Package 'siar'

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Type Package

Title Stable Isotope Analysis in R

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Depends hdrcde, coda, MASS, bayesm, mnormt, spatstat

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Description This package takes data on organism isotopes and fits a Bayesian model to their dietary habits based upon a Gaussian likelihood with a mixture dirichlet-distributed prior on the mean. It also includes SiBER metrics. See siardemo() for an example. Version 4.1.2 contains bug fixes to allow more than isotope numbers other than 2. Version 4.2 fixes a bug that stopped siar working on 64-bit systems

License GPL (>= 2)

LazyLoad yes

NeedsCompilation yes

Repository CRAN

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R topics documented:

`siar-package` *Stable Isotope Analysis in R.*

Description

This package takes data on animal isotopes and fits a Bayesian model to their dietary habits based upon a Gaussian likelihood with a dirichlet prior mixture on the mean. The main function, siarmcmcdirichletv4(), allows the user to specify the data and choose the size of the MCMC run. A wrapper for the package, siarmenu() gives a walkthrough of all the functions contained in the package and produces some pretty plots. Some example data on Geese plasma is included for illustration.

Details

Package:	siar
Type:	Package
Version:	4.2
Date:	2010-04-22
License:	GPL (>= 2)

For a demo of how to use the package, type siarmenu() and then choose option 9,

Author(s)

Andrew Parnell <Andrew.Parnell@tcd.ie>

See Also

siarmenu siarmcmcdirichletv4

Examples

```
## See siarmenu()
```

`allgroups` *The entire set of Geese isotope data*

Description

A 5 column matrix containing isotopic estimates for 251 geese collected at 8 different time points. The first column indicates the time point group, the second and third are d15N (Nitrogen) and d13C (Carbon) isotopic values for the Geese plasma, the third and fourth are d15N and d13C values for the Geese cells. Note that these are raw values; they have not undergone fractionation correction.

Usage

```
data(allgroups)
```

Format

A data frame with 251 observations on the following 5 variables.

`Group` Group number / time point

`d15NPl` d15N plasma

`d13CPl` d13C plasma

`d15NCe` d15N cells

`d13CCe` d13C cells

Examples

```
#see siarmenu() and option 9 for a demo using part of this data
```

bayesMVN *Bayesian MVN*

Description

Fit a Multivariate Normal distribution to bivariate data using Bayesian Inference. Uses the function rmultireg to fit the model to the data.

Usage

```
bayesMVN(x,y,R=10^4)
```

Arguments

x	A vector containing the x coordinates of the data.
y	A vector containing the y coordinates of the data.
R	The number of posterior draws to make. Defaults to 10^4.

Value

b	The posterior draws of the estimated means.
S	The posterior draws of the estimated correlation matrix sigma.

Author(s)

Andrew Jackson

bayestwoNorm *Bayesian Independent Normal Distributions*

Description

Fit two independent Normal distributions to bivariate data using Bayesian Inference. Uses the function runireg to fit the model to the data.

Usage

```
bayestwoNorm(xx,yy,R=10^4)
```

Arguments

xx	A vector containing the x coordinates of the data.
yy	A vector containing the y coordinates of the data.
R	The number of posterior draws to make. Defaults to 10^4.

Value

b	The posterior draws of the estimated independent means.
S	The posterior draws of the estimated independent variances.

Author(s)

Andrew Jackson

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concdepdemo *Concentration dependence values for the geese demo data*

Description

A 5 column, 4 row matrix containing the mean and standard deviation of the concentation dependence values for each of the 2 isotopes used for each different source. Note that the standard deviation is not currently implemened and is set to 0 in this example.

Usage

```
data(concdepdemo)
```

Format

A data frame with 4 observations on the following 5 variables.

`Sources` The source name.

`Meand15N` The mean concentration dependence value for 15N

`SDd15N` The standard deviation concentration dependence value for 15N

`Meand13C` The mean concentration dependence value for 13C

`SDd13C` The standard deviation concentration dependence value for 13C

Examples

```
#see siarmenu() and option 9 for a demo using this data
```

convexhull *Convex Hull*

Description

Calculates the area and coordinates (for plotting) of the convex hull surrounding bivariate data

Usage

```
convexhull(x,y)
```

Arguments

x,y	Bivariate data given as vectors x and y

Author(s)

Andrew Jackson

correctionsdemo *Fractionation correction values for the geese data*

Description

A 5 column, 4 row matrix containing the mean and standard deviation of the correction values for each of the 2 isotopes used for each different source

Usage

```
data(correctionsdemo)
```

Format

A data frame with 4 observations on the following 5 variables.

`Source` The source name.

`Mean15N` The mean correction value for 15N

`Sd15N` The standard deviation correction value for 15N

`Mean13C` The mean correction value for 13C

`Sd13C` The standard deviation correction value for 13C

Examples

```
#see siarmenu() and option 9 for a demo using this data
```

geese1demo *A single group of the geese data*

Description

A 2 column, 9 row matrix containing the plasma data for the first group of geese

Usage

```
data(geese1demo)
```

Format

A data frame with 9 observations on the following 2 variables.

`d15NPl` d15N plasma

`d13CPl` d13C plasma

Examples

```
#see siarmenu() and option 9 for a demo using this data
```

geese2demo *A multi-group version of the geese plasma data*

Description

A 3 column, 251 row matrix which contains the isotopic plasma values of 251 geese over 2 isotopes

Usage

```
data(geese2demo)
```

Format

A data frame with 251 observations on the following 3 variables.

`Group` The group number / time point

`d15NPl` The d15N plasma value

`d13CPl` The d13C plasma value

Examples

```
#see siarmenu() and option 9 for a demo using similar data
```

hullarea *Convex Hull Area*

Description

Utility function to calculate the area enclosed by the convex hull of bivariate data. Not intended for direct use by the user, and is called by `hullarea`

Usage

```
hullarea(x,y)
```

Arguments

`x,y`	Bivariate data given as vectors x and y

Author(s)

Andrew Jackson

laymanmetrics *Isotope-space Niche Width Metrics*

Description

Calculates the 6 metrics for trophic niche width as described by Layman et al. 2007.

Usage

```
laymanmetrics(x,y)
```

Arguments

`x,y`	Bivariate data given as vectors x and y

Value

`dN_range`	Assuming y is delta Nitrogen, then dN_range is the max(delta N
- min(delta N)	
`dC_range`	Assuming x is delta Nitrogen, then dN_range is the max(delta N
- min(delta N)	
`hull`	Contains the area of the convex hull around the data points defined by x and y (hull$TA); the coordinates for plotting of the convex hull (hull$xcoords, hull$ycoords); and the index address of the points in x and y which define the convex hull (hull$chI)

CD	Mean distance to centroid
MNND	Mean Nearest Neighbour Distance
SDNND	Standard Deviation of the Nearest Neighbour Distance

Author(s)

Andrew Jackson

References

Layman, C. A., D. A. Arrington, et al. (2007). Can stable isotope ratios provide for community-wide measures of trophic structure? Ecology 88(1): 42-48.

---

newgraphwindow *Opens a new graphics window on a variety of platforms*

Description

Opens a new graphics window on a variety of platforms

Usage

```
newgraphwindow()
```

Details

Not intended for use outside siarmenu

Author(s)

Andrew Parnell

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overlap *Area of overlap between two estimated ellipses*

Description

Given the coordinates of two bivariate samples, this function calculates (computationally) the area of overlap between two standard ellipses. Note, be sure to use a sufficiently low step size when creating the ellipses (i.e. to ensure that there is no excessive discretising of the elliptical shape). As a result of this process, you will inevitably underestimate the true ellipse areas and hence their overlap (although this bias is likely to be inconsequential) if a suitable fine scale is chosen for the step size. There is no single rule for making this choice as it depends on the angle and shape of the ellipse but a step-size of 1 should be more than sufficient in most cases (N.B. the default steps=5). The ellipses calculated are the small sample size corrected standard ellipses.

Usage

```
overlap(x1,y1,x2,y2,steps = 5)
```

Arguments

x1	A vector containing the x coordinates of the first data.
y1	A vector containing the y coordinates of the first data.
x2	A vector containing the x coordinates of the second data.
y2	A vector containing the y coordinates of the second data.
steps	The number of steps in degrees to estimate points on the curve.

Value

overlap	The area of overlap between the two standard ellipses.
area1	The area of the first ellipse.
area2	The area of the second ellipse.

Author(s)

Andrew Jackson

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panelcontour *Adds contours to a matrix plot*

Description

A simple function used by pairs to produce neat looking matrix plots. Not intended for use by those using siar.

Usage

```
panelcontour(x, y, ...)
```

Arguments

x	A numeric vector containing data with which to produce a contour plot
y	A numeric vector containing data with which to produce a contour plot
...	Other arguments

Author(s)

Andrew Parnell

panelcor *Adds correlations to a matrix plot*

Description

A simple function used by pairs to produce neat looking matrix plots. Not intended for use by those using siar.

Usage

```
panelcor(x, y, digits = 2, prefix = "", cex.cor, ...)
```

Arguments

x	A numeric vector containing data with which to produce correlations
y	A numeric vector containing data with which to produce correlations
digits	Number of digits to display on plot
prefix	Text to add before the correlation
cex.cor	Multiplier for the size of the text on the plot
...	Other arguments

Author(s)

Unknown

panelhist *Adds histograms to the diagonal of a matrix plot*

Description

A simple function used by pairs to produce neat looking matrix plots. Not intended for use by those using siar.

Usage

```
panelhist(x, ...)
```

Arguments

x	A numeric vector containing data over which to compute a histogram
...	Other arguments

Author(s)

Uknown

plotSigmaEllipse *Plot an ellipse based on a correlation matrix*

Description

A utility function for quickly adding an ellipse to an existing graph based on a correlation matrix defining the ellipse's parameters.

Usage

```
plotSigmaEllipse(m,sigma,steps=5,col="black",lwd=1,lty=2)
```

Arguments

m	A vector of length 2 containing the centres of the ellipse (i.e. the means of the ellipse).
sigma	A 2x2 matrix representing the correlation matrix that defines the ellipse.
steps	A visual rendering option that sets the number of step-size and hence resolution of the points used to draw the lines defining the ellipses. The larger the value, the more angular the ellipses will appear.
col	The colour to use in the plot see par.
lty	The line type to use in the plot see par.
lwd	The line width to use in the plot see par.

Author(s)

Andrew Jackson

popSEA *Standard Ellipse Metrics for the Population*

Description

Returns statistics on the standard ellipse based on a population (as opposed to a sample).

Usage

```
popSEA(sigma)
```

Arguments

sigma	A 2x2 matrix defining the correlation structure of bivariate data.

Value

SEA	The area of the standard ellipse.
eccentricity	The eccentricity of the ellipse.
a	The length of the semi-major axis of the ellipse a.
b	The length of the semi-minor axis of the ellipse b.

Author(s)

Andrew Jackson

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siaraddcross *Plotting tool for adding isotope bi-plot data to a figure*

Description

A sub-function for siarplotdata() and not intended for calling directly by the user.

Author(s)

Andrew Parnell and Andrew Jackson

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siardemo *Runs the siar model and some nice plots for the siar package*

Description

A simple function which utilises the loaded in Geese plasma data to run the MCMC on dietary proportions. Can be accessed either directly or through the menu function

Usage

```
siardemo(siarversion = 0)
```

Arguments

siarversion	Not required

Author(s)

Andrew Parnell

`siardensityplot` *SIAR's Custom Density Plot*

Description

generates a custom density plot of the a matrix of data, usually but not exclusively representing the posterior draws of esimated parameters. Based on `hdr.boxplot` in the `hdr` package.

Usage

```
siardensityplot(dat, probs = c(95, 75, 50),
    xlab = "Group", ylab= "Value", xticklabels = NULL, yticklabels = NULL,
    type = "boxes", clr = gray((9:1)/10), scl = 1,
    xspc = 0.5, prn = F, leg = FALSE, ct = "mode",ylims=NULL,
    lbound = -Inf, ubound = Inf, main="",...)
```

Arguments

`dat`	Data to be plotted as a matrix.
`probs`	Define the extent probability intervals for a given parameter.
`xlab`	Specifies the text to print on the x-axis.
`ylab`	Specifies the text to print on the y-axis.
`xticklabels`	Specifies the text to associate with each group defined as ticks on the x-axis.
`yticklabels`	Specifies the text to associate with each tickmark on the y-axis.
`type`	Determines the style of graph. type="boxes" draws boxplot style (default), type="lines" draws overlain lines increasing in thickness
`clr`	Determines the set of colours to use for the boxes. Default is greyscale.
`scl`	Specifies a proportional scaling factor to increase (scl > 1) or decrease (scl < 1) the default width of lines or boxes. Default = 1.
`xspc`	Sets the amount of blank space either side of the first and last (on the x-axis) graphic object.
`prn`	If prn=TRUE the values for the defined probability densities (probs) are returned to the command window. Default is prn=FALSE with no such output.
`leg`	Determines whether a legend is to be drawn (leg=TRUE) or not (default leg=FALSE). Note, currently only supported for type="lines".
`ct`	Plots the specified measure of central tendancy, taking one of: 'mode', 'mean', 'median'
`ylims`	Sets the y axis limits. By default this is inferred from the data
`lbound`	Sets a strict limit on the lower extent of the posterior distribution. E.g. useful for values that must be strictly positive.
`ubound`	Sets a strict limit on the upper extent of the posterior distribution. E.g. useful for proportions that must be strictly less than one.
`main`	A title for the figure.
`...`	Additional parameters to be passed to `plot`.

Author(s)

Andrew Jackson

`siarelicit` *Elicit prior parameters for the Dirichlet distribution.*

Description

Allows users to enter mean estimated proportions and a standard deviation term so that useful prior distributions can be enterred into the `siarmcmcdirichletv4` function.

Usage

```
siarelicit(siardata)
```

Arguments

`siardata`	A list containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. For more details of these inputs see the `siarmenu` function.

Details

Uses standard results from the Dirichlet distibution to turn the estimated mean proportions M_I and a variance term V_1 to give the estimated parameters a_i via:

$$a_i = M_i \left(\frac{M_1(1 - M_1)}{V_1} - 1 \right)$$

Note that V can be given for any of the k sources.

Author(s)

Andrew Parnell

siarhdrs *Creates hdrs and convergence diagnostics from siar output*

Description

Creates highest density regions and convergence diagnostics from siar output. Accessed by the siar menu function and not really intended for use outside that environment

Usage

```
siarhdrs(siardata)
```

Arguments

siardata	A list containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. For more details of these inputs see the siarmenu function.

Details

Not intended for use outside siarmenu

Author(s)

Andrew Parnell

siarhistograms *Produce neat siar histograms*

Description

Produces neat and colourful histograms for siar output.

Usage

```
siarhistograms(siardata, siarversion=0, legloc='topright')
```

Arguments

siardata	A list containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. For more details of these inputs see the siarmenu function.
siarversion	The siar version number as a string.
legloc	The location of the legend - see legend for plotting choices.

Details

Not intended for use outside siarmenu

Author(s)

Andrew Parnell

---

siarloaddata *Loads in siar data*

Description

Loads in siar data via a neat menu-driven interface.

Usage

```
siarloaddata(siarversion)
```

Arguments

siarversion	The siar version number as a string.

Details

Not intended for use outside siarmenu

Author(s)

Andrew Parnell

---

siarmatrixplot *Matrix plots of siar output*

Description

Produces matrix plots of siar output

Usage

```
siarmatrixplot(siardata, siarversion=0)
```

Arguments

siardata	A list containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. For more details of these inputs see the siarmenu function.
siarversion	The siar version number.

Details

Not intended for use outside siarmenu

Author(s)

Andrew Parnell

---

siarmcmcdirichletv4 *MCMC for stable isotope data*

Description

Runs an MCMC on stable isotope data from certain organisms to determine their dietary habits.

Usage

```
siarmcmcdirichletv4(data, sources, corrections = 0, concdep = 0, iterations=200000, burnin=50000, howm
```

Arguments

data	A matrix with each food source as a seperate row and each isotope as a seperate column.
sources	A matrix containing the mean and standard deviations of the fractionated correction values for each of the isotopes. Also allows corrections = 0 for pre-corrected data.
corrections	A matrix containing the mean and standard deviations of the fractional correction values for each of the isotopes. Also allows corrections = 0 for pre-corrected data.
concdep	A matrix containing the mean and standard deviations of the concentration dependence values for each of the isotopes. Also allows concdep = 0 for data with no required concentration dependence. Note that version 4.0 does not use the standard deviations.
iterations	The number of iterations to run.
burnin	The size of the burnin
howmany	How often to report the number of iterations.
thinby	The amount of thinning of the iterations.
prior	The dirichlet distribution prior parameters, the default is rep(1,numsources). New parameters can be estimated via the function siarelicit.
siardata	A list containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. For more details of these inputs see the siarmenu function.

Details

The model assumes that each target value comes from a Gaussian distribution with an unknown mean and standard deviation. The structure of the mean is a weighted combination of the food sources' isotopic values. The weights are made up dietary proportions (which are given a Dirichlet prior distribution) and the concentration depdendencies given for the different food sources. The standard deviation is divided up between the uncertainty around the fractionation corrections (if corrections are given) and the natural variability between target individuals within a defined group (or between all individuals if no grouping structure is specified). The default iterations numbers work well for the demo data sets, but advanced users will want to adjust them to suit their analysis.

Value

A parameter matrix consisting of (iterations-burnin)/thinby rows with numgroups*(numsources+numiso) columns, where numsources is the number of food sources, numiso is the number of isotopes, and numgroups is the number of groups. The parameter matrix is structured so that, for each group, the first columns are those of the proportions of each food source eaten, the next columns are the standard deviations for each isotope. This format repeats across rows to each group. The parameters may then subsequently be used for plotting, convergence checks, summaries, etc, etc.

Author(s)

Andrew Parnell

See Also

siarmenu, siarelicit

Examples

```
# Should take around 10 seconds to run
#out <- siarmcmcdirichletv4(geese1demo,sourcesdemo,correctionsdemo,concdepdemo)
```

---

siarmenu *A list of menu options for running the siar package*

Description

Brings up a list of menu options which allow the user to run MCMC and produce some plots

Usage

```
siarmenu()
```

Details

The internal workings of this function uses a list called siardata containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. Targets, sources and corrections are the isotopic values, source values and fractionation correction values respectively. PATH is the path used to get to the files. TITLE is the title to be used on most of the graphs. Numgroups, numdata, numsources and numiso are the number of groups, number of data points, number of sources and number of isotopes respectively. SHOULDRUN, GRAPHSONLY and EXIT are used to determine which parts of the menu system can be accessed.

Author(s)

Andrew Parnell

See Also

siarmcmcdirichletv4

Examples

```
#siarmenu()
```

---

siarmultigrouprun *siar MCMC for multi-group data*

Description

Runs the siar MCMC with Dirichlet mixture mean for isotopic data

Usage

```
siarmultigrouprun(siardata)
```

Arguments

siardata	A list containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. For more details of these inputs see the siarmenu function.

Details

Not intended for use outside siarmenu

Author(s)

Andrew Parnell

`siarplotdata` *Produces plots of target data and sources*

Description

Produces colourful scatter plots of siar target data and sources.

Usage

```
siarplotdata(siardata, siarversion = 0, grp=1:siardata$numgroups,panel=NULL,isos=c(0,0),leg=1)
```

Arguments

`siardata`	A list containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. For more details of these inputs see the `siarmenu` function.
`siarversion`	The siar version number as a string.
`grp`	A vector containing the groups of target consumer data to be rendered on the graph. Default value NULL draws all groups. Groups are identified by their own data marker.
`panel`	A scalar value that determines if the groups of consumer data are to be drawn on the same graph (default=NULL) or on seperate panels within a single figure. Number of rows and columns of panels can be specified by a 2 element vector. Alternatively, giving a single value e.g. panel=1 will cause the program to attempt to fit a "reasonable" number of panels to each row and column.
`isos`	A two element vector containing the reference to each isotope combination for the x and y axis to be rendered in teh figure. Note, only relevant for datasets contianing >2 isotopes. By default, if there are more than two isotopes, seperate figures will be created for all possible combinations of isotopes.
`leg`	A scalar determining how the legend is to be created. Default leg=1 prompts the user to locate the legend on each figure. leg = 2, puts the legend in a new figure automatically (useful if you want to omit the legend but still want to retain access to the information). leg = 0 omits the legend entirely.

Details

Can be called at any time after running `siarloaddata` or when running `siarmenu`

Author(s)

Andrew Parnell and Andrew Jackson

siarplotdatawrapper *Handles repeated plotting instructions for siarplotdata()*

Description

A sub-function for siarplotdata() and not intended for calling directly by the user.

Author(s)

Andrew Parnell and Andrew Jackson

siarplottarget *Plots the consumers' data in isotope space*

Description

A sub-function for siarplotdata() and not intended for calling directly by the user.

Author(s)

Andrew Parnell and Andrew Jackson

siarproportionbygroupplot *siar proportion plots by group*

Description

Plots boxplots or line plots representing defined credible intervals for each source (x-axis) for a given group. The representation is basically the same as siarhistograms but allows easier comparison of source contribution witin a group. Similar in style to siarproportionbysourceplot().

Usage

```
siarproportionbygroupplot(siardata, siarversion=0,probs=c(95,75,50),xlabels=NULL, grp=NULL, type="bo
```

Arguments

siardata	A list containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. For more details of these inputs see the siarmenu function.
siarversion	The siar version number.
probs	Define the extent probability intervals for a given parameter.
xlabels	Specifies the text to associate with each group defined as ticks on the x-axis.
grp	Specifies which group the graph is drawn for. Default prompts the user for input from the command line.
type	Determines the style of graph. type="boxes" draws boxplot style (default), type="lines" draws overlain lines increasing in thickness
clr	Determines the set of colours to use for the boxes. Default is greyscale.
scl	Specifies a proportional scaling factor to increase (scl > 1) or decrease (scl < 1) the default width of lines or boxes. Default = 1.
xspc	Sets the amount of blank space either side of the first and last (on the x-axis) graphic object.
prn	If prn=TRUE the values for the defined probability densities (probs) are returned to the command window. Default is prn=FALSE with no such output.
leg	Determines whether a legend is to be drawn (leg=TRUE) or not (default leg=FALSE). Note, currently only supported for type="lines".

Author(s)

Andrew Jackson & Andrew Parnell

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siarproportionbysourceplot

siar proportion plots by source

Description

Useful for siar data with multiple groups where the variability of each source over time is of interest.

Usage

```
siarproportionbysourceplot(siardata, siarversion=0,probs=c(95,75,50),xlabels=NULL, grp=NULL, type="b
```

Arguments

siardata	A list containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. For more details of these inputs see the siarmenu function.
siarversion	The siar version number.
probs	Define the extent probability intervals for a given parameter.
xlabels	Specifies the text to associate with each group defined as ticks on the x-axis.
grp	Specifies which source group the graph is drawn for. Default prompts the user for input from the command line.
type	Determines the style of graph. type="boxes" draws boxplot style (default), type="lines" draws overlain lines increasing in thickness
clr	Determines the set of colours to use for the boxes. Default is greyscale.
scl	Specifies a proportional scaling factor to increase (scl > 1) or decrease (scl < 1) the default width of lines or boxes. Default = 1.
xspc	Sets the amount of blank space either side of the first and last (on the x-axis) graphic object.
prn	If prn=TRUE the values for the defined probability densities (probs) are returned to the command window. Default is prn=FALSE with no such output.
leg	Determines whether a legend is to be drawn (leg=TRUE) or not (default leg=FALSE). Note, currently only supported for type="lines".

Author(s)

Andrew Parnell

---

siarsaveoutput *Saves siar output to a file*

Description

Saves created siar output to a file

Usage

```
siarsaveoutput(siardata)
```

Arguments

siardata	A list containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. For more details of these inputs see the siarmenu function.

Details

Not intended for use outside siarmenu

`siarsinglegrouprun` *siar MCMC for single group data*

Description

Runs the siar MCMC with Dirichlet mixture mean for isotopic data

Usage

```
siarsinglegrouprun(siardata)
```

Arguments

siardata	A list containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. For more details of these inputs see the siarmenu function.

Details

Not intended for use outside siarmenu

Author(s)

Andrew Parnell

`siarsolomcmcv4` *MCMC for stable isotope data with only single target organisms*

Description

Runs an MCMC on stable isotope data from certain organisms to determine their dietary habits. This version requires only a single target organism per group

Usage

```
siarsolomcmcv4(data, sources, corrections = 0, concdep = 0, iterations=200000, burnin=50000, howmany=
```

Arguments

data	A matrix with each food source as a seperate row and each isotope as a seperate column.
sources	A matrix containing the mean and standard deviations of the fractionated correction values for each of the isotopes. Also allows corrections = 0 for pre-corrected data.
corrections	A matrix containing the mean and standard deviations of the fractional correction values for each of the isotopes. Also allows corrections = 0 for pre-corrected data.
concdep	A matrix containing the mean and standard deviations of the concentration dependence values for each of the isotopes. Also allows concdep = 0 for data with no required concentration dependence. Note that version 4.0 does not use the standard deviations.
iterations	The number of iterations to run.
burnin	The size of the burnin
howmany	How often to report the number of iterations.
thinby	The amount of thinning of the iterations.
prior	The dirichlet distribution prior parameters, the default is rep(1,numsources). New parameters can be estimated via the function siarelicit.
siardata	A list containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. For more details of these inputs see the siarmenu function.

Details

The model assumes that each target value comes from a Gaussian distribution with an unknown mean and standard deviation. The structure of the mean is a weighted combination of the food sources' isotopic values. The weights are made up dietary proportions (which are given a Dirichlet prior distribution) and the concentration depdendencies given for the different food sources. The standard deviation is divided up between the uncertainty around the fractionation corrections (if corrections are given) and the natural variability between target individuals within a defined group (or between all individuals if no grouping structure is specified). The default iterations numbers work well for the demo data sets, but advanced users will want to adjust them to suit their analysis.

Note that this version is analagous to the Moore and Semmens (2008) MixSIR model except with a Dirichlet prior distribution.

Value

A parameter matrix consisting of (iterations-burnin)/thinby rows with numgroups*(numsources+numiso) columns, where numsources is the number of food sources, numiso is the number of isotopes, and numgroups is the number of groups. The parameter matrix is structured so that, for each group, the first columns are those of the proportions of each food source eaten, the next columns are the standard deviations for each isotope. This format repeats across rows to each group. The parameters may then subsequently be used for plotting, convergence checks, summaries, etc, etc.

Author(s)

Andrew Parnell

References

Moore and Semmens (2008), Incorporating uncertainty and prior information into stable isotope mixing models, Ecology Letters.

See Also

siarmenu, siarelicit

`siarsolomultigrouprun` *siar MCMC for multi-group data with only one target organism per group*

Description

Runs the siar MCMC with Dirichlet mixture mean for isotopic data with only one target organism per group.

Usage

```
siarsolomultigrouprun(siardata)
```

Arguments

`siardata`	A list containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. For more details of these inputs see the `siarmenu` function.

Author(s)

Andrew Parnell

siarsolosinglegrouprun *siar MCMC for single group data with only one organism*

Description

Runs the siar MCMC with Dirichlet mixture mean for isotopic data when there is only one target organism.

Usage

```
siarsolosinglegrouprun(siardata)
```

Arguments

siardata	A list containing some or all of the following parts: targets, sources, corrections, PATH, TITLE, numgroups, numdata, numsources, numiso, SHOULDRUN, GRAPHSONLY, EXIT, and output. For more details of these inputs see the siarmenu function.

Details

Not intended for use outside siarmenu

Author(s)

Andrew Parnell

siber.ellipses *The SIBER method for calculating ellipse based metrics of niche width*

Description

Takes bivariate isotope data in x and y with a grouping variable and returns the posterior draws for the metric SEA.B for each group.

Usage

```
siber.ellipses(x,y,group,R=10^4)
```

Arguments

x	Data for the x-axis.
y	Data for the y-axis.
group	A grouping variable
R	The number of posterior draws to make

Value

SEA.B	A matrix containing the posterior estimate of the Standard Ellipse Area metric for each group by column.

Author(s)

Andrew Jackson

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siber.hull.metrics *The SIBER method for calculating Convex Hull based metrics of niche width*

Description

Takes bivariate isotope data in x and y with a grouping variable and returns a list that contains the posterior distribution of the 6 niche width metrics for application to community type data described by Layman, C.A., Arrington, D.A., Montana, C.G., & Post, D.M. (2007) Can stable isotope ratios provide for community-wide measures of trophic structure? Ecology, 88, 42-48.

Usage

```
siber.hull.metrics(X,Y,G,R=10^4)
```

Arguments

X	Data for the x-axis.
Y	Data for the y-axis.
G	A grouping variable
R	The number of posterior draws to make

Value

metrics	A Rx6 matrix containing the R posterior draws in rows, and the metrics in columns in the order: dNr, dCr, TA, CD, MNND, SDNND.

Author(s)

Andrew Jackson

sourcesdemo *Source (in this case plant) isotope values*

Description

A 3 column, 4 row matrix containing 4 different plants and their measurements on 2 different isotopes

Usage

```
data(sourcesdemo)
```

Format

A data frame with 5 observations on the following 3 variables.

`Sources` The plants name

`Meand15N` d15N mean

`SDd15N` d15N standard deviation

`Meand13C` d13C mean

`SDd13C` d13C standard deviation

Examples

```
#see siarmenu() and option 9 for a demo using this data
```

standard.ellipse *Standard Ellipse*

Description

Fits a standard ellipse to bivariate data analytically using maximum likelihood estimators.

Usage

```
standard.ellipse(x,y,confs=NULL,steps=5)
```

Arguments

x	Vector of x data.
y	Vector of y data.
confs	Optional list of confidence intervals as a vector. If specified will calculate the confidence intervals of the means and store their coordinates in a list (useful for plotting). Defaults to Null.
steps	A visual rendering option that sets the number of step-size and hence resolution of the points used to draw the lines defining the ellipses. The larger the value, the more angular the ellipses will appear.

Value

CEA	The area of the 95 percent confidence ellipse.
SEA	The area of the standard ellipse.
SEAc	The area of the small sample size corrected standard ellipse.
theta	The angle of the semi-major axis of the ellipse with the x-axis.
confs	list of the confidence intervals of the mean, if speficied.
xCEA	x coordinates of the confidence ellipses.
yCEA	y coordinates of the confidence ellipses.
xSEA	x coordinates of the standard ellipse.
ySEA	y coordinates of the standard ellipse.
xSEAc	x coordinates of the small sample size corrected standard ellipse.
ySEAc	y coordinates of the small sample size corrected standard ellipse.
eccentricity	Eccentricity of the ellipse
a	The length of the semi-major axis a
b	The length of the semi-minor axis a
r	The correlation coefficient of the data
ac	The length of the semi-major axis a based on the small sample size correction.
bc	The length of the semi-minor axis b based on the small sample size correction.

Author(s)

Andrew Jackson

Index