Package 'EDFIR'

July 17, 2015

Title Estimating Discrimination Factors

Version 1.0

Date 2015-07-15

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Depends R (>= 2.15.3), lpSolve, geometry, vertexenum, MASS

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Description Functions for reading in data sets of prey and predator isotopic measurements and producing estimates for discrimination factors.

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NeedsCompilation no

Repository CRAN

Date/Publication 2015-07-17 12:44:21

R topics documented:

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build.hull.list   *build.hull.list*

Description

Construct a stacked list of values from a data frame containing multiple prey types. Used for creating input to convhulln.

Usage

```
build.hull.list(frame)
```

Arguments

frame   A data frame containing a list of isotope values for multiple organisms. If there are d isotope values and s organisms, then the frame is assumed to contain ds columns, where for any $1 \leq i \leq s - 1$ the columns di to $d(i + 1) - 1$ contain the isotope measurements for the ith organism. For each organism, the isotopes (columns) must be in the same order.

Value

A $m \times d$ matrix, where m is the total number of isotopic measurements (over all organisms) and d is the number of isotopes.

Author(s)

Robert Robere

See Also

build.normalhull convhulln

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build.isotopeframe   *build.isotopeframe*

Description

Given local filenames leading to tab-delimited files of isotope values, read in the values from the file and store them in a dataframe.

Usage

```
build.isotopeframe(pred.file, prey.file, prey.header=TRUE,
  pred.header=FALSE, sep="\t")
```

Arguments

`pred.file`	The name of the file containing the predator isotope data.
`prey.file`	The name of the file containing the prey isotope data.
`prey.header`	TRUE if the file pointed to by prey.file has a header line.
`pred.header`	TRUE if the file pointed to by pred.file has a header line.
`sep`	The separator used within the isotope files. Defaults to tab.

Details

The isotope measurement files allowable for input by the system must be formatted in one of two ways. The first are files containing raw data: they must contain one measurement per line, with the measurement for each isotope separated into columns. If the prey file contains more than a single species, then the measurements for each species must be appended as additional blocks of columns. The columns for each species must preserve the ordering of the isotopes.

The second file format contain the mean and standard deviation of the isotopic measurements of each species. Each input species will have it's measurements on a single line, organized like so: <name of species> <mean of isotope 1> <sd of isotope 1> <mean of isotope 2> <sd of isotope 2> ...

A final note: predator files may also have more than one species, although any extra predators will be ignored.

Value

`prey.frame`	A data frame containing the prey isotopic measurements (or the mean/sd of each isotope).
`pred.frame`	A data frame containing the predator isotopic measurements (or the mean/sd of each isotope).

Author(s)

Robert Robere

Examples

```
## import data files, assuming the predator file contains header lines
## Not run: input <- build.isotopeframe("pred_dataset.csv",
"prey_dataset.csv", pred.header=TRUE, prey.header=TRUE)
## End(Not run)
```

build.normalhull	*build.normalhull*

Description

Build a convex hull of the data in a data frame using convhulln.

Usage

```
build.normalhull(inputframe)
```

Arguments

inputframe   A data frame, containing isotopic measurements in data frames imported from
                files using build.isotopeframe.

Details

Use the convhulln package to build a convex hull of the isotopic measurements given by the input
data frame. The data frame is assumed to have the measurements presented one per row. If there
are multiple species present in the data frame, they must be added as extra columns, and the order
of the columns for each species must be the same.

Value

Return a $m \times d + 1$ matrix $[A|b]$ representing the convex hull of the system of equations $Ax \leq -b$.

Author(s)

Robert Robere

See Also

convhulln

Examples

```
## Not run: ## read in data from some files
## Not run: input <- build.isotopeframe("predfile", "preyfile")
## Not run: ## get the convex hull of the predator data
## Not run: hull <- build.normalhull(input$pred.frame)
```

---

construct.linearsys *construct.linearsys*

Description

Construct a linear system of inequalities from the predator and prey isotopic data for input to lpSolve.

Usage

```
construct.linearsys(predatorframe, preyframe)
```

Arguments

predatorframe	The data frame containing the isotopic measurements from the predator species.
preyframe	The data frame containing the isotopic measurements from the prey species.

Value

A	The matrix A used as input to the lp solver.
b	The vector b used as input to the lp solver.

Author(s)

Robert Robere

See Also

build.normalhull isotopesolve

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estimate.shiftvec *estimate.shiftvec*

Description

Given two data frames, one containing isotopic measurements from some predator species, and another containing isotopic measurements from a collection of prey species, return num.samples samples of discrimination factors from predators to prey.

Usage

```
estimate.shiftvec(predator, prey, num.samples=1000, num.preysamples=1,
  pred.distinput=FALSE, prey.distinput=TRUE)
```

Arguments

predator	A data frame containing the isotopic measurements (presented as raw data or mean/standard deviation) from a predator species.
prey	A data frame containing the isotopic measurements (presented as raw data or mean/standard deviation) from a prey species.
num.samples	The number of samples of discrimination factors to produce.
num.preysamples	
	The number of samples to draw from each prey source when performing the estimation process.
pred.distinput	TRUE if the predator measurements are in mean/standard deviation form (see [build.isotopeframe](#)).
prey.distinput	TRUE if the prey measurements are in mean/standard deviation form (see [build.isotopeframe](#)).

Value

A matrix with num.samples rows, each of which contains one estimate discrimination factor.

Author(s)

Robert Robere

See Also

[build.isotopeframe](#)

Examples

```
## normally input is read from a file via build.isotopeframe, but here
## we generate the input by hand
## we have three prey species: birds, mice, and bugs
## one predator species: cats
## we are measuring two isotopic values for each: %%C and %%N
## assume that all measurements are normally distributed
bird.samples <- as.data.frame(mvrnorm(n=25, mu=c(2, 2),
  Sigma=diag(c(1, 1), nrow=2)))
mice.samples <- as.data.frame(mvrnorm(n=25, mu=c(4, 4),
  Sigma=diag(c(1, 1), nrow=2)))
bugs.samples <- as.data.frame(mvrnorm(n=25, mu=c(2, 6),
  Sigma=diag(c(1, 1), nrow=2)))

## note that prey are collected into a single data frame,
## as are the predators
## if number of samples differs from species to species,
## the data frame should be padded
## with NAs appropriately (this is done automatically when
## reading in from CSV)
pred.frame <- data.frame(cats=mvrnorm(n=20, mu=c(6, 6),
  Sigma=diag(c(1/2, 1/2), nrow=2)))
prey.frame = data.frame(bird=bird.samples, mice=mice.samples,
```

```
  bugs=bugs.samples)

## now estimate discrimination factors
## in applications, usually the prey measurements are given by mean/sd
## of corresponding gaussian, so we notify the function that we are
## actually providing samples in this example
estimate.shiftvec(pred.frame, prey.frame, num.samples=10,
  prey.distinput=FALSE)
```

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heatmap.samples   *heatmap.samples*

Description

Visualize the output of `estimate.shiftvec` if the data has only two isotope measurements.

Usage

```
heatmap.samples(samples)
```

Arguments

samples   A list of samples of discrimination factors produced by `estimate.shiftvec`.

Author(s)

Robert Robere

See Also

`estimate.shiftvec`

Examples

```
## get the input from a file, where the predator measurements are simple
## raw isotopic measurements, and prey measurements are in mean/sd form
## Heatmap.samples assumes only two isotopes are measured!
## Not run: input <- build.isotopeframe("predator measurements.dat",
"prey measurements.dat")
## End(Not run)

## now get 2000 samples of discrimination factors
## Not run: out <- estimate.shiftvec(input$pred.frame, input$prey.frame,
 num.samples=2000, pred.distinput=FALSE, prey.distinput=TRUE)
## End(Not run)

## now visualize
## Not run: heatmap.samples(out)
```

---

isotopesolve *isotopesolve*

Description

Solve the linear system of inequalities given by construct.linearsys using lpSolve.

Usage

```
isotopesolve(predatorframe, preyframe, maximize="min")
```

Arguments

predatorframe	A data frame containing isotopic measurements for a predator species.
preyframe	A data frame containing isotopic measurements for a set of prey species.
maximize	An optional argument, asking whether or not you would like to maximize or minimize the default objective function.

Value

A summary object output by lp for the system of inequalities produced from the input data.

Author(s)

Robert Robere

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parse.isotopeframe *parse.isotopeframe*

Description

Parse the isotope data frame produced by build.isotopeframe if the input data is in mean/standard deviation form.

Usage

```
parse.isotopeframe(isotope.frame)
```

Arguments

isotope.frame	A data frame of isotope mean/sd measurements to be parsed.

Details

This function is used by the internals of this package for parsing.

Value

mu	A matrix of mean vectors, one for each species.
sigma	A matrix of standard deviations for each isotope and each species.

Author(s)

Robert Robere

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shift.mean   *shift.mean*

Description

Given a collection of predator and prey isotopic measurements, produce the average discrimination factors between the two sets of measurements.

Usage

```
shift.mean(predator.frame, prey.frame)
```

Arguments

predator.frame	A data frame containing isotopic measurements from the predator species.
prey.frame	A data frame containing isotopic measurements from a collection of prey species.

Value

A vector containing the average discrimination factors between the predator and prey sets, or an empty vector otherwise.

Author(s)

Robert Robere

See Also

isotopesolve, estimate.shiftvec

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