

Package ‘QBMS’

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Title Query the Breeding Management System 'BMS'

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Depends R (>= 3.1.0)

Description

Query the Breeding Management System 'BMS' database (using 'BrAPI' calls) to help breeders as targeted end-users retrieving data directly into their analyzing pipelines.

License GPL (>= 3)

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

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

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R topics documented:

brapi_get_call	2
debug_qbms	3
get_crop_locations	3
get_germplasm_data	4
get_germplasm_list	5
get_login_details	6
get_program_studies	6
get_program_trials	7
get_study_data	8
get_study_info	9
get_trial_data	10
get_trial_obs_ontology	11
list_crops	12
list_programs	12
list_studies	13
list_trials	14
login_bms	15
rbindlistx	16
rbindx	17
set_crop	17
set_program	18
set_qbms_config	19
set_study	20
set_trial	21
Index	22

brapi_get_call	<i>Internal function used for core BrAPI GET calls</i>
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Description

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

Usage

```
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 FLASE, then retrived JSON data will be flatten (default is TRUE)

Value

result object returned by JSON API response

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

```
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

```
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

```
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>

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 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](#)

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")
}
```

```
# 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

```
get_login_details()
```

Value

a vector of inserted username and password

Author(s)

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

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
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

```
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	<i>Get the observations data of the current active study</i>
----------------	--

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

```
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

```
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	<i>Get the details/metadata of the current active study</i>
----------------	---

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>

See Also

[login_bms](#), [set_crop](#), [set_program](#), [set_trial](#), [set_study](#)

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

get_trial_data	<i>Get the observations data of the current active trial</i>
----------------	--

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>

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")  
  
  # select a specific environment/location dataset  
  set_study("2018 PVT Environment Number 1")  
  
  # retrieve multi-environment trial data  
  MET <- get_trial_data()  
}
```

`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>

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()
}
```

list_crops	<i>Get the list of supported crops</i>
------------	--

Description

Get the list of supported crops

Usage

```
list_crops()
```

Value

a list of supported crops

Author(s)

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

See Also

[login_bms](#)

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

list_programs	<i>Get the list of breeding programs names</i>
---------------	--

Description

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

Usage

```
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>

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

```
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)
}
```

login_bms

Login to the BMS server

Description

Connect to the BMS 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

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

Arguments

username	the BMS username (optional, default is NULL)
password	the BMS password (optional, default is NULL)

Value

no return value

Author(s)

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

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()  
}
```

rbindlistx

Makes one data.table from a list of many

Description

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

Usage

```
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	<i>Combine data.frames by row, filling in missing columns</i>
--------	---

Description

rbinds a list of data frames filling missing columns with NA

Usage

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

Arguments

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

Value

a single data frame

set_crop	<i>Set the current active crop</i>
----------	------------------------------------

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")
}
```

set_program

Set the current active breeding program

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	<i>Configure BMS server settings</i>
-----------------	--------------------------------------

Description

Set the connection configuration of the BMS server

Usage

```
set_qbms_config(
  url = "http://localhost/ibpworkbench/controller/auth/login",
  path = "bmsapi",
  page_size = 1000,
  time_out = 10
)
```

Arguments

url	URL of the BMS login page (default is "http://localhost/ibpworkbench/")
path	BMS API path (default is "bmsapi")
page_size	Page size (default is 1000)
time_out	Number of seconds to wait for a response until giving up (default is 10)

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	<i>Set the current active study by location name</i>
-----------	--

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	<i>Set the current active trial</i>
-----------	-------------------------------------

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

```
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")
}
```

Index

`brapi_get_call`, 2

`debug_qbms`, 3

`get_crop_locations`, 3

`get_germplasm_data`, 4

`get_germplasm_list`, 5

`get_login_details`, 6

`get_program_studies`, 6

`get_program_trials`, 7

`get_study_data`, 8

`get_study_info`, 9

`get_trial_data`, 10

`get_trial_obs_ontology`, 11

`list_crops`, 12, 17

`list_programs`, 12, 18

`list_studies`, 13, 20

`list_trials`, 7, 14, 21

`login_bms`, 4–15, 15, 17, 18, 20, 21

`rbindlistx`, 16

`rbindx`, 17

`set_crop`, 4–11, 13–15, 17, 18, 20, 21

`set_program`, 4–11, 14, 15, 18, 20, 21

`set_qbms_config`, 19

`set_study`, 5, 8, 9, 20

`set_trial`, 5, 8–11, 14, 20, 21