Package 'rKIN'

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Type Package

Title (Kernel) Isotope Niche Estimation

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URL

BugReports

Depends R (>= 4.1.0), ks, sf

Imports ggplot2, MASS, RColorBrewer, randomcoloR, shades, dplyr

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Description Applies methods used to estimate animal homerange, but
instead of geospatial coordinates, we use isotopic coordinates. The estimation
methods include: 1) 2-dimensional bivariate normal kernel utilization density
estimator, 2) bivariate normal ellipse estimator, and 3) minimum convex polygon
estimator, all applied to stable isotope data. Additionally, functions to
determine niche area, polygon overlap between groups and levels (confidence
contours) and plotting capabilities.

License GPL (>= 3)

LazyData TRUE

RoxygenNote 7.2.3

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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Contents

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bw_hbcv   *Biased cross-validation bandwidth matrix selector for bivariate data.*

Description

A simple wrapper for the ks::Hbcv function.

Usage

```
bw_hbcv(x)
```

Arguments

x   2d matrix of data values.

Value

A numeric vector of estimated x and y bandwidths. Must subset your data if you wish to obtain group specific bandwidths.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

Examples

```
data("rodents")
# Subset the data for a single species
spec1<- rodents[rodents$Species == "Species1", ]
# Calculate the bandwidth
bw_hbcv(as.matrix(spec1[, c("Ave_C", "Ave_N")]))
```

---

bw_hlscv   *Least-squares cross-validation bandwidth matrix selector for multi-*
                            variate data.

Description

A simple wrapper for the ks::Hlscv function.

Usage

```
bw_hlscv(x)
```

Arguments

x   2d matrix of data values.

Value

A numeric vector of estimated x and y bandwidths. Must subset your data if you wish to obtain group specific bandwidths.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

Examples

```
data("rodents")
# Subset the data for a single species
spec1<- rodents[rodents$Species == "Species1", ]
# Calculate the bandwidth
bw_hlscv(as.matrix(spec1[, c("Ave_C", "Ave_N")]))
```

---

bw_hnm   *Normal mixture bandwidth.*

Description

A simple wrapper for the ks::Hnm function.

Usage

```
bw_hnm(x)
```

Arguments

x   2d matrix of data values.

Value

A numeric vector of estimated x and y bandwidths. Must subset your data if you wish to obtain group specific bandwidths.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

Examples

```
data("rodents")
# Subset the data for a single species
spec1<- rodents[rodents$Species == "Species1", ]
# Calculate the bandwidth
bw_hnm(as.matrix(spec1[, c("Ave_C", "Ave_N")]))
```

---

bw_hns   *Normal scale bandwidth using ks::Hns function.*

Description

A simple wrapper for the ks::Hns function.

Usage

```
bw_hns(x)
```

Arguments

x   2d matrix of data values.

Value

A numeric vector of estimated x and y bandwidths. Must subset your data if you wish to obtain group specific bandwidths.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

Examples

```
data("rodents")
# Subset the data for a single species
spec1<- rodents[rodents$Species == "Species1", ]
# Calculate the bandwidth
bw_hns(as.matrix(spec1[, c("Ave_C", "Ave_N")]))
```

---

bw_hpi   *Default Plug-in bandwidth selector using ks::Hpi function.*

Description

A simple wrapper for the ks::Hpi function.

Usage

```
bw_hpi(x)
```

Arguments

x   2d matrix of data values.

Value

A numeric vector of estimated x and y bandwidths. Must subset your data if you wish to obtain group specific bandwidths.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

Examples

```
data("rodents")
# Subset the data for a single species
spec1<- rodents[rodents$Species == "Species1", ]
# Calculate the bandwidth
bw_hpi(as.matrix(spec1[, c("Ave_C", "Ave_N")]))
```

---

bw_hscv   *Smoothed cross-validation bandwidth selector.*

Description

A simple wrapper for the ks::Hscv function.

Usage

```
bw_hscv(x)
```

Arguments

x   2d matrix of data values.

Value

A numeric vector of estimated x and y bandwidths. Must subset your data if you wish to obtain group specific bandwidths.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

Examples

```
data("rodents")
# Subset the data for a single species
spec1<- rodents[rodents$Species == "Species1", ]
# Calculate the bandwidth
bw_hscv(as.matrix(spec1[, c("Ave_C", "Ave_N")]))
```

---

bw_hucv   *Least-squares cross-validation bandwidth matrix selector for multi-variate data.*

Description

A simple wrapper for the ks::Hucv function.

Usage

```
bw_hucv(x)
```

Arguments

x   2d matrix of data values.

Value

A numeric vector of estimated x and y bandwidths. Must subset your data if you wish to obtain group specific bandwidths.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

Examples

```
data("rodents")
# Subset the data for a single species
spec1<- rodents[rodents$Species == "Species1", ]
# Calculate the bandwidth
bw_hucv(as.matrix(spec1[, c("Ave_C", "Ave_N")]))
```

---

bw_ref   *Normal Reference Distribution.*

Description

A simple wrapper for the MASS::bandwidth.nrd function. Divides values by 4 to match the scale of ks methods

Usage

```
bw_ref(x)
```

Arguments

x   2d matrix of data values.

Value

A numeric vector of estimated x and y bandwidths. Must subset your data if you wish to obtain group specific bandwidths.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

Examples

```
data("rodents")
# Subset the data for a single species
spec1<- rodents[rodents$Species == "Species1", ]
# Calculate the bandwidth
bw_hucv(as.matrix(spec1[, c("Ave_C", "Ave_N")]))
```

---

calcOverlap   *Calculate Percent Overlap of Isotopic Niche Space*

Description

Calculates the percent of polygon overlap between each group and level.

Usage

```
calcOverlap(estObj)
```

Arguments

estObj   List object of class estObj containing returned sf data frames from estimating
                functions estKIN, etc.

Value

A data.frame containing the percent of the polygon overlap for each group and level. Rows are the
1st input polygon, columns are the 2nd input, the returned area of overlap is divided by the area of
the 1st polygon (row).

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

Examples

```
library(rKIN)
data("rodents")
#estimate niche overlap between 2 species using kernel UD
test.kin<- estKIN(data=rodents, x="Ave_C", y="Ave_N", group="Species",
                  levels=c(50, 75, 95), scaler=2)
#determine polygon overlap for all polygons
dat.olp<- calcOverlap(test.kin)
```

---

createSPDF   *Internal helper function*

Description

Create empty sf data frame with estObj schema

Usage

```
createSPDF()
```

Value

An empty sf data frame object matching the expected schema of the estKIN function.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

---

estEllipse	*Estimate Bivariate Normal Ellipse Isotope Niche*

Description

Calculates the Bivariate Normal Ellipse Polygon for isotopic values at multiple confidence levels. Returns a list of sf data frames, each list item representing the grouping variable (i.e. species).

Usage

```
estEllipse(data, x, y, group, levels = c(50, 75, 95), smallSamp = FALSE)
```

Arguments

data	data.frame object containing columns of isotopic values and grouping variables
x	character giving the column name of the x coordinates
y	character giving the column name of the y coordinates
group	character giving the column name of the grouping variable (i.e. species)
levels	Numeric vector of desired percent levels (e.g. c(10, 50, 90). Should not be less than 1 or greater than 100)
smallSamp	logical value indicating whether to override minimum number of samples. Currently 10 samples are required.

Value

A list of sf data frames, each list item representing the grouping variable.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

Examples

```
library(rKIN)
data("rodents")
#estimate niche overlap between 2 species using bivariate ellipse
test.elp<- estEllipse(data=rodents, x="Ave_C", y="Ave_N", group="Species",
                   levels=c(50, 75, 95))
#determine polygon overlap for all polygons
plotKIN(test.elp, scaler=2, title="Ellipse Estimates", xlab="Ave_C", ylab="Ave_N")
```

---

estKIN   *Estimate Kernel Isotope Niche*

Description

Calculates the 2D kernel for isotopic values at multiple confidence levels. Returns a list of sf data frames, each list item representing the grouping variable (i.e. species).

Usage

```
estKIN(
  data,
  x,
  y,
  h = "ref",
  hval = NULL,
  group,
  levels = c(50, 75, 95),
  scaler = 10,
  smallSamp = FALSE
)
```

Arguments

data	data.frame object containing columns of isotopic values and grouping variables
x	character giving the column name of the x coordinates
y	character giving the column name of the y coordinates
h	character describing the bandwidth estimator method. Default = "ref". See Details for more information.
hval	numeric vector of length 2 describing the bandwidth in x and y directions. Default = NULL
group	character giving the column name of the grouping variable (i.e. species)
levels	Numeric vector of desired percent levels (e.g. c(10, 50, 90). Should not be less than 1 or greater than 99)
scaler	numeric value to expand the min/max x and y values. This assists with error given smaller sample sizes. Default value = 10
smallSamp	logical value indicating whether to override minimum number of samples. Currently 10 samples are required.

Details

Details For the h argument there are 8 different bandwidth estimation options ("hns", "hpi", "hscv", "hlscv", "hbcv", "hnm", "hucv", "ref"). "ref" = The default MASS::kde2d bandwidth method. The remaining options are obtained from the 'ks' package with the default method being "hpi". For all ks package methods, the default values are accepted and only the x and y values are passed to the

bivariate bandwidth estimating functions. For all bandwidth estimation methods, reducing the data to an individual group will provide the same bandwidths as used during rKIN estimation.

* hpi - Default Plug-in bandwidth selector using ks::Hpi function. Values can be obtained using bw_hpi(). * hns - Normal scale bandwidth using ks::Hns function.Values can be obtained using bw_hns(). * hscv - Smoothed cross-validation bandwidth selector. Values can be obtained using bw_hscv(). * hlscv - Least-squares cross-validation bandwidth matrix selector for multivariate data. Values can be obtained using bw_hlscv(). * hbcv - Biased cross-validation bandwidth matrix selector for bivariate data. Values can be obtained using bw_hbcv(). * hnm - Normal mixture bandwidth. Values can be obtained using bw_hnm(). * hucv - Least-squares cross-validation bandwidth matrix selector for multivariate data. Values can be obtained using bw_hucv(). * ref - Uses MASS::bandwidth.nrd for both x and y separately, dividing values by 4 to match the scale of ks methods. Values can be obtained using bw_ref(). See MASS:kde2d() for details (i.e. the function divides the values by 4).

Value

A class rKIN object containing a list of sf data frames, each list item representing the grouping variable.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

Examples

```
library(rKIN)
data("rodents")
#estimate niche overlap between 2 species using kernel UD
test.kin<- estKIN(data=rodents, x="Ave_C", y="Ave_N", group="Species",
                levels=c(50, 75, 95), scaler=2)
#determine polygon overlap for all polygons
plotKIN(test.kin, scaler=2, title="Kernel Estimates", xlab="Ave_C", ylab="Ave_N")
```

---

estMCP   *Estimate Minimum Convex Polygon (MCP) Isotope Niche*

Description

Calculates the Minimum Convex Polygon for isotopic values at multiple confidence levels. Returns a list of sf data frames, each list item representing the grouping variable (i.e. species).

Usage

```
estMCP(data, x, y, group, levels = c(50, 75, 95), smallSamp = FALSE)
```

Arguments

data	data.frame object containing columns of isotopic values and grouping variables
x	character giving the column name of the x coordinates
y	character giving the column name of the y coordinates
group	character giving the column name of the grouping variable (i.e. species)
levels	Numeric vector of desired percent levels (e.g. c(10, 50, 90). Should not be less than 1 or greater than 100)
smallSamp	logical value indicating whether to override minimum number of samples. Currently 10 samples are required.

Value

A list of sf data frames, each list item representing the grouping variable.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

Examples

```
library(rKIN)
data("rodents")
#estimate niche overlap between 2 species using minimum convex polygons
test.mcp<- estMCP(data=rodents, x="Ave_C", y="Ave_N", group="Species",
                  levels=c(50, 75, 95))
#determine polygon overlap for all polygons
plotKIN(test.mcp, scaler=2, title="Minimum Convex Hull Estimates", xlab="Ave_C", ylab="Ave_N")
```

---

genCircle	*Create a sequence of points on a circle*

Description

This is a helper function that creates a sequence of points on a circle of radius r as a resolution determined by n. This function was directly borrowed from SIBER package (Intended for generating various SIBER ellipses).It is not intended for direct calling. NB not an exported function.

Usage

```
genCircle(n = 100, r)
```

Arguments

n	the number of points to create around the circle. Defaults to 100.
r	the radius of the circle to create.

Value

A 2 x n matrix of x and y coordinates of points on a circle.

---

getArea *Method to extract Niche Polygon Areas*

Description

Extracts the polygon area for an rKIN object for each group and level.

Usage

```
getArea(estObj)
```

Arguments

estObj   List object created from estKIN, estMCP or estEllipse functions

Value

A data.frame() of polygon areas.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

Examples

```
data("rodents")
#estimate niche overlap between 2 species using kernel UD
test.kin<- estKIN(data=rodents, x="Ave_C", y="Ave_N", group="Species",
                  levels=c(50, 75, 95), scaler=2)
#determine polygon sizes/areas
kin.area<- getArea(test.kin)
```

---

getColors   *Create a list of colors for plotKIN function*

Description

The list of colors were obtained from Colorbrewer2.org using single hue. This is run within the function plotKIN()

Usage

```
getColors(groups, levels, colors = NULL)
```

Arguments

groups	The number of groups within grouping variable (i.e. species)
levels	The number of confidence intervals provided by the user
colors	Character vector of hex codes representing desired colors

Value

A character vector of RGB colors

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

---

getKernelThreshold   *Miscellaneous functions to complete kernel 2D estimates: Get contour threshold values*

Description

Obtains the quantile threshold levels for a vector of probabilities from a kernel density estimate.

Usage

```
getKernelThreshold(x, levels = c(50, 75, 95))
```

Arguments

x	Numeric vector of probabilities from a kernel density estimate
levels	Numeric vector of desired percent levels (e.g. c(10, 50, 90). Should not be less than 1 or greater than 99)

Value

A list of threshold values for each percent.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

---

plotKIN   *Plotting function for rKIN polygons*

Description

Using ggplot2 methods, simultaneously plot all of the groups and levels of niche space

Usage

```
plotKIN(
  estObj,
  scaler = 1,
  alpha = 0.3,
  title = "",
  xlab = "x",
  ylab = "y",
  xmin = NULL,
  xmax = NULL,
  ymin = NULL,
  ymax = NULL,
  colors = NULL
)
```

Arguments

estObj	list object created from estKIN, estMCP or estEllipse functions
scaler	numeric value indicating number of isotopic units to expand the x and y axes of the plot. Default is 1.
alpha	numeric value between 0 and 1, representing the amount of transparency of each polygon. 0 is transparent, 1 is opaque.
title	character string for a plot title.
xlab	character or expression string for the x-axis label.
ylab	character or expression string for the y-axis label.
xmin	default is NULL, numeric value of user specified minimum x axis value
xmax	default is NULL, numeric value of user specified maximum x axis value
ymin	default is NULL, numeric value of user specified minimum y axis value
ymax	default is NULL, numeric value of user specified maximum y axis value
colors	default is NULL, character vector of hex codes representing colors for plot

Value

A plot of all groups and levels.

Author(s)

Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

Examples

```
library(rKIN)
data("rodents")
#estimate niche overlap between 2 species using kernel UD
test.kin<- estKIN(data=rodents, x="Ave_C", y="Ave_N", group="Species",
                  levels=c(50, 75, 95), scaler=2)
#determine polygon overlap for all polygons
plotKIN(test.kin, scaler = 1, title = "Kernel Estimates",
        xlab = expression({delta}^13*C~ ('Per Mille')),
        ylab = expression({delta}^15*N~ ('Per Mille')))
```

---

rKIN   *rKIN: A package for computating isotopic niche space*

Description

The rKIN This package applies methods used to estimate animal homerange, but instead of geospatial coordinates, we use isotopic coordinates. The estimation methods include: 1) 2-dimensional bivariate normal kernel utilization density estimator with multiple bandwidth estimation methods, 2) bivariate normal ellipse estimator, and 3) minimum convex polygon estimator, all applied to stable isotope data. Additionally, functions to determine niche area, polygon overlap between groups and levels (confidence contours) and plotting capabilities.

rKIN functions

The rKIN functions: estKIN, estEllipse, estMCP, plot.kin, getArea, calcOverlap

---

rodents   *Isotopic data from rodent blood samples.*

Description

A dataset containing the individual Species, Habitat sampled, and Percent delta C and N.

Usage

```
rodents
```

Format

A data frame with 530 rows and 4 variables:

Species Generic species used as a grouping variable

Habitat Habitat in which the individual was captured

Ave_C Averaged delta 13C present within the blood sample

Ave_N Averaged delta 15N present within the blood sample ...

Source

http://www.uwyo.edu/zoology/people/bendavid.html

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