Package 'fqacalc'

February 6, 2023

Title Calculate FQA Metrics

Version 0.0.0.9000

Description Provides functions for calculating Floristic Quality Assessment (FQA) metrics using regional FQA databases that have been reviewed and certified by the U.S. Army Corps of Engineers (USACE). 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.

License MIT + file LICENSE

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Depends R (>= 2.10)

LazyData true

Imports magrittr,
  dplyr,
  rlang,
  fqadata

URL https://github.com/ifoxfoot/fqacalc

BugReports https://github.com/ifoxfoot/fqacalc/issues

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

R topics documented:

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.
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 wetland 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 frequency/abundance 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	(optional) A character string representing the column in x that contains plot identification values.

Value

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

Examples

```
plant_list <- crooked_island

#with native and non natives
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),
quad_id = c(1, 2, 2))

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))

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", "CAREX FOENEA", "ABIES BIFOLIA"),
cover = c(80, 60, 10))

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.

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

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.
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
)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: `name` or `acronym`.
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 frequency/abundance metrics.

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),
quad_id = c(1, 1, 1, 1, 2, 2, 2))

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

---

cover_mean_c   *Calculate Cover-Weighted Mean C*

Description

cover_mean_c calculates the sum of cover times 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
)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: `name` or `acronym`.
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 frequency/abundance metrics.

Value

A non-negative number

Examples

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

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

---

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 containing the names of regional FQA databases contained in this package as well as their certification status.

Usage

```
db_names()
```

Value

A data frame of regional FQA database names. The column name contains the names of the databases. These are acceptable values for db in other fqacalc functions. The column status notes whether the database has been fully approved or approved with reservations by the US Army Corps of Engineers.

Examples

```
db_names()
```

FQI   *Calculate FQI*

Description

FQI calculates the Floristic Quality Index (FQI) for the site. 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.
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 exotic)
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 conservation coefficient 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.
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 exotic)
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 USFWS Wetland Indicator Status. Negative wetness coefficients indicate a stronger affinity for wetlands, while positive wetland coefficients indicate an affinity for upland.

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.
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 non-native)
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.

Usage

```
physiog_summary(
  x,
  key = "name",
  db,
  cover_class = "percent_cover",
  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.
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.

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),
quad_id = c(1, 1, 1, 1, 2, 2, 2))
```

```
physiog_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),
quad_id = c(1, 1, 1, 1, 1, 2, 2, 2, 2, 2))

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

---

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.
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	(optional) A character string representing the column in x that contains plot identification values.
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),
quad_id = c(1, 1, 1, 1, 2, 2, 2))

plot_summary(transect, key = "acronym", db = "michigan_2014",
cover_class = "percent_cover", plot_id = "quad_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.

Usage

```
relative_cover(
  x,
  key = "name",
  db,
  col = c("species", "family", "physiog"),
  cover_class = "percent_cover",
  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.

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.

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),
quad_id = c(1, 1, 1, 1, 2, 2, 2))

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

#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),
quad_id = c(1, 1, 1, 1, 1, 2, 2, 2, 2, 2))

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

---

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.

Usage

```
relative_frequency(
  x,
  key = "name",
  db,
  col = c("species", "family", "physiog"),
  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.

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.

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),
quad_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 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),
quad_id = c(1, 1, 1, 1, 1, 2, 2, 2, 2, 2))

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

---

relative_importance	*Calculate Relative Importance*

Description

relative_importance calculates the average of relative frequency and relative cover.

Usage

```
relative_importance(
  x,
  key = "name",
  db,
  col = c("species", "family", "physiog"),
  cover_class = "percent_cover",
```

```
  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`.
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.

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),
quad_id = c(1, 1, 1, 1, 1, 2, 2, 2, 2, 2))

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

---

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.
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 exotic)
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
)
```

Arguments

x	A data frame containing a list of plant species. This data frame must have one of the following columns: name or acronym.
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.

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),
quad_id = c(1, 1, 1, 1, 1, 2, 2, 2, 2, 2))

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

---

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

Description

`transect_summary` calculates and prints a summary of both non cover-weighted metrics and cover-weighted metrics. Cover-weighted metrics allow duplicate entries.

Usage

```
transect_summary(
  x,
  key = "name",
  db,
  cover_class = "percent_cover",
  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`.
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.

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),
quad_id = c(1, 1, 1, 1, 2, 2, 2))

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

| 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. This is usually because the plant is unfamiliar to the botanists who assigned the C Values or because there is little known about the plant. 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.
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, either proper name or synonym

name_origin Indicates if the name is the accepted scientific name–"accepted_scientific_name"–or a synonym

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

accepted_scientific_name The accepted/official scientific name

family Taxonomic family of species

nativity Nativity status. native, non-native, and undetermined are values

c Coefficient of Conservatism (C Value)

w Wetland Indicator Rating

physiognomy Categories based on plant habit (architectural characteristics), life history, and certain taxonomic classes

duration Categories based on life cycle

common_name Common name(s) for plant

fqa_db Regional FQA database ...

Examples

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