

Package ‘fqr’

July 22, 2025

Type Package

Title Floristic Quality Assessment Tools for R

Version 0.5.5

Description Tools for downloading and analyzing floristic quality assessment data.
See Freyman et al. (2015) <[doi:10.1111/2041-210X.12491](https://doi.org/10.1111/2041-210X.12491)> for more information
about floristic quality assessment and the associated database.

License MIT + file LICENSE

Encoding UTF-8

Language en-US

LazyData true

Imports dplyr, ggplot2, httr, jsonlite, memoise, rlang, tidyr,
tidyselect

RoxygenNote 7.3.2

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Depends R (>= 4.1.0)

VignetteBuilder knitr

URL <https://github.com/equitable-equations/fqr/>

BugReports <https://github.com/equitable-equations/fqr/issues>

Config/testthat/edition 3

NeedsCompilation no

Author Andrew Gard [aut, cre] (ORCID: <<https://orcid.org/0000-0003-4434-0755>>),
Alexia Myers [aut],
Irene Luwabelwa [aut]

Maintainer Andrew Gard <agard@lakeforest.edu>

Repository CRAN

Date/Publication 2025-06-21 23:30:02 UTC

Contents

assessment_cooccurrences	2
assessment_cooccurrences_summary	4
assessment_glance	5
assessment_inventory	7
assessment_list_glance	8
assessment_list_inventory	10
chicago	11
database_glance	13
database_inventory	14
download_assessment	15
download_assessment_list	15
download_database	16
download_transect	17
download_transect_list	18
index_fqa_assessments	19
index_fqa_databases	19
index_fqa_transects	20
missouri	21
species_acronym	23
species_c	24
species_common_name	25
species_nativity	26
species_phys	27
species_profile	28
species_profile_plot	29
species_w	30
transect_glance	31
transect_inventory	33
transect_list_glance	34
transect_list_inventory	36
transect_phys	37
transect_subplot_inventories	38
Index	39

assessment_cooccurrences

Generate a species co-occurrence matrix from assessment inventories

Description

`assessment_coccurrences()` accepts a list of species inventories downloaded from universalfqa.org and returns a complete listing of all co-occurrences. Repeated co-occurrences across multiple assessments are included, but self co-occurrences are not, allowing for meaningful summary statistics to be computed.

Usage

```
assessment_cooccurrences(inventory_list)
```

Arguments

`inventory_list` A list of site inventories having the format of [assessment_list_inventory\(\)](#)

Value

A data frame with 13 columns:

- `target_species` (character)
- `target_species_c` (numeric)
- `target_species_nativity` (character)
- `target_species_n` (numeric)
- `cospecies_scientific_name` (character)
- `cospecies_family` (character)
- `cospecies_acronym` (character)
- `cospecies_nativity` (character)
- `cospecies_c` (numeric)
- `cospecies_w` (numeric)
- `cospecies_physiognomy` (character)
- `cospecies_duration` (character)
- `cospecies_common_name` (character)

Examples

```
# assessment_cooccurrences is best used in combination with  
# download_assessment_list() and assessment_list_inventory().
```

```
maine <- download_assessment_list(database = 56)  
maine_invs <- assessment_list_inventory(maine)  
maine_cooccurrences <- assessment_cooccurrences(maine_invs)
```

`assessment_cooccurrences_summary`*Generate a summary of co-occurrences in various assessment inventories*

Description

`assessment_cooccurrences_summary()` accepts a list of species inventories downloaded from universalfqa.org and returns a summary of the co-occurrences of each target species. Repeated co-occurrences across multiple assessments are included in summary calculations, but self co-occurrences are not.

Usage

```
assessment_cooccurrences_summary(inventory_list)
```

Arguments

`inventory_list` A list of site inventories having the format of [assessment_list_inventory\(\)](#).

Value

A data frame with 16 columns:

- `target_species` (character)
- `target_species_c` (numeric)
- `target_species_nativity` (character)
- `target_species_n` (numeric)
- `cospecies_n` (numeric)
- `cospecies_native_n` (numeric)
- `cospecies_mean_c` (numeric)
- `cospecies_native_mean_c` (numeric)
- `cospecies_std_dev_c` (numeric)
- `cospecies_native_std_dev_c` (numeric)
- `percent_native` (numeric)
- `percent_nonnative` (numeric)
- `percent_native_low_c` (numeric)
- `percent_native_med_c` (numeric)
- `percent_native_high_c` (numeric)
- `discrepancy_c` (numeric)

Examples

```
# assessment_cooccurrences_summary is best used in combination with
# download_assessment_list() and assessment_list_inventory().

maine <- download_assessment_list(database = 56)
maine_invs <- assessment_list_inventory(maine)
maine_cooccurrences_summary <- assessment_cooccurrences_summary(maine_invs)
```

assessment_glance	<i>Obtain tidy summary information for a floristic quality assessment</i>
-------------------	---

Description

assessment_glance() tidies a floristic quality assessment data set obtained from universalfqa.org.

Usage

```
assessment_glance(data_set)
```

Arguments

data_set A data set downloaded from universalfqa.org either manually or using [download_assessment\(\)](#)

Value

A data frame with 53 columns:

- assessment_id (numeric)
- title (character)
- date (date)
- site_name (character)
- city (character)
- county (character)
- state (character)
- country (character)
- fqa_db_region (character)
- fqa_db_publication_year (character)
- fqa_db_description (character)
- custom_fqa_db_name (character)
- custom_fqa_db_description (character)
- practitioner (character)

- latitude (character)
- longitude (character)
- weather_notes (character)
- duration_notes (character)
- community_type_notes (character)
- other_notes (character)
- private_public (character)
- total_mean_c (numeric)
- native_mean_c (numeric)
- total_fqi (numeric)
- native_fqi (numeric)
- adjusted_fqi (numeric)
- c_value_zero (numeric) Percent of c-values 0
- c_value_low (numeric) Percent of c-values 1-3
- c_value_mid (numeric) Percent of c-values 4-6
- c_value_high (numeric) Percent of c-values 7-10
- native_tree_mean_c (numeric)
- native_shrub_mean_c (numeric)
- native_herbaceous_mean_c (numeric)
- total_species (numeric)
- native_species (numeric)
- non_native_species (numeric)
- mean_wetness (numeric)
- native_mean_wetness (numeric)
- tree (numeric)
- shrub (numeric)
- vine (numeric)
- forb (numeric)
- grass (numeric)
- sedge (numeric)
- rush (numeric)
- fern (numeric)
- bryophyte (numeric)
- annual (numeric)
- perennial (numeric)
- biennial (numeric)
- native_annual (numeric)
- native_perennial (numeric)
- native_biennial (numeric)

Examples

```
# While assessment_glance can be used with a .csv file downloaded manually  
# from the universal FQA website, it is most typically used in combination  
# with download_assessment().
```

```
edison <- download_assessment(25002)  
assessment_glance(edison)
```

assessment_inventory *Obtain species details for a floristic quality assessment*

Description

assessment_inventory() returns a data frame of all plant species included in a floristic quality assessment obtained from universalfqa.org.

Usage

```
assessment_inventory(data_set)
```

Arguments

data_set A data set downloaded from universalfqa.org either manually or using [download_assessment\(\)](#).

Value

A data frame with 9 columns:

- scientific_name (character)
- family (character)
- acronym (character)
- nativity (character)
- c (numeric)
- w (numeric)
- physiognomy (character)
- duration (character)
- common_name (character)

Examples

```
# While assessment_glance can be used with a .csv file downloaded  
# manually from the universal FQA website, it is most typically used  
# in combination with download_assessment().
```

```
edison <- download_assessment(25002)  
assessment_inventory(edison)
```

`assessment_list_glance`*Obtain tidy summary information for multiple floristic quality assessments*

Description

`assessment_list_glance()` tidies a list of floristic quality assessment data sets obtained from universalfqa.org, returning summary information as a single data frame.

Usage

```
assessment_list_glance(assessment_list)
```

Arguments

`assessment_list`

A list of data sets downloaded from universalfqa.org, typically using `download_assessment_list()`.

Value

A data frame with 53 columns:

- `assessment_id` (numeric)
- `title` (character)
- `date` (date)
- `site_name` (character)
- `city` (character)
- `county` (character)
- `state` (character)
- `country` (character)
- `fqa_db_region` (character)
- `fqa_db_publication_year` (character)
- `fqa_db_description` (character)
- `custom_fqa_db_name` (character)
- `custom_fqa_db_description` (character)
- `practitioner` (character)
- `latitude` (character)
- `longitude` (character)
- `weather_notes` (character)
- `duration_notes` (character)
- `community_type_notes` (character)

- other_notes (character)
- private_public (character)
- total_mean_c (numeric)
- native_mean_c (numeric)
- total_fqi (numeric)
- native_fqi (numeric)
- adjusted_fqi (numeric)
- c_value_zero (numeric) Percent of c-values 0
- c_value_low (numeric) Percent of c-values 1-3
- c_value_mid (numeric) Percent of c-values 4-6
- c_value_high (numeric) Percent of c-values 7-10
- native_tree_mean_c (numeric)
- native_shrub_mean_c (numeric)
- native_herbaceous_mean_c (numeric)
- total_species (numeric)
- native_species (numeric)
- non_native_species
- mean_wetness (numeric)
- native_mean_wetness (numeric)
- tree (numeric)
- shrub (numeric)
- vine (numeric)
- forb (numeric)
- grass (numeric)
- sedge (numeric)
- rush (numeric)
- fern (numeric)
- bryophyte (numeric)
- annual (numeric)
- perennial (numeric)
- biennial (numeric)
- native_annual (numeric)
- native_perennial (numeric)
- native_biennial (numeric)

Examples

```
# While assessment_list_glance can be used with a list of .csv file downloaded  
# manually from the universal FQA website, it is most typically used  
# in combination with download_assessment_list().
```

```
maine <- download_assessment_list(database = 56)  
assessment_list_glance(maine)
```

assessment_list_inventory

Obtain species details for a list of floristic quality assessments

Description

assessment_list_inventory() returns a list of data frames, each of which consists of all plant species included in a floristic quality assessment obtained from universalfqa.org.

Usage

```
assessment_list_inventory(assessment_list)
```

Arguments

assessment_list

A list of data sets downloaded from universalfqa.org, typically using [download_assessment_list\(\)](#).

Value

A list of data frames, each with 9 columns:

- scientific_name (character)
- family (character)
- acronym (character)
- nativity (character)
- c (numeric)
- w (numeric)
- physiognomy (character)
- duration (character)
- common_name (character)

Examples

```
# While assessment_list_inventory can be used with a list of .csv file downloaded
# manually from the universal FQA website, it is most typically used
# in combination with download_assessment_list().
```

```
maine <- download_assessment_list(database = 56)
maine_invs <- assessment_list_inventory(maine)
```

chicago

*Chicagoland floristic quality assessment data***Description**

A data set summarizing 786 floristic quality assessments using the 2017 Chicago Region USACE database.

Usage

```
chicago
```

Format

A data frame with 52 columns:

- Title (character)
- Date (date)
- Site Name (character)
- City (character)
- County (character)
- State (character)
- Country (character)
- FQA DB Region (character)
- FQA DB Publication Year (character)
- FQA DB Description (character)
- Custom FQA DB Name (character)
- Custom FQA DB Description (character)
- Practitioner (character)
- Latitude (character)
- Longitude (character)
- Weather Notes (character)

- Duration Notes (character)
- Community Type Notes (character)
- Other Notes (character)
- Private/Public (character)
- Total Mean C (numeric)
- Native Mean C (numeric)
- Total FQI: (numeric)
- Native FQI (numeric)
- Adjusted FQI (numeric)
- % C value 0 (numeric)
- % C value 1-3 (numeric)
- % C value 4-6 (numeric)
- % C value 7-10 (numeric)
- Native Tree Mean C (numeric)
- Native Shrub Mean C (numeric)
- Native Herbaceous Mean C (numeric)
- Total Species (numeric)
- Native Species (numeric)
- Non-native Species
- Mean Wetness (numeric)
- Native Mean Wetness (numeric)
- Tree (numeric)
- Shrub (numeric)
- Vine (numeric)
- Forb (numeric)
- Grass (numeric)
- Sedge (numeric)
- Rush (numeric)
- Fern (numeric)
- Bryophyte (numeric)
- Annual (numeric)
- Perennial (numeric)
- Biennial (numeric)
- Native Annual (numeric)
- Native Perennial (numeric)
- Native Biennial (numeric)

Source

universalfqa.org

database_glance	<i>Obtain tidy summary information for a floristic quality database</i>
-----------------	---

Description

database_glance() tidies a floristic quality database obtained from universalfqa.org.

Usage

```
database_glance(database)
```

Arguments

database A database downloaded from universalfqa.org either manually or using [download_database\(\)](#)

Value

A data frame with 8 columns:

- region (character)
- year (numeric)
- description (character)
- total_species (numeric)
- native_species (numeric)
- non_native_species (numeric)
- total_mean_c (numeric)
- native_mean_c (numeric)

Examples

```
# While database_glance can be used with a .csv file downloaded manually  
# from the universal FQA website, it is most typically used in combination  
# with download_database().
```

```
chicago_db <- download_database(database_id = 1)  
chicago_db_summary <- database_glance(chicago_db)
```

database_inventory	<i>Obtain species details for a floristic quality database</i>
--------------------	--

Description

database_inventory() returns a data frame of all plant species included in a floristic quality database obtained from universalfqa.org.

Usage

```
database_inventory(database)
```

Arguments

database A database downloaded from universalfqa.org either manually or using [download_database\(\)](#).

Value

A data frame with 9 columns:

- scientific_name (character)
- family (character)
- acronym (character)
- nativity (character)
- c (numeric)
- w (numeric)
- physiognomy (character)
- duration (character)
- common_name (character)

Examples

```
# While database_glance can be used with a .csv file downloaded  
# manually from the universal FQA website, it is most typically used  
# in combination with download_database().
```

```
chicago_db <- download_database(database_id = 1)  
chicago_species <- database_inventory(chicago_db)
```

download_assessment	<i>Download a single floristic quality assessment</i>
---------------------	---

Description

download_assessment() retrieves a specified floristic quality assessment from universalfqa.org. ID numbers for assessments in various databases can be found using the [index_fqa_assessments\(\)](#) function.

Usage

```
download_assessment(assessment_id, timeout = 4)
```

Arguments

assessment_id	A numeric identifier of the desired floristic quality assessment, as specified by universalfqa.org . ID numbers for assessments in specified databases can be viewed with the index_fqa_assessments() function.
timeout	Number of seconds to query UniversalFQA before timing out.

Value

An untidy data frame in the original format of the Universal FQA website, except that the assessment id number has been appended in the first row. Use [assessment_glance\(\)](#) for a tidy summary and [assessment_inventory\(\)](#) for species-level data.

Examples

```
databases <- index_fqa_databases() # Database 1 is the original 1994 Chicago edition.

chicago_assessments <- index_fqa_assessments(1) # Edison dune and swale has id number 25002.
edison <- download_assessment(25002)

edison_tidy <- assessment_glance(edison)
```

download_assessment_list	<i>Download multiple floristic quality assessments</i>
--------------------------	--

Description

download_assessment_list() searches a specified floristic quality assessment database and retrieves all matches from universalfqa.org. Download speeds from that website may be slow, causing delays in the evaluation of this function.

Usage

```
download_assessment_list(database_id, ...)
```

Arguments

database_id	Numeric identifier of the desired floristic quality assessment database, as specified by universalfqa.org . Database id numbers can be viewed with the index_fqa_databases() function.
...	dplyr-style filtering criteria for the desired assessments. The following variables may be used: • id (numeric) • assessment (character) • date (date) • location (character) • practitioner (character)

Value

A list of data frames matching the search criteria. Each is an untidy data frame in the original format of the Universal FQA website. Use [assessment_list_glance\(\)](#) for a tidy summary.

Examples

```
databases <- index_fqa_databases() # Database 1 is the original 1994 Chicago edition.
somme_assessments <- download_assessment_list(1, site == "Somme Woods")
somme_summary <- assessment_list_glance(somme_assessments)
```

download_database	<i>Download a single floristic quality database</i>
-------------------	---

Description

`download_database()` retrieves a specified floristic quality database from universalfqa.org. A list of available databases can be found using the [index_fqa_databases\(\)](#) function.

Usage

```
download_database(database_id, timeout = 4)
```

Arguments

database_id	A numeric identifier of the desired floristic quality database, as specified by universalfqa.org . ID numbers for databases recognized this site can be viewed with the index_fqa_databases() function.
timeout	Number of seconds to query UniversalFQA before timing out.

Value

An untidy data frame in the original format of the Universal FQA website. Use [database_glance\(\)](#) for a tidy summary and [database_inventory\(\)](#) for species-level data.

Examples

```
databases <- index_fqa_databases() # Database 1 is the original 1994 Chicago edition.

chicago_database <- download_database(1)
```

download_transect	<i>Download a single floristic quality transect assessment</i>
-------------------	--

Description

`download_transect()` retrieves a specified floristic quality transect assessment from universalfqa.org. ID numbers for transect assessments in various databases can be found using the [index_fqa_transects\(\)](#) function.

Usage

```
download_transect(transect_id, timeout = 4)
```

Arguments

transect_id	A numeric identifier of the desired floristic quality transect assessment, as specified by universalfqa.org . ID numbers for transect assessments in specified databases can be viewed with the index_fqa_transects() function.
timeout	Number of seconds to query UniversalFQA before timing out.

Value

An untidy data frame in the original format of the Universal FQA website, except that the transect id number has been appended in the first row.. Use [transect_glance\(\)](#) for a tidy summary, [transect_phys\(\)](#) for a physiognometric overview, and [transect_inventory\(\)](#) for species-level data.

Examples

```
databases <- index_fqa_databases() # Database 1 is the original 1994 Chicago edition.
chicago_transects <- index_fqa_transects(1) # CBG Sand prairie swale fen A has id number 5932.
cbg <- download_transect(5932, timeout = 10)
```

download_transect_list

Download multiple floristic quality transect assessments

Description

download_transect_list() searches a specified floristic quality assessment database and retrieves all matches from universalfqa.org. Download speeds from that website may be slow, causing delays in the evaluation of this function.

Usage

```
download_transect_list(database_id, ...)
```

Arguments

- | | |
|-------------|---|
| database_id | Numeric identifier of the desired floristic quality assessment database, as specified by universalfqa.org . Database id numbers can be viewed with the index_fqa_databases() function. |
| ... | dplyr-style filtering criteria for the desired transect assessments. The following variables may be used: <ul style="list-style-type: none"> • id (numeric) • assessment (character) • date (date) • site (character) • practitioner (character) |

Value

A list of data frames matching the search criteria. Each is an untidy data frame in the original format of the Universal FQA website. Use [transect_list_glance\(\)](#) for a tidy summary.

Examples

```
databases <- index_fqa_databases() # Database 1 is the original 1994 Chicago edition.
dupont <- download_transect_list(1, site == "DuPont Natural Area")
```

index_fqa_assessments *List all available public floristic quality assessments*

Description

For any given database, `index_fqa_assessments()` produces a data frame of all floristic quality assessments publicly available at universalfqa.org.

Usage

```
index_fqa_assessments(database_id, timeout = 4)
```

Arguments

database_id	A numeric identifier of the desired database, as specified by universalfqa.org . The id numbers can be viewed with the <code>index_fqa_databases()</code> function.
timeout	Number of seconds to query UniversalFQA before timing out.

Value

A data frame with 5 columns:

- id (numeric)
- assessment (character)
- date (date)
- site (character)
- practitioner (character)

Examples

```
databases <- index_fqa_databases() # The 2017 Chicago database has id_number 149
chicago_2017_assessments <- index_fqa_assessments(149)
```

index_fqa_databases *List all available floristic quality assessment databases*

Description

`index_fqa_databases()` produces a data frame showing all floristic quality assessment databases publicly available at universalfqa.org.

Usage

```
index_fqa_databases(timeout = 5)
```

Arguments

timeout Number of seconds to query UniversalFQA before timing out.

Value

A data frame with 4 columns:

- database_id (numeric)
- region (character)
- year (numeric)
- description (character)

Examples

```
databases <- index_fqa_databases()
```

index_fqa_transects *List all available public floristic quality transect assessments*

Description

For any given database, `index_fqa_transects()` produces a data frame of all floristic quality transect assessments publicly available at universalfqa.org.

Usage

```
index_fqa_transects(database_id, timeout = 4)
```

Arguments

database_id A numeric identifier of the desired database, as specified by universalfqa.org. The id numbers can be viewed with the `index_fqa_databases()` function.

timeout Number of seconds to query UniversalFQA before timing out.

Value

A data frame with 5 columns:

- id (numeric)
- assessment (character)
- date (date)
- site (character)
- practitioner (character)

Examples

```
databases <- index_fqa_databases() # The 2017 Chicago database has id_number 149
chicago_2017_transects <- index_fqa_transects(149)
```

missouri

Missouri floristic quality assessment data

Description

A data set summarizing 216 floristic quality assessments using the 2015 Missouri database.

Usage

```
missouri
```

Format

A data frame with 52 columns:

- Title (character)
- Date (date)
- Site Name (character)
- City (character)
- County (character)
- State (character)
- Country (character)
- FQA DB Region (character)
- FQA DB Publication Year (character)
- FQA DB Description (character)
- Custom FQA DB Name (character)
- Custom FQA DB Description (character)
- Practitioner (character)
- Latitude (character)
- Longitude (character)
- Weather Notes (character)
- Duration Notes (character)
- Community Type Notes (character)
- Other Notes (character)
- Private/Public (character)

- Total Mean C (numeric)
- Native Mean C (numeric)
- Total FQI: (numeric)
- Native FQI (numeric)
- Adjusted FQI (numeric)
- % C value 0 (numeric)
- % C value 1-3 (numeric)
- % C value 4-6 (numeric)
- % C value 7-10 (numeric)
- Native Tree Mean C (numeric)
- Native Shrub Mean C (numeric)
- Native Herbaceous Mean C (numeric)
- Total Species (numeric)
- Native Species (numeric)
- Non-native Species
- Mean Wetness (numeric)
- Native Mean Wetness (numeric)
- Tree (numeric)
- Shrub (numeric)
- Vine (numeric)
- Forb (numeric)
- Grass (numeric)
- Sedge (numeric)
- Rush (numeric)
- Fern (numeric)
- Bryophyte (numeric)
- Annual (numeric)
- Perennial (numeric)
- Biennial (numeric)
- Native Annual (numeric)
- Native Perennial (numeric)
- Native Biennial (numeric)

Source

universalfqa.org

species_acronym	<i>Acronym of a species in a specified database</i>
-----------------	---

Description

`species_acronym()` accepts a species and a database inventory and returns the acronym of the species within that database. Either a numeric database ID from universalfqa.org or a homemade inventory with the same format may be specified.

Usage

```
species_acronym(species, database_id = NULL, database_inventory = NULL)
```

Arguments

- | | |
|--------------------|---|
| species | The scientific name of the plant species of interest |
| database_id | ID number of an existing database on universalfqa.org . Use index_fqa_databases() to see a list of all such databases. |
| database_inventory | An inventory of species having the same form as one created using database_inventory() , that is, a data frame with 9 columns: <ul style="list-style-type: none">• scientific_name (character)• family (character)• acronym (character)• nativity (character)• c (numeric)• w (numeric)• physiognomy (character)• duration (character)• common_name (character) |

Value

The acronym of the given species within the given database.

Examples

```
species_acronym("Anemone canadensis", database_id = 149)
```

species_c

*C-value of a species in a specified database***Description**

species_c() accepts a species and a database inventory and returns the c-value of that species. Either a numeric database ID from universalfqa.org or a homemade inventory with the same format may be specified.

Usage

```
species_c(species, database_id = NULL, database_inventory = NULL)
```

Arguments

- | | |
|--------------------|---|
| species | The scientific name of the plant species of interest |
| database_id | ID number of an existing database on universalfqa.org . Use index_fqa_databases() to see a list of all such databases. |
| database_inventory | <p>An inventory of species having the same form as one created using database_inventory(), that is, a data frame with 9 columns:</p> <ul style="list-style-type: none"> • scientific_name (character) • family (character) • acronym (character) • nativity (character) • c (numeric) • w (numeric) • physiognomy (character) • duration (character) • common_name (character) |

Value

The C-value of the given species within the given database.

Examples

```
species_c("Anemone canadensis", database_id = 149)
```

species_common_name	<i>Common name of a species in a specified database</i>
---------------------	---

Description

`species_common_name()` accepts the scientific name of a species and a database inventory and returns the common name of that species. Either a numeric database ID from universalfqa.org or a homemade inventory with the same format may be specified.

Usage

```
species_common_name(species, database_id = NULL, database_inventory = NULL)
```

Arguments

- | | |
|--------------------|---|
| species | The scientific name of the plant species of interest |
| database_id | ID number of an existing database on universalfqa.org . Use index_fqa_databases() to see a list of all such databases. |
| database_inventory | An inventory of species having the same form as one created using database_inventory() , that is, a data frame with 9 columns: <ul style="list-style-type: none">• scientific_name (character)• family (character)• acronym (character)• nativity (character)• c (numeric)• w (numeric)• physiognomy (character)• duration (character)• common_name (character) |

Value

The common name of the given species within the given database.

Examples

```
species_common_name("Anemone canadensis", database_id = 149)
```

species_nativity	<i>Nativity of a species in a specified database</i>
------------------	--

Description

`species_nativity()` accepts a species and a database inventory and returns the nativity of that species. Either a numeric database ID from universalfqa.org or a homemade inventory with the same format may be specified.

Usage

```
species_nativity(species, database_id = NULL, database_inventory = NULL)
```

Arguments

- | | |
|--------------------|---|
| species | The scientific name of the plant species of interest |
| database_id | ID number of an existing database on universalfqa.org . Use index_fqa_databases() to see a list of all such databases. |
| database_inventory | An inventory of species having the same form as one created using database_inventory() , that is, a data frame with 9 columns: <ul style="list-style-type: none"> • scientific_name (character) • family (character) • acronym (character) • nativity (character) • c (numeric) • w (numeric) • physiognomy (character) • duration (character) • common_name (character) |

Value

The nativity of the given species within the given database, either native or non-native.

Examples

```
species_nativity("Anemone canadensis", database_id = 149)
```

species_phys

Physiognomy of a species in a specified database

Description

`species_phys()` accepts a species and a database inventory and returns the physiognomy of that species. Either a numeric database ID from universalfqa.org or a homemade inventory with the same format may be specified.

Usage

```
species_phys(species, database_id = NULL, database_inventory = NULL)
```

Arguments

- | | |
|--------------------|---|
| species | The scientific name of the plant species of interest |
| database_id | ID number of an existing database on universalfqa.org . Use index_fqa_databases() to see a list of all such databases. |
| database_inventory | An inventory of species having the same form as one created using database_inventory() , that is, a data frame with 9 columns: <ul style="list-style-type: none">• scientific_name (character)• family (character)• acronym (character)• nativity (character)• c (numeric)• w (numeric)• physiognomy (character)• duration (character)• common_name (character) |

Value

The physiognomy of the given species within the given database

Examples

```
species_phys("Anemone canadensis", database_id = 149)
```

species_profile	<i>Generate the co-occurrence profile for a species</i>
-----------------	---

Description

`species_profile()` accepts a species and list of inventories like those generated by [assessment_list_inventory\(\)](#) and returns the co-occurrence profile of that species. Repeated co-occurrences across multiple assessments are included in summary calculations but self co-occurrences are not.

Usage

```
species_profile(species, inventory_list, native = FALSE)
```

Arguments

<code>species</code>	The scientific name of the target plant species
<code>inventory_list</code>	A list of site inventories having the format of assessment_list_inventory()
<code>native</code>	Logical indicating whether only native co-occurrences should be considered.

Value

A data frame with 14 columns:

- `target_species` (character)
- `target_species_c` (numeric)
- `cospecies_n` (numeric)
- `cospecies_native_n` (numeric)
- `cospecies_mean_c` (numeric)
- `cospecies_native_mean_c` (numeric)
- `cospecies_std_dev_c` (numeric)
- `cospecies_native_std_dev_c` (numeric)
- `percent_native` (numeric)
- `percent_nonnative` (numeric)
- `percent_native_low_c` (numeric)
- `percent_native_med_c` (numeric)
- `percent_native_high_c` (numeric)
- `discrepancy_c` (numeric)

Examples

```
# species_profile() is best used in combination with  
# download_assessment_list() and assessment_list_inventory().
```

```
ontario <- download_assessment_list(database = 2)  
ontario_invs <- assessment_list_inventory(ontario)  
species_profile("Aster lateriflorus", ontario_invs)
```

species_profile_plot	<i>Plot the co-occurrence profile of a species</i>
----------------------	--

Description

`species_profile_plot()` accepts a species and list of inventories like those generated by [assessment_list_inventory\(\)](#) and generates a histogram of the co-occurrence profile of that species. Repeated co-occurrences across multiple assessments are included in summary calculations but self co-occurrences are not.

Usage

```
species_profile_plot(species, inventory_list, native = FALSE)
```

Arguments

species	The scientific name of the target plant species
inventory_list	A list of site inventories having the format of assessment_list_inventory()
native	Logical indicating whether only native co-occurrences should be considered.

Examples

```
# species_profile_plot() is best used in combination with  
# download_assessment_list() and assessment_list_inventory().
```

```
ontario <- download_assessment_list(database = 2)  
ontario_invs <- assessment_list_inventory(ontario)  
species_profile_plot("Aster lateriflorus", ontario_invs, native = TRUE)
```

species_w

*Wetness value of a species in a specified database***Description**

`species_w()` accepts a species and a database inventory and returns the wetness value of that species. Either a numeric database ID from universalfqa.org or a homemade inventory with the same format may be specified.

Usage

```
species_w(species, database_id = NULL, database_inventory = NULL)
```

Arguments

- | | |
|--------------------|---|
| species | The scientific name of the plant species of interest |
| database_id | ID number of an existing database on universalfqa.org . Use index_fqa_databases() to see a list of all such databases. |
| database_inventory | <p>An inventory of species having the same form as one created using database_inventory(), that is, a data frame with 9 columns:</p> <ul style="list-style-type: none"> • scientific_name (character) • family (character) • acronym (character) • nativity (character) • c (numeric) • w (numeric) • physiognomy (character) • duration (character) • common_name (character) |

Value

The wetness value of the given species within the given database.

Examples

```
species_w("Anemone canadensis", database_id = 149)
```

transect_glance	<i>Obtain tidy summary information for a floristic quality transect assessment</i>
-----------------	--

Description

transect_glance() tidies a floristic quality transect assessment data set obtained from universal-fqa.org.

Usage

```
transect_glance(data_set)
```

Arguments

data_set A data set downloaded from universal-fqa.org either manually or using [download_transect\(\)](#).

Value

A data frame with 1 row and 55 columns:

- transect_id (numeric)
- title (character)
- date (date)
- site_name (character)
- city (character)
- county (character)
- state (character)
- country (character)
- omernik_level_three_ecoregion (character)
- fqa_db_region (character)
- fqa_db_publication_year (character)
- fqa_db_description (character)
- fqa_db_selection_name (character)
- custom_fqa_db_name (character)
- custom_fqa_db_description (character)
- practitioner (character)
- latitude (character)
- longitude (character)
- community_code (character)
- community_name (character)

- community_type_notes (character)
- weather_notes (character)
- duration_notes (character)
- environment_description (character)
- other_notes (character)
- transect_plot_type (character)
- plot_size (numeric) Plot size in square meters
- quadrat_subplot_size (numeric) Quadrat or subplot size in square meters
- transect_length (numeric) Transect length in meters
- sampling_design_description (character)
- cover_method (character)
- private_public (character)
- total_mean_c (numeric)
- cover_weighted_mean_c (numeric)
- native_mean_c (numeric)
- total_fqi (numeric)
- native_fqi (numeric)
- cover_weighted_fqi (numeric)
- cover_weighted_native_fqi (numeric)
- adjusted_fqi (numeric)
- c_value_zero (numeric) Percent of c-values 0
- c_value_low (numeric) Percent of c-values 1-3
- c_value_mid (numeric) Percent of c-values 4-6
- c_value_high (numeric) Percent of c-values 7-10
- total_species (numeric)
- native_species (numeric)
- non_native_species (numeric)
- mean_wetness (numeric)
- native_mean_wetness (numeric)
- annual (numeric)
- perennial (numeric)
- biennial (numeric)
- native_annual (numeric)
- native_perennial (numeric)
- native_biennial (numeric)

Examples

```
# While transect_glance can be used with a .csv file downloaded manually
# from the universal FQA website, it is most typically used in combination
# with download_transect().
```

```
tyler <- download_transect(6352)
transect_glance(tyler)
```

transect_inventory	<i>Obtain species details for a floristic quality transect assessment</i>
--------------------	---

Description

transect_inventory() returns a data frame of all plant species included in a floristic quality transect assessment obtained from universalfqa.org.

Usage

```
transect_inventory(data_set)
```

Arguments

data_set A data set downloaded from universalfqa.org either manually or using [download_transect\(\)](#).

Value

A data frame with 13 columns:

- species (character)
- family (character)
- acronym (character)
- nativity (character)
- c (numeric)
- w (numeric)
- physiognomy (character)
- duration (character)
- frequency (numeric)
- coverage (numeric)
- relative_frequency_percent (numeric)
- relative_coverage_percent (numeric)
- relative_importance_value (numeric)

Examples

```
# while transect_glance can be used with a .csv file downloaded
# manually from the universal FQA website, it is most typically used
# in combination with download_transect().
```

```
tyler <- download_transect(6352)
transect_inventory(tyler)
```

transect_list_glance	<i>Obtain tidy summary information for multiple floristic quality transect assessments</i>
----------------------	--

Description

transect_list_glance() tidies a list of floristic quality transect assessment data sets obtained from universalfqa.org, returning summary information as a single data frame.

Usage

```
transect_list_glance(transect_list)
```

Arguments

transect_list A list of data sets downloaded from universalfqa.org, typically using [download_transect_list\(\)](#).

Value

A data frame with 1 row and 55 columns:

- transect_id (numeric)
- title (character)
- date (date)
- site_name (character)
- city (character)
- county (character)
- state (character)
- country (character)
- omernik_level_three_ecoregion (character)
- fqa_db_region (character)
- fqa_db_publication_year (character)
- fqa_db_description (character)

- fqa_db_selection_name (character)
- custom_fqa_db_name (character)
- custom_fqa_db_description (character)
- practitioner (character)
- latitude (character)
- longitude (character)
- community_code (character)
- community_name (character)
- community_type_notes (character)
- weather_notes (character)
- duration_notes (character)
- environment_description (character)
- other_notes (character)
- transect_plot_type (character)
- plot_size (numeric) Plot size in square meters
- quadrat_subplot_size (numeric) Quadrat or subplot size in square meters
- transect_length (numeric) Transect length in meters
- sampling_design_description (character)
- cover_method (character)
- private_public (character)
- total_mean_c (numeric)
- cover_weighted_mean_c (numeric)
- native_mean_c (numeric)
- total_fqi (numeric)
- native_fqi (numeric)
- cover_weighted_fqi (numeric)
- cover_weighted_native_fqi (numeric)
- adjusted_fqi (numeric)
- c_value_zero (numeric) Percent of c-values 0
- c_value_low (numeric) Percent of c-values 1-3
- c_value_mid (numeric) Percent of c-values 4-6
- c_value_high (numeric) Percent of c-values 7-10
- total_species (numeric)
- native_species (numeric)
- non_native_species (numeric)
- mean_wetness (numeric)
- native_mean_wetness (numeric)

- annual (numeric)
- perennial (numeric)
- biennial (numeric)
- native_annual (numeric)
- native_perennial (numeric)
- native_biennial (numeric)

Examples

```
# While transect_list_glance can be used with a list of .csv file downloaded
# manually from the universal FQA website, it is most typically used in
# combination with download_transect_list().
```

```
transect_list <- download_transect_list(149, id %in% c(3400, 3427))
transect_list_glance(transect_list)
```

transect_list_inventory

Obtain species details for a list of transect assessments

Description

transect_list_inventory() returns a list of data frames, each of which consists of all plant species included in a floristic quality assessment of a transect obtained from universalfqa.org.

Usage

```
transect_list_inventory(transect_list)
```

Arguments

transect_list A list of data sets downloaded from universalfqa.org, typically using [download_transect_list\(\)](#).

Value

A list of data frames, each with 13 columns:

- species (character)
- family (character)
- acronym (character)
- nativity (character)
- c (numeric)
- w (numeric)

- physiognomy (character)
- duration (character)
- frequency (numeric)
- coverage (numeric)
- relative_frequency_percent (numeric)
- relative_coverage_percent (numeric)
- relative_importance_value (numeric)

Examples

```
# While transect_list_inventory can be used with a list of .csv file downloaded
# manually from the universal FQA website, it is most typically used
# in combination with download_transect_list()

chicago <- download_transect_list(database = 149)
chicago_invs <- transect_list_inventory(chicago)
```

transect_phys	<i>Obtain physiognometric information for a floristic quality transect assessment</i>
---------------	---

Description

transect_phys() returns a data frame with physiognometric information for a floristic quality transect assessment obtained from universalfqa.org.

Usage

```
transect_phys(data_set)
```

Arguments

data_set A data set downloaded from universalfqa.org either manually or using [download_transect\(\)](#).

Value

A data frame with 6 columns:

- physiognomy (character)
- frequency (numeric)
- coverage (numeric)
- relative_frequency_percent (numeric)
- relative_coverage_percent (numeric)
- relative_importance_value_percent (numeric)

Examples

```
# While transect_phys can be used with a .csv file downloaded  
# manually from the universal FQA website, it is most typically used  
# in combination with download_transect().
```

```
tyler <- download_transect(6352)  
transect_phys(tyler)
```

transect_subplot_inventories

Extract quadrat/subplot-level inventories from a transect assessment

Description

transect_subplot_inventories() accepts a floristic quality transect assessment data set obtained from universalfqa.org and returns a list of species inventories, one per quadrat/subplot.

Usage

```
transect_subplot_inventories(transect)
```

Arguments

transect A data set downloaded from universalfqa.org either manually or using [download_transect\(\)](#).

Value

A list of data frames, each with 9 columns:

- scientific_name (character)
- family (character)
- acronym (character)
- nativity (character)
- c (numeric)
- w (numeric)
- physiognomy (character)
- duration (character)
- common_name (character)

Examples

```
cbg_fen <- download_transect(5932)  
cbg_inventories <- transect_subplot_inventories(cbg_fen)
```

Index

* datasets

chicago, [11](#)
missouri, [21](#)

assessment_cooccurrences, [2](#)
assessment_cooccurrences_summary, [4](#)
assessment_glance, [5](#)
assessment_glance(), [15](#)
assessment_inventory, [7](#)
assessment_inventory(), [15](#)
assessment_list_glance, [8](#)
assessment_list_glance(), [16](#)
assessment_list_inventory, [10](#)
assessment_list_inventory(), [3](#), [4](#), [28](#), [29](#)

chicago, [11](#)

database_glance, [13](#)
database_glance(), [17](#)
database_inventory, [14](#)
database_inventory(), [17](#), [23–27](#), [30](#)
download_assessment, [15](#)
download_assessment(), [5](#), [7](#)
download_assessment_list, [15](#)
download_assessment_list(), [8](#), [10](#)
download_database, [16](#)
download_database(), [13](#), [14](#)
download_transect, [17](#)
download_transect(), [31](#), [33](#), [37](#), [38](#)
download_transect_list, [18](#)
download_transect_list(), [34](#), [36](#)

index_fqa_assessments, [19](#)
index_fqa_assessments(), [15](#)
index_fqa_databases, [19](#)
index_fqa_databases(), [16](#), [18–20](#), [23–27](#),
[30](#)

index_fqa_transects, [20](#)
index_fqa_transects(), [17](#)

missouri, [21](#)

species_acronym, [23](#)
species_c, [24](#)
species_common_name, [25](#)
species_nativity, [26](#)
species_phys, [27](#)
species_profile, [28](#)
species_profile_plot, [29](#)
species_w, [30](#)

transect_glance, [31](#)
transect_glance(), [17](#)
transect_inventory, [33](#)
transect_inventory(), [17](#)
transect_list_glance, [34](#)
transect_list_glance(), [18](#)
transect_list_inventory, [36](#)
transect_phys, [37](#)
transect_phys(), [17](#)
transect_subplot_inventories, [38](#)