

Package ‘deltabreedquery’

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Type Package

Title Fast, Simple API Tools for Retrieving Data from 'DeltaBreed'

Version 1.0.3

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Description Simplified data retrieval from the 'DeltaBreed' breeding data management platform (<<https://sandbox.breedinginsight.net/>>) via the 'BrAPI' open-source breeding data API (<<https://brapi.org/specification>>). Each of the four main data types stored in 'DeltaBreed' (germplasm, trait variables, experiments/environments, and observations) are handled by a `get_datatype()` function that constructs and executes the request, handles paginated responses, and parses the retrieved data. Responses are reformatted into a consistent, R-friendly data frame format that resembles how the data appears on the 'DeltaBreed' web interface as closely as possible.

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Encoding UTF-8

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check_auth	<i>Validate BrAPI authentication credentials</i>
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Description

Checks if the user has credentials currently stored and validates them by performing a test call to the BrAPI endpoint. Also prints the remaining time until the access token expires, if applicable.

Usage

```
check_auth()
```

Value

No return value, called for side effects (printing status)

Examples

```
check_auth()  
login_deltabreed("example", verbose = FALSE)  
check_auth()
```

filter_observations	<i>Retrieve a filtered list of observation data</i>
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Description

This function retrieves a foo filtered list of observation data using one or more filter values provided by the user, packaging the response into a data frame of the same format as [get_observations\(\)](#).
This function is best used by calling [get_experiments\(\)](#) first, in order to see what experiments are actually present in the target DeltaBreed instance.

Usage

```
filter_observations(
  year = NA,
  location = NA,
  exp_name = NA,
  env_name = NA,
  exp_type = NA,
  page_size = 10000,
  drop_empty_columns = FALSE,
  include_dbids = FALSE,
  verbose = TRUE
)
```

Arguments

year	A year or vector of years.
location	A location name or vector of locations.
exp_name	An experiment name or vector of names.
env_name	An environment name or vector of names.
exp_type	An experiment type or vector of types.
page_size	Page size to use for the response. Larger page sizes may decrease total retrieval time.
drop_empty_columns	Whether to drop all empty columns (including metadata columns) from the returned data frame
include_dbids	Whether to include the DbIds of the observation units, mostly useful for debugging.
verbose	Whether to print short messages about the number of records found.

Value

A data frame of observations using the supplied filters.

Examples

```
login_deltabreed("example", verbose = FALSE)

# the available filters (and values to filter on) correspond to columns of get_experiments()
get_experiments()

all_obs <- get_observations(verbose = FALSE)
manitoba <- filter_observations(location = "Manitoba")
table(all_obs$Location)
table(manitoba$Location)

# all filters can take vectors as arguments
almtis <- filter_observations(location = c("Alma", "Tisdale"))
```

```
table(almtis$Year, almtis$Location)

# filters can be combined as needed
ayt_mb <- filter_observations(exp_type = "AYT", location = "Manitoba")
table(ayt_mb$ExpName, ayt_mb$EnvName)
```

get_experiments	<i>Retrieve experiment/ summary</i>
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Description

Retrieves a summary of all experiments and environments in a given DeltaBreed program. This may include experiments for which no observations have been recorded yet.

Usage

```
get_experiments(verbose = TRUE, include_dbids = FALSE)
```

Arguments

verbose	Whether to print out the number of experiments/environments found.
include_dbids	Whether to include the lengthy unique ID for each experiment/environment. Typically used for debugging or merging data from other sources.

Value

Data frame of experiment/environment metadata.

Examples

```
login_deltabreed("example", verbose = FALSE)

expt <- get_experiments()
expt
```

get_germplasm	<i>Retrieve germplasm records</i>
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Description

Retrieves all germplasm data from the current DeltaBreed instance, reformatting it to match DeltaBreed layout.

Usage

```
get_germplasm(page_size = 10000)
```

Arguments

`page_size` Page size to use for the response. Larger page sizes may decrease total retrieval time.

Value

Data frame of germplasm/accession/entry information.

Examples

```
login_deltabreed("example", verbose = FALSE)

germplasm <- get_germplasm()
head(germplasm)
```

get_observations	<i>Retrieve all observation data</i>
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Description

Retrieves all observation data from a DeltaBreed instance via BrAPI call. This includes observation units with no observations. converting it into a data frame that mimics the appearance of the data tables on the Experiments & Observations tab of DeltaBreed.

Usage

```
get_observations(
  page_size = 10000,
  drop_empty_columns = FALSE,
  include_dbids = FALSE,
  verbose = TRUE
)
```

Arguments

`page_size` Page size to use for the response. Larger page sizes may decrease total retrieval time.

`drop_empty_columns` Whether to drop all empty columns (including metadata columns) from the returned data frame.

`include_dbids` Whether to include the DbIds of the observation units, mostly useful for debugging.

`verbose` Whether to print short messages showing the number of records found.

Value

A data frame of all observation units and any observations (phenotypes).

Examples

```
login_deltabreed("example", verbose = FALSE)
obs <- get_observations()

# phenotype columns will be typed according to the observation variables (trait definitions)
str(obs[,16:20])
get_variables()
```

get_variables	<i>Retrieve observation variables (trait definitions) from a DeltaBreed instance.</i>
---------------	---

Description

Retrieves trait data from a DeltaBreed program via BrAPI, converting it into a data frame that mimics the appearance of the Ontology table in DeltaBreed itself.

Usage

```
get_variables(verbose = TRUE, include_archived = FALSE)
```

Arguments

verbose	Whether to print a short message about the number of traits found.
include_archived	Whether the output should include archived (non-active).

Value

Data frame of trait definitions drawn from BrAPI /variables endpoint.

Examples

```
login_deltabreed("example", verbose = FALSE)

vars <- get_variables()
vars
```

login_deltabreed	<i>Log in to a DeltaBreed instance</i>
------------------	--

Description

This function stores your authentication credentials for a target DeltaBreed instance. To log in, you will require the BrAPI Base URL and a valid authentication token, both of which can be found on the 'BrAPI' tab of DeltaBreed.

The URL and token can be given as arguments or supplied to function prompts. The function performs some basic checks, including verifying that the user has internet access and making some test calls to the BrAPI server.

Usage

```
login_deltabreed(base_url = NULL, access_token = NULL, verbose = TRUE)
```

Arguments

base_url	The BrAPI Base URL, found on the BrAPI tab of DeltaBreed in the BrAPI Information pane.
access_token	A valid Access Token, retrieved from the DeltaBreed user interface.
verbose	Whether to print out success messages.

Details

Access tokens are valid for 24 hours after generation. To check your authorization credentials at any time, use the [check_auth\(\)](#) function.

Value

No return value, called for side effects (storing credentials)

Examples

```
## Not run:  
# function can be run with no arguments to bring up a prompt to enter the URL/token  
login_deltabreed()  
  
# since your program's URL will remain static, you can supply it as an argument, e.g.:  
login_deltabreed("https://app.breedinginsight.net/v1/programs/f152169d-049f-4a7c-b5d8-c725b14e66f0")  
  
## End(Not run)
```

logout_deltabreed	<i>Clear DeltaBreed authentication credentials</i>
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Description

Removes stored credentials (URL and access token) from the package environment. The access token will remain valid for as long as the DeltaBreed instance specifies, but in order to retrieve data the URL/token will need to be-entered with [login_deltabreed\(\)](#).

Usage

```
logout_deltabreed()
```

Value

No return value, called for side effects (clearing credentials)

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