Package ‘fqar’

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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_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 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` *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, 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` *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, 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` *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, 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: • 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 `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_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` *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 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` *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 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` *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)
```

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