Package 'genesysr'

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Version 1.0.1

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>.

Maintainer Matija Obreza <matija.obreza@croptrust.org>

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Imports httr, jsonlite, dplyr, readr

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Suggests knitr, rmarkdown, tidyverse

VignetteBuilder knitr

NeedsCompilation no

Author Global Crop Diversity Trust [cph],
Matija Obreza [aut, cre],
Nora Castaneda [ctb]

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R topics documented:

`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")
```

api2_url *Get full Genesys API v1 URL for a specific path*

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

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 valdator

Examples

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

## End(Not run)
```

check_landorsea *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.*

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 valdator

Examples

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

## End(Not run)
```

---

check_taxonomy *Check MCPD taxonomic data (GENUS, SPECIES, SPAUTHOR, SUBTAXA, SUBTAUTHOR) using https://validator.genesys-pgr.org.*

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 valdator

Examples

```
## 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_pdci *Download PDCI data for one genebank in Excel format and save it to disk.*

Description

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

Usage

```
download_pdci(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 PDCI  data for NGA039
  excelData <- download_pdci("NGA039")

## End(Not run)
```

fetch_accessions *Fetch accession passport data*

Description

Fetch accession passport data

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

Examples

```
## Not run:
  # Retrieve all accession data by country of origin
  accessions <- fetch_accessions(mcpd_filter(ORIGCTY = c("DEU", "SVN")))

  # Fetch Musa
  musa <- genesysr::fetch_accessions(list(taxonomy.genus = c('Musa')))

  # Apply selector function
 accessions <- 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 *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

```
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

```
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

```
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"))
```

---

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

Examples

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

setup_production *Setup for Genesys Production*

Description

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

Usage

```
setup_production()
```

setup_sandbox *Setup for Genesys Sandbox*

Description

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

Usage

```
setup_sandbox()
```

user_login *Login to Genesys as a user*

Description

The authorization URL will open in a browser, ask the user to grant permissions to R and the verification code must be copy-pasted after you grant access to the client.

Usage

```
user_login()
```

See Also

`setup`

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