

Package ‘ctmm’

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<https://groups.google.com/g/ctmm-user>

Depends R (>= 3.5.0)

Imports Bessel, data.table, digest, expm, fasttime, Gmedian, graphics,
grDevices, gsl, manipulate, MASS, methods, numDeriv, parsedate,
pbivnorm, pracma, raster, shape, sf, sp, statmod, stats, terra,
utils

Suggests animation, bit64, dplyr, fftw, knitr, move, parallel,
quadprog, rmarkdown, suncalc

Description Functions for identifying, fitting, and applying continuous-space, continuous-time stochastic-process movement models to animal tracking data.
The package is described in Calabrese et al (2016) <[doi:10.1111/2041-210X.12559](https://doi.org/10.1111/2041-210X.12559)>, with models and methods based on those introduced and detailed in Fleming & Calabrese et al (2014) <[doi:10.1086/675504](https://doi.org/10.1086/675504)>, Fleming et al (2014) <[doi:10.1111/2041-210X.12176](https://doi.org/10.1111/2041-210X.12176)>, Fleming et al (2015) <[doi:10.1103/PhysRevE.91.032107](https://doi.org/10.1103/PhysRevE.91.032107)>, Fleming et al (2015) <[doi:10.1890/14-2010.1](https://doi.org/10.1890/14-2010.1)>, Fleming et al (2016) <[doi:10.1890/15-1607](https://doi.org/10.1890/15-1607)>, Péron & Fleming et al (2016) <[doi:10.1186/s40462-016-0084-7](https://doi.org/10.1186/s40462-016-0084-7)>, Fleming & Calabrese (2017) <[doi:10.1111/2041-210X.12673](https://doi.org/10.1111/2041-210X.12673)>, Péron et al (2017) <[doi:10.1002/ecm.1260](https://doi.org/10.1002/ecm.1260)>, Fleming et al (2017) <[doi:10.1016/j.ecoinf.2017.04.008](https://doi.org/10.1016/j.ecoinf.2017.04.008)>, Fleming et al (2018) <[doi:10.1002/eap.1704](https://doi.org/10.1002/eap.1704)>, Winner & Noonan et al (2018) <[doi:10.1111/2041-210X.13027](https://doi.org/10.1111/2041-210X.13027)>, Fleming et al (2019) <[doi:10.1111/2041-210X.13270](https://doi.org/10.1111/2041-210X.13270)>, Noonan & Fleming et al (2019) <[doi:10.1186/s40462-019-0177-1](https://doi.org/10.1186/s40462-019-0177-1)>, Fleming et al (2020) <[doi:10.1101/2020.06.12.130195](https://doi.org/10.1101/2020.06.12.130195)>, Noonan et al (2021) <[doi:10.1111/2041-210X.13597](https://doi.org/10.1111/2041-210X.13597)>, Fleming et al (2022) <[doi:10.1111/2041-210X.13815](https://doi.org/10.1111/2041-210X.13815)>.

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 Alston & Fleming et al (2023) <[doi:10.1111/2041-210X.14025](https://doi.org/10.1111/2041-210X.14025)>.

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ctmm-package

Continuous-time movement modeling

Description

Functions for identifying, fitting, and applying continuous-space, continuous-time stochastic-process movement models to animal tracking data. The package is described in Calabrese & Fleming (2016) <doi:10.1111/2041-210X.12559> and its models and methods are based on those introduced and detailed in Fleming & Calabrese et al (2014) <doi:10.1086/675504>, Fleming et al (2014) <doi:10.1111/2041-210X.12176>, Fleming et al (2015) <doi:10.1103/PhysRevE.91.032107>, Fleming et al (2015) <doi:10.1890/14-2010.1>, Fleming et al (2016) <doi:10.1890/15-1607>, Péron & Fleming et al (2016) <doi:10.1186/s40462-016-0084-7>, Fleming & Calabrese (2017) <doi:10.1111/2041-210X.12673>, Péron et al (2017) <doi:10.1002/ecm.1260>, Fleming et al (2017) <doi:10.1016/j.ecoinf.2017.04.008>, Fleming et al (2018) <doi:10.1002/eap.1704>, Winner & Noonan et al (2018) <doi:10.1111/2041-210X.13027>, Fleming et al (2019) <doi:10.1111/2041-210X.13270>, Noonan & Fleming et al (2019) <doi:10.1186/s40462-019-0177-1>, Fleming et al (2020) <doi:10.1101/2020.06.12.130195>, Noonan et al (2021) <doi:10.1111/2041-210X.13597>, Fleming et al (2022) <doi:10.1111/2041-210X.13815>, Silva et al (2022) <doi:10.1111/2041-210X.13786>, and Alston & Fleming et al (2023) <doi:10.1111/2041-210X.14025>.

Details

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- [CRAN package](#)
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- [ctmm-FAQ](#)

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 akde

Calculate an autocorrelated kernel density estimate

Description

These functions calculate individual and population-level autocorrelated kernel density home-range estimates from telemetry data and a corresponding continuous-time movement models.

Usage

```
akde(data, CTMM, VMM=NULL, R=list(), SP=NULL, SP.in=TRUE, variable="utilization", debias=TRUE,
      weights=FALSE, smooth=TRUE, error=0.001, res=10, grid=NULL, ...)
```

```
pkde(data, UD, kernel="individual", weights=FALSE, ref="Gaussian", ...)
```

Arguments

data	2D timeseries telemetry data represented as a telemetry object or list of objects.
CTMM	A ctmm movement model from the output of <code>ctmm.fit</code> or list of objects.
VMM	An optional vertical ctmm object for 3D home-range calculation.
R	A named list of raster covariates if CTMM contains an RSF model.
SP	SpatialPolygonsDataFrame object for enforcing hard boundaries.
SP.in	Locations are assumed to be inside the SP polygons if <code>SP.in=TRUE</code> and outside of SP if <code>SP.in=FALSE</code> .
variable	Not yet supported.
debias	Debias the distribution for area estimation (AKDEc).
smooth	"Smooth" out errors from the data.
weights	Optimally weight the data to account for sampling bias (See bandwidth for akde details).

error	Target probability error.
res	Number of grid points along each axis, relative to the bandwidth.
grid	Optional grid specification via raster, UD, or list of arguments (See ‘Details’ below).
...	Arguments passed to akde, bandwidth , and mean.ctmm .
UD	A list of individual UD objects corresponding to data.
kernel	Bandwidths are proportional to the individual covariances if kernel="individual" or to the population covariance if kernel="population".
ref	Include non-Gaussian overlap corrections if ref="AKDE" and weights=TRUE.

Details

For weighted AKDE, please note additional ... arguments passed to [bandwidth](#), which can have a large impact on computation time in certain cases.

When feeding in lists of telemetry and ctmm objects, all UD's will be calculated on the same grid. These UD's can be averaged with the [mean.UD](#) command.

If a UD or raster object is supplied in the grid argument, then the estimate will be calculated on the same grid. Alternatively, a list of grid arguments can be supplied, with any of the following components:

- `r` A list with vectors `x` and `y` that define the grid-cell midpoints.
- `dr` A vector setting the `x` and `y` cell widths in meters. Equivalent to [res](#) for raster objects.
- `extent` The x - y extent of the grid cells, formatted as from the output of [extent](#).
- `align.to.origin` Logical value indicating that cell midpoint locations are aligned to be an integer number of `dr` steps from the projection origin.

Value

Returns a UD object: a list with the sampled grid line locations `r$x` and `r$y`, the extent of each grid cell `dr`, the probability density and cumulative distribution functions evaluated on the sampled grid locations `PDF` & `CDF`, the optimal bandwidth matrix `H`, and the effective sample size of the data in `DOF.H`.

Note

In the case of coarse grids, the value of `PDF` in a grid cell corresponds to the average probability density over the entire rectangular cell.

The `PDF` estimate is not re-normalized to 1, and may fall short of this by the target numerical error. If inspecting quantiles that are very far from the data, the quantiles may hit the grid boundary or become erratic, making it necessary to reduce the numerical error target. However, default arguments should be able to render any quantiles of reasonable accuracy.

Prior to `ctmm` v0.3.2, the default AKDE method was the autocorrelated Gaussian reference function bandwidth. Starting in v0.3.2, the default AKDE method is the autocorrelated Gaussian reference function bandwidth with debiased area.

Prior to `ctmm` v0.3.1, AKDEs included only errors due to autocorrelation uncertainty, which are insignificant in cases such as IID data. Starting in v0.3.1, `akde` calculated an effective sample size `DOF.H` and used this to estimate area uncertainty under a Gaussian reference function approximation. In v0.3.2, this method was further improved to use `DOF.area` from the Gaussian reference function approximation.

Author(s)

C. H. Fleming and K. Winner.

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See Also

[bandwidth](#), [mean.UD](#), [raster](#), [UD-method](#), [revisitation](#)

Examples

```
# Load package and data
library(ctmm)
data(buffalo)
DATA <- buffalo$Cilla

# calculate fit guess object
GUESS <- ctmm.guess(DATA,interactive=FALSE)
# in general, you should be running ctmm.select here instead of ctmm.fit
FIT <- ctmm.fit(DATA,GUESS)

# Compute akde object
UD <- akde(DATA,FIT)

# Plot data with AKDE
plot(DATA,UD=UD)
```


as.telemetry

*Import, coerce, summarize, and combine MoveBank data***Description**

Functions to import MoveBank csv files, data.frame, and Move objects, coerce them into telemetry objects, summarize them, and combine data from multiple tracking devices.

Usage

```
as.telemetry(object,timeformat="auto",timezone="UTC",projection=NULL,datum="WGS84",
             dt.hot=NA,timeout=Inf,na.rm="row",mark.rm=FALSE,keep=FALSE,drop=TRUE,...)

## S3 method for class 'character'
as.telemetry(object,timeformat="auto",timezone="UTC",projection=NULL,datum="WGS84",
             dt.hot=NA,timeout=Inf,na.rm="row",mark.rm=FALSE,keep=FALSE,drop=TRUE,...)

## S3 method for class 'data.frame'
as.telemetry(object,timeformat="auto",timezone="UTC",projection=NULL,datum="WGS84",
             dt.hot=NA,timeout=Inf,na.rm="row",mark.rm=FALSE,keep=FALSE,drop=TRUE,...)

## S3 method for class 'Move'
as.telemetry(object,timeformat="auto",timezone="UTC",projection=NULL,datum="WGS84",
             dt.hot=NA,timeout=Inf,na.rm="row",mark.rm=FALSE,keep=FALSE,drop=TRUE,...)

## S3 method for class 'telemetry'
summary(object,...)

head(x,...)

## S3 method for class 'telemetry'
head(x,n=6L,...)

tail(x,...)

## S3 method for class 'telemetry'
tail(x,n=6L,...)

tbind(...)
```

Arguments

object	A MoveBank CSV filename, MoveBank data.frame object, or Move object to coerce, or a telemetry object to summarize.
timeformat	Format argument for strptime , corresponding to the input data. Alternatively timeformat="auto" will attempt to infer the timestamp format with parse_date .

timezone	Timezone argument for strptime , corresponding to the input data.
projection	Optional PROJ projection argument for the output telemetry object.
datum	Optional argument to specify the input longitude-latitude or UTM datum. The default is WGS84.
dt.hot	Time-interval threshold at which GPS location fixes can be considered as “hot” and location estimate precisions may be smaller (regardless of DOP value) for assigning “hot” and “cold” location classes.
timeout	GPS location fix timeout value (seconds) for assigning a “timed-out” location class.
na.rm	If some values are NA in the data frame, are the rows (times) deleted or are the columns (data types) deleted.
mark.rm	Delete Movebank manually marked outliers. Also see outlie .
keep	Retain additional columns after coercion. keep=TRUE retains all columns, while individual columns to retain can be specified by name.
drop	Only return a telemetry object for one individual if TRUE. Always return a list of telemetry objects if FALSE.
...	telemetry objects or a list of such objects, for tbind() . Optional arguments to be fed to fread or read.csv , in the case of compressed files, for as.telemetry() .
x	telemetry object.
n	Number of rows to return, if positive, or number of rows to omit, if negative.

Details

For data that have not been corralled through Movebank, timestamps either need to be provided in a POSIX format (see the output of `Sys.time()`) or supplied with a `timeformat` argument for interpretation (see [strptime](#)). Alternatively, you can try your luck with `timeformat="auto"`, and [parse_date](#) will attempt to infer the format.

If no projection argument is specified, a two-point equidistant projection is calculated that should be good for most range resident and migratory species. Global migrations that are not along one geodesic (locally straight line) will probably suffer distortion.

`as.telemetry()` assumes **Movebank naming conventions**. Sufficient MoveBank columns include `individual.local.identifier` (or `tag.local.identifier`), `timestamp`, `location.long` and `location.lat`, while the optional Movebank columns include (e-obs) `eobs.horizontal.accuracy.estimate`, (Telonics) `GPS.Horizontal.Error`, `GPS.HDOP`, (Argos) `Argos.orientation`, `Argos.semi.minor` and `Argos.semi.major` or `Argos.location.class`, etc.. To have all columns detected and not overwrite eachother’s information, **it is best to have only one tracking device model per file imported**. Multiple deployments on a single individual can be merged afterwards, using `tbind()`.

Value

`as.telemetry` returns a single telemetry object or list of telemetry objects if multiple animals are identified.

`as.telemetry` will always report the smallest sampling interval, as a message, and the number repeating timestamps, as a warning. Tiny sampling intervals (and repeating timestamps) can sometimes result from misformatted timestamps or an incorrect `timeformat` argument. However, even if genuine, they can necessitate data cleaning ([outlie](#)) or location-error modeling (`vignette('error')`).

Note

Prior to v1.1.1, datum was required to be a full PROJ string, but starting with v1.1.1 datum is just taken to be the PROJ datum argument.

Author(s)

C. H. Fleming, X. Dong, B. Kranstauber, G. Péron, and K. Safi.

See Also

[plot.telemetry](#), [SpatialPoints.telemetry](#), [uere](#).

bandwidth	<i>Calculate the optimal bandwidth matrix of movement data</i>
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Description

This function calculates the optimal bandwidth matrix (kernel covariance) for a two-dimensional animal tracking dataset, given an autocorrelated movement model (Fleming et al, 2015). This optimal bandwidth can fully take into account all autocorrelation in the data, assuming it is captured by the movement model.

Usage

```
bandwidth(data, CTMM, VMM=NULL, weights=FALSE, fast=NULL, dt=NULL, PC="Markov", error=0.01,
          precision=1/2, verbose=FALSE, trace=FALSE, dt.plot=TRUE, ...)
```

Arguments

data	2D timeseries telemetry data represented as a telemetry object.
CTMM	A ctmm movement model as from the output of <code>ctmm.fit</code> .
VMM	An optional vertical ctmm object for 3D bandwidth calculation.
weights	By default, the weights are taken to be uniform, whereas <code>weights=TRUE</code> will optimize the weights.
fast	Use FFT algorithms for weight optimization. <code>fast=NULL</code> will attempt to intelligently decide between the fast and exact algorithms based on computational complexity.
dt	Optional lag bin width for the FFT algorithm.
PC	Preconditioner to use: can be "Markov", "circulant", "IID", or "direct".
error	Maximum grid error for FFT algorithm, if dt is not specified.
precision	Fraction of maximum possible digits of precision to target in weight optimization. <code>precision=1/2</code> results in about 7 decimal digits of precision if the preconditioner is stable.

verbose	Optionally return the optimal weights, effective sample size DOF.H, and other information along with the bandwidth matrix H.
trace	Produce tracing information on the progress of weight optimization.
dt.plot	Execute a diagnostic <code>dt.plot</code> with a red line at dt, if weights=TRUE.
...	Arguments passed to <code>mean.ctmm</code> .

Details

The `weights=TRUE` argument can be used to correct temporal sampling bias caused by autocorrelation. `weights=TRUE` will optimize `n=length(data$t)` weights via constrained & preconditioned conjugate gradient algorithms. These algorithms have a few options that should be considered if the data are very irregular.

`fast=TRUE` is an approximation that discretizes the data with timestep `dt` and applies FFT algorithms, for a computational cost as low as $O(n \log n)$ with only $O(n)$ function evaluations. If no `dt` is specified, then a choice of `dt` will be automated with a message. **If the data contain some very tiny time intervals**, say 1 second among hourly sampled data, then the default `dt` setting can create an excessively high-resolution discretization of time, which will cause slowdown. In this case CTMM should contain a location-error model and `dt` should be increased to a larger fraction of the most-frequent sampling intervals. **If the data are irregular (permitting gaps), then `dt` may need to be several times smaller** than the median to avoid slow down. In this case, try setting `trace=TRUE` and decreasing `dt` below the median until the iterations speed up and the number of feasibility assessments becomes less than $O(n)$.

`fast=FALSE` uses exact time spacing and has a computational cost as low as $O(n^2)$, including $O(n^2)$ function evaluations. With `PC="direct"` this method will produce a result that is exact to within machine precision, but with a computational cost of $O(n^3)$. **`fast=FALSE, PC='direct'` is often the fastest method with small datasets**, where $n \leq O(1,000)$, but scales terribly with larger datasets.

Value

Returns a bandwidth matrix object, which is to be the optimal covariance matrix of the individual kernels of the kernel density estimate.

Note

To obtain a bandwidth scalar representing the variance of each kernel, a `ctmm` object with `isotropic=TRUE` is required. In this case, `bandwidth` will return bandwidth matrix with identical variances along its diagonal. Note that forcing `isotropic=TRUE` will provide an inaccurate estimate for very eccentric distributions.

In v1.0.1 the default `fast`, `dt`, `PC` arguments depend on the sample size, with `fast=FALSE`, `PC="Direct"` for small sample sizes, `fast=FALSE`, `PC="Markov"` for moderate sample sizes, and `fast=TRUE`, `PC="Markov"` for large sample sizes, where `dt` is taken to be the integer fraction of the median sampling interval closest to the minimum sampling interval.

In v0.6.2 the default `dt` was increased from the minimum time difference to a small quantile no less than error times the median.

Author(s)

C. H. Fleming.

References

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- C. H. Fleming, W. F. Fagan, T. Mueller, K. A. Olson, P. Leimgruber, J. M. Calabrese, "Rigorous home-range estimation with movement data: A new autocorrelated kernel-density estimator", *Ecology*, 96:5, 1182-1188 (2015) doi:[10.1890/142010.1](https://doi.org/10.1890/142010.1).
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See Also

[akde](#), [ctmm.fit](#)

 buffalo

African buffalo GPS dataset from Kruger National Park, South Africa.

Description

GPS data on six African buffalo. When using this dataset, please cite the original article by Getz et al (2007) and the Movebank data package (Cross et al, 2016).

Usage

```
data("buffalo")
```

Format

A list of 6 telemetry objects.

Note

In ctmm v0.3.2 the erroneous location fix 606 was removed from buffalo[[4]] "Pepper".

References

- W. M. Getz, S. Fortmann-Roe, P. C. Cross, A. J. Lyons, S. J. Ryan, C. C. Wilmers. LoCoH: Nonparameteric kernel methods for constructing home ranges and utilization distributions. *PLoS ONE* 2:2, e207 (2007).
- P. C. Cross, J. A. Bowers, C. T. Hay, J. Wolhuter, P. Buss, M. Hofmeyr, J. T. du Toit, W. M. Getz. Data from: Nonparameteric kernel methods for constructing home ranges and utilization distributions. Movebank Data Repository. DOI:10.5441/001/1.j900f88t (2016).

See Also

[as.telemetry](#), [plot.telemetry](#), [coati](#), [gazelle](#), [jaguar](#), [pelican](#), [turtle](#), [wolf](#).

Examples

```
# Load package and data
library(ctmm)
data("buffalo")

# Extract movement data for a single animal
Cilla <- buffalo$Cilla

# Plot all sampled locations
plot(Cilla)
```

cluster

Clustering of movement-model parameters

Description

These functions cluster and classify individual movement models and related estimates, including AKDE home-range areas, while taking into account estimation uncertainty.

Usage

```
cluster(x, level=0.95, level.UD=0.95, debias=TRUE, IC="BIC", units=TRUE, plot=TRUE, sort=FALSE,
...)
```

Arguments

x	A list of ctmm movement-model objects, UD objects, or UD summary output, constituting a sampled population, or a list of such lists, each constituting a sampled sub-population.
level	Confidence level for parameter estimates.
level.UD	Coverage level for home-range estimates. E.g., 50% core home range.
debias	Apply Bessel's inverse-Gaussian correction and various other bias corrections.
IC	Information criterion to determine whether or not population variation can be estimated. Can be "AICc", AIC, or "BIC".
units	Convert result to natural units.
plot	Generate a meta-analysis forest plot with two means.
sort	Sort individuals by their point estimates in forest plot.
...	Further arguments passed to plot.

Details

So-far only the clustering of home-range areas is implemented. More details will be provided in an upcoming manuscript.

Value

A list with elements P and CI, where P is an array of individual membership probabilities for sub-population 1, and CI is a table with rows corresponding to the sub-population means, coefficients of variation, and membership probabilities, and the ratio of sub-population means.

Note

The AICc formula is approximated via the Gaussian relation.

Author(s)

C. H. Fleming.

See Also

[akde](#), [ctmm.fit](#), [meta](#).

Examples

```
# load package and data
library(ctmm)
data(buffalo)

# fit movement models
FITS <- AKDES <- list()
for(i in 1:length(buffalo))
{
  GUESS <- ctmm.guess(buffalo[[i]],interactive=FALSE)
  # use ctmm.select unless you are certain that the selected model is OUF
  FITS[[i]] <- ctmm.fit(buffalo[[i]],GUESS)
}

# calculate AKDES on a consistent grid
AKDES <- akde(buffalo,FITS)

# color to be spatially distinct
COL <- color(AKDES,by='individual')

# plot AKDES
plot(AKDES,col.DF=COL,col.level=COL,col.grid=NA,level=NA)

# cluster-analysis of buffalo
cluster(AKDES,sort=TRUE)
```

`coati`*Coatis on Barro Colorado Island, Panama.*

Description

GPS data on 2 coati. When using this dataset, please cite the original article by Powell et al (in preparation) and the Movebank data package (Kays and Hirsch, 2015).

Usage

```
data("coati")
```

Format

A list of 2 telemetry objects.

References

R. A. Powell, S. Ellwood, R. Kays. Stink or swim: techniques to meet the challenges for the study and conservation of small critters that hide, swim or climb and may otherwise make themselves unpleasant. In L. Harrington and D. W. Macdonald; Biology and Conservation of Mustelids and Procyonids (in preparation).

R. Kays, B. T. Hirsch Data from: Stink or swim: techniques to meet the challenges for the study and conservation of small critters that hide, swim or climb and may otherwise make themselves unpleasant. Movebank Data Repository. DOI:10.5441/001/1.41076dq1 (2015).

See Also

[as.telemetry](#), [plot.telemetry](#), [buffalo](#), [gazelle](#), [jaguar](#), [pelican](#), [turtle](#), [wolf](#).

Examples

```
# Load package and data
library(ctmm)
data("coati")

# Plot all sampled locations
plot(coati,col=rainbow(2))
```

color	<i>Color telemetry objects by time</i>
-------	--

Description

These functions facilitate the coloring of tracks by annotating tracking data with time/location specific information and computing color arguments for plot.

Usage

```
annotate(object,by="all",cores=1,...)
```

```
color(object,by="time",col.fn=NULL,alpha=1,dt=NULL,cores=1,...)
```

Arguments

object	A telemetry object or list of objects. color can also take ctm and UD objects.
by	What to annotate or color times by. Options include "individual", "time", "sun", "moon", "season", and "tropic" (see Details below). ctm and UD objects can only be colored by "individual".
col.fn	Optional coloring function that can take a [0,1] interval and alpha channel argument.
alpha	Base alpha channel value.
dt	Sampling interval specification for making oversampled times more transparent. If NULL, the median will be used. Disabled if zero.
cores	Number of annotations or overlap calculations to perform in parallel. cores=0 will use all cores, while cores<0 will reserve abs(cores).
...	Additional arguments.

Details

Annotated telemetry objects are required for color by arguments "sun", "moon", "season", or "tropic".

by="time" colors tracking data with a gradient that increases in time. by="sun" colors according to the sine of the sun's altitude, which is proportional to solar flux during daylight hours. by="moon" colors according to the illuminated fraction of the moon. by="season" colors according to the length of the day, and therefore corresponds to the local season. by="tropic" currently colors according to the calendar day, but will eventually be upgraded to tropical-year cycle. The default col.fn argument runs from blue to red with increasing time, sunlight, moonlight, or day length.

by="individual" assigns colors to minimize the maximum combined spatial and color overlap. Finding the best color assignment is an NP -hard problem that is here approximated in $O(N^3)$ time with a custom greedy algorithm.

Other named columns in the telemetry object can also be used with color, by specifying the column name with by.

Value

annotate returns an annotated telemetry object with extra columns to facilitate coloring. color returns a valid col argument for {plot.telemetry}.

Author(s)

C. H. Fleming.

See Also

[plot.telemetry](#)

Examples

```
# Load package and data
library(ctmm)
data(buffalo)

# assign distinct colors to buffalo
COL <- color(buffalo,by='individual')
# Notice the separation into RGB and CMY for maximum contrast
plot(buffalo,col=COL)

# annotate buffalo with sunlight data and compute colors
buffalo <- annotate(buffalo,cores=2) # CRAN policy limits to 2 cores
COL <- color(buffalo,by='sun')

# use North-preserving projection and plot
projection(buffalo) <- median(buffalo)
plot(buffalo,col=COL)
```

ctmm

Specify, fit, and select continuous-time movement models

Description

These functions allow one to propose hypothetical movement models (with initial estimates), fit those models to the data, and select among those models via an information criterion. The fitting functions wrap around `optim` and `ctmm.loglike` to fit continuous-time movement models to 2D animal tracking data as described in Fleming et al (2014) and Fleming et al (2015), and Fleming et al (2017).

Usage

```
ctmm(tau=NULL,omega=FALSE,isotropic=FALSE,range=TRUE,circle=FALSE,error=FALSE,
      axes=c("x","y"),...)

ctmm.loglike(data,CTMM,REML=FALSE,profile=TRUE,zero=0,verbose=FALSE,compute=TRUE,...)
```

```
ctmm.fit(data, CTMM=ctmm(), method="pHREML", COV=TRUE, control=list(), trace=FALSE)

ctmm.select(data, CTMM, verbose=FALSE, level=1, IC="AICc", MSPE="position", trace=FALSE, cores=1,
...)
```

Arguments

<code>tau</code>	Array of autocorrelation timescales (explained below).
<code>omega</code>	Frequency ($2\pi/\text{period}$) of oscillatory range crossings.
<code>isotropic</code>	A Boolean denoting whether or not the animal's covariance is circular or elliptical.
<code>range</code>	A Boolean denoting whether or not the movement model has a finite range.
<code>circle</code>	(2π divided by) the period it takes the animal to stochastically circle its mean location.
<code>error</code>	A Boolean denoting whether or not to use annotated telemetry error estimates or an estimate of the error's standard deviation if the data are not annotated with error estimates or when $HDOP = 1$.
<code>axes</code>	Spatial dimensions of the movement model.
<code>data</code>	Timeseries data represented as a telemetry object.
<code>CTMM</code>	A ctmm movement-model object containing the initial parameter guesses conforming to the basic structure of the model hypothesis. <code>ctmm.select</code> can accept a list of such objects.
<code>REML</code>	Use residual maximum likelihood if TRUE. Not recommended.
<code>profile</code>	Analytically solve for as many covariance parameters as possible.
<code>zero</code>	Calculates $\log(\text{likelihood}) - \text{zero}$, instead of just $\log(\text{likelihood})$, in a way that maintains numerical precision if the constant zero is close to the log likelihood. Used internally by <code>ctmm.fit</code> .
<code>verbose</code>	Return additional information. See "Value" below.
<code>compute</code>	Only return computational information if FALSE.
<code>method</code>	Fitting method to use: "ML", "HREML", "pREML", "pHREML", or "REML". See "Description" below.
<code>COV</code>	Estimate the autocorrelation parameter covariance matrix.
<code>control</code>	An optional argument list for optimizer .
<code>trace</code>	Report progress updates. Can be among 0:3 with increasing detail.
<code>level</code>	Attempt to simplify a model if a feature's non-existence falls within this level of confidence interval.
<code>IC</code>	Information criterion used for selection. Can be "AICc", "AIC", "BIC", "LOOCV", "HSCV", or none (NA). AICc is approximate.
<code>MSPE</code>	Reject non-stationary features that increase the mean square predictive error of "position", "velocity", or not (NA).
<code>cores</code>	Maximum number of models to fit in parallel. <code>cores=0</code> will use all cores, while <code>cores<0</code> will reserve <code>abs(cores)</code> .
<code>...</code>	Further arguments passed to <code>ctmm.fit</code> .

Details

Model fitting and selection first requires a prototype model with guesstimated parameters (i.e., Brownian motion with a particular diffusion rate). The initial `ctmm` parameter guess can be generated by the output of `ctmm.guess`, `variogram.fit` or manually specified with the function `ctmm(...)`, where the argument `tau` is explained below and additional model options described in `vignette("ctmm")`.

By default, `tau` (τ) is an ordered array of autocorrelation timescales. If `length(tau)==0`, then an IID bi-variate Gaussian model is fit to the data. If `length(tau)==1`, then an Ornstein-Uhlenbeck (OU) model (Brownian motion restricted to a finite home range) is fit to the data, where `tau` is the position autocorrelation timescale. `tau=Inf` then yields Brownian motion (BM). If `length(tau)==2`, then the OUF model (continuous-velocity motion restricted to a finite home range) is fit to the data, where `tau[1]` is again the position autocorrelation timescale and `tau[2]` is the velocity autocorrelation timescale. `tau[1]=Inf` then yields integrated Ornstein-Uhlenbeck (IOU) motion, which is a spatially unrestricted continuous-velocity process.

Two new models were introduced in `ctmm` version 0.5.2 for the case of `tau[1]==tau[2]`, which can happen with short tracks of data. When `tau[1]==tau[2]` and `omega==0`, the model is categorized as OUF—a special case of OUF—and the two `tau` parameters are treated as identical. On the other hand, when `tau[1]==tau[2]` and `omega>0`, an oscillatory model is implemented, which we refer to as $OU\Omega$.

The potential fitting methods—maximum likelihood (ML), residual maximum likelihood (REML), perturbative REML (pREML), hybrid REML (HREML), and perturbative hybrid REML (pHREML)—are described in Fleming et al (2019). In general, pHREML is the best method, though when parameter estimates lie near boundaries it can fail, in which case `ctmm.fit` will fall back to HREML, as reported by the method slot of the resulting fit object.

The control list can take the following arguments, with defaults shown:

`method="pNewton"` The partial-Newton method of `optimizer` is default. See `optim` for alternative methods in multiple dimensions.

`precision=1/2` Fraction of machine numerical precision to target in the maximized likelihood value. MLEs will necessarily have half this precision. On most computers, `precision=1` is approximately 16 decimal digits of precision for the likelihood and 8 for the MLEs.

`maxit=.Machine$integer.max` Maximum number of iterations allowed for optimization.

Model selection in `ctmm.select` proceeds in two phases. If there are a large number of parameters that must be fit numerically (such as when error is modeled), then the target model (argument `CTMM`) is worked toward by first fitting simpler, compatible models. The second phase proceeds by attempting to simplify the autocorrelation model and complexify the deterministic (trend) model until the information criterion fails to improve. The intent of working in these directions is to improve numerical convergence and avoid fitting trends to autocorrelation. Note that simpler models in a nested hierarchy will only be attempted if they appear credible, which can be adjusted with the `level` argument. `level=1` will, therefore, always attempt a simpler model.

The leave-one-out cross validation IC, `IC="LOOCV"`, is (-2 times) the sum of log-likelihoods of the validation data, after fitting to and conditioning on the training data. This information criterion is intended for small amounts of data where AIC/BIC are not valid, and where the questions of interest are targeted at the finest scales of the data, such as speed or occurrence. Unlike other model-selection criteria, the computational complexity of LOOCV is $O(n^2)$, which is very slow

for sample sizes on the order of 10-100 thousand locations. Furthermore, as autocorrelation in the validation data is ignored, this information criterion is not valid for making inferences at scales coarser than the sampling interval, such as home range.

The half-sample cross validation IC, $IC="HSCV"$, is (-2 times) the sum of log-likelihoods of the validation data, after fitting to and conditioning on the training data consisting of the first (and second) halves of the data when split temporally. This information criterion is intended for when few range crossings are observed and AIC/BIC may not be valid.

Value

The function `ctmm` returns a prototype `ctmm` movement-model object. By default, `ctmm.loglike` returns the log-likelihood of the model CTMM. `ctmm.fit` (and `ctmm.loglike` with `verbose=TRUE`) returns the estimated `ctmm` movement-model object with all of the components of CTMM plus the components listed below. `ctmm.select` returns the best model by default, or the sorted list of attempted models if `verbose=TRUE`, with the best model being first in the list.

AICc The approximate corrected Akaike information criterion for multivariate distributions with variable numbers of unknown mean and (structured) covariance parameters (Burnham & Anderson, Eq. 7.91). This formula is only exact for IID data.

loglike The log-likelihood.

sigma The maximum likelihood variance/covariance estimate (possibly debiased). For the endlessly diffusing BM and IOU processes, this is instead the diffusion rate estimate.

mu The maximum likelihood stationary mean vector estimate.

COV.mu The covariance matrix of the `mu` estimate, assuming that the covariance estimate is correct.

DOF.mu The effective number of degrees of freedom in the estimate of `mu`, assuming that the autocorrelation model is correct. This can be much smaller than `length(data$t)` if the data are autocorrelated.

COV Covariance of the autocovariance parameter estimate vector `c(sigma,tau,circle)`, as derived (asymptotically) from the hessian of the log-likelihood function, and where `sigma` is parameterized in terms of its largest variance major, the ratio of the smallest to largest variance minor, and angle of orientation. Typically, `sigma`'s major parameter is extremely correlated to `tau[1]`, and sequential components of `tau` are slightly correlated.

Warnings

The warning "MLE is near a boundary or `optim()` failed" indicates that you should be using `ctmm.select` rather than `ctmm.fit`, because some features are not well supported by the data.

The warning "pREML failure: indefinite ML Hessian" is normal if some autocorrelation parameters cannot be well resolved.

Note

The default optimization method in `ctmm` v0.5.7 and above is `optimizer`'s "pNewton". Anecdotaly, on these problems, `optimizer`'s pNewton method generally outperforms `optim`'s "Nelder-Mead", which generally outperforms `optim`'s "BFGS" and "L-BFGS-B" methods. With default arguments, "pNewton" is about half as fast as "Nelder-Mead", but is resolving about twice as much numerical precision by default.

The AICs/BICs of endlessly diffusing models like BM and IOU cannot be easily compared to the AICs/BICs of range resident models like bivariate Gaussian, OU, and OUF, as their joint likelihood functions are infinitely different. Endlessly diffusing models have to be conditioned off of an initial state, which we derive in `ctmm` by taking the large range limit of a range-restricted process. I.e., BM is the limit $OU(\text{Inf})$ and $IOU(\text{tau})$ is the limit $OUF(\text{Inf}, \text{tau})$. Using comparable likelihood functions gives up statistical efficiency and the objective prior. Moreover, comparing conditional likelihoods—with the objective prior taken from the joint likelihood—does not appear to select the true model with a likelihood ratio test. Different criteria must be used to select between range resident and endlessly diffusing movement models.

Prior to v0.3.6, the univariate AICc formula was (mis)used, with the full parameter count treated as degrees of freedom in the mean. As of v0.3.6, the mean and autocovariance parameters are treated separately in the approximate multivariate AICc formula (Burnham & Anderson, Eq. 7.91). Still, this improved formula is only exact for IID data.

Prior to v0.3.2, `ctmm.select` would consider every possible model. This is no longer feasible with current versions of `ctmm`, as the number of possible models has grown too large.

Author(s)

C. H. Fleming and G. Péron.

References

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- C. H. Fleming, M. J. Noonan, E. P. Medici, J. M. Calabrese, “Overcoming the challenge of small effective sample sizes in home-range estimation”, *Methods in Ecology and Evolution* 10:10, 1679-1689 (2019) [doi:10.1111/2041210X.13270](https://doi.org/10.1111/2041210X.13270).

See Also

[ctmm.boot](#), [ctmm.guess](#), [optimizer](#), [summary.ctmm](#), [variogram.fit](#).

Examples

```
# Load package and data
library(ctmm)
data(buffalo)
DATA <- buffalo$Cilla

GUESS <- ctmm.guess(DATA, interactive=FALSE)
```

```
# in general, you want to run ctmm.select instead
FIT <- ctmm.fit(DATA,GUESS)

# some human-readable information
summary(FIT)
```

ctmm-FAQ

ctmm FAQ

Description

Frequently asked questions for the ctmm package.

Details

General recommendations

1. Work through the vignettes `vignette("variogram")` and `vignette("akde")`. Also, see the help file for the method of interest, and its example.
2. Do not save workspaces between sessions. They will become corrupted over time. In RStudio, go to Tools: Global Options: Workspace, uncheck Restore and set Save to Never.
3. If RStudio is crashing frequently in Windows (or your display driver is crashing), try setting the rendering engine to Software under Tools : Global Options : General : Advanced : Rendering Engine.
4. Never edit or save your CSV in Microsoft Excel. The dates will be reformatted incorrectly and inconsistently.
5. If using Windows, make sure to have the suggested version of “Rtools” installed. If using MacOS, make sure to have “Xcode” installed. If using Ubuntu, make sure to have “build-essential” installed. Otherwise, you can sometimes run into problems when trying to update packages.
6. Upgrade R to the latest version and update all of your packages.
7. The development build can be installed via `remotes::install_github("ctmm-initiative/ctmm")`.
8. Sometimes installing from Github can silently fail to overwrite old files, requiring the package to be manually uninstalled, and then re-installed after restarting.
9. Stable beta releases between the CRAN release are published [here](#) on request.
10. The [ctmm user's group](#) is a good place to find and ask for help.
11. Bug reports and feature requests can be raised at the [Github project page](#).

Help installing packages on Linux

These are the packages I needed in Ubuntu:

```
sudo apt install ffmpeg fftw3 libfftw3-dev libgdal-dev libgeos-dev libgit2-dev libgmp-dev
libgsl-dev libmpfr-dev libproj-dev libnode-dev libudunits2-dev r-base-core
```

as.telemetry **reports abnormal sampling intervals and speeds**

Make sure that you have the correct `timezone` and `timeformat` arguments specified. Also, see [outlie](#).

rdb database corruption, "could not find function", "cannot coerce class", and other weird errors

R might not have installed or loaded the package correctly—e.g., some files may have failed to overwrite previous versions—or the workspace/session might be corrupted. Uninstall `ctmm`, restart R without saving the workspace/session, and install `ctmm` again.

Infinite recursion and stack overflow errors

`ctmm` has no recursive functions, so I am not exactly sure what causes this error, but it only occurs with certain versions of R on certain computer architectures. There are several solutions that have worked for people, including restarting R in a fresh session and updating their software. Alternatively:

1. Reboot your computer.
2. Increase the allowed number of nested expressions within R via `options(expressions=10000)` or some other large number.
3. Try a different computer.

plot complains about the datatype or has weird errors

Namespace collision sometimes occurs between `raster`, `sp`, `move`, and `ctmm`. Either restart R and only load the `ctmm` package, or run `ctmm::plot` instead of `plot`.

North is no longer up after importing data

The default projection in `ctmm` does not preserve the direction of North, but better preserves distances for elongated distributions. See the `projection` argument in [as.telemetry](#) and the example in [projection](#). The [compass](#) function is also useful for pointing north.

projection complains about the datatype and fails

Namespace collision can occur between `raster` and `ctmm`. Either restart R and only load the `ctmm` package, or run `ctmm::projection` instead of `projection`.

ctmm.guess has no save button

Maximize the plot window and/or increase your screen resolution.

manipulate panel does not popup in ctmm.guess or zoom

Click the gear icon in the upper-left corner of the plot window.

Gear icon missing in ctmm.guess or zoom

Recent versions of `manipulate` and/or RStudio seem to have some issues. Sometimes the gear icon does not render unless you re-run the function 2-5 times.

manipulate::isAvailable is not found

You probably have an outdated copy of the `manipulate` package installed. Update R to the latest version and then update all of your packages. This seems to happen frequently with the MacOS release of R.

Author(s)

C. H. Fleming

ctmm.boot

*Parametric bootstrap continuous-time movement models***Description**

This function allows the point estimates and confidence intervals of an initial estimated movement model to be improved by parametric bootstrap, as described in Fleming et al (2019).

Usage

```
ctmm.boot(data, CTMM, method=CTMM$method, AICc=FALSE, iterate=FALSE, robust=FALSE, error=0.01,
          cores=1, trace=TRUE, ...)
```

Arguments

data	Timeseries data represented as a telemetry object.
CTMM	A ctmm movement-model object from the output of <code>ctmm.fit</code> containing the initial parameter estimates.
method	Fitting method to use: "ML", "HREML", "pREML", "pHREML", or "REML". See ctmm.fit for descriptions.
AICc	Run dual set of simulations to approximate AICc values via Kullback–Leibler divergence. Otherwise, only the AIC is updated.
iterate	Iteratively solve for the parameters such that the average estimate (of method) is that of the data, whereas with <code>iterate=FALSE</code> only the first-order correction is calculated from the initial estimate.
robust	Uses robust estimates of the average and covariation for debiasing. Useful when parameters are near boundaries.
error	Relative standard error target for bootstrap ensemble estimates and nonlinear iterations.
cores	Number of simulations to run in parallel. <code>cores=NULL</code> will use all cores, while <code>cores<0</code> will reserve <code>abs(cores)</code> .
trace	Report progress updates. Can be among 0:2 with increasing detail.
...	Further arguments passed to ctmm.fit .

Value

A model fit object with relatively unbiased estimates of location covariance, and autocorrelation timescales (and more accurate CIs than `ctmm.fit`). If `AICc=TRUE`, then, in addition to an updated AICc slot, the model fit object will also contain a `VAR.AICc` slot quantifying the numerical variance in the AICc estimate. This variance can be decreased by decreasing argument `error`.

Author(s)

C. H. Fleming.

References

C. H. Fleming, M. J. Noonan, E. P. Medici, J. M. Calabrese, “Overcoming the challenge of small effective sample sizes in home-range estimation”, *Methods in Ecology and Evolution* 10:10, 1679-1689 (2019) [doi:10.1111/2041210X.13270](https://doi.org/10.1111/2041210X.13270).

See Also

[ctmm.fit](#).

Examples

```
# Load package and data
library(ctmm)
data(gazelle)
DATA <- gazelle[[3]]

GUESS <- ctmm.guess(DATA, interactive=FALSE)
FIT <- ctmm.select(DATA, GUESS)

# some human-readable information
summary(FIT)

# in general, you will want to set iterate=TRUE, trace=TRUE
BOOT <- ctmm.boot(DATA, FIT, iterate=FALSE, trace=FALSE)

# compare to the previous estimate
summary(BOOT)
```

difference

Estimate the proximity of two individuals

Description

Given a pair of telemetry objects and ctmm movement models, predict their location differences or midpoints at shared times and estimate their distances.

Usage

```
difference(data, CTMM, t=NULL, ...)
```

```
midpoint(data, CTMM, t=NULL, complete=FALSE, ...)
```

```
distances(data, CTMM, t=NULL, level=0.95, ...)
```

```
proximity(data, CTMM, t=NULL, GUESS=ctmm(error=TRUE), debias=TRUE, level=0.95, ...)
```

Arguments

<code>data</code>	A list of two telemetry objects.
<code>CTMM</code>	A list of two <code>ctmm</code> movement-model objects.
<code>t</code>	An optional vector of times or range of times over which to predict the location differences.
<code>complete</code>	Additionally calculate timestamps and geographic coordinates.
<code>level</code>	Confidence level for the distance/proximity estimate.
<code>GUESS</code>	An optional <code>ctmm</code> object to specify the candidate model parameters of the location differences.
<code>debias</code>	Include inverse- χ^2 bias corrections.
<code>...</code>	Options passed to <code>ctmm.select</code> .

Details

The difference function predicts the location difference vectors, $(x_A - x_B, y_A - y_B)$, for a pair of individuals, $\{A, B\}$, at overlapping times. The midpoint function predicts the location midpoints, $(x_A + x_B, y_A + y_B)/2$, for a pair of individuals. The distances function further estimates the instantaneous distances between individuals. The proximity function fits an autocorrelation model to the output of difference, and then compares the mean-square distance between the individuals to what you would expect if the two individuals were moving independently.

Value

difference and midpoint output telemetry objects of the location differences and midpoints with prediction covariances. distances outputs a `data.frame` of distance estimates with confidence intervals. proximity outputs a ratio estimate with confidence intervals, where values <1 indicate that the two individuals are closer on average than expected for independent movement, 1 is consistent with independent movement, and values >1 indicate that the individuals are farther from each other on average than expected for independent movement. Therefore, if the CIs contain 1, then the distance is insignificant with a p-value threshold of $1 - \text{level}$ (two-sided) or half that for a one-sided test.

Author(s)

C. H. Fleming.

See Also

[ctmm.select](#), [predict.ctmm](#)

Examples

```
#Load package
library(ctmm)

# load buffalo data
data(buffalo)
```

```

# select two buffalo that overlap in space and time
DATA <- buffalo[c(1,3)]
# plot the two buffalo
plot(DATA,col=c('red','blue'))

FITS <- list()
for(i in 1:2)
{
  GUESS <- ctmm.guess(DATA[[i]],interactive=FALSE)
  # in general, you want to use ctmm.select
  FITS[[i]] <- ctmm.fit(DATA[[i]],GUESS)
}

# calculate difference vectors
DIFF <- difference(DATA,FITS)
# plot the difference vectors with prediction-error ellipses
plot(DIFF)

# calculate the proximity statistic
# disabling location error for speed
proximity(DATA,FITS,GUESS=ctmm(error=FALSE))

```

distance	<i>Calculate the square distance between two distributions or location estimates</i>
----------	--

Description

This function calculates various square distances measures between distributions, including the, Bhattacharyya distance, Mahalanobis distance, and Euclidean distance.

Usage

```
distance(object,method="Mahalanobis",sqrt=FALSE,level=0.95,debias=TRUE,...)
```

Arguments

object	A list of ctmm fit objects or single-location telemetry objects to compare.
method	Square distance measure to return: "Bhattacharyya", "Mahalanobis", or "Euclidean".
sqrt	Return the linear distance.
level	The confidence level desired for the output.
debias	Approximate debiasing of the square distance.
...	Not currently used.

Value

A list with tables DOF, containing the effective samples sizes of the estimates, and CI, containing the confidence intervals of the distance estimates. A value of 0 implies that the two distributions have the same mean location, while larger values imply that the two distributions are farther apart. The (square) Euclidean distance has units of square meters, if `sqr t=FALSE`. The square Mahalanobis and Bhattacharyya distances are unitless. For the Euclidean distance, only the centroids are compared.

Note

The Bhattacharyya distance (BD) is naturally of a squared form and is not further squared.

Author(s)

C. H. Fleming

See Also

[ctmm.fit](#), [overlap](#)

Examples

```
# Load package and data
library(ctmm)
data(buffalo)

# fit models for first two buffalo
GUESS <- lapply(buffalo[1:2], function(b) ctmm.guess(b,interactive=FALSE) )
# using ctmm.fit here for speed, but you should almost always use ctmm.select
FITS <- lapply(1:2, function(i) ctmm.fit(buffalo[[i]],GUESS[[i]]) )
names(FITS) <- names(buffalo[1:2])

# Mahalanobis distance between these two buffalo
distance(FITS)
```

dt.plot

Functions for diagnosing sampling schedules

Description

Produces a log-scale plot of the sorted sampling intervals for inspection.

Usage

```
dt.plot(data,...)
```

Arguments

<code>data</code>	A telemetry object.
<code>...</code>	Additional options passed to plot.

Details

Horizontal lines are included at common sampling intervals (e.g., 1-hour) and dimmed horizontal lines are included at common subdivisions (e.g., 30-minutes).

Author(s)

C. H. Fleming.

See Also

[as.telemetry](#).

Examples

```
# Load package and data
library(ctmm)
data(gazelle)

# Plot the sampling intervals
dt.plot(gazelle)
```

emulate

Draw a random model-fit from the sampling distribution

Description

This function generates random model-fit statistics from the sampling distribution of a given ctmm movement model and sampling schedule. If `fast=FALSE`, the results are exact, though slow to evaluate. Else if `fast=TRUE`, the central-limit theorem is invoked.

Usage

```
emulate(object,...)

## S3 method for class 'ctmm'
emulate(object,data=NULL,fast=FALSE,...)

## S3 method for class 'telemetry'
emulate(object,CTMM,fast=FALSE,...)
```

Arguments

<code>object</code>	telemetry data or ctmm model object.
<code>CTMM</code>	A ctmm movement-model object.
<code>data</code>	Optional telemetry object for exact results.
<code>fast</code>	Whether or not to invoke the central-limit theorem.
<code>...</code>	Arguments passed to ctmm.fit .

Details

Given `fast=FALSE`, which requires the `data` argument specified, new data are simulated from the CTMM movement model with the same sampling schedule and error structure as `data`. A new model, of the same structure as CTMM, is then fit to the simulated data and returned.

Given `fast=TRUE`, a model-fit object is sampled from the central-limit distribution, using the covariance estimates within CTMM. Strictly positive parameters, such as `area`, are log-transformed prior to the normal approximation. Note that this faster method does not adjust for bias.

Value

A `ctmm` movement model with the same structure as CTMM.

Author(s)

C. H. Fleming.

See Also

[ctmm.fit](#), [simulate.ctmm](#)

encounter	<i>Encounter statistics</i>
-----------	-----------------------------

Description

Functions to calculate encounter probabilities and the conditional location distribution of where encounters take place (conditional on said encounters taking place), as described in Noonan et al (2021).

Usage

```
encounter(object,debias=FALSE,level=0.95,normalize=FALSE,self=TRUE,...)
```

```
cde(object,include=NULL,exclude=NULL,debias=FALSE,...)
```

Arguments

<code>object</code>	A list of aligned UD objects.
<code>debias</code>	Approximate bias corrections [IN DEVELOPMENT].
<code>level</code>	Confidence level for relative encounter rates.
<code>normalize</code>	Normalize relative encounter rates by the average uncorrelated self-encounter rate.
<code>self</code>	Fix the self-interaction rate appropriately.
<code>include</code>	A matrix of interactions to include in the calculation (see Details below).
<code>exclude</code>	A matrix of interactions to exclude in the calculation (see Details below).
<code>...</code>	Additional arguments for future use.

Details

Encounter probabilities are standardized to 1 meter, and must be multiplied by the square encounter radius (in meters), to obtain other values. If `normalize=FALSE`, the relative encounter rates have units of $1/m^2$ and tend to be very small numbers for very large home-range areas. If `normalize=TRUE`, the relative encounter rates are normalized by the average uncorrelated self-encounter rate, which is an arbitrary value that provides a convenient scaling.

The `include` argument is a matrix that indicates which interactions are considered in the calculation. By default, `include = 1 - diag(length(object))`, which implies that all interactions are considered aside from self-interactions. Alternatively, `exclude = 1 - include` can be specified, and is by-default `exclude = diag(length(object))`, which implies that only self-encounters are excluded.

Value

`encounter` produces an array of standardized encounter probabilities with CIs, while `cde` produces a single UD object.

Note

Prior to v1.2.0, `encounter()` calculated the CDE and `rates()` calculated relative encounter probabilities.

Author(s)

C. H. Fleming

References

M. J. Noonan, R. Martinez-Garcia, G. H. Davis, M. C. Crofoot, R. Kays, B. T. Hirsch, D. Caillaud, E. Payne, A. Sih, D. L. Sinn, O. Spiegel, W. F. Fagan, C. H. Fleming, J. M. Calabrese, “Estimating encounter location distributions from animal tracking data”, *Methods in Ecology and Evolution* (2021) [doi:10.1111/2041210X.13597](https://doi.org/10.1111/2041210X.13597).

See Also

[akde](#), [overlap](#)

Examples

```
# Load package and data
library(ctmm)
data(buffalo)

# fit models for first two buffalo
GUESS <- lapply(buffalo[1:2], function(b) ctmm.guess(b, interactive=FALSE) )
# in general, you should use ctmm.select here
FITS <- lapply(1:2, function(i) ctmm.fit(buffalo[[i]], GUESS[[i]]) )
names(FITS) <- names(buffalo[1:2])

# create aligned UDs
```



```

UDS <- akde(buffalo[1:2],FITS)

# calculate 100-meter encounter probabilities
P <- encounter(UDS)
P$CI * 100^2

# calculate CDE
CDE <- cde(UDS)

# plot data and encounter distribution
plot(buffalo[1:2],col=c('red','blue'),UD=CDE,col.DF='purple',col.level='purple',col.grid=NA)

```

export

Export ctmm data formats

Description

Functions to export ctmm data formats into common sp, sf, raster, and ESRI formats.

Usage

```

as.sf(x,error=FALSE,...)

## S4 method for signature 'UD'
raster(x,DF="CDF",...)

## method for class 'telemetry'
SpatialPoints.telemetry(object,...)

## method for class 'telemetry'
SpatialPointsDataFrame.telemetry(object,...)

## method for class 'telemetry'
SpatialPolygonsDataFrame.telemetry(object,level.UD=0.95,...)

## method for class 'UD'
SpatialPolygonsDataFrame.UD(object,convex=FALSE,level.UD=0.95,level=0.95,...)

## S4 method for signature 'UD,character'
writeRaster(x,filename,format,DF="CDF",...)

## S4 method for signature 'list,character'
writeVector(x,filename,...)

## S4 method for signature 'list,missing'
writeVector(x,filename,...)

## S4 method for signature 'telemetry,character'

```

```

writeVector(x,filename,filetype="ESRI Shapefile",error=TRUE,level.UD=0.95,...)

## S4 method for signature 'telemetry,missing'
writeVector(x,filename,filetype="ESRI Shapefile",error=TRUE,level.UD=0.95,...)

## S4 method for signature 'UD,character'
writeVector(x,filename,filetype="ESRI Shapefile",convex=FALSE,level.UD=0.95,level=0.95,
            ...)

## S4 method for signature 'UD,missing'
writeVector(x,filename,filetype="ESRI Shapefile",convex=FALSE,level.UD=0.95,level=0.95,
            ...)

```

Arguments

x	telemetry or UD object.
error	Export telemetry location error circles/ellipses as polygons if TRUE.
object	telemetry or UD object.
convex	Export convex coverage areas if TRUE. By default, the highest density regions (HDRs) are exported.
level.UD	Coverage level of the UD area. I.e., the 50% core home range would be given by level.UD=0.50.
level	Confidence level for the magnitude of the above area. I.e., the 95% CI of the core home range area.
DF	Rasterize the probability density function "PDF", probability mass function "PMF", or cumulative distribution function "CDF".
filename	Character name of file for raster or vector file.
format	Output file type (see writeFormats). If this argument is not provided, it is inferred from the filename extension. If that fails, the default 'raster' format is used, which can be changed using rasterOptions .
filetype	A file format associated with a GDAL "driver". See <code>gdal(drivers=TRUE)</code> or the GDAL docs . If filetype=NULL, the filetype is inferred from the filename extension.
...	Optional arguments passed to writeRaster , writeVector , etc..

Details

`as.sf` exports `ctmm` objects to the `sf` format. Arguments to `ctmm Spatial*` export functions can also be used, such as `level.UD` and `level`.

`raster` exports UD object point-estimates distribution functions (DF) to raster objects. `DF="PDF"` gives the average probability density per cell, `DF="PMF"` gives the total probability per cell, and `DF="CDF"` gives the cumulative probability.

`Spatial*` functions export `ctmm` objects to `sp` formats.

`writeRaster` writes a raster file to disk, with pixel values corresponding to the distribution function DF.

`writeVector` writes a shapefile to disk, with UD polygons corresponding to the low-CI, point-estimate, and high-CI home-range area estimates.

Value

`as.sf` returns an `sf` object for the input points or polygons, with individual identity and other information retained.

`raster` returns a raster of the point-estimate distribution function DF, given a UD object.

`SpatialPoints.telemetry` returns a single `SpatialPoints` object for the x-y locations, without individual identity and other information retained.

`SpatialPointsDataFrame.telemetry` returns a `SpatialPointsDataFrame` with the individual identities and other data recorded in the data frame retained.

`SpatialPolygonsDataFrame.telemetry` returns a `SpatialPolygonsDataFrame` that encodes the location estimate's error circles/ellipses.

`SpatialPolygonsDataFrame.UD` returns a `SpatialPolygonsDataFrame` of the low-CI, point-estimate, and high-CI home-range area estimates, in the appropriate order for plotting.

Author(s)

C. H. Fleming and K. Safi.

See Also

[akde](#), [as.telemetry](#), [occurrence](#).

extent	<i>Extent</i>
--------	---------------

Description

Functions to calculate the (x, y) plotting extent (or bounding box) of various `ctmm` objects or list of such objects, for use when plotting multiple `ctmm` objects.

Usage

```
## S4 method for signature 'telemetry'
extent(x, level=1, ...)

## S4 method for signature 'ctmm'
extent(x, level=0.95, level.UD=0.95, ...)

## S4 method for signature 'UD'
extent(x, level=0.95, level.UD=0.95, complete=FALSE, ...)

## S4 method for signature 'variogram'
extent(x, level=0.95, threshold=2, ...)
```

```
## S4 method for signature 'list'
extent(x,...)

## S4 method for signature 'data.frame'
extent(x,level=1,...)

## S4 method for signature 'matrix'
extent(x,level=1,...)
```

Arguments

x	A telemetry, ctm, or UD object.
level	For telemetry objects, this is the fraction of locations bounded, according to two-sided quantiles. For ctm and UD objects, this is confidence level for the magnitude of the utilization area circumscribed by level.UD.
level.UD	Coverage level of the UD area. I.e., the 50% core home range would be given by level.UD=0.50.
complete	Also calculate longitude-latitude extent of UD objects.
threshold	Limit ylim to threshold times the maximum semi-variance, even if the level confidence intervals exceed this amount.
...	Optional arguments for future extensions.

Details

Returns a data.frame with columns x and y with rows min and max. See vignette('akde') for an example of extent used to plot multiple UDs on the same scale.

Author(s)

C. H. Fleming

See Also

[plot.telemetry](#), [plot.variogram](#).

format

Scientific formatting of numbers

Description

Functions for concisely representing dimensionful quantities and uncertain quantities.

Usage

```
dimfig(data,dimension,thresh=1,...)
```

```
sigfig(est,VAR=NULL,SD=NULL,level=0.95,digits=2,...)
```

Arguments

data	A numerical vector of dimensionful quantities represented in SI units.
dimension	One of "length", "area", "time", "frequency", "speed", "diffusion", or "mass".
thresh	Threshold quantity for switching between units. E.g., 100 cm is represented as 1 m only if thresh>=1.
est	Can be either confidence-interval estimates with rows (lower-limit,point-estimate,upper-limit) or point estimates (with VAR or SD also specified).
VAR	Variance in the sampling distribution of x.
SD	Standard deviation in the sampling distribution of x.
level	Confidence level for designating the numerical precision of the significant digits.
digits	Number of significant digits to retain.
...	Not currently used.

Details

dimfig chooses the set of units that provides the most concise representation for data, and sigfig concisely represents statistical estimates with a fixed number of significant digits.

Value

dimfig returns a list with slots for the converted data and the name of the most concise units. sigfig returns a character string that is formatted with the specified number of significant digits.

Author(s)

C. H. Fleming.

See Also

[%#%](#)

Examples

```
# Load package and data
library(ctmm)
data(buffalo)
DATA <- buffalo$Cilla

GUESS <- ctmm.guess(DATA,interactive=FALSE)
# in general, you want to run ctmm.select instead
FIT <- ctmm.fit(DATA,GUESS)

# raw summary (SI units)
summary(FIT,units=FALSE)

# default summary (concise units)
summary(FIT,units=TRUE)
```

```
# text-formatted summary
sigfig( summary(FIT)$CI )
```

gazelle

Mongolian gazelle GPS dataset from the Mongolia's Eastern Steppe.

Description

x-y projected GPS data on 36 Mongolian gazelle.

Usage

```
data("gazelle")
```

Format

A list of 36 telemetry objects.

References

C. H. Fleming, J. M. Calabrese, T. Mueller, K.A. Olson, P. Leimgruber, and W. F. Fagan. Data from: From fine-scale foraging to home ranges: A semi-variance approach to identifying movement modes across spatiotemporal scales. Dryad Digital Repository (2014) [doi:10.5061/dryad.45157](https://doi.org/10.5061/dryad.45157).

See Also

[as.telemetry](#), [plot.telemetry](#), [buffalo](#), [coati](#), [jaguar](#), [pelican](#), [turtle](#), [wolf](#).

Examples

```
# Load package and data
library(ctmm)
data("gazelle")

# Plot a gazelle's locations
plot(gazelle[[18]])
```

homerange	<i>Calculate a range distribution estimate</i>
-----------	--

Description

Estimates the range distributions and suitability from telemetry data and a continuous-time movement model.

Usage

```
homerange(data, CTMM, method="AKDE", ...)
```

```
agde(data=NULL, CTMM=NULL, R=list(), variable="utilization", error=0.001, res=100, grid=NULL, ...)
```

```
suitability(data=NULL, CTMM=NULL, R=list(), level=0.95, grid=NULL, log=FALSE, ...)
```

Arguments

data	2D timeseries telemetry data represented as a telemetry object.
CTMM	A ctmm movement model from the output of <code>ctmm.fit</code> .
method	Which range distribution method to use. Can be "AKDE" or "AGDE".
...	Arguments passed to the method call or bandwidth .
R	A named list of raster covariates if CTMM contains an RSF model
variable	Not yet supported.
error	Target probability error.
res	Number of grid points along each axis, relative to the location covariance.
grid	Grid specification via raster, UD, or list of arguments (See akde for details).
level	Confidence level for output confidence intervals.
log	Calculate the log(suitability).

Details

`homerange` is a wrapper function that calls either [akde](#) or `agde`. Please consult [akde](#) for further details on `method="AKDE"`.

`suitability` calculates a suitability raster from an [rsf.fit](#) object. Population RSF fit objects calculated from [mean](#) will produce a suitability estimate of the population.

`agde` calculates autocorrelated Gaussian and RSF home-range areas.

Value

`homerange` and `agde` return a UD object. `suitability` returns a [brick](#) object.

Author(s)

C. H. Fleming.

See Also

[akde](#), [raster](#), [UD-method](#)

intensity

Compare empirical and theoretical intensity (resource-selection) functions [IN DEVELOPMENT]

Description

This function plots the empirical and theoretical intensity functions with respect to a covariate of interest.

Usage

```
intensity(data,UD,RSF,R=list(),variable=NULL,empirical=FALSE,level=0.95,ticks=TRUE,
          smooth=TRUE,interpolate=TRUE,...)
```

Arguments

data	A telemetry object.
UD	A UD object generated by akde from the same telemetry object as data. If weights were optimized in akde , then they will be adopted by intensity.
RSF	An iRSF model-fit object from <code>rsf.fit</code> or <code>rsf.select</code> .
R	A named list of rasters or time-varying raster stacks [NOT TESTED] to fit Poisson regression coefficients to (under a log link).
variable	Variable of interest from <code>names(R)</code> .
empirical	Plot an empirical estimate of $\log \lambda$ [IN DEVELOPMENT].
level	Confidence level for intensity function estimates.
ticks	Demark used resource values atop the plot.
smooth	Apply location-error smoothing to the tracking data before regression.
interpolate	Whether or not to interpolate raster values during extraction.
...	Arguments passed to plot .

Details

With respect to the Poisson point process likelihood $L(\lambda) = \frac{\lambda(x,y)}{\iint \lambda(x',y') dx' dy'}$, the formula object of a ctm iRSF model corresponds to the covariate dependence of $\log(\lambda)$, which is typically of the form $\beta \cdot \mathbf{R}$. `intensity` plots both empirical (black) and theoretical (red) estimates of the log-intensity (or log-selection) function $\log(\lambda)$ as a function of the covariate variable, which provides a visualization of what the true formula looks like and how the fitted model compares. The empirical estimate is semi-parametric, in that it assumes that RSF is correct for all variables other than variable.

Note

Only relative differences in $\log(\lambda)$ are meaningful.

See Also

[rsf.fit.](#)

jaguar

Jaguar data from the Jaguar movement database.

Description

x-y projected GPS data on 4 jaguar. Please cite Morato et al (2018) when publishing with these data.

Usage

```
data("jaguar")
```

Format

A list of 4 telemetry objects.

References

R. G. Morato et al, "Jaguar movement database: a GPS-based movement dataset of an apex predator in the Neotropic", Ecology, 99:7, 1691-1691 (2018) [doi:10.1002/ecy.2379](#).

See Also

[as.telemetry](#), [plot.telemetry](#), [buffalo](#), [coati](#), [gazelle](#), [pelican](#), [turtle](#), [wolf](#).

Examples

```
# Load package and data
library(ctmm)
data("jaguar")

# Plot all jaguar locations
plot(jaguar,col=rainbow(length(jaguar)))
```

Log

Log transformation of parameter estimates and their uncertainties

Description

Methods for log transforming individual parameter estimates and their uncertainty estimates for use in meta-analytic regression, and then back-transforming mean-log parameter estimates back to mean parameter estimates.

Usage

```
Log(x,variable="area",debias=TRUE,...)
```

```
Exp(est,VAR.est=0,VAR=0,VAR.VAR=0,variable="area",debias=TRUE,level=0.95,units=TRUE,...)
```

Arguments

x	A list of UD objects, UD summary objects, or speed objects.
variable	Can be "area", "diffusion", "speed", "tau position", or "tau velocity".
debias	Apply $\log \chi^2$ and $\log \chi$ bias corrections if TRUE.
...	Further arguments passed.
est	Point estimate of the mean log-parameter.
VAR.est	Uncertainty in the mean log-parameter estimate (square standard error).
VAR	Variance in the log-parameters.
VAR.VAR	Uncertainty in the log-parameter variance estimate (square standard error).
level	Confidence level for parameter estimates.
units	Convert result to natural units.

Value

Log returns a list with two slots, log and VAR.log, corresponding to the point estimates and variance estimates of the logged variables.

Exp returns a confidence intervals for the back-transformed mean parameter estimate.

Author(s)

C. H. Fleming.

See Also

[meta](#), [mean](#).

Examples

```
# load package and data
library(ctmm)
data(buffalo)

# fit movement models
FITS <- AKDES <- list()
for(i in 1:length(buffalo))
{
  GUESS <- ctmm.guess(buffalo[[i]],interactive=FALSE)
  # use ctmm.select unless you are certain that the selected model is OUF
  FITS[[i]] <- ctmm.fit(buffalo[[i]],GUESS)
}

# calculate AKDES on a consistent grid
AKDES <- akde(buffalo,FITS)

# extract 95% areas
AREAS <- lapply(AKDES,summary)

# log transform for further meta-analysis
LOG <- Log(AREAS)

LOG
```

mean.ctmm

Average movement models and autocorrelated kernel density estimates

Description

These functions calculate population averages of continuous-time movement models and utilization distributions.

Usage

```
## S3 method for class 'ctmm'
mean(x,weights=NULL,sample=TRUE,debias=TRUE,IC="AIC",trace=TRUE,...)

## S3 method for class 'UD'
mean(x,weights=NULL,sample=TRUE,...)
```

Arguments

x	A list of ctmm objects calculated in the same projection or UD objects calculated on the compatible grids.
weights	A vector of numeric weights with the same length as x, specifying the relative frequency of each distribution in x.

sample	x represents a sample of a larger population if TRUE, or the entire statistical population if FALSE.
debias	Include $\log -\chi^2$ and REML bias corrections.
IC	Model selection criterion for the anisotropy of the distribution of mean locations and covariance matrices.
trace	Report location and autocovariance model selection results.
...	Additional arguments for future use.

Details

When applied to a list of `ctmm` objects, `mean` calculates an average movement model with population variability estimates. The population model is taken to be multivariate normal and log-normal. The population mean location represents an arithmetic mean, while the population mean home-range areas, RMS speeds, and diffusion rates represent geometric means. Location-error estimates are not correctly averaged yet.

When applied to a list of `UD` objects, `mean` calculates a weighted average of autocorrelated kernel density home-range estimates from `akde`. The point estimates are correct, but the confidence-interval calculation is not yet complete.

By default, uniform weights are used (`weights=rep(1,length(x))`). This can be sensible for averaging over individuals. For averaging over periods of time, users should consider weighting by the proportion of time spent in each distribution. For example, if an animal spends 4 months in its winter range, `x[[1]]`, and 7 months in its summer range, `x[[2]]`, then the annual range (sans migration corridor) would be calculated with `weights=c(4,7)`.

All `UD`s need to be calculated on the same grid (see [overlap](#) for an example).

Value

When applied to a list of `ctmm` objects, `mean` returns a `ctmm` object with additional population variability parameter estimates.

When applied to a list of `UD` objects, `mean` returns a `UD` object: a list with the sampled grid line locations `r$x` and `r$y`, the extent of each grid cell `dr`, the probability density and cumulative distribution functions evaluated on the sampled grid locations `PDF` & `CDF`, the optimal bandwidth matrix `H`, and the effective sample size of the data in `DOF.H`.

Author(s)

C. H. Fleming

See Also

[akde](#), [ctmm.select](#)

mean.variogram	<i>Compute a number-weighted average of variogram objects</i>
----------------	---

Description

This function takes a list of variogram objects and calculates its number-weighted average variogram.

Usage

```
## S3 method for class 'variogram'  
mean(x,...)
```

Arguments

x	A variogram object or list of such objects to be averaged.
...	Additional variograms if specified individually.

Value

Returns a variogram object which is a dataframe containing the lag, the semi-variance estimate at that lag, and the approximate degrees of freedom associated with the semi-variance estimate.

Note

Variogram averaging should only be used when there is a degree of similarity across individual variograms.

Author(s)

J. M. Calabrese and C. H. Fleming

References

C. H. Fleming, J. M. Calabrese, T. Mueller, K.A. Olson, P. Leimgruber, W. F. Fagan, “From fine-scale foraging to home ranges: A semi-variance approach to identifying movement modes across spatiotemporal scales”, *The American Naturalist*, 183:5, E154-E167 (2014) doi:[10.1086/675504](https://doi.org/10.1086/675504).

See Also

[plot.variogram](#), [variogram](#).

Examples

```
# Load package and data
library(ctmm)
data(buffalo)

# Calculate a list of variograms for all similar individuals in the dataset
# the 4th buffalo has a different sampling rate
SVFS <- lapply( buffalo[-4] , variogram )
# alternatively, we could variogram all at coarsest scale with variogram option dt

# Calculate the average variogram
SVF <- mean(SVFS)

# Plot the mean variogram
plot(SVF)
```

meta

Meta-analysis of movement-model parameters

Description

These functions estimate population-level mean parameters from individual movement models and related estimates, including AKDE home-range areas, while taking into account estimation uncertainty.

Usage

```
meta(x,variable="area",level=0.95,level.UD=0.95,method="MLE",IC="AICc",boot=FALSE,
     error=0.01,debias=TRUE,verbose=FALSE,units=TRUE,plot=TRUE,sort=FALSE,mean=TRUE,
     col="black",...)

funnel(x,y,variable="area",precision="t",level=0.95,level.UD=0.95,...)
```

Arguments

x	A named list of ctmm movement-model objects, UD objects, UD summary output, speed output, or 2×2 overlap objects constituting a sampled population, or a named list of such lists, with each constituting a sampled population.
y	An optional named list of telemetry objects for the funnel-plot precision variable.
variable	Biological “effect” variable of interest for ctmm object arguments. Can be “area”, “diffusion”, “speed”, “tau position”, or “tau velocity”.
precision	Precision variable of interest. Can be “t” for sampling time period or time interval, “n” for nominal sample size, “N” or “DOF” for effective sample size.
level	Confidence level for parameter estimates.
level.UD	Coverage level for home-range estimates. E.g., 50% core home range.

method	Statistical estimator used—either maximum likelihood estimation based ("MLE") or approximate 'best linear unbiased estimator' ("BLUE")—for comparison purposes.
IC	Information criterion to determine whether or not population variation can be estimated. Can be "AICc", AIC, or "BIC".
boot	Perform a parametric bootstrap for confidence intervals and first-order bias correction if <code>debias=TRUE</code> .
error	Relative error tolerance for parametric bootstrap.
debias	Apply Bessel's inverse-Gaussian correction and various other bias corrections if <code>method="MLE"</code> , REML if <code>method="BLUE"</code> , and an additional first-order correction if <code>boot=TRUE</code> .
verbose	Return a list of both population and meta-population analyses if <code>TRUE</code> and <code>x</code> is a list of population lists.
units	Convert result to natural units.
plot	Generate a meta-analysis forest plot.
sort	Sort individuals by their point estimates in forest plot.
mean	Include population mean estimate in forest plot.
col	Color(s) for individual labels and error bars.
...	Further arguments passed to <code>plot</code> or <code>meta</code> .

Details

`meta` employs a custom χ^2 -IG hierarchical model to calculate debiased population mean estimates of positive scale parameters, including home-range areas, diffusion rates, mean speeds, and auto-correlation timescales. Model selection is performed between the χ^2 -IG population model (with population mean and variance) and the Dirac- δ population model (population mean only). Population "coefficient of variation" (CoV) estimates are also provided. Further details are given in Fleming et al (2022).

Value

If `x` constitutes a sampled population, then `meta` returns a table with rows corresponding to the population mean and coefficient of variation.

If `x` constitutes a list of sampled populations, then `meta` returns confidence intervals on the population mean variable ratios.

Note

The AICc formula is approximated via the Gaussian relation.

Confidence intervals depicted in the forest plot are χ^2 and may differ from the output of `summary()` in the case of mean speed and timescale parameters with small effective sample sizes.

As mean ratio estimates are debiased, reciprocal estimates can differ slightly.

Author(s)

C. H. Fleming.

References

C. H. Fleming, I. Deznabi, S. Alavi, M. C. Crofoot, B. T. Hirsch, E. P. Medici, M. J. Noonan, R. Kays, W. F. Fagan, D. Sheldon, J. M. Calabrese, “Population-level inference for home-range areas”, *Methods in Ecology and Evolution* 13:5 1027–1041 (2022) doi:[10.1111/2041210X.13815](https://doi.org/10.1111/2041210X.13815).

See Also

[akde](#), [cluster](#), [ctmm.fit](#).

Examples

```
# load package and data
library(ctmm)
data(buffalo)

# fit movement models
FITS <- AKDES <- list()
for(i in 1:length(buffalo))
{
  GUESS <- ctmm.guess(buffalo[[i]],interactive=FALSE)
  # use ctmm.select unless you are certain that the selected model is OUF
  FITS[[i]] <- ctmm.fit(buffalo[[i]],GUESS)
}

# calculate AKDES on a consistent grid
AKDES <- akde(buffalo,FITS)

# color to be spatially distinct
COL <- color(AKDES,by='individual')

# plot AKDEs
plot(AKDES,col.DF=COL,col.level=COL,col.grid=NA,level=NA)

# meta-analysis of buffalo home-range areas
meta(AKDES,col=c(COL,'black'),sort=TRUE)

# funnel plot to check for sampling bias
funnel(AKDES,buffalo)
```

npr

Calculate a non-parametric regression surface

Description

This function estimates the mean value of an annotated covariate as a function of location, using non-parametric regression.

Usage

```
npr(data,UD,variable="speed",normalize=FALSE,debias=TRUE,error=0.001,...)
```


Arguments

data	2D timeseries telemetry data represented as a telemetry object or list of objects.
UD	A UD object from the output of akde .
variable	Variable for mean estimation. Can be a column of data.
normalize	Consider variable as providing a weighted probability distribution.
debias	Correct for oversmoothing if normalize=TRUE.
error	Target probability error.
...	Arguments passed to akde .

Value

Returns a UD object.

Author(s)

C. H. Fleming.

See Also

[akde](#), [occurrence](#)

Examples

```
# Load package and data
library(ctmm)
data(buffalo)
DATA <- buffalo$Cilla

# calculate fit guess object
GUESS <- ctmm.guess(DATA,interactive=FALSE)
# in general, you should be running ctmm.select here instead of ctmm.fit
FIT <- ctmm.fit(DATA,GUESS)

# Compute akde object
UD <- akde(DATA,FIT)

# compute revisitation distribution
RD <- revisitation(DATA,UD)

# Plot data with revisitation distribution
plot(DATA,RD)
```

occurrence

*Calculate a Kriged occurrence distribution estimate***Description**

This function calculates an occurrence distribution from telemetry data and a continuous-time movement model.

Usage

```
occurrence(data, CTMM, R=list(), SP=NULL, SP.in=TRUE, H=0, variable="utilization", res.time=10,
           res.space=10, grid=NULL, cor.min=0.05, dt.max=NULL, buffer=TRUE, ...)
```

Arguments

<code>data</code>	A telemetry object or list of telemetry objects.
<code>CTMM</code>	A ctmm movement model, as from the output of <code>ctmm.select</code> , or a list of ctmm objects.
<code>R</code>	A named list of raster covariates if CTMM contains an RSF model.
<code>SP</code>	SpatialPolygonsDataFrame object for enforcing hard boundaries.
<code>SP.in</code>	Locations are assumed to be inside the SP polygons if <code>SP.in=TRUE</code> and outside of SP if <code>SP.in=FALSE</code> .
<code>H</code>	Optional additional bandwidth matrix for future use.
<code>variable</code>	Either "utilization" or "revisitation". Only utilization is accurately estimated.
<code>res.time</code>	Number of temporal grid points per median timestep.
<code>res.space</code>	Number of grid points along each axis, relative to the average diffusion (per median timestep) from a stationary point.
<code>grid</code>	Optional grid specification via raster, UD, or list of arguments (See akde for details).
<code>cor.min</code>	Velocity correlation threshold for skipping gaps.
<code>dt.max</code>	Maximum absolute gap size (in seconds) for Kriging interpolation. If left NULL, the median of <code>diff(data\$t)</code> will be used.
<code>buffer</code>	Buffer the observation period, according to the minimum gap specified by <code>cor.min</code> and <code>dt.max</code> , to include more probable locations if possible.
<code>...</code>	Not used.

Details

The arguments `cor.min` or `dt.max` are used to prevent the interpolation of large gaps, which would bias the estimate to more resemble the movement model than the data. Because `cor.min` can produce an empty range with fractal movement models, the larger of the two rules is employed for interpolation.

If `buffer=TRUE`, then the data are also extrapolated according to the minimum of the two rules (`cor.min` and `dt.max`) which is limited to cases where persistence of motion is modeled.

Value

Returns a UD object containing the sampled grid line locations `x` and `y`, the probability density and cumulative distribution functions evaluated on the sampled grid locations PDF & CDF, the optional bandwidth matrix `H`, and the area of each grid cell `dA`.

Note

Large gaps have a tendency to slow down computation and blow up the estimate. This can be avoided with the `cor.min` or `dt.max` arguments.

In the case of coarse grids, the value of PDF in a grid cell actually corresponds to the average probability density over the entire rectangular cell.

Prior to `ctmm` v0.5.6, `cor.min` referred to the location correlation, with a default of 50%. In `ctmm` v0.5.6 and above, `cor.min` refers to the velocity correlation, with a default of 5%.

Author(s)

C. H. Fleming.

References

C. H. Fleming, W. F. Fagan, T. Mueller, K. A. Olson, P. Leimgruber, J. M. Calabrese, “Estimating where and how animals travel: An optimal framework for path reconstruction from autocorrelated tracking data”, *Ecology*, 97:3, 576-582 (2016) doi:[10.1890/151607.1](https://doi.org/10.1890/151607.1).

C. H. Fleming, D. Sheldon, E. Gurarie, W. F. Fagan, S. LaPoint, J. M. Calabrese, “Kálmán filters for continuous-time movement models”, *Ecological Informatics*, 40, 8-21 (2017) doi:[10.1016/j.ecoinf.2017.04.008](https://doi.org/10.1016/j.ecoinf.2017.04.008).

See Also

[akde](#), [raster](#), [UD-method](#)

Examples

```
# Load package and data
library(ctmm)
data(buffalo)
Cilla <- buffalo$Cilla

GUESS <- ctmm.guess(Cilla, interactive=FALSE)
FIT <- ctmm.fit(Cilla, GUESS)

# Compute occurrence distribution
UD <- occurrence(Cilla, FIT)

# Plot occurrence UD
plot(UD, col.level=NA)
```

optimizer

*Minimize a function***Description**

This function serves as a wrapper around [optimize](#), [optim](#), and `ctmm`'s partial-Newton optimization routine, with standardized arguments and return values. It finds the optimal parameters that minimize a function, whether it be a cost, loss, risk, or negative log-likelihood function.

Usage

```
optimizer(par,fn,...,method="pNewton",lower=-Inf,upper=Inf,period=FALSE,reset=identity,
          control=list())
```

Arguments

<code>par</code>	Initial parameter guess.
<code>fn</code>	Function to be minimized with first argument <code>par</code> and optional argument <code>zero</code> (see 'Details' below).
<code>...</code>	Optional arguments fed to <code>fn</code> .
<code>method</code>	Optimization algorithm (see 'Details' below).
<code>lower</code>	Lower bound for parameters.
<code>upper</code>	Upper bound for parameters.
<code>period</code>	Period of circular parameters if not <code>FALSE</code> .
<code>reset</code>	Optional function to re-center parameters, if symmetry permits, to prevent numerical underflow.
<code>control</code>	Argument list for the optimization routine (see 'Details' below).

Details

Only `method='pNewton'` will work in both one dimension and multiple dimensions. Any other method argument will be ignored in one dimension, in favor of [optimize](#) with a backup evaluation of [nlm](#) (under a log-link) for cases where [optimize](#) is known to fail. In multiple dimensions, methods other than `pNewton` include those detailed in [optim](#).

`method='pNewton'` is `ctmm`'s partial-Newton optimizer, which is a quasi-Newton method that is more accurate than BFGS-based methods when the gradient of `fn` must be calculated numerically. In short, while BFGS-based methods provide a single rank-1 update to the Hessian matrix per iteration, the partial-Newton algorithm provides `length(par)+1` rank-1 updates to the Hessian matrix per iteration, at the same computational cost. Furthermore, `length(par)` of those updates have better numerical precision than the BFGS update, meaning that they can be used at smaller step sizes to obtain better numerical precision. The `pNewton` optimizer also supports several features not found in other R optimizers: the `zero` argument, the `period` argument, and parallelization.

The `zero` argument is an optional argument in `fn` supported by `method='pNewton'`. Briefly, if you rewrite a negative log-likelihood of the form $fn = \sum_{i=1}^n fn_i$ as $fn = \sum_{i=1}^n (fn_i - zero/n) + zero$,

where zero is the current estimate of the minimum value of `fn`, then the sum becomes approximately "zeroed" and so the variance in numerical errors caused by the difference in magnitude between `fn` and `fn_i` is mitigated. In practice, without the zero argument, log-likelihood functions grow in magnitude with increasing data and then require increasing numerical precision to resolve the same differences in log-likelihood. But absolute differences in log-likelihoods (on the order of 1) are always important, even though most optimization routines more naturally consider relative differences as being important.

The period argument informs `method='pNewton'` if parameters is circular, such as with angles, and what their periods are.

The control list can take the following arguments, with defaults shown:

`precision=1/2` Fraction of machine numerical precision to target in the maximized likelihood value. The optimal `par` will have half this precision. On most computers, `precision=1` is approximately 16 decimal digits of precision for the objective function and 8 for the optimal `par`.

`maxit=.Machine$integer.max` Maximum number of iterations allowed for optimization.

`parscale=pmin(abs(par),abs(par-lower),abs(upper-par))` The natural scale of the parameters such that variations in `par` on the order of `parscale` produce variations in `fn` on the order of one.

`trace=FALSE` Return step-by-step progress on optimization.

`cores=1` Perform `cores` evaluations of `fn` in parallel, if running in UNIX. `cores<=0` will use all available cores, save `abs(cores)`. This feature is only supported by `method='pNewton'` and is only useful if `fn` is slow to evaluate, `length(par)>1`, and the total number of parallel evaluations required does not trigger fork-bomb detection by the OS.

Value

Returns a list with components `par` for the optimal parameters, `value` for the minimum value of `fn`, and possibly other components depending on the optimization routine employed.

Note

`method='pNewton'` is very stringent about achieving its precision target and assumes that `fn` has small enough numerical errors (permitting the use of argument zero) to achieve that precision target. If the numerical errors in `fn` are too large, then the optimizer can fail to converge. `ctmm.fit` standardizes its input data before optimization, and back-transforms afterwards, as one method to minimize numerical errors in `fn`.

Author(s)

C. H. Fleming.

See Also

`optim`, `optimize`, `nlm`

outlie	<i>Methods to facilitate outlier detection.</i>
--------	---

Description

Produces a `data.frame` of speed and distance estimates to analyze, as well as a plot highlighting potential speed and distance outliers in telemetry data.

Usage

```
outlie(data, plot=TRUE, by='d', ...)

## S3 method for class 'outlie'
plot(x, level=0.95, units=TRUE, axes=c('d', 'v'), xlim=NULL, ylim=NULL, ...)
```

Arguments

<code>data</code>	telemetry object.
<code>plot</code>	Output a plot highlighting high speeds (blue) and distant locations (red).
<code>by</code>	Color and size side-effect plot points by 'd', 'v', 'dz', 'vz', for distance from center, minimum speed, vertical distance from center, and minimum vertical speed.
<code>...</code>	Arguments passed to plot.
<code>x</code>	outlie object to plot.
<code>level</code>	Confidence level for error bars.
<code>units</code>	Convert axes to natural units.
<code>axes</code>	<i>x-y</i> axes to plot. Can be any of 'd', 'v', 'dz', 'vz', for time, distance from center, minimum speed, vertical distance from center, and minimum vertical speed.
<code>xlim</code>	<i>x</i> -axis plotting range in SI units.
<code>ylim</code>	<i>y</i> -axis plotting range in SI units.

Details

If `plot=TRUE` in `outlie()`, intervals of high speed are highlighted with blue segments, while distant locations are highlighted with red points.

When plotting the `outlie` object itself, ‘median deviation’ denotes distances from the geometric median, while ‘minimum speed’ denotes the minimum speed required to explain the location estimate’s displacement as straight-line motion. Both estimates account for telemetry error and condition on as few data points as possible. The speed estimates furthermore account for timestamp truncation and assign each timestep’s speed to the most likely offending time, based on its other adjacent speed estimate.

The output `outlie` object contains the above noted speed and distance estimates in a `data.frame`, with rows corresponding to those of the input telemetry object.

Value

Returns an `outlie` object, which is a `data.frame` of distance and speed information. Can also produce a plot as a side effect.

Note

The speed estimates here are tailored for outlier detection and have poor statistical efficiency. The `predict` and `speed` methods are appropriate for estimating speed (after outliers have been removed and a movement model has been selected).

In `ctmm` v0.6.1 the `UERE` argument was deprecated. For uncalibrated data, the initial estimates used by `outlie` are now generated on import and stated by `summary(uere(data))`. These values not be reasonable for arbitrary datasets.

Author(s)

C. H. Fleming.

References

C. H. Fleming et al, “A comprehensive framework for handling location error in animal tracking data”, *bioRxiv* 2020.06.12.130195 (2020) doi:[10.1101/2020.06.12.130195](https://doi.org/10.1101/2020.06.12.130195).

See Also

[as.telemetry](#).

Examples

```
# Load package and data
library(ctmm)
data(turtle)

# look for outliers in a turtle
OUT <- outlie(turtle[[3]])

# look at the distribution of estimates
plot(OUT)
```

Description

This function calculates a useful measure of similarity between distributions known as the *Bhattacharyya coefficient* in statistics and simply the *fidelity* or *overlap* in quantum and statistical mechanics. It is roughly speaking the ratio of the intersection area to the average individual area, but it is a direct comparison between the density functions and does not require an arbitrary quantile to be specified. When applied to ctmm objects, this function returns the overlap of the two Gaussian distributions. When applied to aligned UD objects with corresponding movement models, this function returns the overlap of their (autocorrelated) kernel density estimates.

Usage

```
overlap(object, method="Bhattacharyya", level=0.95, debias=TRUE, ...)
```

Arguments

object	A list of ctmm fit or aligned UD objects to compare.
method	Can be "Bhattacharyya" or "Encounter" (see Details below).
level	The confidence level desired for the output.
debias	Approximate debiasing of the overlap.
...	Not currently used.

Details

The default method="Bhattacharyya" estimates the standard overlap measure $\int \int \sqrt{p(x, y) q(x, y)} dx dy$ between the distributions $p(x, y)$ and $q(x, y)$, while method="encounter" estimates the non-standard measure $\frac{\int \int p(x, y) q(x, y) dx dy}{\sqrt{\int \int p(x', y')^2 dx' dy' \int \int q(x'', y'')^2 dx'' dy''}}$, which has a numerator proportional to the uncorrelated encounter probability. Both measures lie between 0 and 1, where 0 indicates no shared support and 1 indicates identical distributions.

Value

An object with slots DOF, containing the effective sample sizes, and CI containing a table of confidence intervals on the overlap estimates. A value of 1 implies that the two distributions are identical, while a value of 0 implies that the two distributions share no area in common.

Note

In ctmm v0.5.2, direct support for telemetry objects was dropped and the CTMM argument was depreciated for UD objects, simplifying usage.

Uncertainties in the model fits are propagated into the overlap estimate under the approximation that the Bhattacharyya distance is a chi-square random variable. Debiasing makes further approximations noted in Winner & Noonan et al (2018).

Author(s)

C. H. Fleming and K. Winner

References

K. Winner, M. J. Noonan, C. H. Fleming, K. Olson, T. Mueller, D. Sheldon, J. M. Calabrese. “Statistical inference for home range overlap”, *Methods in Ecology and Evolution*, 9:7, 1679-1691 (2018) [doi:10.1111/2041210X.13027](https://doi.org/10.1111/2041210X.13027).

See Also

[akde](#), [ctmm.fit](#), [distance](#), [encounter](#)

Examples

```
# Load package and data
library(ctmm)
data(buffalo)

# fit models for first two buffalo
GUESS <- lapply(buffalo[1:2], function(b) ctmm.guess(b,interactive=FALSE) )
# using ctmm.fit here for speed, but you should almost always use ctmm.select
FITS <- lapply(1:2, function(i) ctmm.fit(buffalo[[i]],GUESS[[i]]) )
names(FITS) <- names(buffalo[1:2])

# Gaussian overlap between these two buffalo
overlap(FITS)

# AKDE overlap between these two buffalo
# create aligned UDS
UDS <- akde(buffalo[1:2],FITS)
# evaluate overlap
overlap(UDS)
```

pelican

Brown Pelican GPS and ARGOS data.

Description

GPS and ARGOS data on a single brown pelican (*Pelecanus occidentalis*). Please contact Autumn-Lynn Harrison (HarrisonAL@si.edu) if you want to publish with these data.

Funding for Brown Pelican tracking was provided by the Friends of the National Zoo Conservation Research Grant and ConocoPhillips Global Signature Program. Field support provided by D. Brinker.

Usage

```
data("pelican")
```

Format

A list of 2 telemetry objects.

See Also

[as.telemetry](#), [plot.telemetry](#), [buffalo](#), [coati](#), [gazelle](#), [jaguar](#), [turtle](#), [wolf](#).

Examples

```
# Load package and data
library(ctmm)
data("pelican")
names(pelican)

# Plot all sampled locations
plot(pelican,col=c('blue','red'))
```

periodogram

Calculate the Lomb-Scargle periodogram of animal-tracking data

Description

This function calculates isotropic Lomb-Scargle periodogram (LSP, Scargle, 1982) from a telemetry object. One of two algorithms is used. The slow $O(n^2)$ algorithm vectorizes the exact relations of Scargle (1982), while the fast $O(n \log n)$ algorithm uses the FFT method described in Péron & Fleming et al (2016). The latter method is exact if the data are evenly scheduled, permitting gaps, and otherwise it can be made arbitrarily precise via the `res.time` option.

Usage

```
periodogram(data,CTMM=NULL,dt=NULL,res.freq=1,res.time=1,fast=NULL,axes=c("x","y"))

## S3 method for class 'periodogram'
plot(x,max=FALSE,diagnostic=FALSE,col="black",transparency=0.25,grid=TRUE,...)
```

Arguments

<code>data</code>	telemetry data object or list of such objects.
<code>CTMM</code>	An optional <code>ctmm</code> model object for specifying the mean.
<code>dt</code>	Sampling interval for frequency cutoff.
<code>res.freq</code>	Multiplier to inflate the frequency resolution.
<code>res.time</code>	Integer multiplier to inflate the temporal resolution. Useful when <code>fast>0</code> and the sampling rate is variable.
<code>fast</code>	Use the exact algorithm if <code>FALSE</code> , the FFT algorithm if <code>TRUE</code> , and further inflate the frequency resolution to a power of two sample size if <code>fast=2</code> .
<code>axes</code>	Array of axes to calculate an average (isotropic) variogram for.
<code>x</code>	Output object of <code>periodogram</code> .
<code>max</code>	Plot only the local maxima of the periodogram. Use only with <code>res>1</code> .
<code>diagnostic</code>	Plot the sampling schedule's periodogram to check for spurious periodicities.

<code>col</code>	Color of periodogram.
<code>transparency</code>	Adds transparency to clustered data if greater than zero. Should be less than one.
<code>grid</code>	Whether or not to plot gridlines at common periodicities.
<code>...</code>	Optional arguments fed to <code>plot</code> .

Details

If no `dt` is specified, the median sampling interval is used. This is typically a good assumption for most data, even when there are gaps and this choice corresponds to the discrete Fourier transform (DFT) periodogram for evenly-sampled data.

At default resolution the frequency grid interval is given by $1/(2*(\text{range}(\text{data}\$t)+dt))$ and the frequency cutoff is given by $1/(2*dt)$, both in accordance with the DFT periodogram. Increasing `res.freq` beyond `res.freq=1` will make for a smooth periodogram, but sequential frequencies will be highly correlated. The `max=TRUE` option to `plot.periodogram` may be useful for `res.freq>1`. Increasing `res.time` beyond `res.time=1` is helpful if there is variability in the sampling rate and `fast>0`.

If a CTMM argument is provided, the ML mean will be detrended from the data prior to calculating the periodogram. Otherwise, the sample mean will be detrended.

If a list of telemetry objects are fed into `periodogram`, then a mean periodogram object will be returned with the default `dt` and base frequency resolution selected on a worst case basis according to the method described by Péron & Fleming et al (2016).

Value

Returns a periodogram object (class `periodogram`) which is a dataframe containing the frequency, `f` and the Lomb-Scargle periodogram at that frequency, `LSP`.

Note

The LSP is totally inappropriate if you in any way alter the sampling rate within the dataset. Stick with variograms in that case. There is a diagnostic option in `plot.periodogram` that can check for spurious periodicities that result from an autocorrelated sampling schedule. This plot will not contain any periodicities if the LSP is appropriate.

`res.time>1` relies on Lagrange interpolation of the sinusoids (not the data), which can suffer from Runge's phenomena. `periodogram` tests for an invalid result and can fail with an error message. For whatever reason, this more frequently seems to happen when `res.time=3`.

Author(s)

C. H. Fleming and G. Péron

References

J. D. Scargle, "Studies in astronomical time-series analysis. II. Statistical aspects of spectral analysis of unevenly-sampled data", The Astrophysical Journal, 263, 835-853 (1952) [doi:10.1086/160554](https://doi.org/10.1086/160554).

G. Péron, C. H. Fleming, R. C. de Paula, J. M. Calabrese, “Uncovering periodic patterns of space use in animal tracking data with periodograms, including a new algorithm for the Lomb-Scargle periodogram and improved randomization tests”, *Movement Ecology*, 4:19 (2016) [doi:10.1186/s4046201600847](https://doi.org/10.1186/s4046201600847).

Examples

```
#Load package and data
library(ctmm)
data(wolf)

#Extract movement data for a single animal
DATA <- wolf$Tay

#Calculate periodogram (fast==2 for a speedy example)
#There is some variability in the sampling frequency, so we increase res.time
LSP <- periodogram(DATA,fast=2,res.time=2)

#Plot the periodogram
plot(LSP,max=TRUE)
```

plot.telemetry

Plotting methods for telemetry objects

Description

Produces simple plots of telemetry objects, possibly overlayed with a Gaussian ctmm movement model or a UD utilization distribution.

Usage

```
plot(x,y,...)

## S3 method for class 'telemetry'
plot(x,CTMM=NULL,UD=NULL,col.bg="white",cex=NULL,col="red",lwd=1,pch=1,type='p',
     error=TRUE,transparency.error=0.25,velocity=FALSE,DF="CDF",col.DF="blue",
     col.grid="white",labels=NULL,convex=FALSE,level=0.95,level.UD=0.95,col.level="black",
     lwd.level=1,SP=NULL,border.SP=TRUE,col.SP=NA,R=NULL,col.R="green",legend=FALSE,
     fraction=1,xlim=NULL,ylim=NULL,ext=NULL,units=TRUE,add=FALSE,...)

## S4 method for signature 'list'
zoom(x,...)

## S4 method for signature 'telemetry'
zoom(x,fraction=1,...)

## S4 method for signature 'UD'
zoom(x,fraction=1,...)
```

Arguments

x	telemetry or UD object.
y	Unused option.
CTMM	Optional Gaussian ctmm movement model from the output of ctmm.fit or list of such objects.
UD	Optional UD object such as from the output of akde or list of such objects.
col.bg	Background color
cex	Relative size of plotting symbols. Only used when error=FALSE, because error=TRUE uses the location-error radius instead of cex.
col	Color option for telemetry data. Can be an array or list of arrays.
lwd	Line widths of telemetry points.
pch	Plotting symbol. Can be an array or list of arrays.
type	How plot points are connected. Can be an array.
error	Plot error circles/ellipses if present in the data. error=2 will fill in the circles and error=3 will plot densities instead. error=FALSE will disable this feature.
transparency.error	Transparency scaling for erroneous locations when error=1:2. trans=0 disables transparency. Should be no greater than 1.
velocity	Plot velocity vectors if present in the data.
DF	Plot the maximum likelihood probability density function "PDF" or cumulative distribution function "CDF".
col.DF	Color option for the density function. Can be an array.
col.grid	Color option for the maximum likelihood akde bandwidth grid. col.grid=NA will disable the plotting of the bandwidth grid.
labels	Labels for UD contours. Can be an array or list of arrays.
convex	Plot convex coverage-area contours if TRUE. By default, the highest density region (HDR) contours are plotted.
level	Confidence levels placed on the contour estimates themselves. I.e., the above 50% core home-range area can be estimated with 95% confidence via level=0.95. level=NA will disable the plotting of confidence intervals.
level.UD	Coverage level of Gaussian ctmm model or UD estimate contours to be displayed. I.e., level.UD=0.50 can yield the 50% core home range within the rendered contours.
col.level	Color option for home-range contours. Can be an array.
lwd.level	Line widths of UD contours.
SP	SpatialPolygonsDataFrame object for plotting a shapefile base layer.
border.SP	Color option for shapefile polygon boundaries.
col.SP	Color option for shapefile polygon regions.
R	Background raster, such as habitat suitability .
col.R	Color option for background raster.

legend	Plot a color legend for background raster.
fraction	Quantile fraction of the data, Gaussian ctmm, or UD range to plot, whichever is larger.
xlim	The x limits c(x1, x2) of the plot (in SI units).
ylim	The y limits c(y1, y2) of the plot (in SI units).
ext	Plot extent alternative to xlim and ylim (see extent).
units	Convert axes to natural units.
add	Setting to TRUE will disable the unit conversions and base layer plot, so that plot.telemetry can be overlayed atop other outputs more easily.
...	Additional options passed to plot.

Details

Confidence intervals placed on the ctmm Gaussian home-range contour estimates only represent uncertainty in the area's magnitude and not uncertainty in the mean location, eccentricity, or orientation angle. For akde UD estimates, the provided contours also only represent uncertainty in the magnitude of the area. With akde estimates, it is also important to note the scale of the bandwidth and, by default, grid cells are plotted with akde contours such that their length and width matches that of a bandwidth kernels' standard deviation in each direction. Therefore, this grid provides a visual approximation of the kernel-density estimate's "resolution". Grid lines can be disabled with the argument `col.grid=NA`.

Value

Returns a plot of x vs. y , and, if specified, Gaussian ctmm distribution or UD. akde UD plots also come with a standard resolution grid. zoom includes a zoom slider to manipulate fraction.

Note

If xlim or ylim are provided, then the smaller or absent range will be expanded to ensure `asp=1`.

Author(s)

C. H. Fleming.

See Also

[akde](#), [ctmm.fit](#), [plot](#), [SpatialPoints.telemetry](#).

Examples

```
# Load package and data
library(ctmm)
data(buffalo)

# Plot the data
plot(buffalo,col=rainbow(length(buffalo)))
```

plot.variogram	<i>Plotting methods for variogram objects.</i>
----------------	--

Description

Produces simple plots of variogram objects (semi-variance vs. time lag) and model semi-variance functions, with approximate confidence intervals around the semi-variance estimates.

Usage

```
## S3 method for class 'variogram'
plot(x, CTMM=NULL, level=0.95, units=TRUE, fraction=0.5, col="black", col.CTMM="red", xlim=NULL,
      ylim=NULL, ext=NULL, ...)

## S4 method for signature 'variogram'
zoom(x, fraction=0.5, ...)
```

Arguments

x	A variogram object calculated using variogram .
CTMM	A ctmm movement model object in the same format as the output of <code>ctmm.fit</code> or <code>variogram.fit</code> .
level	Confidence level of confidence bands (95% default CIs). Can be an array.
units	Convert axes to natural units.
fraction	The proportion of the variogram object, <code>variogram</code> , that will be plotted. By convention, half is shown. The tail end is generally garbage.
col	Color for the empirical variogram. Can be an array.
col.CTMM	Color for the model. Can be an array.
xlim	Range of lags to plot (in SI units).
ylim	Range of semi-variance to plot (in SI units).
ext	Plot extent alternative to <code>xlim</code> and <code>ylim</code> (see extent).
...	Additional plot function parameters.

Value

Returns a plot of semi-variance vs. time lag, with the empirical variogram in black and the ctmm semi-variance function in red if specified. `zoom` includes a log-scale zoom slider to manipulate `fraction`.

Note

The errors of the empirical variogram are correlated. Smooth trends are not necessarily significant.

Author(s)

J. M. Calabrese and C. H. Fleming

References

C. H. Fleming, J. M. Calabrese, T. Mueller, K.A. Olson, P. Leimgruber, W. F. Fagan. From fine-scale foraging to home ranges: A semi-variance approach to identifying movement modes across spatiotemporal scales. *The American Naturalist*, 183:5, E154-E167 (2014) [doi:10.1086/675504](https://doi.org/10.1086/675504).

See Also

[correlogram](#), [ctmm.fit](#), [plot](#), [variogram](#), [variogram.fit](#).

Examples

```
# Load package and data
library(ctmm)
data(buffalo)

# Extract movement data for a single animal
Cilla <- buffalo$Cilla

# Calculate variogram
SVF <- variogram(Cilla)

# Plot the variogram
plot(SVF)
```

projection

Projection

Description

Functions to manipulate the coordinate reference system (CRS) of ctmm objects

Usage

```
## S4 method for signature 'telemetry'
projection(x, asText=TRUE)

## S4 method for signature 'ctmm'
projection(x, asText=TRUE)

## S4 method for signature 'UD'
projection(x, asText=TRUE)

## S4 method for signature 'list'
projection(x, asText=TRUE)
```



```
## S4 method for signature 'NULL'
projection(x,asText=TRUE)

## S4 replacement method for signature 'telemetry'
projection(x) <- value

## S4 replacement method for signature 'list'
projection(x) <- value

## S3 method for class 'telemetry'
median(x,na.rm=FALSE,...)

compass(loc=NULL,cex=3,...)
```

Arguments

<code>x</code>	A telemetry, ctmm, or UD object.
<code>asText</code>	If TRUE, the projection is returned as text. Otherwise a CRS object is returned.
<code>value</code>	Projection to apply. Can also be a data.frame of longitude-latitude foci.
<code>na.rm</code>	Not used.
<code>...</code>	Arguments passed to Gmedian or text .
<code>loc</code>	Optional two-dimensional coordinates (in meters) at which to draw a north-facing compass needle.
<code>cex</code>	Relative size of compass.

Details

`projection(x)` returns the projection information from ctmm object `x`, while `projection(x) <- value` applies the projection value to object `x`. `median(x)` returns the ellipsoidal geometric median of a telemetry object. `compass(c(x,y))` plots a north-pointing compass needle at the coordinates (x, y) .

Note

Plotting UTF-8 chracters in a PDF, like the compass needle, requires specifying a compatible font family. For example:

```
library(ctmm)
data(buffalo)
cairo_pdf(file="buffalo.pdf",family="DejaVu Sans")
plot(buffalo[[1]])
compass()
dev.off()
```

Author(s)

C. H. Fleming

See Also

[as.telemetry.](#)

Examples

```
# Load package and data
library(ctmm)
data(buffalo)

# Apply a 1-point projection that preserves North==up
projection(buffalo) <- median(buffalo)
plot(buffalo)
compass()

# Apply a 2-point projection safer for elongated distributions
projection(buffalo) <- median(buffalo,k=2)
# This is the default projection for ctmm
plot(buffalo)
compass()
```

residuals.ctmm

Calculate model fit residuals and assess their autocorrelation

Description

These functions calculate the residuals of a CTMM or UERE calibration model, which should be standardized and IID if the model correctly specified. A correlogram method is also provided to assess autocorrelation. This function is analogous to `acf`, but can handle missing data and multiple dimensions. Finally, `mag` calculates residual magnitudes, which is useful for comparing against potential covariates.

Usage

```
## S3 method for class 'ctmm'
residuals(object,data,...)

## S3 method for class 'telemetry'
residuals(object,CTMM=NULL,...)

correlogram(data,dt=NULL,fast=TRUE,res=1,axes=c("x","y"),trace=TRUE)

mag(x,...)

## S3 method for class 'telemetry'
mag(x,axes=c('x','y'),...)
```

Arguments

<code>object</code>	ctmm model object or telemetry data object for calculating residuals.
<code>data</code>	telemetry data object or <code>data.frame</code> with time column <code>t</code> and data columns <code>axes</code> .
<code>CTMM</code>	ctmm model object. If <code>NULL</code> , the data is treated as (calibrated) calibration data.
<code>...</code>	Unused arguments.
<code>dt</code>	Lag bin width. An ordered array will yield a progressive coarsening of the lags. Defaults to the median sampling interval.
<code>fast</code>	Use the lag-weighted algorithm if <code>FALSE</code> or the FFT algorithm if <code>TRUE</code> . The slow algorithm outputs a progress bar.
<code>res</code>	Increase the discretization resolution for irregularly sampled data with <code>res>1</code> . Decreases bias at the cost of smoothness.
<code>axes</code>	Array of axes for which to calculate residual correlogram or magnitudes.
<code>trace</code>	Display a progress bar if <code>fast=FALSE</code> .
<code>x</code>	telemetry object from the output of <code>residuals</code> .

Details

Given a telemetry dataset and ctmm model, `residuals` calculates the standardized residuals of the Kalman filter, which can be tested for independence. The residuals object can then be plotted with `plot` or fed into the `correlogram` method to test independence. Output of the correlogram can then be plotted as well, though `zoom` is much more useful.

When calculating correlograms, minimizing bias is more important than producing a overall smooth estimate. If `fast=TRUE`, then `res` needs to be large enough to resolve variability in the sampling interval (missing data is permitted). E.g., if the sampling interval is set to 15 minutes, but can be off by a minute or two, then `res=15` is a good choice.

Value

`residuals` return a residual object (class `telemetry`, but flagged as residual) and `correlogram` returns a correlogram object (class `variogram`, but flagged as an ACF).

Note

If the sampling schedule is irregular, permitting gaps, then the correlogram may not look good even if the model is correctly specified. In this case the correlogram of the residuals should be compared to the correlogram of simulated residuals, using "data" simulated from the fit model and with the same sampling schedule.

Author(s)

C. H. Fleming

References

C. H. Fleming, D. Sheldon, E. Gurarie, W. F. Fagan, S. LaPoint, J. M. Calabrese, “Kálmán filters for continuous-time movement models”, *Ecological Informatics*, 40, 8-21 (2017) [doi:10.1016/j.ecoinf.2017.04.008](https://doi.org/10.1016/j.ecoinf.2017.04.008).

See Also

[plot.variogram](#), [variogram](#).

Examples

```
# Load package and data
library(ctmm)
data(buffalo)
Cilla <- buffalo$Cilla

# fit a model
GUESS <- ctmm.guess(Cilla,interactive=FALSE)
FIT <- ctmm.fit(Cilla,GUESS)

# calculate residuals
RES <- residuals(Cilla,FIT)

# scatter plot of residuals with 50%, 95%, and 99.9% quantiles
plot(RES,col.DF=NA,level.UD=c(.50,.95,0.999))

# calculate correlogram of residuals
# increase the res argument to account for sampling variability
ACF <- correlogram(RES,res=10)

# plot 4 day's worth of lags
plot(ACF[ACF$lag<=4 %## 'day',],fraction=1)
```

revisitation

Calculate an revisitation distribution estimate

Description

This function estimates the distribution of revisitations from telemetry data and a continuous-time movement model.

Usage

```
revisitation(data,UD,debias=TRUE,error=0.001,...)
```

Arguments

<code>data</code>	2D timeseries telemetry data represented as a telemetry object or list of objects.
<code>UD</code>	A UD object from the output of akde .
<code>debias</code>	Correct for oversmoothing.
<code>error</code>	Target probability error.
<code>...</code>	Arguments passed to akde .

Value

Returns a UD object.

Author(s)

C. H. Fleming.

See Also

[akde](#), [occurrence](#)

Examples

```
# Load package and data
library(ctmm)
data(buffalo)
DATA <- buffalo$Cilla

# calculate fit guess object
GUESS <- ctmm.guess(DATA,interactive=FALSE)
# in general, you should be running ctmm.select here instead of ctmm.fit
FIT <- ctmm.fit(DATA,GUESS)

# Compute akde object
UD <- akde(DATA,FIT)

# compute revisitation distribution
RD <- revisitation(DATA,UD)

# Plot data with revisitation distribution
plot(DATA,RD)
```

rsf.fit	<i>Fit integrated resource selection functions (iRSFs) with autocorrelation-adjusted weighted likelihood</i>
---------	--

Description

This function fits integrated resource selection functions with autocorrelation-adjusted weights on the RSF likelihood function, importance sampling, and iterative numerical convergence.

Usage

```
rsf.fit(data, UD, R=list(), formula=NULL, integrated=TRUE, level.UD=0.99,
        reference="auto", debias=TRUE, smooth=TRUE, standardize=TRUE, integrator="MonteCarlo",
        error=0.01, max.mem="1 Gb", interpolate=TRUE, trace=TRUE, ...)
```

```
rsf.select(data, UD, R=list(), formula=NULL, verbose=FALSE, IC="AICc", trace=TRUE, ...)
```

Arguments

data	A telemetry object.
UD	A UD object generated by akde from the same telemetry object as data. If weights were optimized in akde , then they will be adopted by rsf.fit.
R	A named list of rasters or time-varying raster stacks [NOT TESTED] to fit Poisson regression coefficients to (under a log link).
formula	Formula object for $\log(\lambda)$ referencing the elements of R and columns of data (see Details below). If not specified, a linear term will be included for every element of R.
integrated	Fit an integrated RSF model with simultaneously estimated spatial constraints. integrated=FALSE is for comparison purposes only.
level.UD	Coverage probability of UD to sample uniformly from if integrated=FALSE. Can also be a pre-defined spatial polygon object.
reference	When expanding categorical predictors into indicator variables, reference="auto" will choose the most common predictor to be the reference category. Otherwise, the reference category can be specified by this argument.
debias	Apply a post-hoc bias correction to the spatial constraint parameters, and apply bias corrections to the numerical log-likelihood estimates.
smooth	Apply location-error smoothing to the tracking data before regression.
standardize	For numerical stability, predictors are <i>internally</i> standardized, if standardize=TRUE and no formula is specified. (The final outputs are not standardized.) Otherwise, users are responsible for standardizing their predictors.
integrator	Numerical integrator used for likelihood evaluation. Can be "MonteCarlo" or "Riemann" (IN TESTING).
error	Relative numerical error threshold for the parameter estimates and log-likelihood.

<code>max.mem</code>	Maximum amount of memory to allocate for availability sampling.
<code>interpolate</code>	Whether or not to interpolate raster values during extraction.
<code>trace</code>	Report progress on convergence (see Details).
<code>verbose</code>	Returns all candidate models if TRUE. Otherwise, only the IC-best model is returned.
<code>IC</code>	Model selection criterion. Can be AIC, AICc, or BIC.
<code>...</code>	Arguments passed to <code>rsf.fit</code> or <code>optimizer</code> .

Details

For autocorrelated tracking data, the relative weights of the log-likelihood used here are taken from the output of `akde`, which are optimized for non-parametric density estimation (if `weights=TRUE`, and so are approximate here. The absolute weight of the data is taken to be the effective sample size of the integrated spatial parameters, when estimated separately.

Integrated resource selection functions simultaneously estimate the spatially constraining (availability) parameters with the resource selection parameters, rather than first estimating the availability parameters (usually via MCP) and then holding those parameters fixed—as known values—when estimating the resource selection parameters. The “integrated” analysis reduces estimation bias, exposes correlations in the resource and availability estimate uncertainties, and propagates the availability estimate uncertainties into the final outputs.

Instead of specifying a number of “available” points to sample and having an unknown amount of numerical error to contend with, `rsf.fit` specifies an estimation target error and the number of “available” points is increased until this target is met. Moreover, the output log-likelihood is that of the continuous Poisson point process, which does not depend on the number of “available” points that were sampled, though the numerical variance estimate is recorded in the `VAR.loglike` slot of the fit object.

When `trace=TRUE`, a number of convergence estimates are reported, including the standard deviation of the numerical error of the log-likelihood, $SD[\log(\ell)]$, the most recent log-likelihood update, $d\log(\ell)$, and the most recent (relative) parameter estimate updates $d\hat{\beta}/SD[\hat{\beta}]$.

The formula object determines the covariate dependence of $\log(\lambda)$ in the Poisson point process likelihood $L(\lambda) = \frac{\lambda(x,y)}{\iint \lambda(x',y') dx' dy'}$, and can reference static rasters in R, time-dependent raster stacks in R [NOT TESTED], and time-dependent effect modifiers in the columns of data, such as provided by `annotate`. Any offset terms are applied under a log transformation (or multiplicatively to λ), and can be used to enforce hard boundaries, where `offset(raster)=TRUE` denotes accessible points and `offset(raster)=FALSE` denotes inaccessible points [NOT TESTED]. Intercept terms are ignored, as they generally do not make sense for individual Poisson point process models. This includes terms only involving the columns of data, as they lack spatial dependence.

Categorical raster variables are expanded into indicator variables, according to the reference category argument. Upon import via `raster`, categorical variables may need to be assigned with `as.factor`, or else they may be interpreted as numerical variables.

Note

It is much faster to calculate all predictors ahead of time and specifying them in the R list than to reference them in the formula argument, which will calculate them as needed, saving memory.

AIC and BIC values for `integrated=FALSE` models do not include any penalty for the estimated location and shape of the available area, and so their AIC and BIC values are expected to be *worse* than reported.

Author(s)

C. H. Fleming and B. Reineking

References

J. M. Alston, C. H. Fleming, R. Kays, J. P. Streicher, C. T. Downs, T. Ramesh, B. Reineking, & J. M. Calabrese, “Mitigating pseudoreplication and bias in resource selection functions with autocorrelation-informed weighting”, *Methods in Ecology and Evolution* 14:2 643–654 (2023) [doi:10.1111/2041210X.14025](https://doi.org/10.1111/2041210X.14025).

See Also

[ctmm.fit](#), [intensity](#), [optimizer](#), [summary.ctmm](#).

sdm.fit

Fit species distribution models (SDMs) [IN DEVELOPMENT]

Description

This function fits species distribution models, sampling density models, and integrated SDMs.

Usage

```
sdm.fit(data,R=list(),formula=NULL,area=NULL,reference="auto",standardize=TRUE,
        integrator="MonteCarlo",error=0.01,max.mem="1 Gb",interpolate=TRUE,trace=TRUE,...)

sdm.select(data,R=list(),formula=NULL,area=NULL,verbose=FALSE,IC="AICc",trace=TRUE,...)

sdm.integrate(biased=NULL,bias=NULL,unbiased=NULL)
```

Arguments

<code>data</code>	A telemetry object.
<code>R</code>	A named list of rasters or time-varying raster stacks [NOT TESTED] to fit Poisson regression coefficients to (under a log link).
<code>formula</code>	Formula object for $\log(\lambda)$ referencing the elements of <code>R</code> and columns of data (see Details below). If not specified, a linear term will be included for every element of <code>R</code> .
<code>area</code>	A spatial polygon object defining the extent of the SDM. If left <code>NULL</code> , an integrated Gaussian model will be used to define the extent of the SDM, which can be a very bad model for geographic ranges.

reference	When expanding categorical predictors into indicator variables, reference="auto" will choose the most common predictor to be the reference category. Otherwise, the reference category can be specified by this argument.
standardize	For numerical stability, predictors are <i>internally</i> standardized, if rescale=TRUE and no formula is specified. (The final outputs are not standardized.) Otherwise, users are responsible for standardizing their predictors.
integrator	Numerical integrator used for likelihood evaluation. Can be "MonteCarlo" or "Riemann" (IN TESTING).
error	Relative numerical error threshold for the parameter estimates and log-likelihood.
max.mem	Maximum amount of memory to allocate for availability sampling.
interpolate	Whether or not to interpolate raster values during extraction.
trace	Report progress on convergence (see Details).
verbose	Returns all candidate models if TRUE. Otherwise, only the IC-best model is returned.
IC	Model selection criterion. Can be AIC, AICc, or BIC.
...	Arguments passed to <code>rsf.fit</code> or <code>optimizer</code> .
biased	A biased SDM calculated from occurrence records with non-uniform sampling density.
bias	An "SDM" calculated from data representative of the above sampling density.
unbiased	An unbiased SDM or list of RSFs.

Details

Instead of specifying a number of "available" points to sample and having an unknown amount of numerical error to contend with, `rsf.fit` specifies an estimation target error and the number of "available" points is increased until this target is met. Moreover, the output log-likelihood is that of the continuous Poisson point process, which does not depend on the number of "available" points that were sampled, though the numerical variance estimate is recorded in the `VAR.loglike` slot of the fit object.

When `trace=TRUE`, a number of convergence estimates are reported, including the standard deviation of the numerical error of the log-likelihood, $SD[\log(\ell)]$, the most recent log-likelihood update, $d\log(\ell)$, and the most recent (relative) parameter estimate updates $d\hat{\beta}/SD[\hat{\beta}]$.

The `formula` object determines $\log(\lambda)$ and can reference static rasters in R, time-dependent raster stacks in R [NOT TESTED], and time-dependent effect modifiers in the columns of data, such as provided by `annotate`. Any offset terms are applied under a log transformation (or multiplicatively to λ), and can be used to enforce hard boundaries, where `offset(raster)=TRUE` denotes accessible points and `offset(raster)=FALSE` denotes inaccessible points [NOT TESTED]. Intercept terms are ignored, as they generally do not make sense for individual Poisson point process models. This includes terms only involving the columns of data, as they lack spatial dependence.

Categorical raster variables are expanded into indicator variables, according to the reference category argument. Upon import via `raster`, categorical variables may need to be assigned with `as.factor`, or else they may be interpreted as numerical variables.

Note

It is much faster to calculate all predictors ahead of time and specifying them in the R list than to reference them in the formula argument, which will calculate them as needed, saving memory.

AIC and BIC values for `integrated=FALSE` models do not include any penalty for the estimated location and shape of the available area, and so their AIC and BIC values are expected to be *worse* than reported.

Author(s)

C. H. Fleming

References

J. M. Alston, C. H. Fleming, R. Kays, J. P. Streicher, C. T. Downs, T. Ramesh, B. Reineking, & J. M. Calabrese, “Mitigating pseudoreplication and bias in resource selection functions with autocorrelation-informed weighting”, *Methods in Ecology and Evolution* 14:2 643–654 (2023) [doi:10.1111/2041210X.14025](https://doi.org/10.1111/2041210X.14025).

See Also

[rsf.fit](#), [optimizer](#), [summary.ctmm](#).

select

Spatial selection methods for telemetry objects.

Description

Methods to segment or subset telemetry objects based on polygon lasso, rectangular marquee, and time slider selectors.

Usage

```
lasso(object,...)
```

```
marquee(object,...)
```

```
cleave(object,fraction=0.5,name="CLEFT",...)
```

Arguments

<code>object</code>	telemetry object or list of such objects.
<code>fraction</code>	Initial split, as fraction of total time period.
<code>name</code>	Name of list to store cleft telemetry objects to.
<code>...</code>	Additional arguments passed to plot.

Details

lasso and marquee allow the user to subset telemetry data into two groups (interior and exterior), based on a hand-drawn polygon lasso or rectangular marquee. cleave allows the user to split the data into two halves at a particular time selected via slider.

Value

lasso and marquee return a named list telemetry objects, twice the length of the input object, where the first half are the interior subsets and the second half are the exterior subsets. cleave stores a similar list of telemetry objects to name on button press.

Author(s)

C. H. Fleming.

See Also

[plot.telemetry](#)

Examples

```
# This example is interactive
if(interactive())
{
  # Load package and data
  library(ctmm)
  data(wolf)

  # Extract wolf Luna
  DATA <- wolf$Luna

  # Select resident data
  SUB <- lasso(DATA)

  # You can now work with the resident and dispersive data separately
  names(SUB)
}
```

simulate.ctmm

Predict or simulate from a continuous-time movement model

Description

Given a ctmm movement model (and optional telemetry data to condition upon) these functions predict or simulate animal locations over a prescribed set of times.

Usage

```

predict(object,...)

## S3 method for class 'ctmm'
predict(object,data=NULL,VMM=NULL,t=NULL,dt=NULL,res=1,complete=FALSE,...)

## S3 method for class 'telemetry'
predict(object,CTMM=NULL,VMM=NULL,t=NULL,dt=NULL,res=1,complete=FALSE,...)

simulate(object,nsim=1,seed=NULL,...)

## S3 method for class 'ctmm'
simulate(object,nsim=1,seed=NULL,data=NULL,VMM=NULL,t=NULL,dt=NULL,res=1,complete=FALSE,
         precompute=FALSE,...)

## S3 method for class 'telemetry'
simulate(object,nsim=1,seed=NULL,CTMM=NULL,VMM=NULL,t=NULL,dt=NULL,res=1,complete=FALSE,
         precompute=FALSE,...)

```

Arguments

object	A ctmm movement-model or telemetry object, which requires an additional CTMM argument.
data	Optional telemetry object on which the prediction or simulation will be conditioned.
CTMM	A ctmm movement model in the same format as the output of ctmm.fit or variogram.fit .
VMM	An optional vertical ctmm movement model for 3D predictions and simulations.
t	Optional array of numeric time values over which the process will be predicted or simulated.
dt	Timestep to space the prediction or simulation over if data is specified.
res	Average number of locations to predict or simulate per data time.
complete	Additionally calculate timestamps and geographic coordinates.
nsim	Generates a list of nsim simulations.
seed	Optional random seed to fix.
precompute	Precalculate matrices of the Kalman filter (see details).
...	Unused options.

Details

The prediction or simulation necessarily requires a ctmm model object. If a telemetry data object is supplied, the output will be conditional on the data (i.e., simulations that run through the data). If no data is provided then the output will be purely Gaussian, and times t must be provided. Details of the movement model parameters can be found in [ctmm.fit](#).

The `t` argument fixes the output times to a specific array of times. The `dt` and `res` arguments are relative to the sampling schedule present in the optional `telemetry` object. The same span of time will be used, while `dt` will fix the sampling rate absolutely and `res` will fix the sampling rate relative to that of the data.

The `precompute` option can speed up calculations of multiple simulations of the same model, data, and *irregular* sampling schedule. First run `simulate` with `precompute=TRUE` to calculate and store all of the necessary matrices of the Kalman filter. A simulated telemetry object will be produced, as usual, and the precomputed objects are stored in the environment. Subsequent simulations with `precompute=-1` will then apply these precomputed matrices for a computational cost savings. If the sampling schedule is irregular, then this can result in faster simulations.

Value

A simulated animal-tracking telemetry object with components `t`, `x`, and `y`, or a predicted telemetry object that also includes `x-y` covariances for the location point estimates `x` and `y`.

Note

Predictions are autocorrelated and should not be treated as data.

Author(s)

C. H. Fleming.

References

C. H. Fleming, J. M. Calabrese, T. Mueller, K.A. Olson, P. Leimgruber, W. F. Fagan, "From fine-scale foraging to home ranges: A semi-variance approach to identifying movement modes across spatiotemporal scales", *The American Naturalist*, 183:5, E154-E167 (2014) [doi:10.1086/675504](https://doi.org/10.1086/675504).

C. H. Fleming, D. Sheldon, E. Gurarie, W. F. Fagan, S. LaPoint, J. M. Calabrese, "Kálmán filters for continuous-time movement models", *Ecological Informatics*, 40, 8-21 (2017) [doi:10.1016/j.ecoinf.2017.04.008](https://doi.org/10.1016/j.ecoinf.2017.04.008).

See Also

[ctmm.fit](#)

Examples

```
#Load package
library(ctmm)

#prepare simulation parameters
t <- 1:1000
MODEL <- ctmm(tau=c(100,10),sigma=10,mu=c(0,0))

#simulate data
SIM <- simulate(MODEL,t=t)

#plot data with Gaussian model
```

```
plot(SIM, CTMM=MODEL)
```

speed

Estimate the average speed of a tracked animal

Description

Given a `ctmm` movement model and telemetry data, `speed` simulates multiple realizations of the individual's trajectory to estimate the time-averaged speed, which is proportional to distance traveled, while `speeds` estimates instantaneous speeds at a specified array of times `t`. Both tortuosity (non straight-line motion between the data) and telemetry error can be accounted for. Given only a `ctmm` movement model and no data, `speed` calculates the mean speed of the Gaussian movement process. All methods are described in Noonan & Fleming et al (2019).

Usage

```
speed(object,...)
```

```
## S3 method for class 'ctmm'
```

```
speed(object,data=NULL,t=NULL,level=0.95,robust=FALSE,units=TRUE,prior=TRUE,fast=TRUE,
      cor.min=0.5,dt.max=NULL,error=0.01,cores=1,trace=TRUE,...)
```

```
## S3 method for class 'telemetry'
```

```
speed(object,CTMM,t=NULL,level=0.95,robust=FALSE,units=TRUE,prior=TRUE,fast=TRUE,
      cor.min=0.5,dt.max=NULL,error=0.01,cores=1,trace=TRUE,...)
```

```
speeds(object,...)
```

```
## S3 method for class 'ctmm'
```

```
speeds(object,data=NULL,t=NULL,cycle=Inf,level=0.95,robust=FALSE,prior=FALSE,fast=TRUE,
      error=0.01,cores=1,trace=TRUE,...)
```

```
## S3 method for class 'telemetry'
```

```
speeds(object,CTMM,t=NULL,cycle=Inf,level=0.95,robust=FALSE,prior=FALSE,fast=TRUE,
      error=0.01,cores=1,trace=TRUE,...)
```

Arguments

<code>object</code>	A <code>ctmm</code> movement-model or telemetry object, which requires an additional CTMM argument.
<code>data</code>	Optional telemetry object on which the simulations will be conditioned.
<code>CTMM</code>	Movement model object.
<code>t</code>	Array of times to estimate instantaneous speeds at, or range of times to estimate mean speed over.
<code>cycle</code>	Average over time <code>t</code> indices modulo <code>cycle</code> . E.g., for <code>t</code> sequenced by hours, <code>cycle=24</code> gives daily the cycle of speeds. (Not yet supported.)

<code>level</code>	Confidence level to report on the estimated average speed.
<code>robust</code>	Use robust statistics for the ensemble average and its confidence intervals (see Details).
<code>units</code>	Convert result to natural units.
<code>prior</code>	Account for model parameter uncertainty.
<code>fast</code>	Whether or not to invoke the central-limit theorem when propagating parameter uncertainty (see emulate).
<code>cor.min</code>	Velocity correlation threshold for skipping gaps.
<code>dt.max</code>	Absolute gap sizes to skip (in seconds), alternative to <code>cor.min</code> .
<code>error</code>	Target (relative) standard error.
<code>cores</code>	Number of simulations to run in parallel. <code>cores=0</code> will use all cores, while <code>cores<0</code> will reserve <code>abs(cores)</code> .
<code>trace</code>	Display a progress bar.
<code>...</code>	Arguments passed to emulate .

Details

The `cor.min` or `dt.max` arguments are used to constrain the estimate to be derived from simulations near the data, and therefore ensure that the estimate is more reflective of the data than the model.

If data quality is poor and velocity can barely be resolved, then the sampling distribution may occasionally include impersistent motion and its mean will be infinite. In these cases `robust=TRUE` can be used to report the sampling distribution's median rather than its mean. The time average of speed, in either case, is still the mean average of times and the resulting quantity is still proportional to distance traveled. Furthermore, note that medians should be compared to medians and means to means, so the robust option should be the same for all compared individuals.

Value

Returns the estimated mean speed of the sampled trajectory with CIs by default. If `level=NULL`, then the ensemble of mean speeds is returned instead.

Note

The mean speed estimated by `speed` is applicable only during the sampling periods. If an individual is diurnal/nocturnal and only tracked during the day/night, then the output of `speed` will only be the mean speed during the day/night. For instance, if an individual is tracked the 12 hours per day during which it is active, and `speed` reports a mean speed of 10 kilometers per day during those periods, then the average distance traveled per day is only 5 kilometers (from 10 kilometers / day * 12 hours). An average of 10 kilometers would only result if the individual were similarly active for 24 hours a day.

The average speeds estimated here are mean speeds. The speeds reported by [summary.ctmm](#) are root-mean-square (RMS) speeds. These quantities are sometimes proportional, but not equivalent.

Author(s)

C. H. Fleming.

References

M. J. Noonan, C. H. Fleming, T. S. Akre, J. Drescher-Lehman, E. Gurarie, A.-L. Harrison, R. Kays, Justin Calabrese, “Scale-insensitive estimation of speed and distance traveled from animal tracking data”, *Movement Ecology*, 7:35 (2019).

See Also

[emulate](#), [simulate](#)

Examples

```
# Load package and data
library(ctmm)
data(buffalo)
DATA <- buffalo$Gabs

GUESS <- ctmm.guess(DATA,interactive=FALSE)
# in general, you should use ctmm.select instead
FIT <- ctmm.fit(DATA,GUESS)

# stationary Gaussian estimate
speed(FIT)

# conditional estimate
# you will likely want trace=TRUE
speed(FIT,DATA,trace=FALSE)
```

summary.ctmm

Summarize a continuous-time movement model

Description

This function returns a list of biologically interesting parameters in human readable format, as derived from a continuous-time movement model.

Usage

```
## S3 method for class 'ctmm'
summary(object,level=0.95,level.UD=0.95,units=TRUE,IC=NULL,MSPE=NULL,...)
```

Arguments

object	A ctmm movement-model object from the output of <code>ctmm.fit</code> .
level	Confidence level for parameter estimates.
level.UD	Coverage level for the Gaussian home-range area.
units	Convert result to natural units.

IC	Information criteria for sorting lists of ctmm objects. Can be "AICc", "AIC", "BIC", "LOOCV", "HSCV", or none (NA). AICc is approximate.
MSPE	Sort models with the same autocovariance structure by the mean square predictive error of "position", "velocity", or not (NA).
...	Unused options.

Value

If summary is called with a single ctmm object output from `ctmm.fit`, then a list is returned with the effective sample sizes of various parameter estimates (DOF) and a parameter estimate table CI, with low, point, and high estimates for the following possible parameters:

tau The autocorrelation timescales. tau position is also the home-range crossing timescale.

area The Gaussian home-range area, where the point estimate has a significance level of `level.UD`. I.e., the core home range is where the animal is located 50% of the time with `level.UD=0.50`. This point estimate itself is subject to uncertainty, and is given confidence intervals derived from `level`.

This Gaussian estimate differs from the kernel density estimate of `summary.UD`. The Gaussian estimate has more statistical efficiency, but is less related to space use for non-Gaussian processes.

speed The Gaussian root-mean-square (RMS) velocity, which is a convenient measure of average speed but not the conventional measure of average speed (see `speed`).

If summary is called on a list of ctmm objects output from `ctmm.select`, then a table is returned with the model names and IC differences for comparison across autocovariance structures. The mean square prediction error (MSPE) is also returned for comparison across trend structures (with autocovariance structure fixed). For the model names, "IID" denotes the uncorrelated bi-variate Gaussian model, "OU" denotes the continuous-position Ornstein-Uhlenbeck model, "OUF" denotes the continuous-velocity Ornstein-Uhlenbeck-F model, "OUF" denotes the OUF model where the two autocorrelation timescales cannot be statistically distinguished.

Note

Confidence intervals on the autocorrelation timescales assume they are sufficiently greater than zero and less than infinity.

IC="LOOCV" can only be attempted if also specified during `ctmm.select`, as this argument requires additional calculations.

Prior to ctmm v0.6.2, timescale confidence intervals were constructed from normal and inverse-normal sampling distributions, whereas v0.6.2 onward uses gamma and inverse-gamma sampling distributions.

In ctmm v0.5.1 onward the MSPE is averaged over all possible times instead of over all sampled times.

In ctmm v0.3.4 the speed estimate was fixed to be the RMS velocity and not $1/\sqrt{2}$ times the RMS velocity.

Author(s)

C. H. Fleming.

See Also

[ctmm.fit](#), [ctmm.select](#).

Examples

```
# Load package and data
library(ctmm)
data(buffalo)

# Extract movement data for a single animal
DATA <- buffalo$Cilla

# fit model
GUESS <- ctmm.guess(DATA,interactive=FALSE)
FIT <- ctmm.fit(DATA,GUESS)

# Tell us something interpretable
summary(FIT)
```

summary.UD

Summarize a range distribution

Description

This function returns a list of biologically interesting parameters in human readable format, as derived from an autocorrelated kernel density estimate.

Usage

```
## S3 method for class 'UD'
summary(object,convex=FALSE,level=0.95,level.UD=0.95,units=TRUE,...)
```

Arguments

object	An akde autocorrelated kernel-density estimate from the output of akde.
convex	Report convex coverage areas if TRUE. By default, the highest density regions (HDRs) are reported.
level	Confidence level for the above area estimate. E.g., the 95% confidence interval of the 50% core area.
level.UD	Coverage level for the home-range area. E.g., the 50% core area.
units	Convert result to natural units.
...	Unused options.

Value

A list is returned with the effective sample sizes of various parameter estimates (DOF) and a parameter estimate table CI, with low, point, and high estimates for the following possible parameters:

area The home-range area with fraction of inclusion `level.UD`. E.g., the 50% core home range is estimated with `level.UD=0.50`, and 95% confidence intervals are placed on that area estimate with `level=0.95`.

This kernel density estimate differs from the Gaussian estimate of [summary.ctmm](#). The Gaussian estimate has more statistical efficiency, but is less related to space use for non-Gaussian processes.

Note

Prior to `ctmm` v0.3.1, AKDEs included only errors due to autocorrelation uncertainty, which are insignificant in cases such as IID data. Starting in v0.3.1, `akde` calculated an effective sample size `DOF.H` and used this to estimate area uncertainty under a chi-square approximation. Starting in v0.3.2, this method was improved to use `DOF.area` in the Gaussian reference function approximation.

Author(s)

C. H. Fleming.

References

C. H. Fleming, J. M. Calabrese. A new kernel-density estimator for accurate home-range and species-range area estimation. *Methods in Ecology and Evolution*, 8:5, 571-579 (2016) [doi:10.1111/2041210X.12673](https://doi.org/10.1111/2041210X.12673).

See Also

[akde](#).

Examples

```
# Load package and data
library(ctmm)
data(buffalo)

# Extract movement data for a single animal
DATA <- buffalo$Cilla

# Fit a movement model
GUESS <- ctmm.guess(DATA,interactive=FALSE)
FIT <- ctmm.fit(DATA,GUESS)

# Estimate and summarize the AKDE
UD <- akde(DATA,FIT)
summary(UD)
```

turtle	<i>Wood turtle GPS and calibration dataset from Working Land and Seascapes.</i>
--------	---

Description

x-y projected GPS data from 2 calibration runs and 2 wood turtles. Please contact Tom Akre (akret@si.edu) if you want to publish with these data.

Usage

```
data("turtle")
```

Format

A list of 4 telemetry objects.

See Also

[as.telemetry](#), [plot.telemetry](#), [uere](#), [buffalo](#), [coati](#), [gazelle](#), [jaguar](#), [pelican](#), [wolf](#).

Examples

```
# Load package and data
library(ctmm)
data("turtle")

# Plot a turtle's locations
plot(turtle[[3]])
```

uere	<i>Estimate RMS UERE from calibration data</i>
------	--

Description

Functions for estimating and assigning the root-mean-square User Equivalent Range Error (UERE) of a GPS device from calibration data.

Usage

```
uere(data)

uere(data) <- value

uere.fit(data,precision=1/2)

## S3 method for class 'UERE'
summary(object,level=0.95,...)
```

Arguments

<code>data</code>	telemetry object or list of telemetry objects, preferably with DOP columns.
<code>value</code>	RMS UERE value(s) to assign to telemetry data (see details).
<code>precision</code>	Fraction of maximum possible digits of precision to target in categorical error fitting. <code>precision=1/2</code> results in about 7 decimal digits of precision.
<code>object</code>	UERE object to summarize or list of UERE objects to compare.
<code>level</code>	Confidence level for UERE estimate confidence intervals.
<code>...</code>	Further arguments are ignored.

Details

Often times GPS animal tracking devices return HDOP values but do not specify the device's RMS UERE necessary to transform the HDOP values into absolute errors. `uere.fit()` allows users to estimate the RMS UERE from calibration data, where the device was left fixed over a period of time. The calibration RMS UERE can then be applied to tracking data with the `uere()` assignment method. Otherwise, when `error=TRUE` in `ctmm`, `ctmm.fit` will estimate the RMS UERE simultaneously with the movement model, which is less reliable than using calibration data.

`summary()` applied to single UERE object will return RMS UERE parameter estimates and confidence intervals in meters, while `summary()` applied to a list of UERE objects will return a model-selection table, with AICc and reduced Z squared (goodness of fit) values.

Value

The RMS UERE estimate.

Note

The GPS device should be fixed during calibration.

Author(s)

C. H. Fleming

References

C. H. Fleming et al, "A comprehensive framework for handling location error in animal tracking data", bioRxiv 2020.06.12.130195 (2020) doi:[10.1101/2020.06.12.130195](https://doi.org/10.1101/2020.06.12.130195).

See Also

[as.telemetry](#), [residuals.telemetry](#).

Examples

```
# Load package and data
library(ctmm)
data(turtle)

# the first two datasets are calibration data
names(turtle)

# estimate RMS UERE from calibration data
UERE <- uere.fit(turtle[1:2])
# inspect UERE estimate
summary(UERE)

# assign RMS UERE to entire dataset
uere(turtle) <- UERE

# calculate residuals of calibration data
RES <- lapply(turtle[1:2],residuals)

# scatter plot of residuals with 50%, 95%, and 99.9% coverage areas
plot(RES,col.DF=NA,level.UD=c(0.50,0.95,0.999))

# check calibration data for autocorrelation using fast=FALSE because samples are small
ACFS <- lapply(RES,function(R){correlogram(R,fast=FALSE,dt=10 %## 'min',trace=FALSE)})

# pooling ACFs
ACF <- mean(ACFS)

plot(ACF)
```

Unit conversion

*Convert dimensionful quantities to and from SI units***Description**

This function takes a number in some specified units and converts that number to SI units, or from SI units to the specified units. Internally, all ctmm objects are specified in SI units, and so this is a utility function to facilitate working with ctmm objects.

Usage

```
x %## y
```

Arguments

x	A numeric quantity specified in y character labeled units, or a character unit label to convert a numeric quantity y that is specified in SI units.
y	A unit character label for the quantity x to be converted to SI units, or a numeric quantity in SI units to be converted into unit label x.

Details

If x is a number and y is a character unit label, then x is converted from units y to SI units. If x is a character unit label and y is a number, then y is converted from SI units to units x .

The default non-SI units include the mean solar 'day', mean synodic 'month' and mean tropical 'year'. These defaults can be changed to conventional calendar units via `options(time.units='calendar')`.

Value

Returns a numeric in SI units or units specified by character label x .

Author(s)

C. H. Fleming.

See Also

[unit](#)

Examples

```
# one yard -> meters
1 %%% "yard"

# one meter -> yards
"yard" %%% 1

# 1 month -> days
"day" %%% 1 %%% "month"

# 6 miles per hour -> meters per second
"hour" %%% 6 %%% "mile"

# the same conversion in one step
6 %%% "mph"
```

variogram

Calculate an empirical variogram from movement data

Description

This function calculates the empirical variogram of multi-dimensional tracking data for visualizing stationary (time-averaged) autocorrelation structure. One of two algorithms is used. The slow $O(n^2)$ algorithm is based upon Fleming & Calabrese et al (2014), but with interval-weights instead of lag-weights and an iterative algorithm to adjust for calibrated errors. Additional modifications have also been included to accommodate drift in the sampling rate. The fast $O(n \log n)$ algorithm is based upon the FFT method of Marcotte (1996), with some tweaks to better handle irregularly sampled data. Both methods reduce to the unbiased “method of moments” estimator in the case of evenly *scheduled* data, even with missing observations, but they produce slightly different outputs for irregularly sampled data.

Usage

```
variogram(data,dt=NULL,fast=TRUE,res=1,CI="Markov",error=FALSE,axes=c("x","y"),
          precision=1/8,trace=TRUE)
```

Arguments

<code>data</code>	telemetry data object of the 2D timeseries data.
<code>dt</code>	Lag bin width. An ordered array will yield a progressive coarsening of the lags. Defaults to the median sampling interval.
<code>fast</code>	Use the interval-weighted algorithm if FALSE or the FFT algorithm if TRUE. The slow algorithm outputs a progress bar.
<code>res</code>	Increase the discretization resolution for irregularly sampled data with <code>res>1</code> . Decreases bias at the cost of smoothness.
<code>CI</code>	Argument for confidence-interval estimation. Can be "IID" to consider all unique lags as independent, "Markov" to consider only non-overlapping lags as independent, or "Gauss" for an exact calculation (see Details below).
<code>error</code>	Adjust for the effect of calibrated errors.
<code>axes</code>	Array of axes to calculate an average (isotropic) variogram for.
<code>precision</code>	Fraction of machine precision to target when adjusting for telemetry error (<code>fast=FALSE</code> with calibrated errors). <code>precision=1/8</code> returns about 2 decimal digits of precision.
<code>trace</code>	Display a progress bar if <code>fast=FALSE</code> .

Details

If no `dt` is specified, the median sampling interval is used. This is typically a good assumption for most data, even when there are gaps. A `dt` coarser than the sampling interval may bias the variogram (particularly if `fast=TRUE`) and so this should be reserved for poor data quality.

For irregularly sampled data, it may be useful to provide an array of time-lag bin widths to progressively coarsen the variogram. I.e., if you made the very bad choice of changing your sampling interval on the fly from `dt1` to `dt2`, where `dt1 < dt2`, the an appropriate choice would be `dt=c(dt1,dt2)`. On the other hand, if your sampling is itself a noisy process, then you might want to introduce larger and larger `dt` components as the visual appearance of the variogram breaks down with increasing lags. Alternatively, you might try the `fast=FALSE` option or aggregating multiple individuals with [mean.variogram](#).

With irregularly sampled data, different size lags must be aggregated together, and with current fast methods there is a tradeoff between bias and smoothness. The default settings produce a relatively smooth estimate, while increasing `res` (or setting `fast=FALSE`) will produce a less biased estimate, which is very useful for [correlogram](#).

In conventional variogram regression treatments, all lags are considered as independent (`CI="IID"`) for the purposes of confidence-interval estimation, even if they overlap in time. However, in high resolution datasets this will produce vastly underestimated confidence intervals. Therefore, the default `CI="Markov"` behavior is to consider only the maximum number of non-overlapping lags in calculating confidence intervals, though this is a crude approximation and is overly conservative at

large lags. `CI="Gauss"` implements exact confidence intervals under the assumption of a stationary Gaussian process, but this algorithm is $O(n^2 \log n)$ even when `fast=TRUE`.

If `fast=FALSE` and the tracking data are calibrated (see [uere](#)), then with `error=TRUE` the variogram of the movement process (sans the telemetry-error process) is estimated using an iterative maximum-likelihood estimator that downweights more erroneous location estimates (Fleming et al, 2020). The variogram is targeted to have precision fraction of machine precision. If the data are very irregular and location errors are very homoskedastic, then this algorithm can be slow to converge at time lags where there are few data pairs. If `fast=TRUE` and `error=TRUE`, then the estimated contribution to the variogram from location error is subtracted on a per lag basis, which is less ideal for heteroskedastic errors.

Value

Returns a variogram object (class `variogram`) which is a dataframe containing the time-lag, lag, the semi-variance estimate at that lag, SVF, and the approximate number of degrees of freedom associated with that semi-variance, DOF, with which its confidence intervals can be estimated.

Note

Prior to `ctmm` v0.3.6, `fast=FALSE` used the lag-weighted estimator of Fleming et al (2014). Lag weights have been abandoned in favor of interval weights, which are less sensitive to sampling irregularity. The same weighting formulas are used, but with `dt` instead of the current lag.

Author(s)

C. H. Fleming and J. M. Calabrese.

References

- D. Marcotte, "Fast variogram computation with FFT", *Computers and Geosciences* 22:10, 1175-1186 (1996) [doi:10.1016/S00983004\(96\)00026X](#).
- C. H. Fleming, J. M. Calabrese, T. Mueller, K.A. Olson, P. Leimgruber, W. F. Fagan, "From fine-scale foraging to home ranges: A semi-variance approach to identifying movement modes across spatiotemporal scales", *The American Naturalist*, 183:5, E154-E167 (2014) [doi:10.1086/675504](#).
- C. H. Fleming et al, "A comprehensive framework for handling location error in animal tracking data", *bioRxiv* (2020) [doi:10.1101/2020.06.12.130195](#).

See Also

`vignette("variogram")`, [correlogram](#), [mean.variogram](#), [plot.variogram](#), [variogram.fit](#).

Examples

```
#Load package and data
library(ctmm)
data(buffalo)

#Extract movement data for a single animal
DATA <- buffalo$Cilla
```

```
#Calculate variogram
SVF <- variogram(DATA)

#Plot the variogram with 50% and 95% CIs
plot(SVF,level=c(0.5,0.95))
```

variogram.fit

Visually fit a movement model to a variogram

Description

This function plots a variogram object overlayed with a continuous-time movement model guesstimated from the variogram's shape. Sliders are given to adjust the parameter guesstimates and the result can be saved to a global variable. The intention of this function is to facilitate good starting guesses for `ctmm.fit`, starting with a prototype hypothesis argument `CTMM`, which can contain features such as isotropic, range, circle, etc..

Usage

```
ctmm.guess(data,CTMM=ctmm(),variogram=NULL,name="GUESS",interactive=TRUE)

variogram.fit(variogram,CTMM=ctmm(),name="GUESS",fraction=0.5,interactive=TRUE,...)
```

Arguments

<code>data</code>	A telemetry object.
<code>CTMM</code>	Optional model prototype or initial guesstimate of the model parameters, in <code>ctmm</code> object format.
<code>name</code>	Name of the global variable to store the guesstimate in.
<code>interactive</code>	Boolean denoting whether to render the initial guess with interactive sliders or store the result silently.
<code>variogram</code>	A variogram object from the output of <code>variogram</code> .
<code>fraction</code>	Initial fraction of the variogram to render.
<code>...</code>	Optional parameters passed to <code>plot.variogram</code> .

Details

By default, `sigma` is the asymptote of the variogram and `tau` is an array of autocorrelation timescales. The position timescale is roughly the time lag it takes of the variogram to reach 63% of its asymptote. The velocity autocorrelation timescale visually corresponds to width of the concave bowl shape at the beginning of the variogram. If `CTMM=ctmm(range=FALSE)`, `sigma` is the asymptotic slope of the variogram and only the velocity timescale is finite.

By default, parameter values are estimated from the shape of the variogram. If this fails, the `CTMM` option can provide alternative initial guesstimates.

`variogram.fit` is called by `ctmm.guess`, and there is usually no reason to call `variogram.fit` directly.

Note

If the `manipulate` package is unavailable, then `interactive` is set to `FALSE`.

Author(s)

C. H. Fleming.

See Also

`ctmm.fit`, `plot.variogram`, `variogram`.

Examples

```
#Load package and data
library(ctmm)
data(buffalo)

#Extract movement data for a single animal
DATA <- buffalo$Cilla

# generate a visual fit of the variogram (requires RStudio or a guess object is returned)
ctmm.guess(DATA)
```

video

Video record animated telemetry objects.

Description

Produces an MP4 video file by animating telemetry objects.

Usage

```
video(x, ext=extent(x), fps=60, dt=NULL, ghost=0, timestamp=FALSE, file="ctmm.mp4", res=720,
      col="red", pch=1, cex=NULL, lwd=1, par.list=list(), ...)
```

Arguments

<code>x</code>	telemetry object or list of telemetry objects.
<code>ext</code>	Plot extent for all frames.
<code>fps</code>	Frames per viewed second.
<code>dt</code>	Tracked time per frame (not per viewed second). By default, the median timestep will be used.
<code>ghost</code>	Timescale over which image retention (ghosting) decays.
<code>timestamp</code>	Display timestamps on title.
<code>file</code>	File name for MP4 file to save. The full path can also be specified. Otherwise the working directory will be used.

<code>res</code>	Pixel resolution for square videos or pixel <code>c(width,height)</code> for rectangular videos.
<code>col</code>	Color option for telemetry data. Can be an array or list of arrays.
<code>pch</code>	Plotting symbol. Can be an array or list of arrays.
<code>cex</code>	Relative size of plotting symbols. Only used when errors are missing.
<code>lwd</code>	Line widths of telemetry points.
<code>par.list</code>	List of additional arguments passed to <code>par</code> within <code>animate</code> that do not work outside of <code>animate</code> , like <code>mar</code> .
<code>...</code>	Additional options passed to <code>plot.telemetry</code> .

Details

This function does not interpolate locations to make smooth animations. For that, please use `predict` or `simulate` outputs instead of a raw tracking data.

Value

Saves an MP4 file named `file` to the working directory.

Note

Further animation and ffmpeg options can be set via `ani.options`.

Author(s)

C. H. Fleming.

See Also

`plot`, `plot.telemetry`, `ani.options`

Examples

```
# Load package and data
library(ctmm)
data(coati)

# temporary file to store videos for CRAN compliance
FILE <- tempfile("ctmm",fileext=".mp4")
# you will likely want to save your video elsewhere
# the working directory is the default location

# create guess object
GUESS <- ctmm.guess(coati[[2]],interactive=FALSE)
# in general, use ctmm.select instead of ctmm.fit
FIT <- ctmm.fit(coati[[2]],GUESS)

# consider a few hours of consecutive sampling, at 1 minute per frame
t <- seq(coati[[2]]$t[19],coati[[2]]$t[27],by=60)
```

```
# tau[velocity] is a natural scale to demonstrate persistence of motion
ghost <- FIT$tau[2]

# predicted locations each minute
PRED <- predict(coati[[2]],FIT,t=t)

# most likely path
video(PRED,error=FALSE,pch=16,ghost=ghost,file=FILE)

# prediction (distribution)
video(PRED,error=3,file=FILE)

# conditional simulations
SIMS <- lapply(1:6,function(i){simulate(coati[[2]],FIT,t=t)})

# random paths
video(SIMS,pch=16,ghost=ghost,file=FILE)
```

wolf	<i>Maned wolf GPS dataset from The Maned Wolf Conservation Program.</i>
------	---

Description

x-y projected GPS data on 8 Maned wolves. Please contact Rogerio Cunha de Paula (roger-cunha@gmail.com) if you want to publish with these data.

Usage

```
data("wolf")
```

Format

A list of 8 telemetry objects.

See Also

[as.telemetry](#), [plot.telemetry](#), [buffalo](#), [coati](#), [gazelle](#), [pelican](#), [turtle](#).

Examples

```
# Load package and data
library(ctmm)
data("wolf")

# Plot a wolf's locations
plot(wolf[[8]])
```

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