Package ‘QBMS’

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Type Package

Title Query the Breeding Management System(s)

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Description Query the Breeding Management System(s) like BMS <https://bmspro.io>,
      BreeBase <https://breedbase.org>, and GIGWA <https://southgreen.fr/content/gigwa>
      (using 'BrAPI' <https://brapi.org> calls) to help breeders as targeted end-users
      retrieve phenotypic and genotypic data directly into their analyzing pipelines.

License GPL (>= 3)

URL https://github.com/icarda-git/QBMS

BugReports https://github.com/icarda-git/QBMS/issues

Depends R (>= 3.1.0)

Imports httr, jsonlite, tcltk, utils

Suggests knitr, rmarkdown

VignetteBuilder knitr

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**brapi_get_call**  
*Internal function used for core BrAPI GET calls*

**Description**

This function is created for **internal use only** to call BrAPI in GET method and retrieve the rough response data and send back the results. This function takes care of pagination, authentication, encoding, compress, decode JSON response, etc.

**Usage**

```r
brapi_get_call(call_url, page = 0, nested = TRUE)
```

**Arguments**

- **call_url**: BrAPI URL to call in GET method
- **page**: Page number to retrieve in case of multi-paged results (default is 0)
- **nested**: If FALSE, then retrieved JSON data will be flattened (default is TRUE)

**Value**

result object returned by JSON API response

**Author(s)**

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

---

**build_pedigree_table**  
*Building Pedigree Table Recursively*

**Description**

Internal helping function to build the pedigree table recursively.

**Usage**

```r
build_pedigree_table(
    geno_list = NULL,
    pedigree_list = NULL,
    pedigree_df = NULL
)
```
Arguments

- `geno_list`: List of genotypes/germplasms names.
- `pedigree_list`: List of associated pedigree strings.
- `pedigree_df`: Pedigree data.frame as per previous call/iteration.

Value

A data.frame that has three columns correspond to the identifiers for the individual, female parent and male parent, respectively.

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

---

`debug_qbms` *Debug internal QBMS status object*

Description

Return the internal QBMS status object for debugging.

Usage

`debug_qbms()`

Value

an environment object for the package config and status

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

Examples

```r
obj <- debug_qbms()
obj$config
obj$state
```
**get_crop_locations**

*Get the list of locations information of the current selected crop*

**Description**

This function will retrieve the locations information of the current active crop as configured in the internal state object using `set_crop()` function.

**Usage**

```r
get_crop_locations()
```

**Value**

a data frame of the locations information

**Author(s)**

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

**See Also**

`login_bms`, `set_crop`

---

**get_germplasm_data**

*Get the observations data of a given germplasm name*

**Description**

This function will retrieve the observations data of the current active study as configured in the internal state object using `set_study()` function.

**Usage**

```r
get_germplasm_data(germplasm_name)
```

**Arguments**

- `germplasm_name` the name of the germplasm

**Value**

a data frame of the germplasm observations data aggregate from all trials

**Author(s)**

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>
get_germplasm_list

See Also

login_bms, set_crop, set_program

Examples

if(interactive()) {
  # config your BMS connection
  set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

  # login using your BMS account (interactive mode)
  # you can pass BMS username and password as parameters (batch mode)
  login_bms()

  set_crop("maize")

  # select a breeding program by name
  set_program("MC Maize")

  # reetrive observations data of a given germplasm aggregated from all trials
  germplasm_observations <- get_germplasm_data("BASFCORN-2-1")
}

get_germplasm_list  Get the germplasm list of the current active study

Description

This function will retrieve the germplasm list of the current active study as configured in the internal state object using ‘set_study()’ function.

Usage

get_germplasm_list()

Value

a data frame of the study germplasm list

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

See Also

login_bms, set_crop, set_program, set_trial, set_study
**get_login_details**

**Examples**

```r
if(interactive()) {
  # config your BMS connection
  set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

  # login using your BMS account (interactive mode)
  # you can pass BMS username and password as parameters (batch mode)
  login_bms()

  set_crop("maize")

  # select a breeding program by name
  set_program("MC Maize")

  # select a specific study/trial by name
  set_trial("2018 PVT")

  # select a specific environment/location dataset
  set_study("2018 PVT Environment Number 1")

  # retrieve the germplasm list of the selected environment/location
  germplasm <- get_germplasm_list()
}
```

---

**get_login_details**  
*Login pop-up window*

**Description**

Build a GUI pop-up window using Tcl/Tk to insert BMS username and password

**Usage**

```r
get_login_details()
```

**Value**

a vector of inserted username and password

**Author(s)**

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>
get_pedigree_table

get_parents  Get Direct Parents

Description
Internal helping function to split the given pedigree string that provides the parentage through which a cultivar was obtained, and get the pedigrees of the direct parents.

Usage
get_parents(pedigree)

Arguments
pedigree  String provide the parentage through which a cultivar was obtained.

Value
Vector of two items, the direct female and male parents.

Author(s)
Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

get_pedigree_table  Get the Pedigree Table

Description
Get the pedigree table starting from current germplasm list and associated pedigree string that provides the parentage through which a cultivar was obtained.

Usage
get_pedigree_table(
data,
  geno_column = "germplasmName",
  pedigree_column = "pedigree"
)

Arguments
data  germplasm dataset as a data.frame.
geno_column  name of the column that identifies the genotype/germplasm names.
pedigree_column  name of the column that identifies the pedigree strings.
get_pedigree_table

Value

A data.frame that has three columns correspond to the identifiers for the individual, female parent and male parent, respectively. The row giving the pedigree of an individual appears before any row where that individual appears as a parent. Founders use NA in the parental columns.

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

Examples

```r
if(interactive()) {
  # config your BMS connection
  set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

  # login using your BMS account (interactive mode)
  # you can pass BMS username and password as parameters (batch mode)
  login_bms()

  set_crop("maize")

  # select a breeding program by name
  set_program("MC Maize")

  # select a specific study/trial by name
  set_trial("2018 PVT")

  # select a specific environment/location dataset
  set_study("2018 PVT Environment Number 1")

  # retrieve the germplasm list of the selected environment/location
  germplasm <- get_germplasm_list()

  pedigree_table <- get_pedigree_table(germplasm, "germplasmName", "pedigree")

  # nadiv package way
  # library(nadiv)

  # get additive relationship matrix in sparse matrix format
  # A <- nadiv::makeA(pedigree_table)

  # get A inverse matrix using base R function
  # AINV <- solve(as.matrix(A))

  # ASReml-R package way
  # library(asreml)

  # represent A inverse matrix in efficient way using i,j index and Ainverse value
  # actual genotype names of any given index are in the attr(ainv, "rowNames")
  # ainv <- asreml::ainverse(pedigree_table)
```
get_program_studies

Get the list of trials studies locations information of the current selected program

Description

This function will retrieve all environments/locations information of the trials studies in the current active program as configured in the internal state object using 'set_program()' function.

Usage

get_program_studies()

Value

a data frame of locations information for each study in the program trials

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

See Also

login_bms, set_crop, set_program

Examples

if(interactive()) {
    # config your BMS connection
    set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

    # login using your BMS account (interactive mode)
    # you can pass BMS username and password as parameters (batch mode)
    login_bms()

    set_crop("maize")

    # select a breeding program by name
    set_program("MC Maize")

    # retrieve all environments/locations information in the selected program studies/trials
get_program_trials

```r
program_studies <- get_program_studies()
```

get_program_trials  Internal function used to retrieve the rough list of trials

Description

This function created for *internal use only* to retrieve the rough list of trials from the pre-selected (i.e. currently active) crop and breeding program combination as already configured in the internal state object using ‘set_crop()’ and ‘set_program()’ functions respectively.

Usage

```r
get_program_trials()
```

Value

a list of trials information

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

See Also

`login_bms, set_crop, set_program, list_trials`

get_study_data  Get the observations data of the current active study

Description

This function will retrieve the observations data of the current active study as configured in the internal state object using ‘set_study()’ function.

Usage

```r
get_study_data()
```

Value

a data frame of the study observations data

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>
See Also

login_bms, set_crop, set_program, set_trial, set_study

Examples

```r
if(interactive()) {
  # config your BMS connection
  set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

  # login using your BMS account (interactive mode)
  # you can pass BMS username and password as parameters (batch mode)
  login_bms()

  set_crop("maize")

  # select a breeding program by name
  set_program("MC Maize")

  # select a specific study/trial by name
  set_trial("2018 PVT")

  # select a specific environment/location dataset
  set_study("2018 PVT Environment Number 1")

  # retrieve the data of the selected environment/location
  data <- get_study_data()
}
```

get_study_info

Get the details/metadata of the current active study

Description

This function will retrieve the details/metadata of the current active study as configured in the internal state object using `set_study()` function.

Usage

get_study_info()

Value

a data frame of the study details/metadata

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>
get_trial_data

See Also

login_bms, set_crop, set_program, set_trial, set_study

Examples

```r
if(interactive()) {
  # config your BMS connection
  set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

  # login using your BMS account (interactive mode)
  # you can pass BMS username and password as parameters (batch mode)
  login_bms()

  set_crop("maize")

  # select a breeding program by name
  set_program("MC Maize")

  # select a specific study/trial by name
  set_trial("2018 PVT")

  # select a specific environment/location dataset
  set_study("2018 PVT Environment Number 1")

  # retrieve the general information of the selected environment/location
  info <- get_study_info()
}
```

get_trial_data

Get the observations data of the current active trial

Description

This function will retrieve the observations data of the current active trial (i.e. including all studies within) as configured in the internal state object using 'set_trial()' function.

Usage

get_trial_data()

Value

a data frame of the trial observations data

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>
get_trial_obs_ontology

Get the traits ontology/metadata of the current active trial

Description

This function will retrieve the traits ontology/metadata of the current active trial as configured in the internal state object using `set_trial()` function.

Usage

get_trial_obs_ontology()

Value

a data frame of the traits ontology/metadata

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>
gigwa_get_samples

See Also

login_bms, set_crop, set_program, set_trial

Examples

if(interactive()) {
  # config your BMS connection
  set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

  # login using your BMS account (interactive mode)
  # you can pass BMS username and password as parameters (batch mode)
  login_bms()

  set_crop("maize")

  # select a breeding program by name
  set_program("MC Maize")

  # select a specific study/trial by name
  set_trial("2018 PVT")

  # get observation variable ontology
  ontology <- get_trial_obs_ontology()
}

---

gigwa_get_samples  Get the samples list of the current active GIGWA run

Description

This function will retrieve the samples list of the current active run as configured in the internal state object using ‘gigwa_set_run()’ function.

Usage

gigwa_get_samples()

Value

a vector of all samples in the selected run

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

See Also

set_qbms_config, gigwa_set_run
Examples

```r
if(interactive()) {
  # config your GIGWA connection
  set_qbms_config("https://gigwa.southgreen.fr/gigwa/",
                  time_out = 300, engine = "gigwa", no_auth = TRUE)

  # select a database by name
  gigwa_set_db("Sorghum-JGL_v1")

  # select a project by name
  gigwa_set_project("Nelson_et_al_2011")

  # select a specific run by name
  gigwa_set_run("run1")

  # get a list of all samples in the selected run
  samples <- gigwa_get_samples()
}
```

---

**gigwa_get_variants**

**Get variants in the selected GIGWA run**

**Description**

Query the variants (e.g., SNPs markers) in the selected GIGWA run that match a given criteria.

**Usage**

```r
gigwa_get_variants(max_missing = 1, min_maf = 0, samples = NULL)
```

**Arguments**

- `max_missing`: maximum missing ratio (by sample) between 0 and 1 (default is 1 for 100%).
- `min_maf`: minimum Minor Allele Frequency (MAF) between 0 and 1 (default is 0 for 0%).
- `samples`: a list of a samples subset (default is NULL will retrieve for all samples).

**Value**

A data.frame that has the first 4 columns describe attributes of the SNP (`rs#`: variant name, `alleles`: reference allele / alternative allele, `chrom`: chromosome name, and `pos`: position in bp), while the following columns describe the SNP value for a single sample line using numerical coding 0, 1, and 2 for reference, heterozygous, and alternative/minor alleles.

**Author(s)**

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>
Examples

if(interactive()) {
  # config your GIGWA connection
  set_qbms_config("https://gigwa.southgreen.fr/gigwa/",
                  time_out = 300, engine = "gigwa", no_auth = TRUE)

  # select a database by name
  gigwa_set_db("Sorghum-JGI_v1")

  # select a project by name
  gigwa_set_project("Nelson_et_al_2011")

  # select a specific run by name
  gigwa_set_run("run1")

  marker_matrix <- gigwa_get_variants(max_missing = 0.2,
                                       min_maf = 0.35,
                                       samples = c("ind1", "ind3", "ind7"))
}

---

### gigwa_list_dbs

*Get the list of existing databases in the current GIGWA server*

#### Description

Get the list of existing databases in the current GIGWA server

#### Usage

```r
  gigwa_list_dbs()
```

#### Value

a list of existing databases

#### Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

#### See Also

`set_qbms_config`
Examples

```r
if(interactive()) {
  # config your GIGWA connection
  set_qbms_config("https://gigwa.southgreen.fr/gigwa/",
                   time_out = 300, engine = "gigwa", no_auth = TRUE)
  
  # list existing databases in the GIGWA server
  gigwa_list_dbs()
}
```

---

### gigwa_list_projects

*Get the list of all projects in the selected GIGWA database*

Description

This function will retrieve the projects list from the current active database as configured in the internal configuration object using `gigwa_set_db()` function.

Usage

```r
gigwa_list_projects()
```

Value

a list of projects names

Author(s)

Khaled Al-Shamaa, <k.e1-shamaa@cgiar.org>

See Also

`set_qbms_config`, `gigwa_set_db`

Examples

```r
if(interactive()) {
  # config your GIGWA connection
  set_qbms_config("https://gigwa.southgreen.fr/gigwa/",
                   time_out = 300, engine = "gigwa", no_auth = TRUE)

  # select a database by name
  gigwa_set_db("Sorghum-JGI_v1")

  # list existing projects
  gigwa_list_projects()
}
```
gigwa_list_runs

Get the list of run names in the selected GIGWA project

Description

This function will retrieve the runs list from the current active project as configured in the internal configuration object using `gigwa_set_project()` function.

Usage

```r
gigwa_list_runs()
```

Value

a list of runs names

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

See Also

`set_qbms_config`, `gigwa_set_project`

Examples

```r
if(interactive()) {
  # config your GIGWA connection
  set_qbms_config("https://gigwa.southgreen.fr/gigwa/",
                  time_out = 300, engine = "gigwa", no_auth = TRUE)

  # select a database by name
  gigwa_set_db("Sorghum-JGI_v1")

  # select a project by name
  gigwa_set_project("Nelson_et_al_2011")

  # list all runs in the selected project
  gigwa_list_runs()
}
```
gigwa_set_db

Set the current active GIGWA database by name

Description

This function will update the current active database in the internal configuration object (including the brapi connection object).

Usage

```r
gigwa_set_db(db_name)
```

Arguments

- `db_name` the name of the database

Value

no return value

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

See Also

- `set_qbms_config`
- `gigwa_list_dbs`

Examples

```r
if(interactive()) {
  # config your GIGWA connection
  set_qbms_config("https://gigwa.southgreen.fr/gigwa/",
                  time_out = 300, engine = "gigwa", no_auth = TRUE)

  # select a database by name
  gigwa_set_db("Sorghum-JGI_v1")
}
```
gigwa_set_project  

Set the current active GIGWA project

Description

This function will update the current active project in the internal state object using the programDbId retrieved from GIGWA which is associated to the given ‘project_name’ parameter.

Usage

```
gigwa_set_project(project_name)
```

Arguments

- `project_name`: the name of the project

Value

- no return value

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

See Also

- `set_qbms_config`
- `gigwa_set_db`
- `gigwa_list_projects`

Examples

```
if(interactive()) {
  # config your GIGWA connection
  set_qbms_config("https://gigwa.southgreen.fr/gigwa/",
                   time_out = 300, engine = "gigwa", no_auth = TRUE)

  # select a database by name
  gigwa_set_db("Sorghum-JGI_v1")

  # select a project by name
  gigwa_set_project("Nelson_et_al_2011")
}
```
gigwa_set_run

Set the current active GIGWA run

Description

This function will update the current active run in the internal state object using the 'studyDbIds' retrieved from GIGWA which is associated to the given run_name parameter.

Usage

gigwa_set_run(run_name)

Arguments

run_name       the name of the run

Value

no return value

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

See Also

set_qbms_config, gigwa_set_project, gigwa_list_runs

Examples

if(interactive()) {
  # config your GIGWA connection
  set_qbms_config("https://gigwa.southgreen.fr/gigwa/",
                  time_out = 300, engine = "gigwa", no_auth = TRUE)

  # select a database by name
  gigwa_set_db("Sorghum-JGI_v1")

  # select a project by name
  gigwa_set_project("Nelson_et_al_2011")

  # select a specific run by name
  gigwa_set_run("run1")
}

**list_crops**

*Get the list of supported crops*

**Description**

Get the list of supported crops

**Usage**

```r
list_crops()
```

**Value**

a list of supported crops

**Author(s)**

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

**See Also**

`login_bms`

**Examples**

```r
if(interactive()) {
  # config your BMS connection
  set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

  # login using your BMS account (interactive mode)
  # you can pass BMS username and password as parameters (batch mode)
  login_bms()

  # list supported crops in the bms server
  list_crops()
}
```

---

**list_programs**

*Get the list of breeding programs names*

**Description**

This function will retrieve the breeding programs list from the current active crop as configured in the internal configuration object using the `set_crop()` function.

**Usage**

```r
list_programs()
```
Value

a list of breeding programs names

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

See Also

login_bms, set_crop

Examples

if(interactive()) {
  # config your BMS connection
  set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

  # login using your BMS account (interactive mode)
  # you can pass BMS username and password as parameters (batch mode)
  login_bms()

  set_crop("maize")

  # list existing breeding programs
  list_programs()
}

---

list_studies Get the list of studies in the current active trial

Description

This function will retrieve the studies list from the current active trial as configured in the internal state object using `set_trial()` function.

Usage

list_studies()

Value

a list of study and location names

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>
list_trials

See Also

    login_bms, set_crop, set_program, set_trial

Examples

    if(interactive()) {
        # config your BMS connection
        set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

        # login using your BMS account (interactive mode)
        # you can pass BMS username and password as parameters (batch mode)
        login_bms()

        set_crop("maize")

        # select a breeding program by name
        set_program("MC Maize")

        # select a specific study/trial by name
        set_trial("2018 PVT")

        # list all environments/locations information in the selected study/trial
        list_studies()
    }

list_trials  Get the list of trials in the current active breeding program

Description

This function will retrieve the trials list from the current active breeding program as configured in the internal state object using 'set_program()' function.

Usage

    list_trials(year = NULL)

Arguments

    year  the starting year to filter the list of trials (optional, default is NULL)

Value

    a list of trials names

Author(s)

    Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>
See Also

`login_bms, set_crop, set_program`

Examples

```r
if(interactive()) {
  # config your BMS connection
  set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

  # login using your BMS account (interactive mode)
  # you can pass BMS username and password as parameters (batch mode)
  login_bms()

  set_crop("maize")

  # select a breeding program by name
  set_program("MC Maize")

  # list all studies/trials in the selected program
  list_trials()

  # filter listed studies/trials by year
  list_trials(2020)
}
```

Description

Connect to the server. If username or password parameters are missing, then a login window will pop-up to insert username and password.

All other connection parameters (i.e. server IP or domain, connection port, API path, and connection protocol e.g. http://) will retrieve from the qbms_config list.

This function will update both of the qbms_config list (brapi connection object in the con key) and qbms_state list (token value in the token key).

Usage

```r
login_bms(username = NULL, password = NULL)
```

Arguments

- **username** the username (optional, default is NULL)
- **password** the password (optional, default is NULL)
**login_gigwa**

**Value**

no return value

**Author(s)**

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

**Examples**

```r
if(interactive()) {
  # config your BMS connection
  set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

  # login using your BMS account (interactive mode)
  # you can pass BMS username and password as parameters (batch mode)
  login_bms()
}
```

---

**Description**

Connect to the GIGWA server. If username or password parameters are missing, then a login window will pop-up to insert username and password.

All other connection parameters (i.e. server IP or domain, connection port, API path, and connection protocol e.g. http://) will retrieve from the qbms_config list.

This function will update both of the qbms_config list (brapi connection object in the con key) and qbms_state list (token value in the token key).

**Usage**

```r
login_gigwa(username = NULL, password = NULL)
```

**Arguments**

- **username** the GIGWA username (optional, default is NULL)
- **password** the GIGWA password (optional, default is NULL)

**Value**

no return value

**Author(s)**

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>
**Examples**

```r
if(interactive()) {
  # config your GIGWA connection
  set_qbms_config("http://localhost:59395/gigwa/index.jsp", time_out = 300, engine = "gigwa")

  # login using your GIGWA account (interactive mode)
  # you can pass GIGWA username and password as parameters (batch mode)
  login_gigwa()
  login_gigwa("gigwadmin", "nimda")
}
```

---

**rbindlistx**  
*Makes one data.table from a list of many*

**Description**

Same as `do.call("rbind", x)` on data.frames, but much faster.

**Usage**

```r
rbindlistx(x)
```

**Arguments**

- **x**  
  A list containing data.table, data.frame or list objects.

**Value**

an unkeyed data.table containing a concatenation of all the items passed in.

---

**rbindx**  
*Combine data.frames by row, filling in missing columns*

**Description**

`rbinds` a list of data frames filling missing columns with NA

**Usage**

```r
rbindx(..., dfs = list(...))
```

**Arguments**

- **...**  
  the first argument data frame.
- **dfs**  
  input data frames to row bind together.

**Value**

a single data frame
set_crop

---

**set_crop**  
*Set the current active crop*

---

**Description**

This function will update the current active crop in the internal configuration object (including the brapi connection object).

**Usage**

```
set_crop(crop_name)
```

**Arguments**

- **crop_name**: the name of the crop

**Value**

No return value

**Author(s)**

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

**See Also**

- `login_bms`, `list_crops`

**Examples**

```
if(interactive()) {
  # config your BMS connection
  set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

  # login using your BMS account (interactive mode)
  # you can pass BMS username and password as parameters (batch mode)
  login_bms()

  set_crop("maize")
}
```
Description

This function will update the current active breeding program in the internal state object using the programDbId retrieved from BMS which is associated to the given program_name parameter.

Usage

set_program(program_name)

Arguments

program_name the name of the breeding program

Value

no return value

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

See Also

login_bms, set_crop, list_programs

Examples

if(interactive()) {
  # config your BMS connection
  set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

  # login using your BMS account (interactive mode)
  # you can pass BMS username and password as parameters (batch mode)
  login_bms()

  set_crop("maize")

  # select a breeding program by name
  set_program("MC Maize")
}
set_qbms_config

Configure BMS server settings

Description

Set the connection configuration of the BMS server

Usage

set_qbms_config(
  url = "http://localhost/ibpworkbench/controller/auth/login",
  path = NULL,
  page_size = 1000,
  time_out = 120,
  no_auth = FALSE,
  engine = "bms"
)

Arguments

url           URL of the BMS login page (default is "http://localhost/ibpworkbench/")
path          BMS API path (default is NULL)
page_size     Page size (default is 1000)
time_out      Number of seconds to wait for a response until giving up (default is 10)
no_auth       TRUE if the server doesn’t require authentication/login (default is FALSE)
engine        Backend database (qbms default, breedbase, gigwa)

Value

no return value

Author(s)

Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

Examples

set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")
set_study

Set the current active study by location name

Description
This function will update the current active study in the internal state object using the studyDbId retrieved from BMS which is associated to the given study_name parameter.

Usage
set_study(study_name)

Arguments
study_name the name of the study

Value
no return value

Author(s)
Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

See Also
login_bms, set_crop, set_program, set_trial, list_studies

Examples
if(interactive()) {
  # config your BMS connection
  set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

  # login using your BMS account (interactive mode)
  # you can pass BMS username and password as parameters (batch mode)
  login_bms()

  set_crop("maize")

  # select a breeding program by name
  set_program("MC Maize")

  # select a specific study/trial by name
  set_trial("2018 PVT")

  # select a specific environment/location dataset
  set_study("2018 PVT Environment Number 1")
}
**set_trial**  
*Set the current active trial*

**Description**
This function will update the current active trial in the internal state object using the trialDbId retrieved from BMS which is associated to the given trial_name parameter.

**Usage**
```
set_trial(trial_name)
```

**Arguments**
- **trial_name** the name of the trial

**Value**
no return value

**Author(s)**
Khaled Al-Shamaa, <k.el-shamaa@cgiar.org>

**See Also**
- `login_bms`
- `set_crop`
- `set_program`
- `list_trials`

**Examples**
```r
if(interactive()) {
    # config your BMS connection
    set_qbms_config("https://www.bms-uat-test.net/ibpworkbench")

    # login using your BMS account (interactive mode)
    # you can pass BMS username and password as parameters (batch mode)
    login_bms()

    set_crop("maize")

    # select a breeding program by name
    set_program("MC Maize")

    # select a specific study/trial by name
    set_trial("2018 PVT")
}
```
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