Package 'rKIN'

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Type Package

Title (Kernel) Isotope Niche Estimation

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URL `http://github.com/salbeke/rKIN`

BugReports `http://github.com/salbeke/rKIN/issues`

Depends R (>= 2.10), maptools

Imports ggplot2, MASS, sp, rgeos

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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 5.0.1

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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R topics documented:

`calcOverlap` *Calculate Percent Overlap of Isotopic Niche Space*

Description

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

Usage

```
calcOverlap(estObj)
```

Arguments

`estObj`	List object of class estObj containing returned SpatialPolygonDataFrames 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 devided 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 SpatialPolygonsDataFrame with estObj schema

Usage

```
createSPDF()
```

Value

An empty SpatialPolygonsDataFrame object matching the expected schema of the estKIN function.

Author(s)

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

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`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 SpatialPolygonsDataFrame, 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 SpatialPolygonsDataFrame, 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 SpatialPolygonsDataFrame, each list item representing the grouping variable (i.e. species).

Usage

```
estKIN(data, x, y, 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
`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.

Value

A class rKIN object containing a list of SpatialPolygonsDataFrame, 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 SpatialPolygonsDataFrame, 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 SpatialPolygonsDataFrame, 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)
```

Arguments

`groups`	The number of groups within grouping variable (i.e. species)
`levels`	The number of confidence intervals provided by the user

Value

A character vector of RGB colors

Author(s)

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

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`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

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`makeHole` *Miscellaneous functions to complete kernel 2D estimates: make polygon hole when inner circle*

Description

For multipart polygons, set the inner circle to be 'hole=TRUE' after obtaining contour lines from kernel estimate. The hole is determined using the gContainsProper() function from rgeos package. This is run within the 2D-Kernel estimator function estKIN()

Usage

```
makeHole(poly, outer, hole)
```

Arguments

`poly`	The multipart polygon
`outer`	The outer ring of the polygon
`hole`	The inner ring of the polygon

Value

A Polygons object

Author(s)

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

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`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")
```

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.

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~ ('\u2030')),
         ylab = expression({delta}^15*N~ ('\u2030')))
```

`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, 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

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`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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