

# Package: fqr (via r-universe)

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**Type** Package

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**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.

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---

assessment\_cooccurrences

*Generate a species co-occurrence matrix from assessment inventories*

---

### Description

assessment\_cooccurrences() accepts a list of species inventories downloaded from [universalfqa.org](http://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](http://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](http://universalfqa.org).

## Usage

```
assessment_glance(data_set)
```

## Arguments

data\_set      A data set downloaded from [universalfqa.org](http://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](http://universalfqa.org).

## Usage

```
assessment_inventory(data_set)
```

## Arguments

data\_set        A data set downloaded from [universalfqa.org](http://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](http://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](http://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](http://universalfqa.org).

## Usage

```
assessment_list_inventory(assessment_list)
```

## Arguments

assessment\_list

A list of data sets downloaded from [universalfqa.org](http://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](http://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](http://universalfqa.org).

### Usage

```
database_glance(database)
```

### Arguments

database      A database downloaded from [universalfqa.org](http://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](http://universalfqa.org).

### Usage

```
database_inventory(database)
```

### Arguments

database      A database downloaded from [universalfqa.org](http://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](http://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](http://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](http://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](http://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)
```

---

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

---

**Description**

`download_database()` retrieves a specified floristic quality database from [universalfqa.org](http://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](http://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	<i>Download a single floristic quality transect assessment</i>
-------------------	--

---

**Description**

`download_transect()` retrieves a specified floristic quality transect assessment from [universalfqa.org](http://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](http://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](http://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

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

### 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](http://universalfqa.org).

### Usage

```
index_fqa_assessments(database_id)
```

### Arguments

`database_id` A numeric identifier of the desired database, as specified by [universalfqa.org](http://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](http://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](http://universalfqa.org).

**Usage**

```
index_fqa_transects(database_id)
```

**Arguments**

`database_id` A numeric identifier of the desired database, as specified by [universalfqa.org](http://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](http://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](http://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 <a href="http://universalfqa.org">universalfqa.org</a> . Use <a href="#">index_fqa_databases()</a> to see a list of all such databases.
database_inventory	An inventory of species having the same form as one created using <a href="#">database_inventory()</a> , that is, a data frame with 9 columns: <ul style="list-style-type: none"> <li>• scientific_name (character)</li> <li>• family (character)</li> <li>• acronym (character)</li> <li>• nativity (character)</li> <li>• c (numeric)</li> <li>• w (numeric)</li> <li>• physiognomy (character)</li> <li>• duration (character)</li> <li>• common_name (character)</li> </ul>

### 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](http://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 <a href="http://universalfqa.org">universalfqa.org</a> . Use <a href="#">index_fqa_databases()</a> to see a list of all such databases.  |
| database_inventory | An inventory of species having the same form as one created using <a href="#">database_inventory()</a> , that is, a data frame with 9 columns: <ul style="list-style-type: none"> <li>• scientific_name (character)</li> <li>• family (character)</li> <li>• acronym (character)</li> <li>• nativity (character)</li> <li>• c (numeric)</li> <li>• w (numeric)</li> <li>• physiognomy (character)</li> <li>• duration (character)</li> <li>• common_name (character)</li> </ul> |

### 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](http://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 <a href="http://universalfqa.org">universalfqa.org</a> . Use <a href="#">index_fqa_databases()</a> to see a list of all such databases.  |
| database_inventory | An inventory of species having the same form as one created using <a href="#">database_inventory()</a> , that is, a data frame with 9 columns: <ul style="list-style-type: none"><li>• scientific_name (character)</li><li>• family (character)</li><li>• acronym (character)</li><li>• nativity (character)</li><li>• c (numeric)</li><li>• w (numeric)</li><li>• physiognomy (character)</li><li>• duration (character)</li><li>• common_name (character)</li></ul> |

### 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](http://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 <a href="http://universalfqa.org">universalfqa.org</a> . Use <code>index_fqa_databases()</code> to see a list of all such databases.  |
| database_inventory | An inventory of species having the same form as one created using <code>database_inventory()</code> , that is, a data frame with 9 columns: <ul style="list-style-type: none"><li>• scientific_name (character)</li><li>• family (character)</li><li>• acronym (character)</li><li>• nativity (character)</li><li>• c (numeric)</li><li>• w (numeric)</li><li>• physiognomy (character)</li><li>• duration (character)</li><li>• common_name (character)</li></ul> |

### 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](http://universalfqa.org) or a homemade inventory with the same format may be specified.

### Usage

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

### Arguments

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

### 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

species	The scientific name of the target plant species
inventory_list	A list of site inventories having the format of <a href="#">assessment_list_inventory()</a>
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 <a href="#">assessment_list_inventory()</a>
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](http://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 <a href="http://universalfqa.org">universalfqa.org</a> . Use <a href="#">index_fqa_databases()</a> to see a list of all such databases.  |
| database_inventory | An inventory of species having the same form as one created using <a href="#">database_inventory()</a> , that is, a data frame with 9 columns: <ul style="list-style-type: none"> <li>• scientific_name (character)</li> <li>• family (character)</li> <li>• acronym (character)</li> <li>• nativity (character)</li> <li>• c (numeric)</li> <li>• w (numeric)</li> <li>• physiognomy (character)</li> <li>• duration (character)</li> <li>• common_name (character)</li> </ul> |

### 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 [universalfqa.org](http://universalfqa.org).

### Usage

```
transect_glance(data_set)
```

### Arguments

data\_set      A data set downloaded from [universalfqa.org](http://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	<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](http://universalfqa.org).

## Usage

```
transect_inventory(data_set)
```

## Arguments

data\_set      A data set downloaded from [universalfqa.org](http://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](http://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](http://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](http://universalfqa.org).

## Usage

```
transect_list_inventory(transect_list)
```

## Arguments

transect\_list A list of data sets downloaded from [universalfqa.org](http://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](http://universalfqa.org).

### Usage

```
transect_phys(data_set)
```

### Arguments

data\_set      A data set downloaded from [universalfqa.org](http://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](http://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](http://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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