Package ‘genesysr’

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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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R topics documented:

api1_url ................................................................. 2
api2_url ................................................................. 3
authorization .............................................................. 3
check_country ............................................................ 4
check_landorsea .......................................................... 4
check_taxonomy ........................................................... 5
api1_url

Get full Genesys API v1 URL for a specific path

Description

Get full Genesys API v1 URL for a specific path

Usage

api1_url(path)

Arguments

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

Value

Absolute URL to an API call

Examples

api1_url("/me")
**Description**

Get full Genesys API v1 URL for a specific path

**Usage**

api2_url(path)

**Arguments**

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

**Value**

Absolute URL to an API call

**Examples**

api2_url("/me")

---

**authorization**

*Provide OAuth2 token to use for authorization with Genesys*

**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_landorsea

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

Usage

check_landorsea(mcpd)

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)

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_taxonomy

**Arguments**

mcpd Accession passport data in MCPD format

toCurrentTaxa Should obsoleted names be reported?

**Value**

Results from validator

**Examples**

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

---


**Description**

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

**Usage**

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

**Arguments**

mcpd Accession passport data in MCPD format

toCurrentTaxa Should obsoleted names be reported?

**Value**

Results from validator

**Examples**

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

Login to Genesys as a service client (system-to-system)

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

Usage
client_login()

See Also
setup

download_mcpd

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

Description
Download all 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
HTTP response data

Examples
## Not run:
# Download MCPD passport data for NGA039
excelData <- download_mcpd("NGA039")

## End(Not run)
**download_pdcf**

*Description*

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

*Usage*

```r
download_pdcf(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*

HTTP response data

*Examples*

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

---

**fetch_accessions**

*Fetch accession passport data*

*Description*

Fetch accession passport data

*Usage*

```r
call_accessions(filters = list(), page = NULL, size = 1000, selector = NULL, at.least = NULL)
```
filter.DOI

Add filter on accession DOI

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**  
*Add filter by genus*

**Description**  
Add filter by genus

**Usage**  
```r
filter_GENUS(filter = list(), GENUS)
```

**Arguments**  
- `filter`: Existing filters (or blank list if not provided)
- `GENUS`: List of genera

---

**filter_ORIGCTY**  
*Add filter on Country of origin of material*

**Description**  
Add filter on Country of origin of material

**Usage**  
```r
filter_ORIGCTY(filter = list(), ORIGCTY)
```

**Arguments**  
- `filter`: Existing filters (or blank list if not provided)
- `ORIGCTY`: Country of origin

---

**filter_SAMPSTAT**  
*Add filter on Biological status of sample*

**Description**  
Add filter on Biological status of sample

**Usage**  
```r
filter_SAMPSTAT(filter = list(), SAMPSTAT)
```

**Arguments**  
- `filter`: Existing filters (or blank list if not provided)
- `SAMPSTAT`: Biological status of sample
filter_SPECIES    
Add filter on specific epithet

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    
Fetch accession passport data

Description
Fetch accession passport data

Usage
get_accessions(filters = list(), page = 0, size = 1000,
fields = 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
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
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 <- 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)

mcpd_filter

Make or adjust filter using MCPD terminology

Description

See FAO/Bioversity Multi-Crop Passport Descriptors.

Usage

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

Arguments

filter Existing filters (or blank list if not provided)
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"))
setup

me

Who am i?

Description

Who am i?

Usage

me()

print_setup

Print Genesys client configuration

Description

Print Genesys client configuration

Usage

print_setup()

setup

Configure the Genesys environment

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
setup_production

Examples

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

Description

Use the Genesys R Client with <https://api.genesys-pgr.org> requiring `user_login`

Usage

```r
setup_production()
```

setup_sandbox

Description

Use the Genesys R Client with <https://api.sandbox.genesys-pgr.org> requiring `user_login`

Usage

```r
setup_sandbox()
```

user_login

Description

Login to Genesys as a user

Usage

```r
user_login()
```

See Also

`setup`
Index

api1_url, 2
api2_url, 3
authorization, 3

check_country, 4
check_landorsea, 4
check_taxonomy, 5
client_login, 3, 6

download_mcpd, 6
download_pdc, 7

fetch_accessions, 7
filter.DOI, 8
filter.GENUS, 9
filter.ORIGCTY, 9
filter.SAMPSTAT, 9
filter.SPECIES, 10

get_accessions, 10

mcpd_filter, 10, 11
me, 12

print_setup, 12

setup, 6, 12, 13
setup_production, 12, 13
setup_sandbox, 12, 13

user_login, 3, 13, 13