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.
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LazyData FALSE
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R topics documented:

bio.infer-package .................................................. 2
bcnt.emapw ....................................................... 3
bcnt.OR .......................................................... 4
bcnt.otu.OR ....................................................... 4
bcnt.tax.OR ........................................................ 5
coef.east.sed ..................................................... 5
coef.west.wt ..................................................... 6
correct.taxanames ................................................ 7
envdata.emapw .................................................... 7
envdata.OR ........................................................ 8
flist.data .......................................................... 9
flist.match ........................................................ 9
formtomat ......................................................... 10
### Description

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

### Details

<table>
<thead>
<tr>
<th>Package</th>
<th>bio.infer</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>Package</td>
</tr>
<tr>
<td>Version</td>
<td>1.0</td>
</tr>
<tr>
<td>Date</td>
<td>2006-10-31</td>
</tr>
<tr>
<td>License</td>
<td>GPL version 2 or newer</td>
</tr>
</tbody>
</table>
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

---

**Description**

Benthic count data for streams in the western United States.

**Usage**

```r
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**

```r
data(bcnt.emapw)
```
**bcnt.OR**

*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**

*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
bcnt.tax.OR

Source
Oregon Department of Environmental Quality

Examples
data(bcnt.otu.OR)

cbnt.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)

cbnt.tax.OR  Benthic count with taxonomic hierarchy

Description
Regression coefficients for eastern U.S. sediment

Usage
data(coef.east.sed)

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)

c 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.0R)`
Format
A data frame with 1674 observations on the following 8 variables.

ID  Unique sample code
ntl  Total nitrogen concentration
no3  Nitrate concentration
ptl  Total phosphorus concentration
sed  Percent sands and fines
tempre  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(bcct, optlist = NULL, ndc = TRUE, outputFile = "sum.otu.txt",
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**: File name for summary output file.

- **gui**: Logical indicating whether to use gui interface.

Details

`get.otu` makes decisions out 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, Falceon, 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

```r
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(bcni)

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.taxononomic

Merge benthic count data with the ITIS taxonomy table

Description
get.taxononomic 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.taxononomic(bcni)

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)

g.get.valid.names | Get taxon names from benthic count file

Description

Identifies valid names from parsed name matrix.

Usage

g.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**

**Usage**
```
data(itis.ttable)
```

**Source**

**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**

```r
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**

```r
load.revised.species(bcnt.tax, fname)
```
locate.dupes

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
makess

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
gt.otu, load.revised.otu
Examples

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

**Description**

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

**Usage**

```r
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**

```r
data(coef.west.wt)
data(ss.OR)
in.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**

```r
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
Details provides the list of data files available to the user.

Value
Value selected file name.

Author(s)
Author(s) Lester L. Yuan

---

**ss.OR**

*site-OTU matrix for western Oregon*

---

Description
Description matrix with each row representing a distinct sample and each column representing a different OTU for western Oregon benthic count data.

Usage
Usage `data(ss.OR)`

Source
Source Oregon Department of Environmental Quality

Examples
Examples `data(ss.OR)`

---

**taxon.env**

*Estimate taxon-environment relationships*

---

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

Usage
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 ml.solve to infer environmental conditions.

Value:

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

generate.taxonomic
Examples

```r
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**

```r
tklist.modal(title, elements0, returnValOnCancel="IDCancelar" , 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**

```r
## 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**

```r
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/](http://pubs.usgs.gov/ds/ds187/).

**Source**

Yuan, L.L.

**Examples**

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

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

**Description**

Habit classifications for different benthic invertebrates.

**Usage**

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

**Format**

A data frame with two columns.

- **TAXON**  Character vector with the names of each taxon.
- **TRAITVAL**  Value of trait classification
trait.stat

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(bc.nt.ou, 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
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 explanatory variable are displayed as line plots, and models with two explanatory variables are displayed as contour plots. Plots are 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

*Topic datasets
bcnt.emapw, 3
bcnt.OR, 4
bcnt.otu.OR, 4
bcnt.tax.OR, 5
coeff.east.sed, 5
coeff.west.wt, 6
endata.emapw, 7
endata.OR, 8
itis.ttable, 17
ss.OR, 27
trait.feeding, 30
trait.habit, 30

*Topic models
bio.infer, 2
correct.taxanames, 7
flist.data, 9
flist.match, 9
formtomat, 10
get.dupe.sel, 11
get.otu, 11
get.taxon.names, 13
get.taxonomic, 13
get.valid.names, 14
in.ITIS, 15
incorp.correct, 16
infergui, 16
load.itis, 17
load.revised.otu, 18
load.revised.species, 18
locate.dupes, 19
make.fulltab1, 20
make.species, 20
makess, 21
mlsolve, 22
modalDialog, 23
output.tax.table, 24
parse.taxon.name, 24
remove.dupes, 25
resolve.multi, 26
sel.coeffile, 26
taxon.env, 27
tklist.modal, 29
trait.stat, 31
view.te, 32
bcnt.emapw, 3
bcnt.OR, 3, 4, 4
bcnt.otu.OR, 4
bcnt.tax.OR, 5
bio.infer (bio.infer-package), 2
bio.infer-package, 2
coeff.east.sed, 5
coeff.west.wt, 3, 6, 32
correct.taxanames, 7
enidata.emapw, 7
enidata.OR, 8
fix, 14
flist.data, 9
flist.match, 9
formtomat, 10
get.dupe.sel, 11
get.otu, 3, 4, 11, 18, 21, 22, 31
glm, 28
in.ITIS, 15
incorp.correct, 16
infergui, 16
itis.ttable, 14, 17
load.itis, 17
load.revised.otu, 12, 18, 21
load.revised.species, 14, 18
locate.dupes, 19
make.fulltab1, 20
make.species, 20
makess, 3, 21, 22
mlsolve, 3, 22
modalDialog, 23
optim, 22
output.tax.table, 24
parse.taxon.name, 24
remove.dupes, 25
resolve.mult, 26
sel.coeffile, 26, 31
ss.OR, 27
taxon.env, 22, 27
tklist.modal, 29
trait_FEEDING, 30
trait.habit, 30
trait.stat, 31
view.te, 32