

Package ‘genesysr’

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Version 0.9.2

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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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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| | |
|--------------------------|--|
| <code>.check_auth</code> | <i>Ensure that environment has OAuth token</i> |
|--------------------------|--|

Description

Ensure that environment has OAuth token

Usage

```
.check_auth()
```

| | |
|-------------------------------------|--|
| <code>.fetch_accessions_page</code> | <i>Fetch accession passport data (paginated)</i> |
|-------------------------------------|--|

Description

Fetch accession passport data (paginated)

Usage

```
.fetch_accessions_page(filters = list(), page = 0, size = 1000,
  selector = NULL)
```

Arguments

| | |
|-----------------------|--|
| <code>filters</code> | an R structure with Genesys filters |
| <code>page</code> | the page index (0-based) |
| <code>size</code> | number of records to load per page (page size) |
| <code>selector</code> | NULL or a function to "select" variables of interest |

Value

Paged data structure

See Also

[mcpd_filter](#)

Examples

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

| | |
|--------------------|------------------------------|
| .MAX_ALLOWED_PAGES | <i>Max pages to retrieve</i> |
|--------------------|------------------------------|

Description

Max pages to retrieve

Usage

```
.MAX_ALLOWED_PAGES
```

Format

An object of class numeric of length 1.

| | |
|---------|---|
| .onLoad | <i>Configure package defaults on load</i> |
|---------|---|

Description

Configure package defaults on load

Usage

```
.onLoad(libname, pkgname)
```

Arguments

| | |
|---------|--------------|
| libname | Library name |
| pkgname | Package name |

`.post` *HTTP POST method*

Description

HTTP POST method

Usage

```
.post(path, query = NULL, body = NULL,
      content.type = "application/json")
```

Arguments

| | |
|---------------------------|---|
| <code>path</code> | API path |
| <code>query</code> | query string parameters |
| <code>body</code> | request body (will be serialized to JSON) |
| <code>content.type</code> | Content-Type of the body |

Value

httr response

`api_url` *Get full Genesys API URL for a specific path*

Description

Get full Genesys API URL for a specific path

Usage

```
api_url(path)
```

Arguments

| | |
|-------------------|--|
| <code>path</code> | relative path of the API endpoint (e.g. /me) |
|-------------------|--|

Value

Absolute URL to an API call

Examples

```
api_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](#)

| | |
|--------------|--|
| 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](#)

| | |
|------------------|--------------------------------------|
| fetch_accessions | <i>Fetch accession passport data</i> |
|------------------|--------------------------------------|

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> |
|------------|------------------------------------|

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> |
|----------------|--|

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 *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)
```

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 *Who am i?*

Description

Who am i?

Usage

```
me()
```

print_setup *Print Genesys client configuration*

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 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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