Package ‘rKIN’

January 24, 2017

Type Package
Title (Kernel) Isotope Niche Estimation
Version 0.1
Date 2017-01-16

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

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

Depends R (>= 2.10), maptools
Imports ggplot2, MASS, sp, rgeos

Maintainer Shannon E Albeke <salbeke@uwyo.edu>

Description Applies methods used to estimate animal home range, 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

Author Shannon E Albeke [aut, cre]

Repository CRAN

Date/Publication 2017-01-24 01:01:39
\textbf{R topics documented:}

\begin{itemize}
  \item \texttt{calcOverlap} \hspace{2cm} 2
  \item \texttt{createSPDF} \hspace{2cm} 3
  \item \texttt{estEllipse} \hspace{2cm} 3
  \item \texttt{estKIN} \hspace{2cm} 4
  \item \texttt{estMCP} \hspace{2cm} 5
  \item \texttt{genCircle} \hspace{2cm} 6
  \item \texttt{getArea} \hspace{2cm} 7
  \item \texttt{getColors} \hspace{2cm} 8
  \item \texttt{getKernelThreshold} \hspace{2cm} 8
  \item \texttt{makeHole} \hspace{2cm} 9
  \item \texttt{plotKIN} \hspace{2cm} 9
  \item \texttt{rKIN} \hspace{2cm} 10
  \item \texttt{rodents} \hspace{2cm} 11
\end{itemize}

\section*{Index}

\begin{tabular}{ll}
\texttt{calcOverlap} & \textit{Calculate Percent Overlap of Isotopic Niche Space} \\
\end{tabular}

\section*{Description}

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

\section*{Usage}

\texttt{calcOverlap(estObj)}

\section*{Arguments}

\begin{itemize}
  \item \texttt{estObj} \hspace{2cm} List object of class \texttt{estObj} containing returned \texttt{SpatialPolygonDataFrames} from estimating functions \texttt{estKIN}, etc.
\end{itemize}

\section*{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).

\section*{Author(s)}

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

```r
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**

```r
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

---

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**

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

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.
getArea

Value

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

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

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.
**makeHole**

Author(s)
Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

---

**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 

\texttt{gContainsProper()} function from rgeos package. This is run within the 2D-Kernel estimator function \texttt{estKIN()}

**Usage**

\texttt{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 Polylines object

**Author(s)**
Shannon E. Albeke, Wyoming Geographic Information Science Center, University of Wyoming

---

**plotKIN**

*Plotting function for rKIN polygons*

---

**Description**

Using \texttt{ggplot2} methods, simultaneously plot all of the groups and levels of niche space

**Usage**

\texttt{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

```r
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)^13C - ('\u2030\u2030')),
         ylab = expression((delta)^15N - ('\u2030\u2030')))
```

Description

The rKIN 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
rodents

---

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](http://www.uwyo.edu/zoology/people/bendavid.html)
Index

*T Topic **datasets**
   rodents, 11

calcOverlap, 2
createSPDF, 3

estEllipse, 3
estKIN, 4
estMCP, 5

genCircle, 6
getArea, 7
getColors, 8
getKernelThreshold, 8

makeHole, 9

plotKIN, 9

rKIN, 10
rKIN-package (rKIN), 10
rodents, 11