.org>

**See Also**

See [which.ltraj](#) to identify the relocations fulfilling a condition.

**Examples**

```
## Load puehcirc data and add some infolocs:
data(puehcirc)
info <- list(data.frame(A = rnorm(80), B = runif(80), C = rpois(80,
  1)), data.frame(A = rnorm(69, 10), B = runif(69, 10, 11),
  C = rpois(69, 10)), data.frame(A = rnorm(66, -10), B = runif(66,
  -10, -9), C = rpois(66, 100)))
## Watch the row names:
info <- mapply(function(x, y) {
  row.names(x) <- row.names(y)
  return(x)
}, info, puehcirc, SIMPLIFY = FALSE)
infolocs(puehcirc) <- info

## Different subsets:
```

```
(xsub1 <- subset(x, dist > 200, rec = FALSE))
(xsub2 <- subset(x, C == 3, rec = TRUE))
(xsub3 <- subset(x, C == 3, rec = FALSE))
```

trajdyn

*Interactive Display of Objects of Class ltraj*

## Description

Modified version of [trajdyn](#), which allows to 1) increment by by points/steps, 2) only display k previous points/steps, 3) show the current step as a vector, 4) to modify point and line display, 5) show the current burst/loc/(infolocs) and 6) to update interactively a new or existing variable in infolocs.

## Usage

```
trajdyn(x, burst = attr(x[[1]], "burst"), na.rm = TRUE, hscale = 1,
  vscale = 1, addvec = 1, by = 1, only = Inf, recycle = TRUE,
  ppar = list(pch = 16), lpar = list(lwd = 2), nvar = NULL,
  display = c("guess", "windows", "tk"), ...)
```

## Arguments

na.rm	Logical, whether to remove missing locations.
addvec	Numeric, whether to highlight the current location (1, default), the current step (2) or nothing (0).
by	The number of previous points/steps to increment at each step. Default is an increment of 1 point/step.
only	The number of previous points/steps to display. Default is Inf, i.e. all points/steps.
ppar	A list of arguments that allows the user to modify point display, using any argument available to points. Default is <code>list(pch = 16)</code> . See Details.
lpar	A list of arguments that allows the user to modify line display, using any argument available to lines. Default is <code>list(lwd = 2)</code> . See Details.
nvar	A character string giving the name of a variable.

## Details

y selects the number of previous points/steps to increment at each step. It defaults to 1, i.e. an increment of 1 point/step. Choosing anything different than a positive number sets it back to 1.

k selects the number of previous points/steps to display. It defaults to Inf, i.e. all points/steps. Choosing anything different than a positive number sets it back to Inf.

v shows (or removes) the current step as a vector. Note that the vector connects the current location to the next available location (even if there are NAs in the data set).

s shows the current buffer and localisation numbers, together with the associated infolocs (if it exists). If a nvar is requested, only this variable is shown.

The argument `nvar` allows to work on a given variable: if a variable of that name already exists in `infolocs(x)`, the values of the variable are retrieved from there; otherwise, a variable filled with NAs is used. If a `nvar` is requested, `d` "deletes" the value and resets it to NA; every other letter not in use in any option is saved in `nvar`. The letters available are: "c", "e", "f", "h", "j", "m", "t", "u", "w", "x".

On a QWERTY keyboard:

`w e t u f h j x c m`

On a AZERTY keyboard:

`e t u f h j m w x c`

It is possible to use point and line parameters globally for every trajectory displayed. In this case, `ppar` and `lpar` need just be a list of graphical parameters, such as `list(pch = 21, col = "black", bg = "white")`. It is also possible to use parameters for single steps, using as graphical parameter a list of vectors of length equal to each trajectory. Such information can be based on `infolocs`, see Example.

## Value

If a `nvar` is provided, return the original `ltraj` with updated values in `infolocs(nvar)`.

## Author(s)

Modified by Mathieu Basille <basille@ase-research.org>

## Examples

```
## Not run:
data(puechcirc)

## Use of `by` and `only` to select the previous k points/steps:
trajdyn(puechcirc, by = 10, only = 20)

## Use of `ppar` and `lpar` globally:
trajdyn(puechcirc, ppar = list(col = "red"), lpar = list(col = "blue"))

## Create some random `infolocs`:
infolocs(puechcirc) <- list(data.frame(col = sample(c("red",
  "grey"), 80, rep = TRUE), stringsAsFactors = FALSE),
  data.frame(col = sample(c("blue", "darkred"),
    69, rep = TRUE), stringsAsFactors = FALSE),
  data.frame(col = sample(c("darkgreen", "purple"),
    66, rep = TRUE), stringsAsFactors = FALSE))

## Use the infolocs to color points and steps:
trajdyn(puechcirc, by = 1, only = 20, ppar = list(pch = 19,
  col = infolocs(puechcirc, "col", simplify = TRUE)),
  lpar = list(col = infolocs(puechcirc, "col", simplify = TRUE)))

## The same without removing the missing locations:
trajdyn(puechcirc, by = 1, only = 20, ppar = list(pch = 19,
  col = infolocs(puechcirc, "col", simplify = TRUE)),
  lpar = list(col = infolocs(puechcirc, "col", simplify = TRUE)),
```

```
na.rm = FALSE)

## Use of `nvar` to dynamically fill in new data:
(newtraj <- trajdyn(puechcirc, nvar = "Var"))

## End(Not run)
```

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