**Package ‘dragDBI’**

**Type** Package

**Title** Calculation of Dragonfly Biotic Index for Odonata communities

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**Description** The “dragDBI” package calculates a set of DBI values for dragonfly communities, based on species-level identification. Indices that can be calculated are sum DBI, mean DBI, DBI potential, true DBI potential, and permutational DBI potential. The DBI values can be calculated for the Central European Dataset, South African Dataset or for user´s uploaded checklist with DBI values. The definitions of these indices are given in the paper Šigutová et al. 2022.

**Depends** R

**LazyData** TRUE

**Suggests** knitr

**URL** <https://github.com/VeronikaPrielozna/dragDBI>

**VignetteBuilder** knitr

**NeedsCompilation** no

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# dragDBI-package *dragDBI: A package for calculation of Dragonfly Biotic Index for Odonata communities*

**Description**

The “dragDBI” package provides the main calculation function, wrapper functions for easy calculation of particular DBI indices, reference checklists with DBI values for Central European and South African dragonflies, and a three data uploading functions that can be used to i) load data, ii) quality-check, annotation of DBI values to particular species, and preparation of data for analysis, iii) or for uploading set of user-defined DBI values

**Main function**

The main function is “CalculateDBI” which allows the calculation of the set of DBI indices implemented.

**Wrapper functions**

A function is provided for each of the individual DBI indices to allow for quick calculations. An example is “PermDBI” which implements the calculation of the permutational DBI potential.

**Data uploading functions**

The first function “LoadDBI” allows for uploading a user-defined checklist of dragonflies with a user-defined set of DBI values. The second function “LoadData” checks and converts the input data into the format needed by the package.

# Stormwaters *Highway stormwater and control ponds dataset*

**Descriptions**

The dataset is derived from the research project of Aleš Dolný, which was used in the publication: Highway stormwater ponds as islands of Odonata diversity in an agricultural landscape (Šigutová et al., 2022).

**Format**

Dataframe

**Author(s)**

Šigutová et al., 2022

**References**

Šigutová, H., Pyszko, P., Valušák, J., Dolný, A., 2022. Highway stormwater ponds as islands of Odonata diversity in an agricultural landscape. Sci. Total Environ. 837, 155774. <https://doi.org/10.1016/j.scitotenv.2022.155774>.

# DBI\_CE *Central European checklist with DBI values*

**Descriptions**

Checklist of all Central European dragonfly species with assigned DBI values according to Dolný et al. 2012. Contains 68 species (in total 73 species, containing DBI with NA values).

**Format**

Dataframe

**Author(s)**

Dolný et al., 2012

**References**

Dolný, A., Harabiš, F., Bárta, D., Lhota, S., Drozd, P., 2012. Aquatic insects indicate terrestrial habitat degradation: Changes in taxonomical structure and functional diversity of dragonflies in tropical rainforest of East Kalimantan. Trop. Zool. 25, 141–157.

# DBI\_SA *South African checklist with DBI values*

**Descriptions**

Checklist of all South Africa dragonfly species with assigned DBI values according to Samways et al. 2016. Contains 164 species.

**Format**

Dataframe

**Author(s)**

Samways et al., 2016

**References**

Samways, M.J., Simaika, J.P., 2016. Manual of freshwater assessment for South Africa: Dragonfly Biotic Index. Suricata 2. South African National Biodiversity Institute, Pretoria.

# LoadDBI *Uploading function for user-defined DBI checklist*

**Descriptions**

The function allows for uploading a user-defined checklist of dragonflies with a user-defined set of DBI values.

**Usage**

LoadDBI(attrib=T)

**Arguments**

attrib Logical, if true creating attributes (number of species).

**Value**

A data frame uploaded by user containing a list of taxa in the first column and user-defined DBI values in the second column.

**Example**

# Uploading user-defined DBI checklist. Saved as DBI\_UD.

DBI\_UD<-LoadDBI()

# LoadData *Data uploading function*

**Descriptions**

The function allows for simple loading of user data and converting NA values into null.

**Usage**

LoadData(attrib=T, na2null=T)

**Arguments**

attrib Logical, if true creating attributes (number of species and number of samples).

na2null Logical, if true converting NA values into null.

**Value**

A data frame uploaded by user containing a list of taxa in the first column, and abundance or presence/absence data in following columns with sample names in the column’s header.

**Example**

# Uploading data containing species of Central Europe. Saved as x\_CE.

x\_CE<-LoadData()

# UniteData *Unification of user dataset and DBI data*

**Descriptions**

The function allows for quality-checking of the correctness of species naming, and automated assignment of DBI values to the user dataset based on the comparison with checklists with DBI values for Central European or South African dragonflies. Check the list of taxa present in the sample dataset against the checklist of taxa within package to identify any non-scoring taxa in the samples (or spelling mistakes).

**Usage**

UniteData(df, DBI\_val, DBI\_UD)

**Arguments**

df A data frame containing uploaded user dataset (list of taxa in first column, followed by columns of abundances with sample names in a header).

DBI\_val Indicates checklist which should be used for comparison. “CE” indicates the Central European checklist with DBI values. “SA” indicates the South African checklist with DBI values. “UD” indicates user defined/uploaded checklist.

DBI\_UD In case, that “UD” is defined for the type, the name of user loaded data frame should be specified here.

**Value**

A data frame consisting of user´s dataset and checklist of DBI values. In case, that “CE” or “SA” is defined for the type, there will be also columns with values of distribution, threat and sensitivity of specific species.

**Example**

# Unification of Highway stormwater and control ponds dataset and Central European checklist with DBI values. Saved as StormwatersDBI.

StormwatersDBI<-UniteData(Stormwaters, DBI\_val = "CE")

# CalculateDBI *Main function calculating set of DBI values for dragonfly communities*

**Descriptions**

Calculates sum of DBI, mean of DBI, DBI potential, true DBI potential, and permutational DBI potential for dragonfly community samples.

**Usage**

CalculateDBI(df, DBI\_val, DBI\_UD, NAval=F, sim=10000)

**Arguments**

df A data frame created by “UniteData” function, containing a list of taxa in the first column, followed by the columns of distribution, threat and sensitivity subindices of DBI (in case of use of package´s checklist in “UniteData” function), by the column of DBI values and columns of abundances with sample names in the rows.

DBI\_val Indicates checklist which should be used for comparison. “CE” indicates the Central European checklist with DBI values. “SA” indicates the South African checklist with DBI values. “UD” indicates user defined/uploaded checklist.

DBI\_UD In case, that “UD” is defined for the type, the name of user loaded data frame should be specified here.

NAval Logical, true in case of NA values in user defined checklist.

sim The number of simulations identifies how many permutations should be made to randomly assemble communities with the same species richness as the compared community. The probability weights for each DBI is set on 2^-DBI, i.e. a species with a DBI higher by one unit has half the probability of being selected into a random community than a species with a lower DBI value.

**Value**

A data frame consisting of the columns of index values (sum of DBI, mean of DBI, DBI potential, true DBI potential, and permutational DBI potential) with samples in rows.

**Example**

# Calculate set of DBI values for the Highway stormwater and control ponds dataset

CalculateDBI(StormwatersDBI, DBI\_val = "CE")

# StandardDBI *Standard DBI values for dragonfly communities*

**Descriptions**

Calculates sum or mean of DBI for dragonfly community samples.

**Usage**

StandardDBI(df, UD=F, type, data="DBI", plot=F)

**Arguments**

df A data frame created by “UniteData” function, containing a list of taxa in the first column, followed by the columns of distribution, threat and sensitivity (in case of use of package´s checklist in “UniteData” function), by the column of DBI values and columns of abundances with sample names in the rows.

UD Logical, true in case of user´s uploaded checklist is used. By default, false.

type Indicates if sum of DBI (“sum”) or mean of DBI (“mean”) should be calculated.

data In case, that user´s checklist is used in “UniteData” function, the “StandardDBI” function is able to calculate with DBI values (“DBI”), values of sensitivity (“SENS”), threat (“THR”) and distribution (DIST).

plot Should a barplot for results of calculations be plotted? By default, the plot is not rendered.

**Value**

A data frame consisting of a column of index values with samples in rows.

**Example**

# Calculate the sum DBI index for the Highway stormwater and control ponds dataset.

StandardDBI(StormwatersDBI, type = "sum")

# Calculate the mean DBI index for the Highway stormwater and control ponds dataset.

StandardDBI(StormwatersDBI, type = "mean")

# PermDBI *Permutational DBI potential for dragonfly communities*

**Descriptions**

Calculates permutational DBI potential for dragonfly community samples.

**Usage**

PermDBI(df, DBI\_val, DBI\_UD, NAval=T, sim=10000, plot=F)

**Arguments**

df A data frame created by “UniteData” function, containing a list of taxa in the first column, followed by the columns of distribution, threat and sensitivity (in case of use of package´s checklist in “UniteData” function), by the column of DBI values and columns of abundances with sample names in the rows.

DBI\_val Indicates checklist which should be used for comparison. “CE” indicates the Central European checklist with DBI values. “SA” indicates the South African checklist with DBI values. “UD” indicates user defined/uploaded checklist.

DBI\_UD In case, that “UD” is defined for the type, the name of user loaded data frame should be specified here.

NAval Logical, true in case of NA values in user´s defined checklist.

sim The number of simulations identifies how many permutations should be made to randomly assemble communities with the same species richness as the compared community.

plot Should a histogram for randomly assembled communities be plotted for each compared community, completed with a vertical abline representing the given community? By default, the plot is not rendered.

**Value**

A data frame consisting of a column of index values with samples in rows.

**Example**

# Calculate the permutational DBI potential for the Highway stormwater and control ponds dataset, comparing the given community to 10,000 randomly assembled communities.

PermDBI(StormwaterDBI, DBI\_val = "CE", sim = 10000)

# PotDBI *DBI potential for dragonfly communities*

**Descriptions**

Calculates DBI potential and true DBI potential for dragonfly community samples.

**Usage**

PotDBI (df, DBI\_val, DBI\_UD, type="def", NAval=F, plot=F)

**Arguments**

df A data frame created by “UniteData” function, containing a list of taxa in the first column, followed by the columns of distribution, threat and sensitivity (in case of use of package´s checklist in “UniteData” function), by the column of DBI values and columns of abundances with sample names in the rows.

type Indicates if “tpDBI”, i.e. true DBI potential or “pDBI”, i.e. DBI potential should be calculated. By default, DBI potential, true DBI potential, sum of DBI and probable maximum value of sum of DBI are calculated.

DBI\_val Indicates checklist which should be used for comparison. “CE” indicates the Central European checklist with DBI values. “SA” indicates the South African checklist with DBI values. “UD” indicates user defined/uploaded checklist.

DBI\_UD In case, that “UD” is defined for the type, the name of user loaded data frame should be specified here.

NAval Logical, true in case of NA values in user´s defined checklist.

plot Should a plot displaying range between probable maximum and minimum values of sum of DBI and position of sum of DBI in the range be plotted? By default, the plot is not rendered.

**Value**

A data frame consisting of a column of index values with samples in rows.

**Example**

# Calculate the true DBI potential for the Highway stormwater and control ponds dataset.

PotDBI(StormwatersDBI, DBI\_val = "CE", type = "tpDBI")

**Do vignettu:**

**Introduction**

The “dragDBI” package provides the main calculation function, wrapper functions for easy calculation of DBI indices, reference checklists with DBI values for Central European and South African dragonflies, and a data uploading function that can be used to load, quality-check, and prepare data for analysis.

**Installation**

The current release version (1.0.) of the package can be installed from GitHub. The homepage of the package is <https://github.com/VeronikaPrielozna/dragDBI>. To install the package, you need to first install the “devtools” package.

Install.packages("devtools")

After that, you must load the “devtools” package and use the “install\_github” function. For building vignettes, the argument build\_vignettes must be equal to ‘T’.

library("devtools")

install\_github("VeronikaPrielozna/dragDBI", build\_vignettes = T)

**Input format**

A dataset containing a list of taxa in the first column, and abundance or presence/absence data in following columns with sample names in the column’s header.

# Load library

library(dragDBI)

# Show the format of the built-in dataset

head(Stormwaters)

**Functions**

The first function you are supposed to use is “LoadData”. This function checks and converts the input data into the format needed by the package. To match the input taxa names based on species-level identification with their values for DBI from the checklists, you have to use “UniteData” function. The main function of “dragDBI” package is “CalculateDBI”, which calculates the sum of DBI, mean of DBI, DBI potential, true DBI potential, and permutational DBI potential for dragonfly community samples.

LoadDBI, LoadData, UniteData, CalculateDBI

**Individual index functions**

StandardDBI, PermDBI, PotDBI

**Reporting problems**

The package has been extensively tested using different test datasets, but if you come across an error or bug, then please [email me] (verca.prielozna@gmail.com).

**Paper and citation**

cff-version: 1.0.0

message: "If you use this software, please cite it as below."

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