Package: fqacalc (via r-universe)

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Title Calculate Floristic Quality Assessment Metrics

Version 1.1.1.9000

Description A collection of functions for calculating Floristic Quality Assessment (FQA) metrics using regional FQA databases that have been approved or approved with reservations as ecological planning models by the U.S. Army Corps of Engineers (USACE). For information on FQA see Spyreas (2019) <doi:10.1002/ecs2.2825>. These databases are stored in a sister R package, 'fqadata'. Both packages were developed for the USACE by the U.S. Army Engineer Research and Development Center's Environmental Laboratory.

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`accepted_entries` *Return A Data Frame of Plant Species That Successfully Match to the Regional FQA Database of choice*

Description

`accepted_entries` takes a data frame of user-entered plant species and returns a data frame of plant species that are successfully matched to the regional FQA database of choice. Regional databases are stored in the `fqadata` R package. `accepted_entries` is a utility function that is used in all other metric-calculating functions in this package.

Usage

```
accepted_entries(
  x,
  key = "name",
  db,
  native = c(TRUE, FALSE),
  wetland_warning = TRUE,
  cover_weighted = FALSE,
  cover_class = "percent_cover",
  allow_duplicates = FALSE,
  allow_no_c = FALSE,
```

```
  allow_non_veg = FALSE,
  plot_id = NULL
)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.
key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.
native	Boolean (TRUE or FALSE). If TRUE, calculate metrics using only native species.
wetland_warning	Boolean (TRUE or FALSE). If TRUE, show user messages regarding issues with wetness coefficients.
cover_weighted	Boolean (TRUE or FALSE). If TRUE, keep cover column in output. Note: if cover_weighted = TRUE, x must have a column named cover. This parameter is used to calculate cover-weighted metrics such as plot mean c, transect mean c, and cover-weighted FQI.
cover_class	a character string representing the cover classification used. Acceptable cover classes are: "percent_cover", "carolina_veg_survey", "braun-blanquet", "daubenmire", and "usfs_ecodata". "percent_cover" is the default.
allow_duplicates	Boolean (TRUE or FALSE). If TRUE, allow x to have duplicate observations for the same species. This is only recommended for calculating transect and relative frequency/abundance metrics. For non cover-weighted (inventory) assessments allow_duplicates is always FALSE. For cover-weighted functions, allow_duplicates can be set to TRUE for transect level metrics or FALSE for plot level metrics.
allow_no_c	Boolean (TRUE or FALSE). If TRUE, allow species that are found in the regional FQA database but have not been assigned a C Values. If FALSE, omit species that have not been assigned C Values.
allow_non_veg	Boolean (TRUE or FALSE). If TRUE, allow input to contain un-vegetated ground and un-vegetated water.
plot_id	A character string representing the column in x that contains plot identification values. plot_id is a required argument in plot_summary, where it acts as a grouping variable. plot_id is optional but highly recommended for cover-weighted functions and relative functions. If plot_id is set in a cover-weighted function or a relative function, it only prevents duplicates from occurring in the same plot. It does not act as a grouping variable.

Value

A data frame containing the key column–either acronym or name–as well as columns from the relevant FQA database. These columns include name_origin accepted_name, family, nativity, c (which represents the C Value), w (which represents wetness score), physiognomy, duration, and common_name

Examples

```
plant_list <- crooked_island

#with native and introduced species
accepted_entries(x = plant_list, key = "acronym", db = "michigan_2014", native = FALSE)

#with only native species
accepted_entries(x = plant_list, key = "acronym", db = "michigan_2014", native = TRUE)

#an example with duplicates allowed
duplicate_df <- data.frame(acronym  = c("ABEESC", "ABIBAL", "ABIBAL"),
cover = c(60, 50, 50))

accepted_entries(x = duplicate_df, key = "acronym",
db = "michigan_2014", native = FALSE, allow_duplicates = TRUE)

#an example of duplicates not allowed
accepted_entries(x = duplicate_df, key = "acronym",
db = "michigan_2014", native = FALSE, allow_duplicates = FALSE)

#an example of duplicates not allowed, adding cover values
accepted_entries(x = duplicate_df, key = "acronym",
db = "michigan_2014", native = FALSE, allow_duplicates = FALSE,
cover_weighted = TRUE)

#an example where some entries are synonyms shared by more than one species
same_syn <- data.frame(name = c("CAREX MURICATA", "POTENTILLA NANA", "ABIES BIFOLIA"),
cover = c(80, 60, 10))

#produces a warning saying CAREX MURICATA is a synonym to multiple species and will be omitted.
#To include this species, use the accepted scientific name.
accepted_entries(x = same_syn, key = "name",
db = "wyoming_2017", native = FALSE)

#an example where species is both a synonym and an accepted name
same_syn2 <- data.frame(name = c("CAREX FOENEA", "ABIES BIFOLIA"),
cover = c(80, 10))

#produces a warning saying CAREX FOENEA is an accepted scientific name and a synonym.
#It will default to accepted scientific name.
accepted_entries(x = same_syn2, key = "name",
db = "wyoming_2017", native = FALSE)
```

adjusted_FQI *Calculate Adjusted FQI*

Description

adjusted_FQI calculates the Adjusted Floristic Quality Index. Adjusted FQI is found by multiplying 100 by the Native Mean C divided by 10 and then multiplied by the square root of Native Species Richness over Total Species Richness.

Usage

```
adjusted_FQI(x, key = "name", db)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.
key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.

Value

A non-negative integer

Examples

```
plant_list <- crooked_island
adjusted_FQI(x = plant_list, key = "acronym", db = "michigan_2014")
```

all_metrics *Print a Summary of Non-Weighted FQA Metrics*

Description

all_metrics calculates and prints a summary of all non cover-weighted metrics, including Species Richness, Native Species Richness, Introduced Species Richness, % of species within C value ranges, Mean C, Native Mean C, Total FQI, Native FQI, Adjusted FQI, Mean Wetness, Native Mean Wetness and % Hydrophytes.

Usage

```
all_metrics(x, key = "name", db, allow_no_c = TRUE)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.
key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.
allow_no_c	Boolean (TRUE or FALSE). If TRUE, allow species that are found in the regional FQA database but have not been assigned a C Values. If FALSE, omit species that have not been assigned C Values.

Value

A data frame

Examples

```
plant_list <- crooked_island
all_metrics(x = plant_list, key = "acronym", db = "michigan_2014")
```

---

cover_FQI *Calculate Cover-Weighted FQI*

Description

cover_FQI calculates cover-weighted mean C multiplied by the square root of species richness.

Usage

```
cover_FQI(
  x,
  key = "name",
  db,
  native = FALSE,
  cover_class = "percent_cover",
  allow_duplicates,
  plot_id = NULL
)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.
key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.
native	Boolean (TRUE or FALSE). If TRUE, calculate metrics using only native species.
cover_class	a character string representing the cover classification used. Acceptable cover classes are: "percent_cover", "carolina_veg_survey", "braun-blanquet", "daubenmire", and "usfs_ecodata". "percent_cover" is the default.
allow_duplicates	Boolean (TRUE or FALSE). If TRUE, allow x to have duplicate observations for the same species. This is only recommended for calculating transect and relative frequency/abundance metrics. For non cover-weighted (inventory) assessments allow_duplicates is always FALSE. For cover-weighted functions, allow_duplicates can be set to TRUE for transect level metrics or FALSE for plot level metrics.
plot_id	A character string representing the column in x that contains plot identification values. plot_id is a required argument in plot_summary, where it acts as a grouping variable. plot_id is optional but highly recommended for cover-weighted functions and relative functions. If plot_id is set in a cover-weighted function or a relative function, it only prevents duplicates from occurring in the same plot. It does not act as a grouping variable.

Value

A non-negative number

Examples

```
transect <- data.frame(acronym  = c("ABEESC", "ABIBAL", "AMMBRE", "ANTELE",
"ABEESC", "ABIBAL", "AMMBRE"),
cover = c(50, 4, 20, 30, 40, 7, 60),
plot_id = c(1, 1, 1, 1, 2, 2, 2))

cover_FQI(x = transect, key = "acronym", db = "michigan_2014",
native = FALSE, allow_duplicates = TRUE, plot_id = "plot_id")
```

cover_mean_c *Calculate Cover-Weighted Mean C*

Description

cover_mean_c calculates the sum of cover multiplied by the C value per each species, divided by the sum of cover values for all species.

Usage

```
cover_mean_c(
  x,
  key = "name",
  db,
  native = FALSE,
  cover_class = "percent_cover",
  allow_duplicates,
  plot_id = NULL
)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.
key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.
native	Boolean (TRUE or FALSE). If TRUE, calculate metrics using only native species.
cover_class	a character string representing the cover classification used. Acceptable cover classes are: "percent_cover", "carolina_veg_survey", "braun-blanquet", "daubenmire", and "usfs_ecodata". "percent_cover" is the default.
allow_duplicates	Boolean (TRUE or FALSE). If TRUE, allow x to have duplicate observations for the same species. This is only recommended for calculating transect and relative frequency/abundance metrics. For non cover-weighted (inventory) assessments allow_duplicates is always FALSE. For cover-weighted functions, allow_duplicates can be set to TRUE for transect level metrics or FALSE for plot level metrics.
plot_id	A character string representing the column in x that contains plot identification values. plot_id is a required argument in plot_summary, where it acts as

a grouping variable. `plot_id` is optional but highly recommended for cover-weighted functions and relative functions. If `plot_id` is set in a cover-weighted function or a relative function, it only prevents duplicates from occurring in the same plot. It does not act as a grouping variable.

Value

A non-negative number

Examples

```
plot <- data.frame(acronym  = c("ABEESC", "ABIBAL", "AMMBRE", "ANTELE"),
cover = c(50, 4, 20, 30),
plot_id = c(1, 1, 2, 2))

cover_mean_c(x = plot, key = "acronym", db = "michigan_2014", native = FALSE,
allow_duplicates = FALSE, plot_id = "plot_id")
```

---

crooked_island *A List of Plants from Crooked Island, MI*

Description

A plant list from a site assessment conducted on crooked island, MI in open dune habitat. The data was collected in the summer of 2022 by Joshua Cohen, Jesse Lincoln, Tyler Bassett, and Scott Warner as part of a project for the National Wildlife Refuge.

Usage

```
crooked_island
```

Format

A data frame with 35 rows and 3 variables:

name Latin names for each plant

acronym Unique acronyms for each plant

common_name Common names for each plant

Source

https://universalfqa.org/

db_names *Look Up the Names of Regional FQA Databases*

Description

Create a data frame of regional FQA database names, approval status, notes, and citations. The column `fqa_db` contains the names of the databases. These are acceptable values for `db` in other `fqacalc` functions.

Usage

```
db_names()
```

Format

A data frame with 44 rows and 4 variables:

fqa_db Regional FQA database

recommendation Indicates if the regional FQA database was recommended for use by the U.S. Army Corps of Engineers in 2020

notes Notes on the limitations or recommended usage of the regional FQA database

citation A citation for the regional FQA database

Value

A data frame.

Examples

```
db_names()
```

FQI *Calculate FQI*

Description

`FQI` calculates the Floristic Quality Index (FQI) for the area of concern. FQI is found by multiplying the mean C by the square root of the species richness. If `native = TRUE`, `FQI` will calculate the Native FQI.

Usage

```
FQI(x, key = "name", db, native = FALSE)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.
key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.
native	Boolean (TRUE or FALSE). If TRUE, calculate metrics using only native species.

Value

A non-negative integer

Examples

```
plant_list <- crooked_island

#FQI of all species (native and introduced)
FQI(x = plant_list, key = "acronym", db = "michigan_2014", native = FALSE)

#FQI of native species
FQI(x = plant_list, key = "acronym", db = "michigan_2014", native = TRUE)
```

---

mean_c *Calculate Mean C*

Description

mean_c calculates the mean coefficient of conservatism for all species in the inventory or along the transect.

Usage

```
mean_c(x, key = "name", db, native = FALSE)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.

key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.
native	Boolean (TRUE or FALSE). If TRUE, calculate metrics using only native species.

Value

A non-negative integer

Examples

```
plant_list <- crooked_island

#mean c of all species (native and introduced)
mean_c(x = plant_list, key = "acronym", db = "michigan_2014", native = FALSE)

#mean c of native species
mean_c(x = plant_list, key = "acronym", db = "michigan_2014", native = TRUE)
```

---

mean_w *Calculate the Mean Wetness Coefficient*

Description

mean_w calculates the mean wetness coefficient for all species in the site assessment. The wetness coefficient is based on wetland indicator status. Negative wetness coefficients indicate a stronger affinity for wetlands, while positive wetness coefficients indicate an affinity for uplands.

Usage

```
mean_w(x, key = "name", db, native = FALSE, allow_no_c = TRUE)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.
key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.

native	Boolean (TRUE or FALSE). If TRUE, calculate metrics using only native species.
allow_no_c	Boolean (TRUE or FALSE). If TRUE, allow species that are found in the regional FQA database but have not been assigned a C Values. If FALSE, omit species that have not been assigned C Values.

Value

A non-negative integer

Examples

```
plant_list <- crooked_island

#mean wetness of all species (native and introduced)
mean_w(x = plant_list, key = "acronym", db = "michigan_2014", native = FALSE)

#mean wetness of native species
mean_w(x = plant_list, key = "acronym", db = "michigan_2014", native = TRUE)
```

---

physiog_summary *Create a cover-Weighted Summary of Physiognomic Groups*

Description

physiog_summary produces a table summarizing physiognomic groups' frequency, total cover, relative frequency, relative cover, and relative importance. Physiognomic groups include shrub, tree, forb, sedge, grass, rush, fern, vine, and bryophyte. If the regional database does not have information on species physiognomy, the function will return a data frame with a single NA category.

Usage

```
physiog_summary(
  x,
  key = "name",
  db,
  cover_class = "percent_cover",
  allow_no_c = TRUE,
  allow_non_veg = TRUE,
  plot_id = NULL
)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.

key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.
cover_class	a character string representing the cover classification used. Acceptable cover classes are: "percent_cover", "carolina_veg_survey", "braun-blanquet", "daubenmire", and "usfs_ecodata". "percent_cover" is the default.
allow_no_c	Boolean (TRUE or FALSE). If TRUE, allow species that are found in the regional FQA database but have not been assigned a C Values. If FALSE, omit species that have not been assigned C Values.
allow_non_veg	Boolean (TRUE or FALSE). If TRUE, allow input to contain un-vegetated ground and un-vegetated water.
plot_id	A character string representing the column in x that contains plot identification values. plot_id is a required argument in plot_summary, where it acts as a grouping variable. plot_id is optional but highly recommended for cover-weighted functions and relative functions. If plot_id is set in a cover-weighted function or a relative function, it only prevents duplicates from occurring in the same plot. It does not act as a grouping variable.

Value

A data frame where each row is a physiognomic group and each column is a metric about that species based on the input data frame.

Examples

```
transect <- data.frame(
acronym  = c("ABEESC", "ABIBAL", "AMMBRE", "ANTELE", "ABEESC", "ABIBAL", "AMMBRE"),
cover = c(50, 4, 20, 30, 40, 7, 60),
plot_id = c(1, 1, 1, 1, 2, 2, 2))

physiog_summary(transect, key = "acronym", db = "michigan_2014", plot_id = "plot_id")


#can also include bare ground and unvegetated water
transect_unveg <- data.frame(acronym  = c("GROUND", "ABEESC", "ABIBAL", "AMMBRE",
"ANTELE", "WATER", "GROUND", "ABEESC", "ABIBAL", "AMMBRE"),
cover = c(60, 50, 4, 20, 30, 20, 20, 40, 7, 60),
plot_id = c(1, 1, 1, 1, 1, 2, 2, 2, 2, 2))

physiog_summary(transect_unveg, key = "acronym", db = "michigan_2014",
plot_id = "plot_id")
```

plot_summary *Calculate Plot-level Summary Statistics*

Description

Input a transect with one or more plots (designated with a unique plot ID) as a single data frame and the output will be a data frame with plot-level species richness, native species richness, mean c, native mean c, FQI, native FQI, adjusted FQI, cover-weighted FQI, and native cover-weighted FQI.

Usage

```
plot_summary(
  x,
  key = "name",
  db,
  cover_class = "percent_cover",
  plot_id,
  allow_no_c = TRUE,
  allow_non_veg = TRUE
)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.
key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.
cover_class	a character string representing the cover classification used. Acceptable cover classes are: "percent_cover", "carolina_veg_survey", "braun-blanquet", "daubenmire", and "usfs_ecodata". "percent_cover" is the default.
plot_id	A character string representing the column in x that contains plot identification values. plot_id is a required argument in plot_summary, where it acts as a grouping variable. plot_id is optional but highly recommended for cover-weighted functions and relative functions. If plot_id is set in a cover-weighted function or a relative function, it only prevents duplicates from occurring in the same plot. It does not act as a grouping variable.
allow_no_c	Boolean (TRUE or FALSE). If TRUE, allow species that are found in the regional FQA database but have not been assigned a C Values. If FALSE, omit species that have not been assigned C Values.
allow_non_veg	Boolean (TRUE or FALSE). If TRUE, allow input to contain un-vegetated ground and un-vegetated water.

Value

A data frame where each row is a plot and columns contain FQI and cover-weighted FQI statistics.

Examples

```
transect <- transect <- data.frame(
acronym  = c("ABEESC", "ABIBAL", "AMMBRE", "ANTELE", "ABEESC", "ABIBAL", "AMMBRE"),
cover = c(50, 4, 20, 30, 40, 7, 60),
plot_id = c(1, 1, 1, 1, 2, 2, 2))

plot_summary(transect, key = "acronym", db = "michigan_2014",
cover_class = "percent_cover", plot_id = "plot_id")
```

---

relative_cover *Calculate Relative Cover*

Description

relative_cover calculates the total cover per group of interest (species, taxonomic family, or physiognomic group) divided by the total cover for all observations, then multiplied by 100. If the regional database does not have information on species family or physiognomy, the function will return a data frame with a single NA category.

Usage

```
relative_cover(
  x,
  key = "name",
  db,
  col = c("species", "family", "physiog"),
  cover_class = "percent_cover",
  allow_no_c = TRUE,
  allow_non_veg = TRUE,
  plot_id = NULL
)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.
key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.

col	A character string representing the categorical variable to calculate the relative cover of. Can be set to "species", "family" or "physiog" (for physiognomy).
cover_class	a character string representing the cover classification used. Acceptable cover classes are: "percent_cover", "carolina_veg_survey", "braun-blanquet", "daubenmire", and "usfs_ecodata". "percent_cover" is the default.
allow_no_c	Boolean (TRUE or FALSE). If TRUE, allow species that are found in the regional FQA database but have not been assigned a C Values. If FALSE, omit species that have not been assigned C Values.
allow_non_veg	Boolean (TRUE or FALSE). If TRUE, allow input to contain un-vegetated ground and un-vegetated water.
plot_id	A character string representing the column in x that contains plot identification values. plot_id is a required argument in plot_summary, where it acts as a grouping variable. plot_id is optional but highly recommended for cover-weighted functions and relative functions. If plot_id is set in a cover-weighted function or a relative function, it only prevents duplicates from occurring in the same plot. It does not act as a grouping variable.

Value

A data frame with categorical variables set by the col argument and their relative cover.

Examples

```
transect <- data.frame(
acronym  = c("ABEESC", "ABIBAL", "AMMBRE", "ANTELE", "ABEESC", "ABIBAL", "AMMBRE"),
cover = c(50, 4, 20, 30, 40, 7, 60),
plot_id = c(1, 1, 1, 1, 2, 2, 2))

relative_cover(transect, key = "acronym", db = "michigan_2014", col = "species",
plot_id = "plot_id")

#can also include bare ground and unvegetated water
transect_unveg <- data.frame(acronym  = c("GROUND", "ABEESC", "ABIBAL", "AMMBRE",
"ANTELE", "WATER", "GROUND", "ABEESC", "ABIBAL", "AMMBRE"),
cover = c(60, 50, 4, 20, 30, 20, 20, 40, 7, 60),
plot_id = c(1, 1, 1, 1, 1, 2, 2, 2, 2, 2))

relative_cover(transect_unveg, key = "acronym", db = "michigan_2014",
col = "species", plot_id = "plot_id")
```

---

relative_frequency *Calculate Relative Frequency*

Description

relative_frequency calculates the frequency of one species, taxonomic family, or physiognomic group, divided by the frequency of all observations, then multiplied by 100. If the regional database does not have information on species family or physiognomy, the function will return a data frame with a single NA category.

Usage

```
relative_frequency(
  x,
  key = "name",
  db,
  col = c("species", "family", "physiog"),
  allow_no_c = TRUE,
  allow_non_veg = TRUE,
  plot_id = NULL
)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.
key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.
col	A character string representing the categorical variable to calculate the relative frequency of. Can be set to "species", "family" or "physiog" (for physiognomy).
allow_no_c	Boolean (TRUE or FALSE). If TRUE, allow species that are found in the regional FQA database but have not been assigned a C Values. If FALSE, omit species that have not been assigned C Values.
allow_non_veg	Boolean (TRUE or FALSE). If TRUE, allow input to contain un-vegetated ground and un-vegetated water.
plot_id	A character string representing the column in x that contains plot identification values. plot_id is a required argument in plot_summary, where it acts as a grouping variable. plot_id is optional but highly recommended for cover-weighted functions and relative functions. If plot_id is set in a cover-weighted function or a relative function, it only prevents duplicates from occurring in the same plot. It does not act as a grouping variable.

Value

A data frame with categorical variables set by the col argument and their relative frequency.

Examples

```
transect <- data.frame(
acronym  = c("ABEESC", "ABIBAL", "AMMBRE", "ANTELE", "ABEESC", "ABIBAL", "AMMBRE"),
cover = c(50, 4, 20, 30, 40, 7, 60),
plot_id = c(1, 1, 1, 1, 2, 2, 2))
```

```
relative_frequency(transect, key = "acronym", db = "michigan_2014", col = "physiog")

#can also include bare ground and unvegetated water
transect_unveg <- data.frame(acronym  = c("GROUND", "ABEESC", "ABIBAL", "AMMBRE",
"ANTELE", "WATER", "GROUND", "ABEESC", "ABIBAL", "AMMBRE"),
cover = c(60, 50, 4, 20, 30, 20, 20, 40, 7, 60),
plot_id = c(1, 1, 1, 1, 1, 2, 2, 2, 2, 2))

relative_frequency(transect_unveg, key = "acronym", db = "michigan_2014",
col = "physiog", plot_id = "plot_id")
```

`relative_importance` *Calculate Relative Importance*

Description

`relative_importance` calculates relative frequency added to relative cover, and divided by two. If the regional database does not have information on species family or physiognomy, the function will return a data frame with a single NA category.

Usage

```
relative_importance(
  x,
  key = "name",
  db,
  col = c("species", "family", "physiog"),
  cover_class = "percent_cover",
  allow_no_c = TRUE,
  allow_non_veg = TRUE,
  plot_id = NULL
)
```

Arguments

`x`	A data frame containing a list of plant species. This data frame must have one of the following columns: `name` or `acronym`. For cover-weighted or relative functions, this data frame must also have a column called `cover` containing cover values and ideally a column containing plot IDs.
`key`	A character string representing the column that will be used to join the input data frame `x` with the regional FQA database. If a value is not specified, the default is `"name"`. `"name"` and `"acronym"` are the only acceptable values for `key`.
`db`	A character string representing the regional FQA database to use. See `db_names` for a list of potential values and the `fqadata` R package where the databases are hosted.

col	A character string representing the categorical variable to calculate the relative frequency of. Can be set to "species", "family" or "physiog" (for physiognomy).
cover_class	a character string representing the cover classification used. Acceptable cover classes are: "percent_cover", "carolina_veg_survey", "braun-blanquet", "daubenmire", and "usfs_ecodata". "percent_cover" is the default.
allow_no_c	Boolean (TRUE or FALSE). If TRUE, allow species that are found in the regional FQA database but have not been assigned a C Values. If FALSE, omit species that have not been assigned C Values.
allow_non_veg	Boolean (TRUE or FALSE). If TRUE, allow input to contain un-vegetated ground and un-vegetated water.
plot_id	A character string representing the column in x that contains plot identification values. plot_id is a required argument in plot_summary, where it acts as a grouping variable. plot_id is optional but highly recommended for cover-weighted functions and relative functions. If plot_id is set in a cover-weighted function or a relative function, it only prevents duplicates from occurring in the same plot. It does not act as a grouping variable.

Value

A data frame with categorical variables set by the col argument and their relative importance.

Examples

```
transect <- data.frame(
acronym  = c("ABEESC", "ABIBAL", "AMMBRE", "ANTELE", "ABEESC", "ABIBAL", "AMMBRE"),
cover = c(50, 4, 20, 30, 40, 7, 60),
quad_id = c(1, 1, 1, 1, 2, 2, 2))

relative_importance(transect, key = "acronym", db = "michigan_2014", col = "family")

#can also include bare ground and unveg water
transect_unveg <- data.frame(acronym  = c("GROUND", "ABEESC", "ABIBAL", "AMMBRE",
"ANTELE", "WATER", "GROUND", "ABEESC", "ABIBAL", "AMMBRE"),
cover = c(60, 50, 4, 20, 30, 20, 20, 40, 7, 60),
plot_id = c(1, 1, 1, 1, 1, 2, 2, 2, 2, 2))

relative_importance(transect_unveg, key = "acronym", db = "michigan_2014",
col = "family", plot_id = "plot_id")
```

---

species_richness *Calculate Number of Species*

Description

species_richness calculates the total number of species.

Usage

```
species_richness(x, key = "name", db, native = FALSE, allow_no_c = TRUE)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.
key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.
native	Boolean (TRUE or FALSE). If TRUE, calculate metrics using only native species.
allow_no_c	Boolean (TRUE or FALSE). If TRUE, allow species that are found in the regional FQA database but have not been assigned a C Values. If FALSE, omit species that have not been assigned C Values.

Value

A non-negative integer

Examples

```
plant_list <- crooked_island

#number of species (native and introduced)
species_richness(x = plant_list, key = "acronym", db = "michigan_2014", native = FALSE)

#number of native species
species_richness(x = plant_list, key = "acronym", db = "michigan_2014", native = TRUE)
```

---

species_summary *Create A Cover-Weighted Summary of Species*

Description

species_summary produces a table summarizing species' frequency, total cover, relative frequency, relative cover, and relative importance.

Usage

```
species_summary(
  x,
  key = "name",
  db,
  cover_class = "percent_cover",
  allow_no_c = TRUE,
  allow_non_veg = TRUE,
  plot_id = NULL
)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.
key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.
cover_class	a character string representing the cover classification used. Acceptable cover classes are: "percent_cover", "carolina_veg_survey", "braun-blanquet", "daubenmire", and "usfs_ecodata". "percent_cover" is the default.
allow_no_c	Boolean (TRUE or FALSE). If TRUE, allow species that are found in the regional FQA database but have not been assigned a C Values. If FALSE, omit species that have not been assigned C Values.
allow_non_veg	Boolean (TRUE or FALSE). If TRUE, allow input to contain un-vegetated ground and un-vegetated water.
plot_id	A character string representing the column in x that contains plot identification values. plot_id is a required argument in plot_summary, where it acts as a grouping variable. plot_id is optional but highly recommended for cover-weighted functions and relative functions. If plot_id is set in a cover-weighted function or a relative function, it only prevents duplicates from occurring in the same plot. It does not act as a grouping variable.

Value

A data frame where each row is a species and each column is information about that species based on the input data frame.

Examples

```
transect <- data.frame(
acronym  = c("ABEESC", "ABIBAL", "AMMBRE", "ANTELE", "ABEESC", "ABIBAL", "AMMBRE"),
```

```
cover = c(50, 4, 20, 30, 40, 7, 60),
quad_id = c(1, 1, 1, 1, 2, 2, 2))

species_summary(transect, key = "acronym", db = "michigan_2014")

#can also include bare ground and unveg water
transect_unveg <- data.frame(acronym  = c("GROUND", "ABEESC", "ABIBAL", "AMMBRE",
"ANTELE", "WATER", "GROUND", "ABEESC", "ABIBAL", "AMMBRE"),
cover = c(60, 50, 4, 20, 30, 20, 20, 40, 7, 60),
plot_id = c(1, 1, 1, 1, 1, 2, 2, 2, 2, 2))

species_summary(transect_unveg, key = "acronym", db = "michigan_2014",
plot_id = "plot_id")
```

`transect_summary` *Print a Summary of Cover-Weighted FQA Metrics*

Description

`transect_summary` calculates and prints a summary of both inventory metrics and cover-weighted metrics, including Species Richness, Native Species Richness, Introduced Species Richness, % of species within C value ranges, Mean C, Native Mean C, Cover-weighted Mean C, Native Cover-Weighted Mean C, Total FQI, Native FQI, Cover-Weighted FQI, Native Cover-weighted FQI, Adjusted FQI, Mean Wetness, Native Mean Wetness and % Hydrophytes. Cover-weighted metrics allow duplicate entries for transect level summary metrics.

Usage

```
transect_summary(
  x,
  key = "name",
  db,
  cover_class = "percent_cover",
  allow_no_c = TRUE,
  plot_id = NULL
)
```

Arguments

`x`	A data frame containing a list of plant species. This data frame must have one of the following columns: `name` or `acronym`. For cover-weighted or relative functions, this data frame must also have a column called `cover` containing cover values and ideally a column containing plot IDs.
`key`	A character string representing the column that will be used to join the input data frame `x` with the regional FQA database. If a value is not specified, the default is `"name"`. `"name"` and `"acronym"` are the only acceptable values for `key`.

db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.
cover_class	a character string representing the cover classification used. Acceptable cover classes are: "percent_cover", "carolina_veg_survey", "braun-blanquet", "daubenmire", and "usfs_ecodata". "percent_cover" is the default.
allow_no_c	Boolean (TRUE or FALSE). If TRUE, allow species that are found in the regional FQA database but have not been assigned a C Values. If FALSE, omit species that have not been assigned C Values.
plot_id	A character string representing the column in x that contains plot identification values. plot_id is a required argument in plot_summary, where it acts as a grouping variable. plot_id is optional but highly recommended for cover-weighted functions and relative functions. If plot_id is set in a cover-weighted function or a relative function, it only prevents duplicates from occurring in the same plot. It does not act as a grouping variable.

Value

A data frame

Examples

```
transect <- data.frame(
acronym  = c("ABEESC", "ABIBAL", "AMMBRE", "ANTELE", "ABEESC", "ABIBAL", "AMMBRE"),
cover = c(50, 4, 20, 30, 40, 7, 60),
plot_id = c(1, 1, 1, 1, 2, 2, 2))

transect_summary(x = transect, key = "acronym", db = "michigan_2014",
plot_id = "plot_id")
```

---

unassigned_plants *Return Data Frame of Plant Species That Have No C Value*

Description

Some regional FQA lists contain species which have not been assigned a C Value. unassigned_plants returns a data frame of plants in x that can be matched to a regional FQA database but have no C Value. These observations can optionally be discarded in other fqacalc functions.

Usage

```
unassigned_plants(x, key = "name", db)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and ideally a column containing plot IDs.
key	A character string representing the column that will be used to join the input data frame x with the regional FQA database. If a value is not specified, the default is "name". "name" and "acronym" are the only acceptable values for key.
db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.

Value

A data frame

Examples

```
no_c_test <- data.frame(name = c("ABRONIA FRAGRANS", "ACER GLABRUM",
"ACER GRANDIDENTATUM", "ACER PLATANOIDES"))

unassigned_plants(no_c_test, key = "name", db = "montana_2017")
```

---

view_db *View a Regional FQA Database*

Description

Create a data frame containing an entire regional FQA database.

Usage

```
view_db(db)
```

Arguments

db	A character string representing the regional FQA database to use. See db_names for a list of potential values and the fqadata R package where the databases are hosted.

Value

A data frame with 12 variables:

name Latin name for species, either accepted name or synonym

name_origin Indicates if the name is the accepted scientific name or a synonym

acronym A unique acronym for each species. Not always consistent between FQA databases

accepted_scientific_name The accepted botanical nomenclature

family Taxonomic family of species

nativity Nativity status. Native, introduced, and undetermined are possible values

c Coefficient of Conservatism (C Value)

w Wetness Coefficient

wetland_indicator Wetland indicator status

physiognomy Structure or physical appearance of species

duration Lifespan of species

common_name Common name(s) for species

fqa_db Regional FQA database

Source

See `db_names` function for citations

Examples

```
view_db("michigan_2014")
```

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