

Package: genesysr (via r-universe)

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Title Genesys PGR Client

Description Access data on plant genetic resources from genebanks around the world published on Genesys (<<https://www.genesys-pgr.org>>). Your use of data is subject to terms and conditions available at <<https://www.genesys-pgr.org/content/legal/terms>>.

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BugReports <https://gitlab.croptrust.org/genesys-pgr/genesysr/-/issues>

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api1_url

Get partial API v1 URL for the provided path

Description

Get partial API v1 URL for the provided path

Usage

api1_url(path)

Arguments

path relative path of the API v1 endpoint (e.g. /me)

Value

Returns `"/api/v1" + path`

Examples

```
api1_url("/me")
```

api2_url	<i>Get partial API v2 URL for the provided path</i>
----------	---

Description

Get partial API v2 URL for the provided path

Usage

```
api2_url(path)
```

Arguments

path relative path of the API v2 endpoint (e.g. /me)

Value

Returns `"/api/v2" + path`

Examples

```
api2_url("/me")
```

authorization	<i>Provide OAuth2 token to use for authorization with Genesys</i>
---------------	---

Description

Provide OAuth2 token to use for authorization with Genesys

Usage

```
authorization(authorization)
```

Arguments

authorization OAuth2 Authorization header obtained from somewhere else (e.g. an ENV variable)

See Also

[user_login](#), [client_login](#)

check_country	<i>Run Land-or-Sea check on MCPD data. Uploads only rows where ORIGCTY, DECLATITUDE and DECLONGITUDE are provided.</i>
---------------	--

Description

Run Land-or-Sea check on MCPD data. Uploads only rows where ORIGCTY, DECLATITUDE and DECLONGITUDE are provided.

Usage

```
check_country(mcpd)
```

Arguments

mcpd	Accession passport data in MCPD format
------	--

Value

Results from validator

Examples

```
## Not run:
geoCheck <- genesysr:::check_country(mcpd)

## End(Not run)
```

check_landorsea	<i>Run Land-or-Sea check on MCPD data using https://validator.genesys-pgr.org. Uploads only rows where DECLATITUDE and DECLONGITUDE are provided. In practice it is better to use 'check_country' if ORIGCTY data exists.</i>
-----------------	---

Description

Run Land-or-Sea check on MCPD data using <https://validator.genesys-pgr.org>. Uploads only rows where DECLATITUDE and DECLONGITUDE are provided. In practice it is better to use 'check_country' if ORIGCTY data exists.

Usage

```
check_landorsea(mcpd)
```

Arguments

mcpd Accession passport data in MCPD format

Value

Results from validator

Examples

```
## Not run:  
waterCheck <- genesysr::check_landorsea(mcpd)  
  
## End(Not run)
```

check_taxonomy	<i>Check MCPD taxonomic data (GENUS, SPECIES, SPAUTHOR, SUB-TAXA, SUBTAUTHOR) using https://validator.genesys-pgr.org.</i>
----------------	--

Description

Duplicate input rows are removed using `dplyr::distinct()` and results are returned for unique rows.

Usage

```
check_taxonomy(mcpd, toCurrentTaxa = FALSE)
```

Arguments

mcpd Accession passport data in MCPD format
toCurrentTaxa Should obsoleted names be reported?

Value

Results from validator

Examples

```
## Not run:  
taxaCheck <- genesysr::check_taxonomy(mcpd)  
  
## End(Not run)
```

client_login	<i>Login to Genesys as a service client (system-to-system)</i>
--------------	--

Description

The client must be enabled for Client Credential grant on Genesys.

Usage

```
client_login()
```

See Also

[setup](#)

download_mcpd	<i>Download passport data for one genebank in Excel format and save it to disk</i>
---------------	--

Description

Download passport data for one genebank in Excel format and save it to disk

Usage

```
download_mcpd(instituteCode, file = NULL)
```

Arguments

instituteCode	FAO WIEWS institute code
file	Target file name. Defaults to Genesys-provided file name in the current working directory.

Value

The downloaded MCPD file name

Examples

```
## Not run:  
# Download MCPD passport data for NGA039  
excelFile <- download_mcpd("NGA039")  
  
## End(Not run)
```

download_pdc	<i>Download PDCI data for one genebank in Excel format and save it to disk.</i>
--------------	---

Description

Download PDCI data for one genebank in Excel format and save it to disk.

Usage

```
download_pdc(instituteCode, file = NULL)
```

Arguments

instituteCode	FAO WIEWS institute code
file	Target file name. Defaults to Genesys-provided file name in the current working directory.

Value

The downloaded PDCI file name

Examples

```
## Not run:  
# Download PDCI data for NGA039  
excelData <- download_pdc("NGA039")  
  
## End(Not run)
```

fetch_accessions	<i>Fetch accession passport data and return the paged data structure for further processing. get_accessions might be more useful as it returns a data table.</i>
------------------	--

Description

Fetch accession passport data and return the paged data structure for further processing. [get_accessions](#) might be more useful as it returns a data table.

Usage

```
fetch_accessions(  
  filters = list(),  
  page = NULL,  
  size = 1000,  
  selector = NULL,  
  at.least = NULL  
)
```

Arguments

filters	an R structure with Genesys filters
page	the page index (0-based)
size	number of records to load per page (page size)
selector	NULL or a function to "select" variables of interest
at.least	stop fetching when at.least records are received from Genesys

Value

Paged data structure

See Also

[get_accessions](#)

Examples

```
## Not run:  
# Retrieve all accession data by country of origin  
accessions <- genesysr::fetch_accessions(mcpd_filter(ORIGCTY = c("DEU", "SVN")))  
  
# Fetch Musa  
musa <- genesysr::fetch_accessions(list(taxonomy.genus = c('Musa')))  
  
# Apply selector function  
accessions <- genesysr::fetch_accessions(  
  mcpd_filter(ORIGCTY = c("DEU", "SVN")),  
  selector = function(x) {  
    list(id = x$id, acceNumb = x$acceNumb, instCode = x$institute$code)  
  }  
)  
  
## End(Not run)
```

filter_DOI	<i>Add filter on accession DOI</i>
------------	------------------------------------

Description

Add filter on accession DOI

Usage

```
filter_DOI(filter = list(), DOI)
```

Arguments

filter	Existing filters (or blank list if not provided)
DOI	Accession DOI

filter_GENUS	<i>Add filter by genus</i>
--------------	----------------------------

Description

Add filter by genus

Usage

```
filter_GENUS(filter = list(), GENUS)
```

Arguments

filter	Existing filters (or blank list if not provided)
GENUS	List of genera

filter_INSTCODE	<i>Add filter by genus</i>
-----------------	----------------------------

Description

Add filter by genus

Usage

```
filter_INSTCODE(filter = list(), INSTCODE)
```

Arguments

filter	Existing filters (or blank list if not provided)
INSTCODE	List of WIEWS institute codes

filter_ORIGCTY	<i>Add filter on Country of origin of material</i>
----------------	--

Description

Add filter on Country of origin of material

Usage

```
filter_ORIGCTY(filter = list(), ORIGCTY)
```

Arguments

filter	Existing filters (or blank list if not provided)
ORIGCTY	Country of origin

filter_SAMPSTAT	<i>Add filter on Biological status of sample</i>
-----------------	--

Description

Add filter on Biological status of sample

Usage

```
filter_SAMPSTAT(filter = list(), SAMPSTAT)
```

Arguments

filter	Existing filters (or blank list if not provided)
SAMPSTAT	Biological status of sample

filter_SPECIES	<i>Add filter on specific epithet</i>
----------------	---------------------------------------

Description

Add filter on specific epithet

Usage

```
filter_SPECIES(filter = list(), SPECIES)
```

Arguments

filter	Existing filters (or blank list if not provided)
SPECIES	List of specific epithets

get_accessions	<i>Get accession passport data as a data table.</i>
----------------	---

Description

Get accession passport data as a data table.

Usage

```
get_accessions(  
  filters = list(),  
  page = 0,  
  size = 1000,  
  fields = NULL,  
  exclude = NULL,  
  selector = NULL,  
  at.least = NULL  
)
```

Arguments

filters	an R structure with Genesys filters
page	the page index (0-based)
size	number of records to load per page (page size)
fields	list of fields to fetch from Genesys
exclude	list of field prefixes to exclude from the Genesys response
selector	NULL or a function to "select" variables of interest
at.least	stop fetching when at.least records are received from Genesys

Value

Data table

See Also

[mcpd_filter](#)

Examples

```
## Not run:  
# Retrieve all accession data by country of origin (Slovenia, Ivory Coast)  
accessions <- genesysr::get_accessions(list(countryOfOrigin = list(code3 = c('SVN', 'CIV'))))  
  
# Fetch Musa, but only geographic data and accessionNumber  
musa <- genesysr::get_accessions(list(taxonomy = list(genus = c('Musa'))),  
  fields = c("accessionNumber", "geo"))
```

```

# Apply selector function
accessions <- genesysr::get_accessions(mcpd_filter(ORIGCTY = c('DEU', 'SVN')),
  selector = function(x) {
    list(id = x$id, acceNumb = x$accessionNumber, instCode = x$instituteCode)
  }, at.least = 100)

## End(Not run)

```

list_crops	<i>Fetch Genesys crops. Note that the list of Genesys crops does not fully correspond with various CROPNAME in MCPD provided by genebanks.</i>
------------	--

Description

Fetch Genesys crops. Note that the list of Genesys crops does not fully correspond with various CROPNAME in MCPD provided by genebanks.

Usage

```
list_crops()
```

Value

Genesys crops

Examples

```

## Not run:
# Retrieve all Genesys crops
crops <- genesysr::list_crops()

## End(Not run)

```

list_institutes	<i>List FAO WIEWS institutes.</i>
-----------------	-----------------------------------

Description

Institute filters: - code: list of WIEWS institute codes - accessions: boolean, TRUE list only institutes with accessions in Genesys, FALSE without accessions - country\$code3: list of ISO3166 country codes

Usage

```
list_institutes(filters = list(), at.least = NULL)
```

Arguments

filters an R structure with Institute filters
at.least stop fetching when at.least records are received from Genesys

Value

List of institutes

See Also

[mcpd_filter](#)

Examples

```
## Not run:  
# Retrieve taxa of selected accessions  
filters <- c();  
filters$accessions = TRUE; # Has accessions in Genesys  
institutes <- genesysr::list_institutes(filters)  
  
## End(Not run)
```

list_species	<i>Fetch taxonomic data of selected accessions.</i>
--------------	---

Description

Fetch taxonomic data of selected accessions.

Usage

```
list_species(filters = list())
```

Arguments

filters an R structure with Genesys filters

Value

Taxonomic records of selected accessions

See Also

[mcpd_filter](#)

Examples

```
## Not run:
# Retrieve taxa of selected accessions
taxa <- genesysr::list_species(mcpd_filter(INSTCODE = c("LBN002", "MEX002")))

## End(Not run)
```

mcpd_filter

Make or adjust filter using MCPD terminology

Description

See FAO/Bioersivity Multi-Crop Passport Descriptors.

Usage

```
mcpd_filter(
  filter = list(),
  INSTCODE = NULL,
  DOI = NULL,
  ORIGCTY = NULL,
  SAMPSTAT = NULL,
  GENUS = NULL,
  SPECIES = NULL
)
```

Arguments

filter	Existing filters (or blank list if not provided)
INSTCODE	WIEWS Institute Code of the holding institute
DOI	Accession DOI
ORIGCTY	Country of origin
SAMPSTAT	Biological status of sample
GENUS	List of genera
SPECIES	List of specific epithets (within specified genera)

Examples

```
# Filter accessions from Mexico and Slovenia
mcpd_filter(ORIGCTY = c("MEX", "SVN"))
```

me	<i>Who am i? Loads and prints the user profile from Genesys as JSON. You need to be logged in.</i>
----	--

Description

Who am i? Loads and prints the user profile from Genesys as JSON. You need to be logged in.

Usage

```
me()
```

Examples

```
## Not run:  
# Login  
setup_production()  
user_login()  
me()  
  
## End(Not run)
```

print_setup	<i>Print Genesys client configuration</i>
-------------	---

Description

Print Genesys client configuration

Usage

```
print_setup()
```

setup	<i>Configure the Genesys environment</i>
-------	--

Description

Configure the Genesys environment

Usage

```
setup(server = NULL, client_id = NULL, client_secret = NULL)
```

Arguments

server	Server base URL (e.g. "https://api.genesys-pgr.org" or "https://api.sandbox.genesys-pgr.org")
client_id	OAuth client ID
client_secret	OAuth client secret

See Also

See utility methods [setup_production](#), [setup_sandbox](#)

Examples

```
# Link with sandbox
setup_sandbox()
```

setup_production	<i>Setup for Genesys Production</i>
------------------	-------------------------------------

Description

Use the Genesys R Client with <https://api.genesys-pgr.org> requiring [user_login](#)

Usage

```
setup_production()
```

setup_sandbox	<i>Setup for Genesys Sandbox</i>
---------------	----------------------------------

Description

Use the Genesys R Client with <<https://api.sandbox.genesys-pgr.org>> requiring [user_login](#)

Usage

```
setup_sandbox()
```

user_login	<i>Login to Genesys as a user</i>
------------	-----------------------------------

Description

The authorization URL will open in a browser, ask the user to grant permissions to R. After successful authentication the browser will display a message:

Usage

```
user_login(redirect_uri = "http://127.0.0.1:48913")
```

Arguments

`redirect_uri` a custom `redirect_uri` to submit as part of the authentication request. This is most useful if the default port is blocked and you wish to specify another port: `redirect_uri = "http://127.0.0.1:44211"` Note that `"http://127.0.0.1"` is required and that `"http://localhost"` will not work.

Details

““ Authentication complete. Please close this page and return to R. ““

Close the browser and return to R.

See Also

[setup](#)

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