

# Package ‘divDyn’

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**Type** Package

**Title** Diversity Dynamics using Fossil Sampling Data

**Version** 0.7.1

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**Description** Functions to describe sampling and diversity dynamics of fossil occurrence datasets (e.g. from the Paleobiology Database). The package includes methods to calculate range- and occurrence-based metrics of taxonomic richness, extinction and origination rates, along with traditional sampling measures. A powerful subsampling tool is also included that implements frequently used sampling standardization methods in a multiple bin-framework. The plotting of time series and the occurrence data can be simplified by the functions incorporated in the package, as well other calculations, such as environmental affinities and extinction selectivity testing. Details can be found in: Kocsis, A.T.; Reddin, C.J.; Alroy, J. and Kiessling, W. (2019) <doi:10.1101/423780>.

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affinity                      *Environmental affinities of taxa*

---

**Description**

This function will return the preferred environment of the taxa, given the distribution of occurrences.

**Usage**

```
affinity(dat, tax, bin, env, coll = NULL, method = "binom",
         alpha = 1, reldat = NULL, na.rm = FALSE, bycoll = FALSE)
```

### Arguments

dat	(data.frame) The occurrence dataset containing the taxa with unknown environmental affinities.
tax	(character) The column name of taxon names.
bin	(character) The column name of bin names.
env	(character) The environmental variable of the occurrences.
coll	(character) The column name of collection identifiers (optional). If this is provided, then then the multiple entries of a taxon within the collections will be treated as 1.
method	(character) The method used for affinity calculations. Can be either "binom" or "majority".
alpha	(numeric) The alpha value of the binomial tests. By default binomial testing is off (alpha=1) and the methods returns that environment as the preferred one, which has the highest likelihood (odds ratio).
reldat	(data.frame) Database with the same structure as dat. dat is typically a subset of reldat. If given, the occurrence distribution of reldat is used as the null model of sampling. Defaults to NULL, which means that dat itself will be used as reldat.
na.rm	(logical) Should the NA entries in the relevant columns of dat be omitted automatically?
bycoll	(logical) If set to TRUE, the number of collections (or samples, in coll) will be used rather than the number of occurrences.

### Details

Sampling patterns have an overprinting effect on the frequency of taxon occurrences in different environments. The environmental affinity (Foote, 2006; Kiessling and Aberhan, 2007; Kiessling and Kocsis, 2015) expresses whether the taxa are more likely to occur in an environment, given the sampling patterns of the dataset at hand. The function returns the likely preferred environment for each taxon as a vector. NA outputs indicate that the environmental affinity is equivocal based on the selected method.

#### The following methods are implemented:

'majority': Environmental affinity will be assigned based on the number of occurrences of the taxon in the different environments, without taking sampling of the entire dataset into account. If the taxon has more occurrences in *environment 1*, the function will return *environment 1* as the preferred habitat.

'binom': The proportion of occurrences of a taxon in *environment 1* and *environment 2* will be compared to a null model, which is based on the distribution of all occurrences from the stratigraphic range of the taxon (in dat or if provided, in reldat). Then a binomial test is run on with the numbers of the most likely preference (against all else). The alpha value indicates the significance of the binomial tests, setting alpha to 1 will effectively switch the testing off: if the ratio of occurrences for the taxon is different from the ratio observed in the dataset, an affinity will be assigned. This is the default method. If an environment is not sampled at all in the dataset to which the taxon's occurrences are compared to, the binomial method returns NA for the taxon's affinity.

## References

- Foote, M. (2006). Substrate affinity and diversity dynamics of Paleozoic marine animals. *Paleobiology*, 32(3), 345-366.
- Kiessling, W., & Aberhan, M. (2007). Environmental determinants of marine benthic biodiversity dynamics through Triassic–Jurassic time. *Paleobiology*, 33(3), 414-434.
- Kiessling, W., & Kocsis, Á. T. (2015). Biodiversity dynamics and environmental occupancy of fossil azooxanthellate and zooxanthellate scleractinian corals. *Paleobiology*, 41(3), 402-414.

## Examples

```
data(corals)
# omit values where no occurrence environment entry is present, or where unknown
fossils<-subset(corals, stg!=95)
fossilEnv<-subset(fossils, bath!="uk")
# calculate affinities
aff<-affinity(fossilEnv, env="bath", tax="genus", bin="stg", alpha=1)
```

---

bins

*The 10 million year resolution timescale of the Paleobiology Database*

---

## Description

Roughly 10 million year timescale used in some analyses.

## Usage

bins

## Format

A data.frame with 49 observations and 9 variables:

**X10** The name of the bin: Period and number.

**ocean** The primary state of the oceans from the point of carbonate precipitation. ar indicates aragonitic, cc indicates calcitic conditions. Based on §

**ocean2** §

**climate** Primary climatic characteristic: w denotes warm, c denotes cold.

**bottom** Numeric ages of the bottom boundaries (earliest ages) of the bins.

**mid** Numeric ages midpoints of the bins, the averages of bottom and top.

**top** Numeric ages of the tops (latest ages) of the bins.

**dur** Numeric ages of the durations of the bins.

**bin** Integer number identifiers of the bins. §correct to num!

## Details

This is an example time scale object that can be used in the Phanerozoic scale analyses. This time scale comprises 49 bins, roughly 10 million years of durations that result from the combination of certain standard stages.

## Source

Executive committee meeting (2015) of old Paleobiology Database. Additional variables were added by Wolfgang Kiessling.

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binstat	<i>Sampling statistics and diversity indices in every bin</i>
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---

## Description

This function will return the basic sampling summaries of a dataset

## Usage

```
binstat(dat, tax = "genus", bin = "stg", coll = NULL, ref = NULL,
        noNAstart = FALSE, duplicates = NULL, x = NULL, indices = FALSE)
```

## Arguments

dat	(data.frame): The occurrence dataset.
tax	(character): The column name of taxon names.
bin	(character): The column name of bin names.
coll	(character): The column name of collection numbers. (optional)
ref	(character): The column name of reference numbers. (optional)
noNAstart	(logical) Useful when the dataset does not start from bin no. 1, but positive integer bin numbers are provided. Then noNAstart=TRUE will cut the first part of the resulting table, so the first row will contain the estimates for the lowest bin number. In case of positive integer bin identifiers, and if noNAstart=FALSE, the index of the row will be the bin number.
duplicates	(logical): The function will check whether there are duplicate occurrences (multiple species/genera). When set to NULL, nothing will happen, but the function will notify you if duplicates are present. If set to TRUE, the function will not do anything with these, if set to FALSE, the duplicates will be omitted.
x	(numeric): Argument of the OxW subsampling type ( <a href="#">subtrialOxW</a> ). Setting this parameter to a valid numeric value will return the maximum quota for x.
indices	(logical): Setting this value to TRUE will calculate all indices implemented in ( <a href="#">indices</a> ).

## Details

Secondary function of the package that calculates a number of sampling related variables and diversity estimators for each bin. In contrast to the (`divDyn`) function, the bins are treated independently in this function. The function also returns the maximum subsampling quota for OxW subsampling (`subtrialOxW`) with a given  $x$  value.

By setting `total` to `FALSE` (default), the following results are output:

`occs`: The number of occurrences in each time bin.

`colls`: The number of collections in each time bin.

`xQuota`: The maximum quota for OxW subsampling (`subtrialOxW`) with the given  $x$  value. The number of occurrences in each collection is tabulated, and is raised to the power of  $x$ . The `xQuota` value is the sum of these values across all collections in a time slice.

`refs`: The number of references in each time bin.

`SIBs`: The number of Sampled-In-Bin taxa in each time bin.

`occ1`: The number of taxa in each time bin, that occur in only 1 collection.

`ref1`: The number of taxa in each time bin, that occur in only 1 reference.

`occ2`: The number of taxa in each time bin, that occur in exactly 2 collections.

`ref2`: The number of taxa in each time bin, that occur in exactly 2 references.

`u`: Good's  $u$ , coverage estimator based on the number of single-collection taxa (`occ1`).

`uPrime`: Good's  $u$ , coverage estimator based on the number of single-reference taxa (`ref1`).

`chao1occ`: Chao1 extrapolation estimator, based on the the number of single-collection and two-collection taxa (`occ1`).

`chao1ref`: Chao1 extrapolation estimator, based on the the number of single-reference and two-reference taxa (`occ2`).

## Examples

```
data(corals)
# slice-specific sampling
basic <- binstat(corals, tax="genus", bin="stg")

# subsampling diagnostic
subStats <- subsample(corals, method="cr", tax="genus", FUN=binstat,
  bin="stg", q=100,noNAStart=FALSE)

# maximum quota with x
more <- binstat(corals, tax="genus", bin="stg", coll="collection_no", x=1.4)
```

---

 categorize

*Mapping multiple entries to categories*


---

### Description

This basic function replaces groups of values in a vector with single values with the help of a key object.

### Usage

```
categorize(x, key, incbound = "lower")
```

### Arguments

x	(vector) Object containing the values to be replaced.
key	(list) A list of vectors. Each vector includes the possible elements that will be replaced in a group, the names of the vectors will be the replacement values. Also has to include an element named 'default' with a single value. (see examples)
incbound	(character) Either "lower" or "higher". Interval identifiers will be treated with different interval rules. "lower" will treat the lowest entry as included, "higher" works the opposite. The argument will be renamed to 'include.lowest' to make the interface easier to remember.

### Details

Online datasets usually contain overly detailed information, as enterers intend to conserve as much data in the entry process, as possible. However, in analyses some values are treated to represent the same, less-detailed information, which is then used in further procedures. The map function allows users to do this type of multiple replacement using a specific object called a 'key'.

A key is an informal class and is essentially a list of vectors. In the case of character vectors as x, each vector element in the list corresponds to a set of entries in x. These will be replaced by the name of the vector in the list, to indicate their assumed identity.

In the case of numeric x vectors, if the list elements of the key are numeric vectors with 2 values, then this vector will be treated as an interval. The same value will be assigned to the entries that are in this interval (Example 2). If x contains values that form the boundary of an interval, than either only the one of the two boundary values can be considered to be in the interval (see the incbound argument to set which of the two). The elements of key are looped through in sequence. If values of x occur in multiple elements of key, than the last one will be used (Example 3).

Examples of this data type have been included ([keys](#)) to help process Paleobiology Database occurrences.

## Examples

```
# Example 1
# x, as character
set.seed(1000)
toReplace <- sample(letters[1:6], 15, replace=TRUE)
# a and b should mean 'first', c and d 'second' others: NA
key<-list(first=c("a", "b"), second=c("c", "d"), default=NA)
# do the replacement
categorize(toReplace, key)

# Example 2 - numeric entries and mixed types
# basic vector to be grouped
toReplace2<-1:16

# replacement rules: 5,6,7,8,9 should be "more", 11 should be "eleven" the rest: "other"
key2<-list(default="other", more=c(5,10),eleven=11)
categorize(toReplace2, key2)

# Example 3 - multiple occurrences of same values
# a and b should mean first, a and should mean 'second' others: NA
key3<-list(first=c("a", "b"), second=c("a", "d"), default=NA)
# do the replacement (all "a" entries will be replaced with "second")
categorize(toReplace, key3)
```

---

cleansp

*Cleanse Species Name Vector*


---

## Description

This function will take a vector of binomial names with various qualifiers of open nomenclatures, and removes them from the vector entries. Only the the genus and species names will remain.

## Usage

```
cleansp(vec, debug = FALSE, collapse = "_", subgenera = FALSE,
        misspells = TRUE, stems = TRUE)
```

## Arguments

vec	(character): the vector containing species names with qualifiers of open taxonomy.
debug	(logical): FALSE will return the cleaned species name vector, TRUE returns a data table that allows one by one checking.
collapse	(character): This argument will be passed to the paste function's argument of the same name. The character value to be inserted between the genus and species names.



subgenera	(logical): FALSE omits subgenus information (in parentheses) and will construct a unique binomen based on the genus and species names alone. TRUE will promote the subgenus names and it will create a new binomen based on the subgenus rather than the genus name.
misspells	logical: Resolution of common spelling mistakes, such as diphtongs and alternate spellings: 'ue' is replaced with 'u', 'ae' is replaced with 'e', 'll' with 'l', 'ss' with 's' and 'y' with 'i'.
stems	(logical): Setting this to TRUE will omit the adjective declination suffices from the species names.

### Details

This version will not keep subgenera, and will assign species to the base genus. The following qualifiers will be omitted: "n.", "sp.", "?", "gen.", "aff.", "cf.", "ex gr.", "subgen.", "spp" and informal species designated with letters. Entries with "informal" and "indet." in them will also be invalidated.

Functions called by the misspells and stems arguments were written by Gwen Antell.

### Examples

```
examp <- c("Genus cf. species", "Genus spp.", "Family indet.",
          "Mygenus yourspecies", "Okgenus ? questionsp",
          "Genus (cf. Subgenus) aff. species")
cleansp(examp)
```

---

corals	<i>Fossil occurrences of scleractinian (stony) corals from the Paleobiology Database</i>
--------	--

---

### Description

Example dataset to illustrate the package's basic functionalities.

### Usage

```
corals
```

### Format

A data.frame with 29775 observations and 38 variables:

genus Genus names of the occurrences. Cross referenced with a compiled table, the simplified version of this can be found in the supplementary material of Kiessling and Kocsis (2015).

collection\_no The number of the collection of the occurrence in the PaleoDB.

family Family name of the occurrence.

abund\_value Abundance value.

abund\_unit Unit of abundance values.  
 reference\_no The reference number of the occurrence in the PaleoDB.  
 life\_habit The lifestyle of the occurring taxon.  
 diet The diet of the occurring taxon.  
 country Country of occurrence.  
 geoplate Plate id of the occurrence.  
 lat Present day latitude of the occurrence.  
 lng Present day longitude of the occurrence.  
 paleolat Reconstructed paleolatitude of the occurrence.  
 paleolng Reconstructed paleolongitude of the occurrence.  
 period Period of origin.  
 epoch Epoch of origin.  
 subepoch Subepoch of origin.  
 stage Geologic stage of the embedding rocks.  
 early\_interval Early interval name registered in the PaleoDB dynamic time scale.  
 late\_interval Late interval name registered in the PaleoDB dynamic time scale.  
 max\_ma Maximum estimated age based on the PaleoDB dynamic time scale.  
 min\_ma Minimum estimated age based on the PaleoDB dynamic time scale.  
 stg Bin number in the stage-level timescale [stages](#).  
 Bin Bin number in the PaleoDB 10 million year resolution timescale [bins](#).  
 env Environment of the occurrence: reefal (r), non-reefal (nr) or unknown (uk), based on [keys](#).  
 lith Substrate of the occurrence: carbonate (c), siliciclastic (s) or unknown (uk), based on [keys](#).  
 latgroup Latitude of the occurrence: tropical (t) or non-tropical (nt).  
 bath Inferred depth of the occurrence: deep (deep), shallow (shal) or unknown (uk), based on [keys](#).  
 gensp The binomen of the occurrence.  
 ecology Symbiotic status of the occurring coral: zooxanthellate (z) or azooxanthellate (az, including apozooxanthellates).  
 ecologyMostZ Symbiotic status of the occurring coral, incorporating the uncertainty of inferred symbiotic status. This variable includes assignment with the maximum likely number of zooxanthellate genera.  
 ecologyMostAZ Symbiotic status of the occurring coral, incorporating the uncertainty of inferred symbiotic status. This variable includes assignment with the maximum likely number of azooxanthellate genera.  
 growth Growth type of the coral: colonial or solitary.  
 integration Integration of corallites from the scale of 0 to 4. solitary corals are marked with 0s.

## Details

This particular dataset was used in a study by Kiessling and Kocsis (2015). All occurrences of Scleractinia were downloaded from the Paleobiology Database (PaleoDB, <http://www.paleobiodb.org/>) on 23 September 2014, originally comprising 32420 occurrences. They were then cross-checked with data from CoralloSphere (<http://corallosphere.org>). See the article text for details.

### References

Kiessling, W., & Aberhan, M. (2007). Environmental determinants of marine benthic biodiversity dynamics through Triassic–Jurassic time. *Paleobiology*, 33(3), 414-434.

## Source

<http://www.paleobiodb.org/>

---

divDyn

*Time series from metrics of diversity dynamics*

---

## Description

This function calculates various metrics from occurrence datasets in the form of time series.

## Usage

```
divDyn(dat, tax, bin, ages = FALSE, breaks = NULL,
       coll = "collection_no", ref = "reference_no", om = NULL,
       noNAstart = FALSE, data.frame = TRUE, filterNA = FALSE)
```

## Arguments

dat	(data.frame) Fossil occurrence table.
tax	(character) Variable name of the occurring taxa (variable type: factor or character - such as "genus")
bin	(character) Variable name of the bin numbers of the occurrences. This variable should be numeric.
ages	(logical) Argument for setting the direction of time in bin. The default setting, FALSE will execute the function with higher numbers corresponding to later intervals. TRUE will reverse the direction of values in the bins variable, making originations extinctions and vice versa (use this for age input!, e.g 400 Ma, see examples).
breaks	(numeric) If NULL (default) the used values in the bin variable will designate independent time slices that follow each other in succession. If a vector is provided, then the numeric entries in bin will be binned similarly to the <a href="#">hist</a> or <a href="#">cut</a> function. The order of elements in this vector is arbitrary.
coll	(character) The variable name of the collection identifiers. (optional, only for use with the internal <a href="#">omit</a> function)

ref	(character) The variable name of the reference identifiers. (optional, only for use with the internal <code>omit</code> function)
om	(character) The <code>om</code> argument of the <code>omit()</code> function. If set to <code>NULL</code> (default), then no occurrences will be omitted before the execution of the function.
noNAstart	(logical) Useful when the entries in the <code>bin</code> variable do not start from bin no. 1, but positive integer bin numbers are provided. Then <code>noNAstart=TRUE</code> will cut the first part of the resulting table, so the first row will contain the estimates for the lowest bin number. In case of positive integer bin identifiers, and if <code>noNAstart=FALSE</code> , the index of the row will be the bin number.
data.frame	(logical) Should the output be a <code>data.frame</code> or a <code>matrix</code> ?
filterNA	(logical) The <code>filterNA</code> parameter of the <code>omit</code> function.

## Details

The following variables are produced:

`bin`: Bin number, or the numeric identifier of the bin.

`tThrough`: Number of through-ranging taxa, taxa that have first occurrences before, and last occurrences after the focal bin.

`tOri`: Number of originating taxa, taxa that have first occurrences in the focal bin, and last occurrences after.

`tExt`: Number of taxa getting extinct. These are taxa that have first occurrences before the focal bin, and last occurrences after it.

`tSing`: Number of stratigraphic singleton (single-interval) taxa, taxa that only occur in the focal bin.

`t2d`: Number of lower two timers (Alroy, 2008; 2014), taxa that are present in the  $i-1$ th and the  $i$ th bin (focal bin).

`t2u`: Number of upper two timers (Alroy, 2008; 2014), taxa that are present in the  $i$ th (focal) and the  $i+1$ th bin. (Alroy, 2008; 2014)

`tGFu`: Number of upper gap-fillers (Alroy, 2014), taxa that occur in bin  $i+2$  and  $i-1$ , but were not found in  $i+1$ . (Alroy, 2014)

`tGFd`: Number of lower gap-fillers (Alroy, 2014), taxa that occur in bin  $i-2$  and  $i+1$ , but were not found in  $i-1$ . (Alroy, 2014)

`t3`: Number of three timer taxa (Alroy, 2008; 2014), present in bin  $i-1$ ,  $i$ , and  $i+1$ . (Alroy, 2008; 2014)

`tPart`: Part timer taxa (Alroy, 2008; 2014), present in bin  $i-1$ , and  $i+1$ , but not in bin  $i$ .

`extProp`: Proportional extinctions including single-interval taxa:  $(tExt + tSing) / (tThrough + tOri + tExt + tSing)$ .

`oriProp`: Proportional originations including single-interval taxa:  $(tOri + tSing) / (tThrough + tOri + tExt + tSing)$ .

`extPC`: Per capita extinction rates of Foote (1999).  $-\log(tExt/(tExt + tThrough))$ . Values are not normalized with bin lengths. Similar equations were used by Alroy (1996) but without taking the logarithm.

oriPC: Per capita origination rates of Foote (1999).  $-\log(tOri/(tOri + tThrough))$ . Values are not normalized with bin lengths. Similar equations were used by Alroy (1996) but without taking the logarithm.

ext3t: Three-timer extinction rates of Alroy (2008).  $\log(t2d/t3)$ .

ori3t: Three-timer origination rates of Alroy (2008).  $\log(t2u/t3)$ .

extC3t: Corrected three-timer extinction rates of Alroy (2008).  $ext3t[i] + \log(samp3t[i+1])$ .

oriC3t: Corrected three-timer origination rates of Alroy (2008).  $ori3t[i] + \log(samp3t[i-1])$ .

divSIB: Sampled-in-bin diversity (richness), the number of genera sampled in the focal bin.

divCSIB: Corrected sampled-in-bin diversity (richness).  $divSIB/samp3t*totSamp3t$ , where  $totSamp3t$  is total three-timer sampling completeness of the dataset (Alroy, 2008).

divBC: Boundary-crosser diversity (richness), the number of taxa with ranges crossing the boundaries of the interval.  $tExt + tOri + tThrough$ .

divRT: Range-through diversity (richness), all taxa in the interval, based on the range-through assumption.  $(tSing + tOri + tExt + tThrough)$ .

sampRange: Range-based sampling probability (Foote),  $(divSIB - tExt - tOri - tSing)/tThrough$

samp3t: Three-timer sampling completeness of Alroy (2008).  $t3/(t3+tPart)$

extGF: Gap-filler extinction rates of Alroy(2014).  $\log((t2u + tPart)/(t3+tPart+tGFd))$

oriGF: Gap-filler origination rates of Alroy(2014).  $\log((t2u + tPart)/(t3+tPart+tGFd))$

E2f3: Second-for-third extinction proportions of Alroy (2015). As these metrics are based on an algorithmic approach, for the equations please refer to the Alroy (2015, p. 634, right column and Eq. 4). See source code (<http://www.github.com/adamkocsis/divDyn>) for the exact implementation, found in the Metrics function in the diversityDynamics.R file.

O2f3: Second-for-third origination proportions of Alroy (2015). Please see E2f3.

ext2f3: Second-for-third extinction rates (based on Alroy, 2015). Transformed to the usual rate form with  $\log(1/(1-E2f3))$ .

ori2f3: Second-for-third origination rates (based on Alroy, 2015). Transformed to the usual rate form with  $\log(1/(1-O2f3))$ .

### References:

Foote, M. (1999) Morphological Diversity In The Evolutionary Radiation Of Paleozoic and Post-Paleozoic Crinoids. *Paleobiology* 25, 1–115. doi:10.1017/S0094837300020236.

Alroy, J. (2008) Dynamics of origination and extinction in the marine fossil record. *Proceedings of the National Academy of Science* 105, 11536-11542. doi: 10.1073/pnas.0802597105

Alroy, J. (2014) Accurate and precise estimates of origination and extinction rates. *Paleobiology* 40, 374-397. doi: 10.1666/13036

Alroy, J. (2015) A more precise speciation and extinction rate estimator. *Paleobiology* 41, 633-639. doi: 10.1017/pab.2015.26

### Examples

```
# import data
data(corals)
data(stages)
```

```

# calculate metrics of diversity dynamics
dd <- divDyn(corals, tax="genus", bin="stg")

# plotting
tsplot(stages, shading="series", boxes="sys", xlim=c(260,0),
       ylab="range-through diversity (genera)", ylim=c(0,230))
lines(stages$mid, dd$divRT, lwd=2)

# with omission of single reference taxa
ddNoSing <- divDyn(corals, tax="genus", bin="stg", om="ref")
lines(stages$mid, ddNoSing$divRT, lwd=2, col="red")

# using the estimated ages (less robust) - 10 million years
# mean ages
corals$me_ma <- apply(corals[, c("max_ma", "min_ma")], 1, mean)
# ages reverse the direction of time! set ages to TRUE in this case
ddRadio10 <- divDyn(corals, tax="genus", bin="me_ma",
breaks=seq(250,0,-10), ages=TRUE)
lines(ddRadio10$bin, ddRadio10$divRT, lwd=2, col="green")

# legend
legend("topleft", legend=c("all", "no single-ref. taxa", "all, estimated ages"),
       col=c("black", "red", "green"), lwd=c(2,2,2), bg="white")

```

---

fadlad

*FAD - LAD matrix from occurrence data*


---

## Description

Function to generate range data from an occurrence dataset.

## Usage

```
fadlad(dat, tax, bin, ages = FALSE, na.rm = TRUE, zerodur = TRUE)
```

## Arguments

dat	(data.frame): Occurrence data.
tax	(character): The column name of taxon names.
bin	(character): The column name of bin variable. If two column names are entered, then they will interpreted as the minimum and maximum age uncertainty. (see examples)
ages	(logical): Are the bin entries ages (reversed time axis)? Setting ages to TRUE will replace the entries in 'bin' column(s) with their additive inverses.

na.rm	(logical): Should taxa that have no valid FADs or LADs (due to only NA entries) be removed from the output?
zerodur	(logical): If set to TRUE, single-interval taxa will 0 durations. Setting this argument to FALSE will add 1 to the durations of all taxa, which can be useful for binned data.

### Details

The function will output First and Last Appearance Data of the taxa in the dataset. Keep in mind that incomplete sampling will influence these data and will make the ranges appear shrunken.

The following variables are produced:

attribute row.names: The names of the taxa.

FAD: First appearance data, given in time slice numbers.

LAD: Last appearance data, given in time slice numbers.

duration: optionally, the duration of taxa in numeric ages. It is given for single-interval taxa as well assuming that the taxa's range span over the entire time slice.

### Examples

```
data(corals)

# binned data
flBinned <- fadlad(corals, tax="genus", bin="stg")

# using basic bin lengths
flDual <- fadlad(corals, tax="genus", bin=c("max_ma", "min_ma"), ages=TRUE)

# single age estimate
data(stages)
corals$mid <- stages$mid[corals$stg]
flSingle <- fadlad(corals, tax="genus", bin="mid", ages=TRUE)
```

---

fill	<i>Filling of missing values in a vector, based on the marginal values of the gaps</i>
------	--

---

### Description

The function will loop through a vector and will substitute NA values with the value it last encountered or replaced.

### Usage

```
fill(x, forward = TRUE, inc = 0)
```

**Arguments**

x	(vector) Vector to be filled.
forward	(logical) Should the loop go forward or backward?
inc	(numeric) Only if x is numeric, the function will increase the substituted value by this amount (useful for filling in sequences).

**Details**

NAs won't be substituted when they are the first values the loop encounters.

**Examples**

```
# forward, replace with previous
dummy<- c(TRUE, FALSE, NA, TRUE, FALSE, NA)
fill(dummy)

# forward, replace with previous+1
dummy2 <- c(1,NA, 3, 1, 2, NA, NA, 9, NA,3)
fill(dummy2, inc=1)

# backward, replace with previous in loop direction
fill(dummy2, inc=0, forward=FALSE)
```

---

georange

*Estimation of geographic ranges from occurrence data*


---

**Description**

Geographic range as a function of a set of coordinates or sample/site/cell memberships.

**Usage**

```
georange(dat, lng = NULL, lat = NULL, loc = NULL, method = "co")
```

**Arguments**

dat	(data.frame) Occurrence table containing the coordinates/locality memberships as variables.
lng	(character) The variable name of the longitudes, required for the "co", "mst" and "mgcd" methods.
lat	(character) The variable name of the latitudes, required for the "co", "mst" and "mgcd" methods.
loc	(character) The variable name of the locality entries: cells, site or samples, required for the "lo" method.



method (character) Geographic range estimator method. Can take multiple entries (concatenating the results in a vector). The following methods are implemented: "co": coordinate-based occupancy, the number of different coordinate pairs; "lo": locality-based occupancy for sites, samples or geographic cells, number of different entries in a variable. "mst", the total length of a minimum spanning tree of the point cloud, based on the great circle distances between points (requires the 'vegan' and 'icsa' packages). "mgcd", maximum great-circle distance that can be measured in the point cloud (this version is limited to half the circumference of the equator, requires the 'icsa' package).

### Details

Multiple estimators of geographic ranges are implemented based on coordinates or cell identifiers. The function outputs a vector of the results based on the calculation methods specified in methods.

### Examples

```
data(corals)
# select a taxon from a certain time slice
bitax <- corals[corals$stg==69 & corals$genus=="Microsolena",]
georange(bitax, lng="paleolng", lat="paleolat", method="co")
```

---

indices

*Scalar indices of diversity*

---

### Description

This function includes some indices that characterize a species-abundance/occurrence distribution.

### Usage

```
indices(x, samp = NULL, method = NULL)
```

### Arguments

x either a character vector of occurrences or a table of counts (*matrix*).

samp (vector): Only applicable if x is vector of occurrence entries. The id of the sampling units. A necessary variable for SCOR.

method (character): The type of metric that is to be calculated. The default value (NULL) will calculate all implemented metrics.

## Details

This set is not complete and does not intend to supercede additional R packages (e.g. `vegan`). However, some metrics are presented here as they are not implemented elsewhere or because they are invoked more frequently. The following entries can be added to the `method` argument of the function, which are also named accordingly in the output table/vector.

"richness": The number of sampled species.

"shannon": The Shannon entropy.

dom: The Berger-Parker dominance index, the proportion of occurrences in the time bin that belong to the most frequent taxon.

"hill2": The second order Hill number (Jost, 2006;  $q=2$ ), which will be calculated by default. You can specify additional Hill numbers with adding "hillXX" to the `method` argument, such as "hill3" for ( $q=3$ ). The first Hill number is defined as the exponential version of Shannon entropy (Eq. 3 in Jost, 2006).

"squares": The 'squares' richness estimator of J. Alroy (2018).

"chao2": The Chao2 estimator for incidence-based data.

"SCOR": The Sum Common Species Occurrence rate of Hannisdal et al. (2012). This method will only be calculated if the occurrences entries (vector) a collection vector is provided (see examples).

## References

Alroy, J. 2018. Limits to species richness in terrestrial communities. *Ecology Letters*.

Hannisdal, B., Henderiks, J., & Liow, L. H. (2012). Long-term evolutionary and ecological responses of calcifying phytoplankton to changes in atmospheric CO<sub>2</sub>. *Global Change Biology*, 18(12), 3504–3516. <https://doi.org/10.1111/gcb.12007>

Jost, L. (2006). Entropy and diversity. *Oikos*, 113, 363–375. <https://doi.org/10.1111/j.2006.0030-1299.14714.x>

## Examples

```
# the coral data
data(corals)

# Pleistocene subset
plei <- corals[corals$stg==94,]

# calculate everything
pleiIndex<-indices(plei$genus, plei$coll)
```

---

keys	<i>Keys to process stratigraphic, environmental and lithological information from the Paleobiology Database</i>
------	---

---

### Description

Lists of entries treated as indicators of similar characteristics

### Usage

keys

### Format

A list of 7 lists:

**binInt** A list of vectors. Entries in the `early_interval` and `late_interval` variables of PaleoDB downloads indicate the collections' positions in the dynamic time scale. These entries were linked to 10 million year-resolution time scale stored in `bins`. These links were compiled using a download from the FossilWorks website (<http://fossilworks.org/>), on 08 June, 2018. You can check the lookup table `stratkeys` here. This is version 0.9.2

**stgInt** A list of vectors. Entries in the `early_interval` and `late_interval` variables of PaleoDB downloads indicate the collections' positions in the dynamic time scale. These entries were linked to stage-resolution time scale stored in `stages`. See `binInt` for version information. These entries are reliable only in the Post-Ordovician!

**reefs** A list of vectors. Entries in the `environment` field of the PaleoDB download indicate information regarding the likely reefal origin of carbonatic rocks. See the vignette ('\$PhaneroCurve') on the exact use of these data. v0.9.

**lith** A list of vectors. Entries in the `lithology1` field of the PaleoDB download indicate information regarding the substrate of the embedding rocks. This key maps the entries to `siliciclastic`, `carbonate` or `unknown` substrates. v0.9.

**lat** A list of vectors. Entries in the `paleolat` field of the PaleoDB download indicate information regarding paleolatitude of the occurrences. This key maps the entries to `tropical` or `non-tropical` latitudes. v0.9.

**grain** A list of vectors. Entries in the `lithology1` field of the PaleoDB download indicate information regarding the grain sizes of the depositional environment. This key maps the entries to `coarse`, `fine` or `unknown` grain sizes. v0.9.

### Details

Entries in the stratigraphic, lithological and environment fields of current Paleobiology Database downloads are too numerous to form the basis of analyses without transformations. This variable includes potential groupings of entries that represent similar characteristics. These objects can be used by the `categorize` function to create new variables of stratigraphic, environmental and lithological information.

**Source**

Stratigraphic assignments are based on the download of collection data from Fossilworks (<http://fossilworks.org/>) and the dynamic time scale of the Paleobiology Database, written by J. Alroy. The assignment of numeric values were done by A. Kocsis. Environmental variables were grouped by W. Kiessling.

---

 modeltab

---

*Origination/extinction response table for statistical modelling.*


---

**Description**

This function takes an occurrence dataset and reformats it to a table that can be used as input for logistic models.

**Usage**

```
modeltab(dat, tax, bin, taxvars = NULL, rt = FALSE,
         singletons = FALSE)
```

**Arguments**

dat	(data.frame) Fossil occurrence table.
tax	(character) Variable name of the occurring taxa (variable type: factor or character - such as "genus")
bin	(character) Variable name of the bin numbers of the occurrences. This variable should be numeric and should increase as time passes by (use negative values for age estimates). The current version only supports discreet, non-negative integer interval numbers.
taxvars	(character) Taxon-specific column names of the variables that should be included in the output table. Only one entry/taxon is used, make sure that the data are clean.
rt	(logical) Should the range-through assumption be applied within the function? If set to TRUE then missing occurrences will be interpolated with FALSE values in both the ext and ori variables. .
singletons	(logical) Should single-interval taxa be removed from the final table? This is recommended, as it is impossible to get a FALSE response for these taxa.

**Details**

Every entry in the output table corresponds to one cell in the bin/tax matrix. This function omits duplicates and concatenates two logical vectors (response variables) to the occurrence dataset: The ori vector is TRUE in the interval when the taxon first appeared, and FALSE in all others. The ext vector is TRUE in the interval the taxon appeared for the last time, and FALSE in the rest.

## Examples

```
# load necessary data
data(corals)
# simple table
modTab<-modeltab(corals, bin="stg", tax="genus", taxvars=c("ecology", "family"))
```

---

omit

*Omission of taxa that have a poor occurrence record*

---

## Description

Function to quickly omit single-collection and single-reference taxa.

## Usage

```
omit(dat, tax = "genus", bin = "bin", coll = "collection_no",
      ref = "reference_no", om = "ref", filterNA = FALSE)
```

## Arguments

dat	(data.frame) Occurrence dataset, with bin, tax and coll as column names.
tax	(character) The name of the taxon variable.
bin	(character) The name of the bin variable (has to be numeric for the function to run). For time series, this is the time slice variable.
coll	(character) The variable name of the collection identifiers.
ref	(character) The variable name of the reference identifiers (optional).
om	(character) The type of omission. "coll" omits occurrences of taxa that occur only in one collection. "ref" omits occurrences of taxa that were described only in one reference. "binref" will omit the set of single reference taxa that were described by more than one references, but appear in only one reference in a time bin.
filterNA	(logical) Additional entries can be added to influence the dataset that might not have reference or collection information (NA entries). These occurrences are treated as single-collection or single-reference taxa if the na.rm argument is set to FALSE (default). Setting this argument to TRUE will keep these entries. (see example)

## Details

The function returns a logical vector, with a value for each row. TRUE values indicate rows to be omitted, FALSE values indicate rows to be kept. The function is embedded in the `divDyn` function, but can be called independently.

## Examples

```
# omit single-reference taxa
data(corals)
data(stages)
toOmit <- omit(corals, bin="stg", tax="genus", om="ref")
dat <- corals[!toOmit,]

# within divDyn
# plotting
tsplot(stages, shading="series", boxes="sys", xlim=c(260,0),
  ylab="range-through diversity (genera)", ylim=c(0,230))
# multiple ref/slice required
ddNoSing <- divDyn(corals, tax="genus", bin="stg", om="binref")
lines(stages$mid, ddNoSing$divRT, lwd=2, col="red")

# with the recent included (NA reference value)
ddNoSingRec <- divDyn(corals, tax="genus", bin="stg",
  om="binref", filterNA=TRUE)
lines(stages$mid, ddNoSingRec$divRT, lwd=2, col="blue")

# legend
legend("topleft", legend=c("no single-ref. taxa",
  "no single-ref. taxa,\n with recent"),
  col=c("red", "blue"), lwd=c(2,2))
```

---

parts

*Plot time series counts or proportions as polygons*

---

## Description

This function plots the changing shares of categories in association with an independent variable.

## Usage

```
parts(x, b = NULL, ord = "up", prop = FALSE, plot = TRUE,
  col = NULL, xlim = NULL, border = NULL, ylim = c(0, 1),
  na.valid = FALSE, labs = T, labs.args = NULL, vertical = FALSE)
```

## Arguments

- x (numeric): The independent variable through which the proportion is tracked. Identical entries are used to assess which values belong together to a set. Their values represent the x coordinate over the plot.
- b (character or factor): A single vector with the category designations. This vector will be segmented using the entries of x.
- ord (character): The parameter of the variable order. Either "up" (increasing alphabetical order), "down" (decreasing alphabetical order) or the vector of categories in the desired order.

prop	(logical): Should the diagram show proportions (TRUE) or counts (FALSE)?
plot	(logical): If set to TRUE, then the function will plot the output. If set to FALSE, then a matrix with the relevant values will be returned. This output is similar to the output of <code>table</code> , but handles proportions instantly.
col	(character): The color of polygons, has to be a vector with as many entries as there are categories in <code>b</code> . By default ( <code>col=NULL</code> ) this is grayscale.
xlim	(numeric): Two values, analogous to the <code>xlim</code> argument of <code>plot</code> , and has to exceed the range of <code>x</code> . The polygons that represent non-zero values with the lowest and highest values of <code>x</code> will be extended to these <code>x</code> coordinates.
border	(character): The a single color of the polygon borders. By default ( <code>border=NA</code> ), no borders are drawn.
ylim	(numeric): If <code>prop=TRUE</code> , then the argument controls the position of the proportions in the plotting area (useful to show proportions as a sub plot in a plot). If <code>prop=FALSE</code> , then the entire plotting area will be shifted by a single <code>ylim</code> value.
na.valid	(logical): If TRUE, then the missing values will be treated as an independent category. Entries where <code>x</code> is NA will be omitted either way.
labs	(logical): Should the category names be plotted?
labs.args	(list): Arguments for the <code>text</code> function. If one entry for each argument is provided, then it will be applied to all labels. If the number of elements in an argument equals the number of categories to be plotted, then one to one assignment will be used. For example, for 4 categories in total, if the <code>labs.args</code> list contains a <code>col</code> vector element with 4 values, see examples).
vertical	(logical): Horizontal or vertical plotting? If FALSE, the independent variable will be horizontal, if TRUE, the count/proportion variable will be horizontal. In the latter case <code>xlim</code> and <code>ylim</code> has reversed roles.

## Details

This function is useful for displaying the changing proportions of a category as time progresses. Check out the examples for the most frequent implementations.

To be added: missing portions are omitted in this version, but should be represented as gaps in the polygons.

## Examples

```
# dummy examples
# independent variable
slc<-c(rep(1, 5), rep(2,7), rep(3,6))

# the categories as they change
v1<-c("a", "a", "b", "c", "c") # 1
v2<-c("a", "b", "b", "b", "c", "d", "d") # 2
v3<-c("a", "a", "a", "c", "c", "d") #3
va<-c(v1, v2,v3)
```

```

# basic function
plot(NULL, NULL, ylim=c(0,1), xlim=c(0.5, 3.5))
parts(slc, va, prop=TRUE)

# vertical plot
plot(NULL, NULL, xlim=c(0,1), ylim=c(0.5, 3.5))
parts(slc, va, col=c("red", "blue", "green", "orange"), xlim=c(0.5,3.5),
      labs=TRUE, prop=TRUE, vertical=TRUE)

# intensive argumentation
plot(NULL, NULL, ylim=c(0,10), xlim=c(0.5, 3.5))
parts(slc, va, ord=c("b", "c", "d", "a"), col=c("red", "blue", "green", "orange"),
      xlim=c(0.5,3.5), labs=TRUE, prop=FALSE,
      labs.args=list(cex=1.3, col=c("black", "orange", "red", "blue")))

# just the values
parts(slc, va, prop=TRUE,plot=FALSE)

# real example
# the proportion of coral occurrences through time in terms of bathymetry
data(corals)
data(stages)

# time scale plot
tsplot(stages, shading="series", boxes="sys", xlim=c(250,0),
       ylab="proportion of occurrences", ylim=c(0,1))

# plot of proportions
cols <- c("#55555588", "#88888888", "#BBBBBB88")
types <- c("uk", "shal", "deep")

parts(x=stages$mid[corals$stg], b=corals$bath,
      ord=types, col=cols, prop=TRUE, border=NA, labs=FALSE)

# legend
legend("left", inset=c(0.1,0), legend=c("unknown", "shallow", "deep"), fill=cols,
      bg="white", cex=1.4)

```

---

ranges

*Plotting ranges and occurrence distributions through time*

---

## Description

Visualization of occurrence data

## Usage

```

ranges(dat, bin = NULL, tax = NULL, xlim = NULL, ylim = c(0, 1),
      total = "", filt = "include", occs = FALSE, labs = FALSE,

```



```
decreasing = TRUE, group = NULL, gap = 0, labels.args = NULL,
ranges.args = NULL, occs.args = NULL, total.args = NULL)
```

### Arguments

<code>dat</code>	( <code>data.frame</code> ): The occurrence dataset or the FAD-LAD dataset that is to be plotted. The FAD dataset must have numeric variables named "FAD" and "LAD". Taxon ranges will be searched for in the <code>row.names</code> attribute of the table.
<code>bin</code>	( <code>character</code> ): The column(s) containing the entries of the time dimension. Use one column name if you have one estimate for the occurrences and use two if you have a minimum and a maximum estimate. Reversed axis (ages) are supported too.
<code>tax</code>	( <code>character</code> ): The column containing the taxon entries.
<code>xlim</code>	( <code>numeric</code> ): This argument is used for the subsetting of the taxa. Only those taxa are shown that have ranges within the interval (but ranges are displayed outside of it, if you do not want to plot anything within an interval, use the <code>clip</code> function)
<code>ylim</code>	( <code>numeric</code> ): Ranges will be distributed equally between the assigned <code>ylim</code> values. If set to <code>NULL</code> , than it will be based on the plotting area of the open device.
<code>total</code>	( <code>character</code> ): The name of the range group to be plotted. When multiple groups are used (see <code>group</code> argument), this is set by the character values in the column.
<code>filt</code>	( <code>character</code> ): When <code>xlim</code> filters the taxa, how should they be filtered. "include" (default) will show all ranges that have parts within the <code>xlim</code> interval. "orig" will show only those taxa that originate within the interval.
<code>occs</code>	( <code>logical</code> ): Should the occurrence data be plotted? If you entered two <code>bin</code> column names, than occurrences will be plotted with the ranges of the estimates (segments).
<code>labs</code>	( <code>character</code> ): Should the taxon labels be plotted?
<code>decreasing</code>	( <code>logical</code> ): This parameter sets whether the series of ranges should start from the top <code>decreasing=TRUE</code> or bottom of the plot <code>decreasing=FALSE</code> .
<code>group</code>	( <code>character</code> ): By default, all ranges in the plot are treated as parts of the same group. However, one subsetting variable can be named, by which the ranges will be grouped. This has to be a column name in the dataset (see examples).
<code>gap</code>	( <code>numeric</code> ): Evaluated only when the <code>group</code> argument points to a valid column. The amount of space between the group-specific range charts, expressed as the proportion of the entire plotting area.
<code>labels.args</code>	( <code>list</code> ): Arguments that will be passed to the <code>text</code> function that draws the labels of taxa. If valid grouping is present (see argument <code>group</code> ), then vector entries will be distributed across the groups (see examples.)
<code>ranges.args</code>	( <code>list</code> ): Arguments that will be passed to the <code>segments</code> function that draws ranges. If valid grouping is present (see argument <code>group</code> ), then vector entries will be distributed across the groups (see examples.)

`occs.args` (list): Arguments that will be passed to the `points` or `segments` functions that draw the occurrence points/lines. If you provided two bin columns, occurrence lines will be drawn instead of points. If valid grouping is present (see argument `group`), then vector entries will be distributed across the groups (see examples.)

`total.args` (list): Arguments that will be passed to the `text` function that draws the total label. If valid grouping is present (see argument `group`), then vector entries will be distributed across the groups (see examples.)

### Details

This function will draw a visual representation of the occurrence dataset. The interpolated ranges will be drawn, as well as the occurrence points.

### Examples

```
# import
data(stages)
data(corals)

# all ranges - using the age uncertainties of the occurrences
tsplot(stages, boxes="sys", xlim=c(250,0))
ranges(corals, bin=c("max_ma", "min_ma"), tax="genus", occs=FALSE)

# or use single estimates: assign age estimates to the occurrences
corals$est<-stages$mid[corals$stg]

# all ranges (including the recent!!)
tsplot(stages, boxes="sys", xlim=c(250,0))
ranges(corals, bin="est", tax="genus", occs=FALSE)

# closing on the Cretaceous, with occurrences
tsplot(stages, boxes="series", xlim=c(145,65), shading="short")
ranges(corals, bin="est", tax="genus", occs=TRUE, ranges.args=list(lwd=0.1))

# z and az separately
tsplot(stages, boxes="series", xlim=c(145,65), shading="short")
ranges(corals, bin="est", tax="genus", occs=FALSE, group="ecology",
  ranges.args=list(lwd=0.1))

# same, show only taxa that originate within the interval
tsplot(stages, boxes="series", xlim=c(105,60), shading="short")
ranges(corals, bin="est", tax="genus", occs=TRUE, group="ecology", filt="orig" ,
  labs=TRUE, labels.args=list(cex=0.5))

# same using the age uncertainties of the occurrence age estimates
tsplot(stages, boxes="series", xlim=c(105,60), shading="short")
ranges(corals, bin=c("max_ma", "min_ma"), tax="genus", occs=TRUE, group="ecology", filt="orig" ,
  labs=TRUE, labels.args=list(cex=0.5))

# fully customized/ annotated
tsplot(stages, boxes="series", xlim=c(105,60), shading="short")
ranges(
```

```

corals, # dataset
bin="est", # bin column
tax="genus", # taxon column
occs=TRUE, # occurrence points will be plotted
group="growth", # separate ranges based on growth types
filt="orig" , # show only taxa that originate in the interval
ranges.args=list(
  lwd=1, # set range width to 1
  col=c("darkgreen", "darkred") # set color of the ranges (by groups)
),
total.args=list(
  cex=2, # set the size of the group identifier labels
  col=c("darkgreen", "darkred") # set the color of the group identifier labels
),
occs.args=list(
  col=c("darkgreen", "darkred"),
  pch=3
),
labs=TRUE, # taxon labels will be plotted
labels.args=list(
  cex=0.4, # the sizes of the taxon labels
  col=c("darkgreen", "darkred") # set the color of the taxon labels by group
)
)

```

---

ratesplit

*Test of rate split (selectivity)*

---

### Description

This function will determine whether there are meaningful differences between the taxonomic rates in the individual time bins of two subsets of an occurrence database.

### Usage

```

ratesplit(dat, sel, tax = "genus", bin = "stg", rate = "pc",
  method = "AIC", AICc = TRUE, na.rm = TRUE, alpha = NULL,
  output = "simple")

```

### Arguments

dat	(data.frame): The fossil occurrence data.
sel	(character): Variable name to do the splitting of the dataset. Can have only two levels.
tax	(character): Variable name of the occurring taxa (variable type: factor or character).

bin	(character): Variable name of the bin numbers of the particular occurrences (numeric). Bin numbers should be in ascending order, can contain NAs, it can start from a number other than 1 and must not start with 0.
rate	(character): The rate metric. Currently only the per capita rates of Foote (1999) are available (rate="pc").
method	(character): Either "AIC", "binom" or "combine". The "AIC" method calculates the Akaike weights of the single and dual rate models. The "binom" method assumes a binomial error distribution of the counts that are necessary for the rate calculations. The "combine" method shows slices that pass both tests, the "AIC" being usually the stronger.
AICc	(logical): Only applicable for the "AIC" method. Toggles whether the small sample corrected AIC (AICc) should be used instead of the regular one.
na.rm	(logical): Argument indicating whether the function should proceed when NAs are found in the sel column. Setting this argument to TRUE will proceed with the omission of these entries, while FALSE will coerce the function to output a single NA value.
alpha	(numeric): Threshold to discriminate between meaningful and meaningless split. If method="AIC", the value corresponds to the minimum weight value the dual model should have. By default it is 0.89, which corresponds to the likelihood ratio of 8. If method="binom", the value corresponds to the alpha value of the binomial test (default: 0.05). If method="combine" then two alpha values are required (1st for the AIC, 2nd for the binomial test). If alpha is NULL, then the default values will be used.
output	(character): Either "simple" or "full". "simple" returns the indices of the series where selectivity can be suggested. "full" returns a matrix of Akaike weights, or binomial probabilities.

## Details

Splitting an occurrence database to its subsets decreases the amount of information passed to the rate calculations and therefore the precision of the individual estimates. Therefore, our ability to tell apart two similar values decreases with the number of sampled taxa. In order to assess the subsets individually and compare them, it is advised to test whether the split into two subsets is meaningful, given the total data. Examples of this use can be found in Kiessling and Simpson (2011) and Kiessling and Kocsis (2015). The meaningfulness of the split is dependent on the estimate accuracy and the magnitude of the difference. Two different methods are implemented: `binom` and `combine`.

## References

- Foote, M. (1999) Morphological Diversity In The Evolutionary Radiation Of Paleozoic and Post-Paleozoic Crinoids. *Paleobiology* 25, 1–115. doi:10.1017/S0094837300020236.
- Kiessling, W., & Simpson, C. (2011). On the potential for ocean acidification to be a general cause of ancient reef crises. *Global Change Biology*, 17(1), 56-67.
- Kiessling, W., & Kocsis, A. T. (2015). Biodiversity dynamics and environmental occupancy of fossil azooxanthellate and zooxanthellate scleractinian corals. *Paleobiology*, 41(3), 402-414.

**Examples**

```

# example with the coral dataset of Kiessling and Kocsis (2015)
data(corals)
data(stages)

# split by ecology
z<-corals[corals$ecology=="z",]
az<-corals[corals$ecology=="az",]

# calculate diversity dynamics
ddZ<-divDyn(z, tax="genus", bin="stg")
ddAZ<-divDyn(az, tax="genus", bin="stg")

# origination rate plot
tsplot(stages, boxes="sys", shading="series", xlim=54:95,
  ylab="raw per capita originations")
lines(stages$mid, ddZ$oriPC, lwd=2, lty=1, col="blue")
lines(stages$mid, ddAZ$oriPC, lwd=2, lty=2, col="red")
legend("topright", inset=c(0.1,0.1), legend=c("z", "az"),
  lwd=2, lty=c(1,2), col=c("blue", "red"), bg="white")

# The ratesplit function
rs<-ratesplit(rbind(z, az), sel="ecology", tax="genus", bin="stg")
rs

# display selectivity with points
# select the higher rates
selIntervals<-cbind(ddZ$oriPC[rs$ori], ddAZ$oriPC[rs$ori])
groupSelector<-apply(selIntervals, 1, function(x) x[1]<x[2])
# draw the points
points(stages$mid[rs$ori[groupSelector]], ddAZ$oriPC[rs$ori[groupSelector]],
  pch=16, col="red", cex=2)
points(stages$mid[rs$ori[!groupSelector]], ddZ$oriPC[rs$ori[!groupSelector]],
  pch=16, col="blue", cex=2)

```

---

seqduplicated

*Determination and omission of consecutive duplicates in a vector.*


---

**Description**

seqduplicated() The function determines which elements of a vector are duplicates (similarly to [duplicated](#)) in consecutive rows.

collapse() Omits duplicates similarly to [unique](#), but only in consecutive rows, so the sequence of state changes remains, but without duplicates.

**Usage**

```
seqduplicated(x, na.rm = FALSE, na.breaks = TRUE)
```

```
collapse(x, na.rm = FALSE, na.breaks = TRUE)
```

**Arguments**

x	(vector): input object.
na.rm	(logical): Are NA entries to be treated as duplicates (TRUE) or just like a normal value (FALSE)?
na.breaks	(logical): If na.rm=TRUE and the NA values are surrounded by the same values, should the streak be treated as broken? Running seqduplicated(, na.rm=TRUE) on (2, 1, NA, 1) while setting na.breaks to TRUE will return (FALSE, FALSE, TRUE, FALSE), and with TRUE it will return (FALSE, FALSE, TRUE, TRUE). The results with the same argumentation of collapse() will be (2, 1) and (2, 1, 1).

**Details**

These functions are essentially about checking whether a value in a vector at index is the same as the value at the previous index. This seemingly primitive task had to be rewritten with Rcpp for speed and the appropriate handling of NA values.

**Examples**

```
# example vector
examp <- c(4,3,3,3,2,2,1,NA,3,3,1,NA,NA,5, NA, 5)

# seqduplicated()
seqduplicated(examp)

# contrast with
duplicated(examp)

# with NA removal
seqduplicated(examp, na.rm=TRUE)

# the same with collapse()
collapse(examp)

# contrast with
unique(examp)

# with NA removal
collapse(examp, na.rm=TRUE)

# with NA removal, no breaking
collapse(examp, na.rm=TRUE, na.breaks=FALSE)
```

---

shades *Quantile plot of time series*

---

**Description**

This intermediate-level function will plot a time series with the quantiles shown with transparency values.

**Usage**

```
shades(x, y, col = "black", res = 10, border = NA,
       interpolate = FALSE, method = "symmetric", na.rm = FALSE)
```

**Arguments**

x	(numeric): The x coordinates.
y	(numeric matrix): The series of distributions to be plotted. Every row represents a distribution of values. The number of rows must equal to the length of x.
col	(character): The color of the quantiles, currently just a single color is allowed.
res	(numeric): If a single value is entered, than this argument represents the number of quantiles to be shown (coerced to 150, if higher is entered). If it is vector of values, it will be interpreted as the vector of quantiles to be shown. If method="symmetric", only an odd number of quantiles are plotted.
border	(character): The color of the quantile lines. A single value, by default, no lines are drawn (border=NA).
interpolate	(logical): In case the symmetric method is chosen, the series of quantile values can be interpolated with a LOESS function.
method	(character): The default "symmetric" method will plot the mid quantile range with highest opacity and the shades will be more translucent at the tails of the distributions. The "decrease" method will decrease the opacity with higher quantiles, which can make more sense for bottom-bounded distributions (e.g. exponential).
na.rm	(logical): If set to FALSE, than rows that are missing from the dataset will be plotted as gaps in the shading. If set to TRUE, than these gaps will be skipped.

**Examples**

```
# some random values accross the Phanerozoic
data(stages)
tsplot(stages, boxes="sys", shading="series", ylim=c(-5,5), ylab=c("normal distributions"))
  randVar <- t(sapply(1:95, FUN=function(x){rnorm(150, 0,1)}))
  shades(stages$mid, randVar, col="blue", res=10,method="symmetric")

# a bottom-bounded distribution (log normal)
tsplot(stages, boxes="sys", shading="series", ylim=c(0,30), ylab="log-normal distributions")
```

```
randVar <- t(sapply(1:95, FUN=function(x){rlnorm(150, 0,1)}))
shades(stages$mid, randVar, col="blue", res=c(0,0.33, 0.66, 1),method="decrease")
```

---

singletons

*List of singleton taxa*


---

## Description

The function returns lists of taxa that occur with only one particular entry in a given variable.

## Usage

```
singletons(dat, tax = "clgen", var = NULL, bin = NULL,
  bybin = FALSE, na.rm = TRUE)
```

## Arguments

dat	(data.frame): Occurrence dataset, with bin, tax and coll as column names.
tax	(character): The name of the taxon variable.
var	(character): The variable that is used to define singletons. Use the reference variable for single-reference taxa, and the collection variable for single-collection taxa, the bin identifier for single-interval taxa and so forth. If you set this to the default NULL, the function will return single-occurrence taxa.
bin	(character): Lists of taxa can be tabulated in every bin. Rows with NA entries in this column will be omitted.
bybin	(logical): The type of the filtering process. Was it supposed to be applied to bin-specific subsets (TRUE), or the whole data (FALSE)? Setting this argument to TRUE will return a list class object, where every element of the list is a bin-specific character vector. This setting also removes all NA entries from bin variable.
na.rm	(logical): If var is not NULL, setting this argument to TRUE removes all rows where var is NA. Otherwise these will be returned as singletons.

## Details

Singletons are defined in number of ways in the literature. True singletons are species that are represented by only one specimen, but one can talk about single-occurrence, single-interval, single-reference or single collection taxa as well. These can be returned with this function.

As the time bin has particular importance, it is possible to filter singleton taxa in the context of a single bin. These can be returned with the bybin argument, that constrains and iterates the filtering to every bin. If this argument is set to TRUE and the variable in question is a references, than single-reference taxa will be taxa that occurred in only one reference within each bin - it does not necessarily mean that only one reference describes the taxon in the total database!



**Examples**

```

# load example dataset
data(corals)

# Example 1. single-occurrence taxa
singOcc <- singletons(corals, tax="genus", bin="stg")

# Example 2. output for every bin
singOccBin <- singletons(corals, tax="genus", bin="stg", bybin=TRUE)

# Example 3. single-interval taxa (all)
singInt <- singletons(corals, tax="genus", var="stg")

# Example 4. single interval taxa (for every bin)
singIntBin <- singletons(corals, tax="genus", var="stg", bin="stg", bybin=TRUE)

# Example 5. single reference taxa (total dataset)
singRef <- singletons(corals, tax="genus", var="reference_no")

# Example 6. single reference taxa (see description for differences )
singRefBin <- singletons(corals, tax="genus", var="reference_no", bin="stg", bybin=TRUE)

```

---

stages	<i>95 bin Phanerozoic time scale based on the stratigraphic stages of Ogg et al. (2016).</i>
--------	--

---

**Description**

Stage-level (age-level) timescale used in some analyses.

**Usage**

stages

**Format**

A data frame with 95 observations and 10 variables:

sys Abbreviations of geologic systems.

system Geologic periods.

series Geologic series.

stage Names of geologic stages.

short Abbreviations of geologic stages.

bottom Numeric ages of the bottoms boundaries (earliest ages) of the bins.

mid Numeric age midpoints of the bins, the averages of bottom and top.

top Numeric ages of the tops (latest ages) of the bins.  
 dur Numeric ages of the durations for the bins.  
 stg Integer number identifiers of the bins.  
 systemCol Hexadecimal color code of the systems.  
 seriesCol Hexadecimal color code of the series.  
 col Hexadecimal color code of the stages.

### Details

This is an example time scale object that can be used in the Phanerozoic-scale analyses. Example occurrence datasets related to the package use the variable `stg` when referring to this timescale.

### References

Ogg, J. G., G. Ogg, and F. M. Gradstein. 2016. A concise geologic time scale: 2016. Elsevier.

### Source

Based on Ogg et al. (2016), compiled by Wolfgang Kiessling.

---

stratkeys	<i>The FossilWorks-based lookup table for the stratigraphic assignments of collections in the Paleobiology Database</i>
-----------	---

---

### Description

Table including the user-chosen interval data and the stratigraphic units of the dynamic timescale.

### Usage

stratkeys

### Format

A data.frame with 761 observations of 8 variables:

interval The names of the registered intervals in the early\_interval/max\_interval and late\_interval/min\_interval columns.  
 period The period containing the interval.  
 epoch The epoch containing the interval.  
 X10\_my\_bin The 10 million year time scale interval containing the interval.  
 bin Numeric identifier of the 10 million year interval in the `bins` object.  
 stage The stage containing the interval.  
 stg Numeric identifier of the interval in the stage-level time scale provided as `stages` object.

## Details

Since the separation of the FossilWorks (<http://fossilworks.org/>) portal from the Paleobiology Database (<http://www.paleobiodb.org/>) the access to the stratigraphic information in the database have been problematic. This table includes groupings of `early_interval`/`max_interval` entries of the dynamic timescale that users can choose during collection entry. The table assigns these intervals to some corresponding stratigraphic units from different time scales. These entries were distilled from those collections that only have a `max_interval` value. As there is a mismatch between the data Paleobiology Database and FossilWorks this list is not comprehensive and a couple entries are probably missing. For this reason, this dataset is expected to be updated in the future.

This particular version (v0.9.2) is based on a download of all collections in FossilWorks between the Ediacaran and the Holocene. The download took place on 22 June, 2018. The entries were transformed to `keys` to be used with the `categorize` function. Some entries were corrected manually.

## Source

<http://fossilworks.org/>

---

streaklog	<i>Utility functions for slicing gappy time series</i>
-----------	--

---

## Description

The function returns where the continuous streaks start and how long they are, which can be used for efficient and flexible subsetting.

## Usage

```
streaklog(x)
```

```
whichmaxstreak(x, which = -1)
```

## Arguments

<code>x</code>	(vector) A vector with missing values.
<code>which</code>	(integer) In case multiple streaks of the same length are found, which of them should be returned by the vector (integer).

## Details

The output list of `streaklog` contains the following elements:

`starts`: the indices where the streaks start.

`streaks`: the lengths of the individual streaks (number of values).

`runs`: the number of streaks.

The function `whichmaxstreak()` will return the indices of those values that are in the longest continuous streak.

## Examples

```
# generate a sequence of values
b<-40:1
# add some gaps
b[c(1:4, 15, 19, 23:27)] <- NA
# the functions
streaklog(b)
whichmaxstreak(b)
```

---

subsample

*Serial subsampling wrapper function*


---

## Description

The function will take a desired function that has an occurrence dataset as an argument, and reruns it iteratively on the subsets of the dataset.

## Usage

```
subsample(dat, q, tax = "genus", bin = "stg", FUN = divDyn,
  coll = NULL, ref = NULL, iter = 50, type = "cr", keep = NULL,
  rem = NULL, duplicates = TRUE, output = "arit",
  useFailed = FALSE, ...)
```

## Arguments

dat	(data.frame): Occurrence dataset, with bin, tax and coll as column names.
q	(numeric): Subsampling level argument (mandatory). Depends on the subsampling function, it is the number of occurrences for "cr", and the number of desired occurrences to the power of x for $O^xW$ . It is also the quorum of the SQS method.
tax	(character): The name of the taxon variable.
bin	(character): The name of the subsetting variable (has to be integer). For time series, this is the time-slice variable. Rows with NA entries in this column will be omitted.
FUN	(function): The function to be iteratively executed on the results of the subsampling trials. If set to NULL, no function will be executed, and the subsampled datasets will be returned as a list. By default set to the <a href="#">divDyn</a> function. The function must have an argument called dat, that represents the dataset resulting from a subsampling trial (or the entire dataset). Arguments of the subsample function call will be searched for potential arguments of this function, which means that already provided variables (e.g. bin and tax) will also be used. You can also provide additional arguments (similarly to the <a href="#">apply</a> iterator). Functions that allow arguments to pass through (that have argument '...') are not allowed, as well as functions that have the same arguments as subsample but would require different values.

coll	(character): The variable name of the collection identifiers.
ref	(character): The name of the reference variable, optional - depending on the subsampling method.
iter	(numeric): The number of iterations to be executed.
type	(character): The type of subsampling to be implemented. By default this is classical rarefaction ("cr"). ("oxw") stands for occurrence weighted by-list subsampling. If set to ("sqs"), the program will execute the shareholder quorum subsampling algorithm as it was suggested by Alroy (2010). Setting the argument to "none" will invoke no subsampling, but the applied function will be iterated on the trials, nevertheless.
keep	(numeric): The bins, which will not be subsampled but will be added to the subsampling trials. NIf the number of occurrences does not reach the subsampling quota, by default it will not be represented in the subsampling trials. You can force their inclusion with the keep argument separately (for all, see the useFailed argument).
rem	(numeric): The bins, which will be removed from the dataset before the subsampling trials.
duplicates	(logical ): Toggles whether multiple entries from the same taxon ("tax") and collection ("coll") variables should be omitted. Useful for omitting occurrences of multiple species-level occurrences of the same genus. By default these are allowed through analyses (duplicates=TRUE), setting this to FALSE will require you to provide a collection variable. (coll)
output	(character): If the function output are vectors or matrices, the "arit" and "geom" values will trigger simple averaging with arithmetic or geometric means. If the function output of a single trial is again a vector or a matrix, setting the output to "dist" will return the calculated results of every trial, organized in a list of independent variables (e.g. if the function output is value, the return will contain a single vector, if it is a vector, the output will be a list of vectors, if the function output is a data.frame, the output will be a list of matrix class objects). If output="list", the structure of the original function output will be retained, and the results of the individual trials will be concatenated to a list.
useFailed	(logical): If the bin does not reach the subsampling quota, should the bin be used?
...	arguments passed to FUN and the type-specific subsampling functions: <a href="#">subtrialCR</a> , <a href="#">subtrialOXW</a> , <a href="#">subtrialSQS</a>

## Details

The `subsample` function implements the iterative framework of the sampling standardization procedure. The function 1. takes the dataset `dat`, 2. runs function `FUN` on the dataset and creates a container for results of trials 3. runs one of the subsampling trial functions (e.g. [subtrialCR](#)) to get a subsampled 'trial dataset' 4. runs `FUN` on the trial dataset and 5. averages the results of the trials. For a detailed treatment on what the function does, please see the vignette ('Handout to the R package 'divDyn' v0.5.0 for diversity dynamics from fossil occurrence data'). Currently the Classical Rarefaction ("cr", Raup, 1975), the occurrence weighted by-list subsampling ("oxw", Alroy et al., 2001) and the Shareholder Quorum Subsampling methods are implemented ("sqs", Alroy, 2010).

**References:**

Alroy, J., Marshall, C. R., Bambach, R. K., Bezusko, K., Foote, M., Fürsich, F. T., ... Webber, A. (2001). Effects of sampling standardization on estimates of Phanerozoic marine diversification. *Proceedings of the National Academy of Science*, 98(11), 6261-6266.

Alroy, J. (2010). The Shifting Balance of Diversity Among Major Marine Animal Groups. *Science*, 329, 1191-1194. <https://doi.org/10.1126/science.1189910>

Raup, D. M. (1975). Taxonomic Diversity Estimation Using Rarefaction. *Paleobiology*, 1, 333-342. <https://doi.org/10.2307/2400135>

**Examples**

```

data(corals)
data(stages)
# Example 1-calculate metrics of diversity dynamics
dd <- divDyn(corals, tax="genus", bin="stg")
rarefDD<-subsample(corals,iter=50, q=50,
tax="genus", bin="stg", output="dist", keep=95)

# plotting
tsplot(stages, shading="series", boxes="sys", xlim=c(260,0),
ylab="range-through diversity (genera)", ylim=c(0,230))
lines(stages$mid, dd$divRT, lwd=2)
shades(stages$mid, rarefDD$divRT, col="blue")
legend("topleft", legend=c("raw","rarefaction"),
col=c("black", "blue"), lwd=c(2,2), bg="white")

# Example 2-SIB diversity
# draft a simple function to calculate SIB diversity
sib<-function(dat, bin, tax){
  calc<-tapply(INDEX=dat[,bin], X=dat[,tax], function(y){
    length(levels(factor(y)))
  })
  return(calc[as.character(stages$stg)])
}
sibDiv<-sib(corals, bin="stg", tax="genus")

# calculate it with subsampling
rarefSIB<-subsample(corals,iter=50, q=50,
tax="genus", bin="stg", output="arit", keep=95, FUN=sib)
rarefDD<-subsample(corals,iter=50, q=50,
tax="genus", bin="stg", output="arit", keep=95)

# plot
tsplot(stages, shading="series", boxes="sys", xlim=c(260,0),
ylab="SIB diversity (genera)", ylim=c(0,230))

lines(stages$mid, rarefDD$divSIB, lwd=2, col="black")

```

```

lines(stages$mid, rarefSIB, lwd=2, col="blue")

# Example 3 - different subsampling types with default function (divDyn)
# compare different subsampling types
# classical rarefaction
cr<-subsampling(corals,iter=50, q=20,tax="genus", bin="stg", output="dist", keep=95)
# by-list subsampling (unweighted) - 3 collections
UW<-subsampling(corals,iter=50, q=3,tax="genus", bin="stg", coll="collection_no",
  output="dist", keep=95, type="oxw", x=0)
# occurrence weighted by list subsampling
OW<-subsampling(corals,iter=50, q=20,tax="genus", bin="stg", coll="collection_no",
  output="dist", keep=95, type="oxw", x=1)

SQS<-subsampling(corals,iter=50, q=0.4,tax="genus", bin="stg", output="dist", keep=95, type="sqs")

# plot
tsplot(stages, shading="series", boxes="sys", xlim=c(260,0),
  ylab="range-through diversity (genera)", ylim=c(0,100))
shades(stages$mid, cr$divRT, col="red")
shades(stages$mid, UW$divRT, col="blue")
shades(stages$mid, OW$divRT, col="green")
shades(stages$mid, SQS$divRT, col="cyan")

legend("topleft", bg="white", legend=c("CR (20)", "UW (3)", "OW (20)", "SQS (0.4)"),
  col=c("red", "blue", "green", "cyan"), lty=c(1,1,1,1), lwd=c(2,2,2,2))

```

---

subtrialCR

*Subsampling trial functions*


---

## Description

These functions create one subsampling trial dataset with a desired subsampling method

## Usage

```
subtrialCR(dat, bin, q, unit = NULL, keep = NULL, useFailed = FALSE,
  showFailed = FALSE)
```

```
subtrialOXW(dat, bin, q, coll, x = 1, keep = NULL, useFailed = FALSE,
  showFailed = FALSE)
```

```
subtrialSQS(dat, bin, tax, q, coll = NULL, ref = NULL,
  singleton = "occ", excludeDominant = FALSE, largestColl = FALSE,
  fcorr = "good", byList = FALSE, keep = NULL, useFailed = FALSE,
  showFailed = FALSE, appr = "under")
```

**Arguments**

<code>dat</code>	( <code>data.frame</code> ): Occurrence dataset, with <code>bin</code> , <code>tax</code> and <code>coll</code> as column names.
<code>bin</code>	( <code>character</code> ): The name of the subsetting variable (has to be integer). For time series, this is the time-slice variable. Rows with NA entries in this column will be omitted.
<code>q</code>	( <code>numeric</code> ): Subsampling level argument (mandatory). Depends on the subsampling function, it is the number of occurrences for "cr", and the number of desired occurrences to the power of $x$ for $O^xW$ . It is also the quorum of the SQS method.
<code>unit</code>	( <code>character</code> ): Argument of the CR subsampling type. The name of the variable that designates the subsampling units. In every bin, CR selects a certain number (quota) of entries from the dataset. By default ( <code>unit=NULL</code> ), the units will be the rows, and the <code>q</code> number of rows will be selected in each bin. However, this can be a higher level category that has multiple entries in the each bin. If <code>unit</code> is a valid column of the dataset <code>dat</code> , then CR will select <code>q</code> number entries in this variable, and will return all the corresponding rows.
<code>keep</code>	( <code>numeric</code> ): The bins, which will not be subsampled but will be added to the subsampling trials. NIf the number of occurrences does not reach the subsampling quota, by default it will not be represented in the subsampling trials. You can force their inclusion with the <code>keep</code> argument separately (for all, see the <code>useFailed</code> argument).
<code>useFailed</code>	( <code>logical</code> ): If the bin does not reach the subsampling quota, should the bin be used?
<code>showFailed</code>	( <code>logical</code> ): Toggles the output of the function. If set to <code>TRUE</code> the output will be a list, including both the default output (logical vector of rows) and the <code>numeric</code> vector of bins that did not have enough entries to reach the quota <code>q</code> .
<code>coll</code>	( <code>character</code> ): The variable name of the collection identifiers.
<code>x</code>	( <code>numeric</code> ): Argument of the $OxW$ type. The exponent of by-list subsampling, by default it is 1.
<code>tax</code>	( <code>character</code> ): The name of the taxon variable.
<code>ref</code>	( <code>character</code> ): The name of the reference variable, optional - depending on the subsampling method.
<code>singleton</code>	( <code>character</code> ): A parameter of SQS. Either "ref", "occ" or <code>FALSE</code> . If set to "occ", the coverage estimator (e.g. Good's $u$ ) will be calculated based on the number of single-occurrence taxa. If set to "ref" the number of occurrences belonging to single-reference taxa will be used instead. In case of the inexact algorithm, if set to <code>FALSE</code> then coverage corrections of frequencies will not be applied.
<code>excludeDominant</code>	( <code>logical</code> ): Argument of SQS. This parameter sets whether the dominant taxon should be excluded from all calculations involving frequencies (this is the second correction of Alroy, 2010).
<code>largestColl</code>	( <code>logical</code> ): Parameter of SQS. This parameter sets whether the occurrences of taxa only ever found in the most diverse collection should be excluded from the



	count of single-publication occurrences. (this is the third correction of Alroy, 2010) Note that largestColl=TRUE is dependent on excludeDominant=TRUE. Setting excludeDominant to FALSE will turn this correction off.
fcorr	(character): Parameter for the inexact method of SQS. either "good" or "alroy". This argument changes the frequency correction procedure of the 'inexact' version of SQS (Alroy 2010). As not all taxa are present in the samples, the sampled frequencies of taxa tend overestimate their frequencies in the sampling pool. In Alroy (2010) these are corrected using Good's u ("good", default), in the later versions of SQS this metric is changed to a different method using single occurrence and double occurrence taxa ("alroy").
byList	(character): A parameter of the "inexact" method of SQS. Sets whether occurrences should be subsampled with (FALSE) or without (TRUE) breaking the collection integrity.
appr	(character): A parameter of the inexact method of SQS. Either "over" (default) or ("under"). The current version is not concerned with small fluctuations around the drawn subsampling quorum. Therefore, in the inexact algorithm, sampling is finished when the subset either is immediately below the quorum ("under") or above it ("over").

## Details

The essence of these functions are present within the subsampling wrapper function `subsample`. Each function implements a certain subsampling type. The return value of the functions by default is a logical vector indicating which rows of the original dataset should be present in the subsample. The inexact method for SQS is implemented here as it is computationally less demanding.

### References:

Alroy, J., Marshall, C. R., Bambach, R. K., Bezusko, K., Foote, M., Fürsich, F. T., ... Webber, A. (2001). Effects of sampling standardization on estimates of Phanerozoic marine diversification. *Proceedings of the National Academy of Science*, 98(11), 6261-6266.

Alroy, J. (2010). The Shifting Balance of Diversity Among Major Marine Animal Groups. *Science*, 329, 1191-1194. <https://doi.org/10.1126/science.1189910>

Raup, D. M. (1975). Taxonomic Diversity Estimation Using Rarefaction. *Paleobiology*, 1, 333-342. <https://doi.org/10.2307/2400135>

## Examples

```
#one classical rarefaction trial
data(corals)
# return 5 references for each stage
bRows<-subtrialCR(corals, bin="stg", unit="reference_no", q=5)
# control
unCor<-unique(corals[bRows,c("stg", "reference_no")])
table(unCor$stg)
# classical rarefaction can also be used to do by reference subsampling of collections
fossils <- corals[corals$stg!=95, ]
# rows in the sampling standardization
threeCollPerRef <- subtrialCR(dat=fossils, unit="collection_no",
  bin="reference_no", q=3, useFailed=TRUE)
```

```
# check: table of collections/references in the new subset (with failed!!)
crosstab<-unique(fossils[threeCollPerRef,c("collection_no", "reference_no")])
table(crosstab$reference_no)
```

---

sumstat

*Occurrence database summary*


---

## Description

The function calculates global statistics of the entire database

## Usage

```
sumstat(dat, tax = "genus", bin = "stg", coll = NULL, ref = NULL,
        duplicates = NULL)
```

## Arguments

dat	(data.frame): The occurrence dataset.
tax	(character): The column name of taxon names.
bin	(character): The column name of bin names.
coll	(character): The column name of collection numbers. (optional)
ref	(character): The column name of reference numbers. (optional)
duplicates	(logical): The function will check whether there are duplicate occurrences (multiple species/genera). When set to NULL, nothing will happen, but the function will notify you if duplicates are present. If set to TRUE, the function will not do anything with these, if set to FALSE, the duplicates will be omitted.

## Details

The function returns the following values.

bins: The total number of bins sampled.

occs: The total number of sampled occurrences.

colls: The total number of sampled collections.

refs: The total number of sampled references.

taxa: The total number of sampled taxa.

gappiness: The proportion of sampling gaps in the ranges of the taxa (without the range-endpoints).

## Examples

```
data(corals)
sumstat(corals, tax="genus", bin="stg", coll="collection_no", ref="reference_no")
```

---

survivors *Proportions of survivorship*

---

### Description

This function will calculate both forward and backward survivorship proportions from a given occurrence dataset or FAD-LAD matrix.

### Usage

```
survivors(dat, tax = "genus", bin = "stg", method = "forward",
          noNAstart = FALSE, fl = NULL)
```

### Arguments

dat	(data.frame) The data frame containing fossil occurrences.
tax	(character) The variable name of the occurring taxa (variable type: factor or character).
bin	(character) The variable name of the time slice numbers of the particular occurrences (variable type: numeric). Bin numbers should be in ascending order, can contain NAs, it can start from a number other than 1 and must not start with 0.
method	(character) Either "forward" or "backward".
noNAstart	(logical) Useful when the dataset does not start from bin 1. Then noNAstart=TRUE will cut the first part of the resulting table, so the first row will contain the estimates for the lowest bin number.
fl	(matrix or data.frame). If so desired, the function can be run on an FAD-LAD dataset, output by the <a href="#">fadlad</a> function.

### Details

Proportions of survivorship are great tools to visualize changes in the composition of a group over time (Raup, 1978). The curves show how a once coexisting set of taxa, called a cohort, loses its participants (forward survivorship) as time progress, or gains its elements as time is analyzed backwards. Each value corresponds to a cohort in a bin (*a*) and one other bin (*b*). The value expresses what proportion of the analyzed cohort (present together in bin *a*) is present in bin *b*.

References:

Raup, D. M. (1978). Cohort analysis of generic survivorship. *Paleobiology*, 4(1), 1-15.

### Examples

```
data(corals)
surv<-survivors(corals, tax="genus", bin="stg", method="forward")

# plot
```

```

data(stages)
tsplot(stages, shading="series", boxes="sys", xlim=c(260,0),
       ylab="proportion of survivors present", ylim=c(0.01,1),plot.args=list(log="y"))

for(i in 1:ncol(surv)) lines(stages$mid, surv[,i])

```

---

tabinate

*Apply function to TAXON/BIN subset of occurrences and iterATE*


---

### Description

The function takes another function and reruns it on every taxon- and/or bin-specific subsets of an occurrence dataset.

### Usage

```
tabinate(dat, bin = NULL, tax = NULL, FUN = NULL, ...)
```

### Arguments

dat	(data.frame) Fossil occurrence table.
bin	(character) Variable name of the bin numbers of the occurrences. This variable should be numeric.
tax	(character) Variable name of the occurring taxa (variable type: factor or character - such as "genus")
FUN	(function) The function applied to the subset of occurrences. The subset of occurrence data will be passed to this function as dat.
...	arguments passed to FUN

### Details

The main tabinate function acts as a wrapper for any type of function that requires a subset of the occurrence dataset that represents either one bin or one tax entry or both. For example, the iterator can be used to calculate geographic ranges from occurrence coordinates (georange).

The output structure of FUN should be independent from the input subset, or the function will return an error. Setting both bin If bin=NULL and codetax=NULL, will run FUN on the entire dataset (no effect). Providing either bin or tax and keeping the other NULL will iterate FUN for every bin or tax entry (whichever is presented). The function returns a vector of values if the return value of FUN is a single value. In case it is a vector, the final output will be a matrix. When both bin and tax is presented, the function output will be a matrix (one output value for a taxon/bin subset) or an array (3d, when FUN returns a vector). Setting FUN to NULL will return the occurrence dataset as lists.

**Examples**

```

data(corals)

# the number of different coordinate pairs in every time slice
tabinate(corals, bin="stg", FUN=georange, lat="paleolat",
         lng="paleolng", method="co")
# geographic range (site occupancy) of every taxon in every bin
tabinate(corals, bin="stg", tax="genus", FUN=georange,
         lat="paleolat", lng="paleolng", method="co")

```

---

tsplot

*Time series plotting using a custom time scale*


---

**Description**

This function allows the user to quickly plot a time scale data table

**Usage**

```

tsplot(tsdat, ylim = c(0, 1), xlim = NULL, prop = 0.05, gap = 0,
       bottom = "bottom", top = "top", xlab = "age (Ma)", ylab = "",
       boxes = NULL, boxes.col = NULL, shading = NULL,
       shading.col = c("white", "gray80"), plot.args = NULL,
       boxes.args = NULL, labels = TRUE, labels.args = NULL,
       lplab = TRUE, rplab = TRUE)

```

**Arguments**

tsdat	(data frame): The time scale data frame.
ylim	(numeric): The vertical extent of the plot, analogous to the same argument of <a href="#">plot</a> . By default it is set to the $[0, 1]$ interval.
xlim	(numeric): The horizontal extent of the plot, analogous to the same argument of <a href="#">plot</a> . By default it is set to plot the entire table. If a numeric vector with two values is supplied, it will be interpreted as the standard <code>xlim</code> argument and the plot will be displayed based on numerically constrained ages. If it is an integer vector with more than two values are plotted, the interval corresponding to the row indices of the table will be plotted.
prop	(numeric): Proportion of the vertical extent of the plot to display the the time scale at the bottom.
gap	(numeric): Proportion of the vertical extent of the plot that should be a gap between the time scale and the plot.
bottom	(character): Column name of the table for the variable that contains the older ages of intervals.
top	(character): Column name of the table for the variable that contains the earliest ages of intervals.

xlab	(character): The label of the time axis.
ylab	(character): The label of the data axis.
boxes	(character): Column name indicating the names that should be plotted as boxes of the timescale.
boxes.col	(character): Column name of the colour codes for the boxes. Each entry in this column has to correspond to an entry in the boxes column. It also overrides the col entries in the boxes.args argument.
shading	(character): Column name used for the shading. By default, no shading will be drawn (shading = NULL).
shading.col	(character): Colors that will be used for the shading, if shading is set. It is either a single column of the tsdat object with color codes, or multiple color entries. The provided colors will be repeated as many times as necessary.
plot.args	(list): Arguments that will be passed to the main plot function. Can be useful for the suppression of axes, font change etc.
boxes.args	(list): Arguments that will be passed to the rect function that draws the rectangles of time intervals.
labels	(logical): Should the labels within the boxes be drawn? Setting this argument to FALSE will not call the text function that draws the labels.
labels.args	(list): Arguments that will be passed to the text function that draws the labels. Can be lists of lists if multiple series of “boxes“ are used.
lplab	logical: When the left boundary of the plot does not match with any of the boundaries of the time scale boxes (and labels=TRUE), should the label of the partially drawn box be plotted?
rplab	logical: When the right boundary of the plot does not match with any of the boundaries of the time scale boxes (and labels=TRUE), should the label of the partially drawn box be plotted?

## Details

As most analysis use an individually compiled time scale object, in order to ensure compatibility between the analyzed and plotted values, the time scale table used for the analysis could be plotted rather than a standardized table. Two example tables have been included in the package ([stages](#) and [bins](#)) that can serve as templates.

## Examples

```
data(stages)
  tsplo(stages, boxes="sys", shading="series")
# same with colours
  tsplo(stages, boxes="sys", shading="series", boxes.col="systemCol")

# only the Mesozoic, custom axes
  tsplo(stages, boxes="system", shading="stage", xlim=52:81,
    plot.args=list(axes=FALSE, main="Mesozoic"))
  axis(1, at=seq(250, 75, -25), labels=seq(250, 75, -25))
  axis(2)
```

```
# only the Triassic, use the supplied abbreviations
tsplo(stages, boxes="short", shading="stage", xlim=c(250,199),
      ylab="variable", labels.args=list(cex=1.5, col="blue"),
      boxes.args=list(col="gray95"))

# colourful plot with two levels of hierarchy
tsplo(stages, boxes=c("short", "system"), shading="series",
      boxes.col=c("col", "systemCol"), xlim=c(52:69))
```

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