Package 'bio.infer'

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Type Package

Title Predict Environmental Conditions from Biological Observations

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Description Imports benthic count data, reformats this data, and
computes environmental inferences from this data.

Depends R (>= 2.10), tcltk

LazyLoad FALSE

LazyData FALSE

License GPL (>= 2)

Repository CRAN

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R topics documented:

bio.infer-package   *Scripts for computing biological inferences*

Description

Reformats raw benthic count files, combines them with existing taxon-environment relationships, and computes inferences of environmental conditions.

Details

Package:	bio.infer
Type:	Package
Version:	1.0
Date:	2006-10-31
License:	GPL version 2 or newer

Use this package to import benthic count data, reformat the data, and compute inferences of environmental conditions using taxon-environment relationships.

Typically, the user will start by loading a local benthic count data file (see `bcnt.OR` for an example of the required format). This benthic count file will be merged with standardized taxonomic hierarchy information using `get.taxonomic`. Then, operational taxonomic units will be assigned, based on the number of occurrences of different taxa and based on the identity of taxa for which environmental preferences have been quantified. (See `get.otu` for the OTU assignment script, and `coef.west.wt` for an example file of environmental preferences.)

Once OTUs have been assigned, the benthic count file is reformatted as a site-taxon matrix (`makess`). This file can then be used to compute biological inferences (`mlsolve`).

This package was developed in Windows but should be fully functional in other operating systems.

Author(s)

Lester L. Yuan

---

bcnt.emapw　　　　　　　　*Benthic count data for the western United States*

Description

Benthic count data for streams in the western United States.

Usage

```
data(bcnt.emapw)
```

Format

Three fields are included.

`ID.NEW` Unique sample code

`Taxaname` Name of the observed taxon

`Abundance` Abundance of the observed taxon

Source

U.S. Environmental Protection Agency Environmental Monitoring and Assessment Program

Examples

```
data(bcnt.emapw)
```

---

bcnt.OR	*Benthic count data for western Oregon*

Description

Benthic count data for streams in western Oregon.

Usage

```
data(bcnt.OR)
```

Format

Three fields are included.

SVN Unique sample code

Taxon Name of the observed taxon

CountValue Abundance of the observed taxon

Source

Oregon Department of Environmental Quality

Examples

```
data(bcnt.OR)
```

---

bcnt.otu.OR	*Benthic count data with OTU*

Description

Benthic count data from western Oregon with operational taxonomic units assigned by get.otu.

Usage

```
data(bcnt.otu.OR)
```

Format

Five fields are included.

SVN Unique sample identifier

Taxon Original taxon name, same as in bcnt.OR

CountValue Taxon abundance

TNAME Taxon name after processing by get.taxonomic

OTU Operational taxonomic unit. Taxon name selected with associated taxon-environment data and selected to eliminate double-counting

Source

Oregon Department of Environmental Quality

Examples

```
data(bcnt.otu.OR)
```

---

bcnt.tax.OR	*Benthic count with taxonomic hierarchy*

Description

Benthic count data from western Oregon with full taxonomic hierarchy assigned by `get.taxonomic`.

Usage

```
data(bcnt.tax.OR)
```

Source

Oregon Department of Environmental Quality

Examples

```
data(bcnt.tax.OR)
```

---

coef.east.sed	*Regression coefficients for eastern U.S. sediment*

Description

Regression coefficients describing relationships between different taxa and percent sands/fines.

Usage

```
data(coef.west.wt)
```

Format

A list of with following four elements is provided.

tnames Character vector with the names of each taxon modelled.

csave Matrix of regression coefficients for each taxon. Number of rows is the same as the number of taxa modelled and the number of columns is 6.

xvar Character vector with the names of variables modelled.

xlims List of limits for each of the environmental variables.

form Regression formula used to estimate coefficients.

Details

These regression coefficients were computed using logistic regression.

Source

Yuan, L.L.

Examples

```
data(coef.east.sed)
```

---

coef.west.wt   *Weighted regression coefficients for western U.S.*

Description

Regression coefficients describing relationships between different taxa and percent sands/fines and stream temperature.

Usage

```
data(coef.west.wt)
```

Format

A list of with following four elements is provided.

tnames Character vector with the names of each taxon modelled.

csave Matrix of regression coefficients for each taxon. Number of rows is the same as the number of taxa modelled and the number of columns is 6.

xvar Character vector with the names of variables modelled.

xlims List of limits for each of the environmental variables.

form Regression formula used to estimate coefficients.

Details

These regression coefficients were computed using logistic regression weighted by the number of stream miles represented by each sample.

Source

Yuan, L.L.

Examples

```
data(coef.west.wt)
```

---

correct.taxanames   *Correct unrecognized taxon names*

Description

Prompts user to correct unrecognized taxon names

Usage

```
correct.taxanames(tname.old, get.tax.env)
```

Arguments

tname.old	Character vector of unrecognized names
get.tax.env	Environment for ITIS taxon table

Details

Prompts user to enter corrections to names via a tcltk dialog box.

Value

Character vector of corrected names

Author(s)

Lester L. Yuan

---

envdata.emapw   *Environmental data from the western United States*

Description

Environmental data for stream sampled in the western United States.

Usage

```
data(envdata.OR)
```

Format

A data frame with 1674 observations on the following 8 variables.

ID.NEW Unique sample code

ntl Total nitrogen concentration

no3 Nitrate concentration

ptl Total phosphorus concentration

sed Percent sands and fines

tempres Corrected temperature

STRMTEMP Grab temperature

jday Julian sampling day

Source

U.S. Environmental Protection Agency Environmental Monitoring and Assessment Program.

Examples

```
data(envdata.emapw)
```

---

envdata.OR   *Environmental data from western OR*

Description

Environmental data for stream sampled in western Oregon.

Usage

```
data(envdata.OR)
```

Format

A data frame with 245 observations on the following 13 variables.

STRM.ID Unique sample code

jday Sampling day

lon Longitude in decimal degrees

lat Latitude in decimal degrees

sed Percent sands and fines

elev Log-transformed elevation

slope Slope

area Log-transformed catchment area

sed.log Log-transformed percent sands and fines

temp Grab stream temperature

temp.avg Seven day average maximum temperature

elev.ut Elevation

sp Estimate of unit stream power

Source

Oregon Department of Environmental Quality

Examples

```
data(envdata.OR)
```

---

flist.data   *List available data*

Description

Lists available data in the package

Usage

```
flist.data()
```

Value

List of data files.

Author(s)

Lester L. Yuan

---

flist.match   *Selects data files matching search string*

Description

Select data files matching search string

Usage

```
flist.match(pattern = NULL)
```

Arguments

    pattern   Character string to be matched.

Value

    List of matched data files.

Author(s)

    Lester L. Yuan

---

    formtomat   *Analyze formula string*

Description

    Analyzes formula string that defines the regression models for taxon-environment relationships. Returns a numerical representation of the formula and the derivative of the formula that can be used by `mlsolve`.

Usage

```
formtomat(a, xvar)
```

Arguments

    a   Character string defining regression formula.

    xvar   Character vector with variable names.

Details

    Internal function to `mlsolve`.

Value

    List of transformations.

Author(s)

    Lester L. Yuan

---

get.dupe.sel   *Get duplicate selection*

Description

Prompt user to select correct version from duplicated entries

Usage

```
get.dupe.sel(sumstr)
```

Arguments

sumstr   Character vector summarizing duplicated taxon names

Details

Prompts the user via a tcltk window to select appropriate name from duplicate taxon names.

Value

Returns integer indicating which names are selected.

Author(s)

Lester L. Yuan

---

get.otu   *Defines operational taxonomic units (OTUs)*

Description

`get.otu` generates OTUs for benthic count data using a simple algorithm that is designed to maximize the amount of taxonomic information retained across the entire data set, while eliminating redundant taxonomic identifications.

Usage

```
get.otu(bcnt, optlist = NULL, ndc = TRUE, outputFile = FALSE,
gui = FALSE)
```

Arguments

`bcnt`	benthic count data frame that includes the full taxonomic hierarchy for each taxon. Typically, bcnt is the output from `get.taxonomic`.
`optlist`	vector of taxon names for which trait or tolerance value is available. Specify `optlist = NULL` for cases in which OTU are computed without regard for any additional taxon specific information, e.g. for developing a RIVPACS model.
`ndc`	Logical flag indicating whether OTU should be computed that eliminate double-counting of taxa.
`outputFile`	Logical indicating whether to output summary information
`gui`	Logical indicating whether to use gui interface.

Details

`get.otu` makes decisions about OTU according to the following rule. The number samples in which a given taxonomic group (e.g. Baetidae) is observed, is compared to the number of samples in which members of the that same group are identified to a higher taxonomic level (e.g., Baetis, Fallceon, Acentrella, etc.). If more samples are observed with the coarser identification, then all identifications are downgraded to the coarse identification. If more samples are observed at the finer level of identification, then those sample are retained, and all identifications at the coarser level are omitted. Before deciding on OTU assignments, the script first reviews the species names that are listed in the benthic count file and matches them with the species names provided in `optlist`.

Value

Final OTU decisions are returned as tab-delimited text file, sum.otu.txt, which is best viewed using a spreadsheet. A new benthic count file is also returned in R, including the original benthic count information and a new field specifying the OTU designation for each taxon. Manual revisions to the assigned OTUs can be recorded in sum.otu.txt and loaded with `load.revised.otu`

Author(s)

Lester L. Yuan

See Also

`get.taxonomic`

Examples

```
data(bcnt.tax.OR)
data(coef.west.wt)
bcnt.otu.OR <- get.otu(bcnt.tax.OR, coef.west.wt)
```

---

get.taxon.names   *Get taxon names from benthic count file*

Description

Get taxon names from benthic count file

Usage

```
get.taxon.names(bcnt)
```

Arguments

bcnt   Benthic count file with taxon names in second column

Details

Checks to see if second column is factor or character.

Value

Returns character vector of taxon names.

Author(s)

Lester L. Yuan

---

get.taxonomic   *Merge benthic count data with the ITIS taxonomy table*

Description

get.taxonomic merges the taxon names provided in a benthic count data file with a standardized taxonomy table. The purpose of this function is to provide the complete taxonomic hierarchy for each taxon.

Usage

```
get.taxonomic(bcnt)
```

Arguments

bcnt   A benthic count data frame with the following three fields: a sample identifier, taxon name, and abundance. The three fields must be ordered as listed. Sample identifier is typically a character string that is a unique identifier for a given sample. Taxon name is a character string that specifies the name of the taxon observed in the sample, and abundance is the number of individuals of that taxon that were observed.

Details

`get.taxonomic` attempts to match taxon names provided in a benthic count data file with taxa listed in ITIS. The script automatically corrects for the most common conventions in taxonomic naming. For example, taxon names are converted to all capital letters, and trailing strings such as "SP." and "SPP." are deleted.

The script lists taxa remaining that are not matched to entries in the ITIS database using `fix`. The user can then enter a corrected spelling for the taxon name.

The script provides a final summary of the unmatched taxon names, and the user can continue revising names, or complete the program.

Value

A final taxonomic table is returned as tab-delimited text in the file `sum.tax.table.txt`. This file is best viewed using a spreadsheet. Within R, the script returns a benthic count file with the original taxon name associated with a full taxonomic hierarchy for that taxon. The assigned species names can be modified by hand in `sum.tax.table.txt` and the revised information loaded with `load.revised.species`.

Author(s)

Lester L. Yuan

See Also

`itis.ttable`

Examples

```
data(bcnt.OR)
data(itis.ttable)
## Not run:
bcnt.tax.OR <- get.taxonomic(bcnt.OR)

## End(Not run)
```

---

get.valid.names   *Get taxon names from benthic count file*

Description

Identifies valid names from parsed name matrix.

Usage

```
get.valid.names(df.parse, get.tax.env)
```

Arguments

`df.parse`	Parsed name matrix
`get.tax.env`	Environment for ITIS taxon table

Details

Searches for taxon names in ITIS and splits name matrix into list with first element being the matrix of valid names and the second element being the matrix of invalid names.

Value

List of two taxon name matrices.

Author(s)

Lester L. Yuan

---

in.ITIS	*Check to see if taxon name is in ITIS*

Description

Checks to see if taxon names are listed in the ITIS taxon table.

Usage

```
in.ITIS(df.parse, get.tax.env, col.sel = NULL)
```

Arguments

`df.parse`	Character vector or matrix character vectors of names that need to be checked for presence in ITIS
`get.tax.env`	Environment variable where the full ITIS taxon table is available
`col.sel`	Integer allowing selection of a particular column of the matrix of names to check.

Value

Returns a list in which each element of the list is a successive character string from the parsed names.

Author(s)

Lester L. Yuan

---

incorp.correct   *Incorporate taxon name revisions*

Description

Incorporates corrected taxon names into parse.list

Usage

```
incorp.correct(tname.new, parse.list)
```

Arguments

tname.new	Character vector of corrected taxon names
parse.list	List of parsed taxon names

Value

Revised parse.list.

Author(s)

Lester L. Yuan

---

infergui   *Graphical User Interface for biological inferences*

Description

Provides a graphical user interface that allows users to compute biological inferences using existing taxon-environment relationships.

Usage

```
infergui()
```

Value

None. Used for its side effects.

Author(s)

Lester L. Yuan

| itis.ttable | *ITIS taxonomic hierarchy table* |

Description

Full taxonomic hierarchy to genus for the Kingdom Animalia. Retrieved November 21, 2008 from the Integrated Taxonomic Information System on-line database, <http://www.itis.gov>.

Usage

```
data(itis.ttable)
```

Source

Integrated Taxonomic Information System, U.S. Department of Agriculture.

Examples

```
data(itis.ttable)
```

| load.itis | *Load ITIS taxon table* |

Description

Load ITIS taxon table to the specified environment.

Usage

```
load.itis(get.tax.env)
```

Arguments

get.tax.env   Environment variable.

Details

Loads full ITIS taxonomic table into specified environment.

Value

None. Used for side effects.

Author(s)

Lester L. Yuan

---

load.revised.otu   *Loads a user-revised OTU table*

Description

If manual correction of the OTU selections is desired, these corrections should be made on the "sum.otu.txt" file provided by get.otu. The corrections should be saved as tab-delimited text, and then load.revised.otu run.

Usage

```
load.revised.otu(bcnt.otu, otufname = "sum.otu.txt")
```

Arguments

bcnt.otu	Original benthic count file with OTU designations. Output from get.otu
otufname	File name of revised OTU assignments.

Details

The benthic count data frame is assumed to be the original output from get.otu, and therefore has a field called TNAME.

Value

The script returns a new benthic count file that incorporates the corrections to the OTU table.

Author(s)

Lester L. Yuan

See Also

get.otu

---

load.revised.species   *Loads a user-revised list of species names*

Description

If manual correction of the species names assigned by get.taxonomic is desired, these corrections should be made on the sum.tax.table.txt file. The corrections should be saved as tab-delimited text, and then load.revised.species run.

Usage

```
load.revised.species(bcnt.tax, fname)
```

Arguments

bcnt.tax	benthic count data frame that includes the full taxonomic hierarchy for each taxon.
fname	Character string containing file name for the revised, tab-delimited, file in the format of sum.tax.table.txt. See get.taxonomic.

Details

The script prompts the user to enter the name of the text file containing the revised species names. The original "SPECIES" column in bcnt.tax is deleted and the new, revised version is merged into bcnt.tax.

Value

The script returns a new benthic count file that incorporates the corrections to the species names

Author(s)

Lester L. Yuan

See Also

get.taxonomic

---

locate.dupes   *Locate duplicated taxon names*

Description

Locate taxon names that match multiple records in ITIS.

Usage

```
locate.dupes(fulltab)
```

Arguments

fulltab	Full taxonomic table for matched taxon names

Details

Finds duplicate names in fulltab

Value

Returns string that summarizes duplicates and their row numbers.

Author(s)

Lester L. Yuan

---

make.fulltab1   *Make full taxonomic table*

Description

Merge full ITIS taxonomy with names in benthic count file

Usage

```
make.fulltab1(df.parse, get.tax.env)
```

Arguments

df.parse   Matrix with valid taxon names in the second column

get.tax.env   Environment variable where the full ITIS taxon table is available

Details

Initial merge of taxon names with full ITIS table.

Value

Returns the current list of valid taxon names merged with the full taxonomic hierarchy.

Author(s)

Lester L. Yuan

---

make.species   *Generate species names*

Description

Generate species names from possibilities in the parsed taxa name table.

Usage

```
make.species(df.parse, fulltab)
```

Arguments

df.parse   Matrix with valid taxon names in the second column

fulltab   Full taxonomic table for matched taxon names

Details

Generates likely species names from matched taxon names that are identified as Genus level names.

Value

Returns full taxonomic table with SPECIES field appended.

Author(s)

Lester L. Yuan

---

makess   *Make a site-OTU matrix*

Description

`makess` generates a site-OTU matrix based on a benthic count file. The script assumes that the benthic count file has a field entitled 'OTU' on which the matrix is based.

Usage

```
makess(bcnt, tname = "OTU", plothist=FALSE, prints = FALSE, nview = 0)
```

Arguments

bcnt	a benthic count file that results from running get.otu or load.revised.otu.
tname	Character string specifying the field in bcnt in which the name of the taxon is stored.
plothist	Set to TRUE to plot a histogram of the proportion of abundance at each site that is included in the OTU designations
prints	Set to TRUE to view statistics on the proportion of abundance at each site that is included in the OTU designations
nview	Selects the number of sites to view in which the proportion of abundance included is low

Value

A site-OTU matrix.

Author(s)

Lester L. Yuan

See Also

get.otu, load.revised.otu

Examples

```
data(bcnt.otu.OR)
ss.OR <- makess(bcnt.otu.OR)
```

---

mlsolve   *Maximum likelihood inferences*

Description

mlsolve uses maximum likelihood estimation to infer environmental conditions from biological observations.

Usage

```
mlsolve(ss, coef0, site.sel = "all", bruteforce = FALSE)
```

Arguments

ss	A site-species matrix, with sample identifiers in the first column, and abundances. Typically, the result of makess.
site.sel	Character vector of sample id's at which inferences should be computed. Default selection of 'all' forces script to compute inferences for all samples in the matrix.
coef0	Coefficient file with model specifications and regression coefficients defining taxon-environment relationships. See taxon.env for more details.
bruteforce	Logical flag. Select TRUE to compute solution by brute force rather than by conjugate gradients. Provides a means of examining likelihood contours when needed.

Details

mlsolve uses maximum likelihood estimation to infer environmental conditions from biological observations. Maximum likelihood estimation in this context is a constrained optimization problem, in which we wish find the point at which the likelihood function is maximized, constrained by the range of the environmental variables in the calibration data. mlsolve formulates the likelihood function and calls optim to solve the optimization problem.

The option bruteforce can be used to check the performance of the iterative solver. When bruteforce is set to be TRUE, the script also computes likelihood values for a uniformly-spaced grid that spans the ranges of the environmental variables. This is a time-consuming calculation, and therefore should only be attempted on a few samples. Once the grid is computed, though, contours of the likelihood surface are plotted.

mlsolve requires that the taxa included in ss each have associated taxon-environment information in coef0. The best way to ensure that this condition is satisfied is to make sure that get.otu is run with the same coef0 as used in mlsolve, and that the results from get.otu are used to generate ss (see makess).

Value

The script returns a dataframe containing inferences for each sample as well as a logical flag indicating whether solutions computing with four different starting locations are consistent with one another.

Author(s)

Lester L. Yuan

Examples

```
data(coef.west.wt)
data(ss.OR)
inf.out <- mlsolve(ss.OR, coef.west.wt)
```

---

modalDialog	*Modal dialog box using TclTK*

Description

`modalDialog` generates a dialog box prompting the user to enter a list of text before the process continues. Based on scripts provided in http://bioinf.wehi.edu.au/~wettenhall/RTclTkExamples/

Usage

```
modalDialog(title,itemlist,entryInit,entryWidth=20,
                        returnValOnCancel="ID_CANCEL")
```

Arguments

title   Title for the dialog box

itemlist   Character vector of names that the user must correct

entryInit   Default string to fill in the entries

entryWidth   Width of entry string

returnValOnCancel
                 Value for script to return if canceled

Value

Character vector of user entries.

Author(s)

Lester L. Yuan

---

output.tax.table	*Output final taxonomic table*

Description

Output final taxonomic table as tab-delimited text

Usage

```
output.tax.table(finaltab, tlevs)
```

Arguments

finaltab	Merged taxonomic table
tlevs	Character vector of taxonomic levels in ITIS

Details

Outputs final table to file.

Value

None. Used for side effects.

Author(s)

Lester L. Yuan

---

parse.taxon.name	*Parse taxon name*

Description

Parses taxon names from benthic count file to facilitate matching with ITIS.

Usage

```
parse.taxon.name(tname.orig)
```

Arguments

tname.orig	Character vector of taxon names

Details

Parses compound names typically found in benthic count files into a list of strings for each name.

Value

Returns a matrix in which each row corresponds with a different element of the provided character vector, and each column corresponds to distinct strings in each element.

Author(s)

Lester L. Yuan

---

remove.dupes	*Remove unselected duplicates from taxon table*

Description

Remove unselected duplicate taxon names from taxon table.

Usage

```
remove.dupes(fulltab, dupe.list, dupe.sel)
```

Arguments

fulltab	Full taxon table for matched taxon names.
dupe.list	List of duplicated entries.
dupe.sel	Character vector of taxa selected by user.

Details

Deletes rows from fulltab that are not selected by user

Value

Returns revised fulltab.

Author(s)

Lester L. Yuan

---

resolve.mult   *Resolve cases in which two taxa are found in ITIS*

Description

Resolves cases in which two taxa listed on the same entry are both found in ITIS.

Usage

```
resolve.mult(parse.list, get.tax.env)
```

Arguments

parse.list   List of taxa that are found in ITIS (position 1)and taxa that are still unresolved
              (position 2).

get.tax.env   Environment variable where the full ITIS taxon table is available

Details

The most likely reason for two valid taxa being listed in the same entry is that the taxonomist
could only identify a specimen down to two possibilities. In these cases, the script downgrades the
identification to a coarser level that is the same for both taxa.

Value

Updates parse.list so that resolved multiple listings are included in position 1.

Author(s)

Lester L. Yuan

---

sel.coeffile   *Select coefficient file*

Description

Prompt user to select coefficient file from those available in data directory

Usage

```
sel.coeffile(fstring = "coef")
```

Arguments

fstring   Character string for filtering files in data directory

Details

Provides the list of data files available to the user.

Value

Selected file name.

Author(s)

Lester L. Yuan

---

ss.OR   *site-OTU matrix for western Oregon*

Description

Matrix with each row representing a distinct sample and each colum representing a different OTU for western Oregon benthic count data.

Usage

```
data(ss.OR)
```

Source

Oregon Department of Environmental Quality

Examples

```
data(ss.OR)
```

---

taxon.env   *Estimate taxon-environment relationships*

Description

taxon.env estimates taxon-environment relationships using logistic regression.

Usage

```
taxon.env(form, bcnt, envdata, bcnt.siteid, bcnt.abndid,
env.siteid,tlevs = "all", dumpdata = FALSE)
```

Arguments

form	Regression formula for model. Format is identical to that used for `glm`.
bcnt	A benthic count file with a full taxonomic hierarchy that results from running [get.taxonomic]().
envdata	Environmental data file
bcnt.siteid	Field name for `bcnt` unique site identifier.
bcnt.abndid	Field name for `bcnt` taxon abundance.
env.siteid	Field name for `envdata` unique site identifier.
tlevs	Taxonomic levels to compute taxon-environment relationships.
dumpdata	Logical field specifying whether data used to estimate taxon-environment relationships should be included in the output.

Details

This script generates logistic regression models for taxa at various levels of taxonomic resolution (as specified by the user). The script computes the degrees of freedom specified by the model (df) and selects taxa that occur in at least 10 times df and is absent from at least 10 times df sites. Then, logistic regression models based on the formula specified by the user are computed for each taxon using [glm](). The user can select the taxonomic levels (e.g., CLASS, ORDER, SPECIES, etc.) at which taxon-environment relationships are computed using the parameter `tlevs`. The default value for `tlevs` computes relationships at all levels.

Value

Regression coefficient file that can be used with `mlsolve` to infer environmental conditions.

tnames	Taxon names for which models are calculated
csave	Matrix of regression coefficients
xvar	Character vector with names of explanatory variables
xlims	Range of each explanatory variable
form	Model formula
roc	Area under receiver operator curve for model for each taxon.
raw.data	Data used to estimate relationships. Only included if `dumpdata = T`.

Author(s)

Lester L. Yuan

See Also

[get.taxonomic]()

Examples

```
data(envdata.OR)
data(bcnt.tax.OR)
coef <- taxon.env(~sed + sed^2, bcnt.tax.OR, envdata.OR, "SVN",
"CountValue", "STRM.ID")
```

---

tklist.modal	*Modal select list dialog using TclTk*

Description

tklist.modal generates a dialog box that prompts the user to select from a list of options. This script uses TclTk tools that should be operable on different operating systems.

Usage

```
tklist.modal(title, elements0, returnValOnCancel="ID_CANCEL",selectmode =
"single")
```

Arguments

title	Title for the list box.
elements0	Character vector of elements listing different choices
returnValOnCancel	
	Character string returned by the script if the dialog box is canceled
selectmode	Set to multiple to allow for multiple selections.

Value

A TclTk dialog box.

Author(s)

Lester L. Yuan

Examples

```
## Not run:
tklist.modal("Select a color", c("red", "green", "blue"))

## End(Not run)
```

`trait.feeding` *Feeding traits for benthic invertebrates*

Description

Feeding classifications for different benthic invertebrates.

Usage

```
data(trait.feeding)
```

Format

A data frame with two columns.

TAXON Character vector with the names of each taxon.

TRAITVAL Value of trait classification

Details

These trait classifications were summarized from the USGS data set prepared by Viera et al. http://pubs.usgs.gov/ds/ds187/.

Source

Yuan, L.L.

Examples

```
data(trait.feeding)
```

`trait.habit` *Habit traits for benthic invertebrates*

Description

Habit classifications for different benthic invertebrates.

Usage

```
data(trait.habit)
```

Format

A data frame with two columns.

TAXON Character vector with the names of each taxon.

TRAITVAL Value of trait classification

Details

These trait classifications were summarized from the USGS data set prepared by Viera et al. `http://pubs.usgs.gov/ds/ds187/`.

Source

Yuan, L.L.

Examples

```
data(trait.habit)
```

---

trait.stat	*Compute trait metrics*

Description

Compute trait metrics from benthic count data.

Usage

```
trait.stat(bcnt.otu, coefs)
```

Arguments

bcnt.otu	Benthic count file with OTU defined consistently with selected trait file
coefs	Trait file

Details

OTUs appropriate for the selected trait file must first be assigned using `get.otu`. A list of trait files provided in the library can be obtained using `sel.coeffile`. Script will compute richness, relative richness, and relative abundance of each trait group. Note that many taxa in a benthic count file are often not assigned to traits, and so relative richness and relative abundance values within a given sample may not sum to 1.

Value

Data frame of trait metrics.

Author(s)

Lester L. Yuan

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view.te   *View taxon-environment relationships*

Description

Viewer for taxon-environment relationships.

Usage

```
view.te(coef, plotform = "pdf")
```

Arguments

coef	Taxon-environment coefficient file (e.g. coef.west.wt)
plotform	Specify output plot format. Options include pdf and windows.

Details

Generates contour plots that show taxon-environment relationships represented by taxon-environment coefficients. Models with a single explanaotry variable are displayed as line plots, and models with two explanatory variables are displayed as contour plots. Plots are returned returned the file taxon.env.pdf is plotform = "pdf".

Value

None. Used for side effects.

Author(s)

Lester L. Yuan

Examples

```
## Not run:
data(coef.west.wt)
view.te(coef.west.wt)
## End(Not run)
```

Index