Package 'fqar'

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Type Package

Title Floristic Quality Assessment Tools for R

Version 0.5.4

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

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VignetteBuilder knitr

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BugReports https://github.com/equitable-equations/fqar/issues

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Contents

`assessment_cooccurrences`

Generate a species co-occurrence matrix from assessment inventories

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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_coccurrences_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` *Obtain tidy summary information for a floristic quality assessment*

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 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_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 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_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 *Obtain tidy summary information for a floristic quality database*

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` *Obtain species details for a floristic quality database*

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 *Download a single floristic quality assessment*

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)
```

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.

Value

An untidy data frame in the original format of the Universal FQA website. 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)
edison_species <- assessment_inventory(edison)
```

download_assessment_list *Download multiple floristic quality assessments*

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 *Download a single floristic quality database*

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)
```

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.

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 *Download a single floristic quality transect assessment*

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)
```

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.

Value

An untidy data frame in the original format of the Universal FQA website. 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)
```

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: • 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)
```

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.

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()
```

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)
```

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.

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` *Acronym of a species in a specified database*

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: • 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	An inventory of species having the same form as one created using database_inventory(), that is, 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)

Value

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

Examples

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

`species_common_name` *Common name of a species in a specified database*

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: • 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` *Nativity of a species in a specified database*

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:

- 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:

- 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` *Generate the co-occurrence profile for a species*

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

`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.

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 *Plot the co-occurrence profile of a species*

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`	An inventory of species having the same form as one created using `database_inventory()`, that is, 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)

Value

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

Examples

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

`transect_glance` *Obtain tidy summary information for a floristic quality transect assessment*

Description

`transect_glance()` tidies a floristic quality transect assessment data set obtained from universalfqa.org.

Usage

```
transect_glance(data_set)
```

Arguments

`data_set`	A data set downloaded from universalfqa.org either manually or using `download_transect()`.

Value

A data frame with 1 row and 54 columns:

- 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` *Obtain species details for a floristic quality transect assessment*

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

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 54 columns:

- 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` *Obtain physiognometric information for a floristic quality transect assessment*

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)
```

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