

# Package ‘fqacalc’

February 23, 2023

**Title** Calculate Floristic Quality Assessment Metrics

**Version** 0.0.0.9000

**Description** A collection of functions for calculating Floristic Quality Assessment (FQA) metrics using regional FQA databases that have been reviewed and certified as ecological planning models 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/ifaxfoot/fqacalc>

**BugReports** <https://github.com/ifaxfoot/fqacalc/issues>

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**NeedsCompilation** no

**Author** Iris Foxfoot [aut],  
Ecological Modeling Team [cre]

**Maintainer** Ecological Modeling Team <ecomodteam@usace.army.mil>

## R topics documented:

accepted_entries . . . . .	2
adjusted_FQI . . . . .	4
all_metrics . . . . .	5
cover_FQI . . . . .	6
cover_mean_c . . . . .	7
crooked_island . . . . .	8
db_names . . . . .	9
FQI . . . . .	9

mean_c . . . . .	10
mean_w . . . . .	11
physiog_summary . . . . .	12
plot_summary . . . . .	13
relative_cover . . . . .	14
relative_frequency . . . . .	16
relative_importance . . . . .	17
species_richness . . . . .	19
species_summary . . . . .	20
transect_summary . . . . .	21
unassigned_plants . . . . .	22
view_db . . . . .	23

---

accepted_entries	<i>Return A Data Frame of Plant Species That Successfully Match to the Regional FQA Database of choice</i>
------------------	--

---

## 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 optionally 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 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 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))

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 optionally 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")
```

---

<code>all_metrics</code>	<i>Print a Summary of Non-Weighted FQA Metrics</i>
--------------------------	--

---

### 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 optionally 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 optionally 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 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)
```

---

cover_mean_c	<i>Calculate Cover-Weighted Mean C</i>
--------------	--

---

**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 optionally 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 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 useage 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 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. For cover-weighted or relative functions, this data frame must also have a column called cover containing cover values and optionally 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	<i>Calculate Mean C</i>
--------	-------------------------

---

**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 optionally 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	<i>Calculate the Mean Wetness Coefficient</i>
--------	---

---

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

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

#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\_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 optionally 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 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 <- 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 optionally 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 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")

#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")

```

---

relative_frequency	<i>Calculate Relative Frequency</i>
--------------------	-------------------------------------

---

### 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 optionally 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 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")
```

---

relative_importance	<i>Calculate Relative Importance</i>
---------------------	--------------------------------------

---

### 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**

<code>x</code>	A data frame containing a list of plant species. This data frame must have one of the following columns: <code>name</code> or <code>acronym</code> . For cover-weighted or relative functions, this data frame must also have a column called <code>cover</code> containing cover values and optionally a column containing plot IDs.
<code>key</code>	A character string representing the column that will be used to join the input data frame <code>x</code> with the regional FQA database. If a value is not specified, the default is <code>"name"</code> . <code>"name"</code> and <code>"acronym"</code> are the only acceptable values for <code>key</code> .
<code>db</code>	A character string representing the regional FQA database to use. See <code>db_names</code> for a list of potential values and the <code>fqadata</code> R package where the databases are hosted.
<code>col</code>	A character string representing the categorical variable to calculate the relative frequency of. Can be set to <code>"species"</code> , <code>"family"</code> or <code>"physiog"</code> (for physiognomy).
<code>cover_class</code>	a character string representing the cover classification used. Acceptable cover classes are: <code>"percent_cover"</code> , <code>"carolina_veg_survey"</code> , <code>"braun-blanquet"</code> , <code>"daubenmire"</code> , and <code>"usfs_ecodata"</code> . <code>"percent_cover"</code> is the default.
<code>allow_no_c</code>	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.
<code>allow_non_veg</code>	Boolean (TRUE or FALSE). If TRUE, allow input to contain un-vegetated ground and un-vegetated water.
<code>plot_id</code>	A character string representing the column in <code>x</code> that contains plot identification values. <code>plot_id</code> is a required argument in <code>plot_summary</code> , where it acts as a grouping variable. <code>plot_id</code> is optional for cover-weighted functions and relative functions. If <code>plot_id</code> 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),
  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	<i>Calculate Number of Species</i>
------------------	------------------------------------

---

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

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

---

transect_summary	<i>Print a Summary of Cover-Weighted FQA Metrics</i>
------------------	--

---

## 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 optionally 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 Value. 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 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")
```

---

unassigned_plants	<i>Return Data Frame of Plant Species That Have No C Value</i>
-------------------	--

---

### 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 optionally 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 <code>db_names</code> for a list of potential values and the <code>fqadata</code> 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	<i>View a Regional FQA Database</i>
---------	-------------------------------------

---

**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")
```