The siar Package

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Type Package

Title Stable Isotope Analysis in R

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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. Latest version (4.0) includes the feature to add in concentration dependence. See siardemo() for an example.

License GPL (>= 2)

R topics documented:

`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
```

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
```

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
```

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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
```

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

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

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:	3.2
Date:	2008-06-12
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()
```

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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

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

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siarhistograms *Produce neat siar histograms*

Description

Produces neat and colourful histograms for siar output.

Usage

```
siarhistograms(siardata, siarversion)
```

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.

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
```

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,
```

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()
```

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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(
```

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, g
```

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,
```

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

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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, burr
```

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

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
```

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