

Package ‘genesysr’

June 14, 2018

Version 0.9.1

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>>.

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Depends R (>= 3.1.0)

Imports httr, jsonlite

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RoxygenNote 6.0.1

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

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

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2018-06-14 19:24:54 UTC

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api_url	<i>Get full Genesys API URL for a specific path</i>
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Description

Get full Genesys API URL for a specific path

Usage

api_url(path)

Arguments

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

Absolute URL to an API call

Examples

```
api_url("/me")
```

authorization	<i>Provide OAuth2 token to use for authorization with Genesys</i>
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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](#)

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

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

Usage

```
client_login()
```

See Also

[setup](#)

fetch_accessions	<i>Fetch accession passport data</i>
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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	<i>Add filter on accession DOI</i>
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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_ORIGCTY	<i>Add filter on Country of origin of material</i>
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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

mcpd_filter	<i>Make or adjust filter using MCPD terminology</i>
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Description

See FAO/Bioversity Multi-Crop Passport Descriptors.

Usage

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

Arguments

filter	Existing filters (or blank list if not provided)
DOI	Accession DOI
ORIGCTY	Country of origin
SAMPSTAT	Biological status of sample

Examples

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

me	<i>Who am i?</i>
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Description

Who am i?

Usage

me()

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

Description

Print Genesys client configuration

Usage

print_setup()

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

Configure the Genesys environment

Usage

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

Arguments

server	Server base URL (e.g. "https://www.genesys-pgr.org" or "https://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>
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Description

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

Usage

```
setup_production()
```

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

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

Usage

```
setup_sandbox()
```

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