Package: GalaxyR (via r-universe)

May 21, 2026

Title 'Galaxy' API Implementation

Version 0.1.1

Description On 'Galaxy' platforms like 'Galaxy Europe' <https://usegalaxy.eu>, many tools and workflows can run directly on a high-performance computer. 'GalaxyR' connects R with 'Galaxy' platforms API <https://usegalaxy.eu/api/docs> and allows credential management, uploading data, invoking workflows or tools, checking their status, and downloading results.

URL https://github.com/JulFrey/GalaxyR

BugReports https://github.com/JulFrey/GalaxyR/issues

License GPL-3

Encoding UTF-8

Imports httr, jsonlite, methods

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Depends R (>= 4.1.0)

Config/pak/sysreqs libssl-dev

Repository https://julfrey.r-universe.dev

Date/Publication 2026-04-21 19:55:38 UTC

RemoteUrl https://github.com/julfrey/galaxyr

RemoteRef HEAD

RemoteSha 97f52abe1991e788063d930ba05ca155fbfe4dfb

Contents

`galaxy` *Create a Galaxy session object*

Description

Constructor for a `Galaxy` S4 object used for pipe-based workflows. The returned object carries identifiers such as `history_id`, `input_dataset_id` and `invocation_id` through subsequent calls.

Usage

```
galaxy(history_name = "R API request", galaxy_url = "https://usegalaxy.eu")
```

Arguments

`history_name`	Character. Default name to give to a new history, stored in the object and used by `galaxy_initialize()` if you don't override it.
`galaxy_url`	Character. Base URL of the Galaxy instance. If the environment variable `GALAXY_URL` is set, it takes precedence.

Value

A `Galaxy` object in state `"new"`.

`Galaxy-class` *Galaxy session object*

Description

An S4 class used to carry state across a pipe-based workflow against a Galaxy instance.

Slots

- `history_name` Default name to give to a new history.
- `history_id` Encoded ID of the history on the server.
- `input_dataset_id` Encoded ID of the last uploaded input dataset.
- `inputs` A list of tool/workflow inputs to be applied on the next call.
- `invocation_id` Encoded ID of the last workflow invocation.
- `output_dataset_ids` Character vector of encoded output dataset IDs.
- `state` One of `"new"`, `"pending"`, `"success"` or `"error"`.
- `galaxy_url` Base URL of the Galaxy instance.

`galaxy_delete_dataset` *Delete a Galaxy dataset by ID*

Description

Delete a dataset (HDA) from a Galaxy instance using the Galaxy API.

Usage

```
galaxy_delete_dataset(
  dataset_id,
  purge = TRUE,
  verbose = FALSE,
  galaxy_url = "https://usegalaxy.eu"
)
```

Arguments

`dataset_id`	Character. The Galaxy dataset ID to delete.
`purge`	Logical. If `TRUE` the API call will include `purge=true` to permanently remove the dataset and free space. If `FALSE` the dataset may be only soft-deleted depending on Galaxy configuration. Default: `TRUE`.
`verbose`	Logical. If `TRUE` a message with the HTTP status code will be printed. Default: `TRUE`.
`galaxy_url`	Character. Base URL of the Galaxy instance (for example `"https://usegalaxy.eu"`). If the environment variable `GALAXY_URL` is set, it takes precedence.

Details

This function performs an HTTP DELETE against the Galaxy /api/datasets/id endpoint. By default it requests a purge (permanent removal) by adding ?purge=true. The Galaxy API key is read from the environment variable `GALAXY_API_KEY`.

- Make sure `Sys.getenv("GALAXY_API_KEY")` is set to a valid API key..
- Use caution when running with `purge = TRUE` as this permanently removes data.

Value

A named list with elements:

success Logical. `TRUE` for 2xx responses, otherwise `FALSE`.

status Integer. HTTP status code returned by the API.

content Character. The raw response body (text).

Examples

```
input_file <- tempfile(fileext = ".txt")
test_text <- "This is an example \nfile."
writeLines(test_text,input_file)
history_id <- galaxy_initialize()
dataset_id <- galaxy_upload_https(input_file, history_id)

galaxy_delete_dataset(dataset_id)
```

`galaxy_delete_datasets`

Delete multiple Galaxy datasets by ID

Description

Convenience wrapper that deletes a vector of dataset IDs using `galaxy_delete_dataset`. Requests are paced with a small sleep between calls to avoid overwhelming the server.

Usage

```
galaxy_delete_datasets(
  output_ids,
  purge = TRUE,
  sleep = 0.2,
  galaxy_url = "https://usegalaxy.eu"
)
```

Arguments

`output_ids`	Character vector of dataset IDs to delete.
`purge`	Logical. Passed to `galaxy_delete_dataset`. Default: `TRUE`.
`sleep`	Numeric. Seconds to wait between API calls. Default: `0.2`.
`galaxy_url`	Character. Base URL of the Galaxy instance (for example `"https://usegalaxy.eu"`). If the environment variable `GALAXY_URL` is set, it takes precedence.

Value

A named list where each element is the return value from `galaxy_delete_dataset` for the corresponding dataset ID.

Examples

```
input_file <- tempfile(fileext = ".txt")
input_file2 <- tempfile(fileext = ".txt")
test_text <- "This is an example \nfile."
writeLines(test_text,input_file)
writeLines(test_text,input_file2)
history_id <- galaxy_initialize("test upload")
dataset_id <- galaxy_upload_https(input_file, history_id)
dataset_id2 <- galaxy_upload_https(input_file2, history_id)

galaxy_delete_datasets(list(output_ids = c(dataset_id, dataset_id2)))
```

`galaxy_download_result`

Generic for downloading files from a history

Description

`galaxy_download_result()` is an S4 generic. With `x` as a character vector of HDA output IDs, all corresponding datasets are downloaded into `out_dir` using their Galaxy names; duplicate names are disambiguated by appending `_<i>` before the extension. Existing files are not overwritten if `overwrite = FALSE`, and a warning is issued when a name is adjusted. With `x` as a `Galaxy` object its `output_dataset_ids` and `galaxy_url` are used; the object is returned invisibly after performing the downloads.

Usage

```
galaxy_download_result(
  x,
  out_dir = ".",
  galaxy_url = "https://usegalaxy.eu",
  overwrite = FALSE
)
```

```
## S4 method for signature 'character'
galaxy_download_result(
  x,
  out_dir = ".",
  galaxy_url = "https://usegalaxy.eu",
  overwrite = FALSE
)

## S4 method for signature 'Galaxy'
galaxy_download_result(x, out_dir = ".", overwrite = FALSE)
```

Arguments

`x`	A vector of HDA output IDs (`character`), or a `Galaxy` object.
`out_dir`	Directory in which to save the downloaded files.
`galaxy_url`	Base URL of the Galaxy instance, used by the character method.
`overwrite`	Logical; if `FALSE` (default), do not overwrite existing files but choose unique names instead.

Value

For the character method, a list of `httr` responses; for the `Galaxy` method, the (unchanged) `Galaxy` object invisibly.

`galaxy_download_rocrate` *Generic for downloading a history as an RO-Crate*

Description

`galaxy_download_rocrate()` is an S4 generic. With `x` as a history ID (`character`) it requests an export in RO-Crate format, polls until ready, and downloads the archive to `dest_file`. With `x` as a `Galaxy` object, its `history_id` and `galaxy_url` are used and the object is returned invisibly after performing the download.

Usage

```
galaxy_download_rocrate(
  x,
  dest_file = tempfile(fileext = ".zip"),
  galaxy_url = "https://usegalaxy.eu",
  format = "rocrate.zip",
  poll_interval = 5,
  timeout = 600
)
```

```
## S4 method for signature 'character'
galaxy_download_rocrate(
  x,
  dest_file = tempfile(fileext = ".zip"),
  galaxy_url = "https://usegalaxy.eu",
  format = "rocrate.zip",
  poll_interval = 30,
  timeout = 600
)

## S4 method for signature 'Galaxy'
galaxy_download_rocrate(
  x,
  dest_file = tempfile(fileext = ".zip"),
  format = format,
  poll_interval = 5,
  timeout = 600
)
```

Arguments

`x`	A history ID (`character`), or a `Galaxy` object.
`dest_file`	Path to save the downloaded RO-Crate (defaults to a temporary `.zip` file).
`galaxy_url`	Base URL of the Galaxy instance, used by the character method. If `GALAXY_URL` is set it takes precedence.
`format`	Format for the history export. Possible formats depend on the Galaxy server. Typical inputs are 'tgz', 'tar', 'tar.gz', 'bag.zip', 'bag.tar', 'bag.tgz', 'rocrate.zip' or 'bco.json'. Defaults to 'rocrate.zip'.
`poll_interval`	Seconds between status checks.
`timeout`	Maximum time to wait in seconds before giving up.

Value

For the character method, the path to the downloaded file. For the `Galaxy` method, the (unchanged) `Galaxy` object invisibly.

Examples

```
hid <- "0123456789abcdef"
crate <- galaxy_download_rocrate(hid, dest_file = "history_rocrate.zip")
g <- galaxy()
g <- galaxy_initialize(g)
g <- galaxy_download_rocrate(g, dest_file = "history_rocrate.zip")
```

`galaxy_get_file_info` *Get information for one or more Galaxy datasets*

Description

Retrieves metadata for one or more Galaxy history datasets (HDAs), including name, size, type, state, and deletion status.

Usage

```
galaxy_get_file_info(file_ids, galaxy_url = "https://usegalaxy.eu")
```

Arguments

`file_ids`	Character vector of Galaxy dataset IDs.
`galaxy_url`	Character. Base URL of the Galaxy instance (for example `"https://usegalaxy.eu"`). If the environment variable `GALAXY_URL` is set, it takes precedence.

Details

This function queries the `/api/datasets/{id}` endpoint for each provided dataset ID. If a dataset cannot be retrieved, its fields are returned as `NA`.

Value

A data.frame with one row per dataset and the columns: `id`, `name`, `size_bytes`, `human_size`, `file_type`, `state`, `deleted`, `stringsAsFactors`.

Examples

```
tmp_dir <- tempdir()
f_name <- "iris.csv"
f_path <- paste(tmp_dir, f_name, sep = "\\")
write.csv(datasets::iris, f_path, row.names = FALSE)

history_id <- galaxy_initialize("IRIS")
file_id <- galaxy_upload_https(f_path, history_id)
galaxy_get_file_info(file_id)
```

`galaxy_get_tool` *Retrieve detailed metadata for a Galaxy tool*

Description

Retrieve detailed metadata for a Galaxy tool

Usage

```
galaxy_get_tool(
  tool_id,
  galaxy_url = "https://usegalaxy.eu",
  tool_version = NULL
)
```

Arguments

`tool_id`	Character. The Galaxy tool ID (for example `"toolshed.g2.bx.psu.edu/repos/devteam/fastqc/fast`
`galaxy_url`	Character. Base URL of the Galaxy instance (for example `"https://usegalaxy.eu"`). If the environment variable `GALAXY_URL` is set, it takes precedence.
`tool_version`	Optional character string to request a specific version. If `NULL`, Galaxy will return the default/latest version metadata.

Value

A list containing the tool metadata as returned by the Galaxy API (inputs, outputs, help text, etc.).

Examples

```
tool_id <- galaxy_get_tool_id("FastQC")[1]
fastqc_tool <- galaxy_get_tool(tool_id)
fastqc_tool$description
```

`galaxy_get_tool_id` *Retrieve Galaxy tool IDs by name*

Description

Retrieve Galaxy tool IDs by name

Usage

```
galaxy_get_tool_id(
  name,
  tools = NULL,
  ignore_case = TRUE,
  galaxy_url = "https://usegalaxy.eu",
  panel_id = NULL
)
```

Arguments

`name`	Character string to search for in tool names.
`tools`	Optional list as returned by `galaxy_list_tools`. If `NULL`, the function will fetch tools on the fly by calling `galaxy_list_tools`.
`ignore_case`	Logical. Whether matching should ignore case. Default: `TRUE`.
`galaxy_url`	Character. Base URL of the Galaxy instance (for example `"https://usegalaxy.eu"`). If the environment variable `GALAXY_URL` is set, it takes precedence.
`panel_id`	Optional character. Passed through to `galaxy_list_tools` when `tools` is `NULL` so you can restrict the search to a panel/section.

Value

Character vector of matching tool IDs in decreasing order (usually highest version first). Returns `character(0)` if no tools match.

Examples

```
# Fetch the full tool list once, then lookup
tools <- galaxy_list_tools()
galaxy_get_tool_id("FastQC", tools = tools)

# Or let the helper fetch on demand
galaxy_get_tool_id("FastQC")

# Exact, case-sensitive match inside a specific panel
galaxy_get_tool_id("Concatenate datasets",
ignore_case = FALSE, panel_id = "Text Manipulation")
```

`galaxy_get_workflow` *Receive workflow metadata from the API*

Description

Receive workflow metadata from the API

Usage

```
galaxy_get_workflow(workflow_id, galaxy_url = "https://usegalaxy.eu")
```

Arguments

`workflow_id`	Character. Galaxy workflow ID.
`galaxy_url`	Character. Base URL of the Galaxy instance (for example `"https://usegalaxy.eu"`). If the environment variable `GALAXY_URL` is set, it takes precedence.

Value

a structured list with all metadata

Examples

```
## Not run:
galaxy_get_workflow("f2db41e1fa331b3e")

## End(Not run)
```

`galaxy_get_workflow_inputs`

Retrieve input definitions for a Galaxy workflow

Description

Retrieves and summarizes the input steps required by a Galaxy workflow.

Usage

```
galaxy_get_workflow_inputs(workflow_id, galaxy_url = "https://usegalaxy.eu")
```

Arguments

`workflow_id`	Character. Galaxy workflow ID.
`galaxy_url`	Character. Base URL of the Galaxy instance (for example `"https://usegalaxy.eu"`). If the environment variable `GALAXY_URL` is set, it takes precedence.

Details

This function queries `/api/workflows/{workflow_id}` and extracts workflow input steps (data and parameter inputs). The returned `step_id` values must be used as names in the `inputs` argument of `galaxy_start_workflow`.

Value

A data.frame with one row per workflow input and the columns: `step_id`, `name`, `type`, `optional`, `default`.

Examples

```
## Not run:
galaxy_get_workflow_inputs("f2db41e1fa331b3e")

## End(Not run)
```

`galaxy_has_key` *Check whether a Galaxy API key is available*

Description

Check whether the environment variable `GALAXY_API_KEY` is set and non-empty.

Usage

```
galaxy_has_key()
```

Value

Logical. `TRUE` if an API key is available, otherwise `FALSE`.

Examples

```
galaxy_has_key() # returns true if api key is set
```

`galaxy_history_size` *Galaxy history size Get the disk usage / size of a Galaxy history*

Description

The function first tries to read a size/disk_usage field from the history summary endpoint. If that is not present it fetches the history contents and sums dataset sizes (robust to a few different field names used by different Galaxy versions). Results are returned as a data.frame with bytes and a human-readable size.

Usage

```
galaxy_history_size(
  history_id,
  galaxy_url = "https://usegalaxy.eu",
  include_deleted = FALSE
)
```

Arguments

`history_id`	Galaxy history ID.
`galaxy_url`	Character. Base URL of the Galaxy instance (for example `"https://usegalaxy.eu"`). If the environment variable `GALAXY_URL` is set, it takes precedence.
`include_deleted`	Logical; whether to include deleted datasets when summing (default FALSE)

Value

data.frame with columns history_id, bytes, human_size

Examples

```
histories <- galaxy_list_histories()
if(nrow(histories > 0)){
  galaxy_history_size(histories$history_id[1])
} else {
  message("No histories found for current user.")
}
```

`galaxy_initialize` *Create a new Galaxy history*

Description

`galaxy_initialize()` is an S4 generic. With no `x` supplied it creates a new history on the given Galaxy instance and returns its encoded ID. When called with a `Galaxy` object it uses the object's `history_name` and `galaxy_url`, creates the history, and updates the object with the new `history_id` and state `"pending"`.

Usage

```
galaxy_initialize(
  x,
  name = "R API request",
  galaxy_url = "https://usegalaxy.eu"
)
```

```
## S4 method for signature 'missing'
galaxy_initialize(name, galaxy_url)

## S4 method for signature 'Galaxy'
galaxy_initialize(x)
```

Arguments

`x`	A `Galaxy` object, or missing to use the default method.
`name`	Name of the history to create. Ignored when `x` is a `Galaxy`, in which case `x@history_name` is used.
`galaxy_url`	Base URL of the Galaxy instance. Ignored when `x` is a `Galaxy`, in which case `x@galaxy_url` is used.

Details

A valid Galaxy API key is required and must be available via the `GALAXY_API_KEY` environment variable.

Value

For the default method (`x` missing), a character scalar history ID. For the `Galaxy` method, the modified `Galaxy` object.

Examples

```
history_id <- galaxy_initialize("My history name")
g <- galaxy(history_name = "My history name")
g <- galaxy_initialize(g)
```

`galaxy_list_histories` *List Galaxy histories (name and history id)*

Description

List Galaxy histories (name and history id)

Usage

```
galaxy_list_histories(galaxy_url = "https://usegalaxy.eu")
```

Arguments

`galaxy_url`	Character. Base URL of the Galaxy instance (for example `"https://usegalaxy.eu"`). If the environment variable `GALAXY_URL` is set, it takes precedence.

Value

data.frame with columns: history_name, history_id

Examples

```
histories <- galaxy_list_histories()
```

`galaxy_list_invocations` *List workflow invocations for a given workflow*

Description

List workflow invocations for a given workflow

Usage

```
galaxy_list_invocations(workflow_id, galaxy_url = "https://usegalaxy.eu")
```

Arguments

`workflow_id`	The Galaxy workflow ID to list invocations for.
`galaxy_url`	Character. Base URL of the Galaxy instance (for example `"https://usegalaxy.eu"`). If the environment variable `GALAXY_URL` is set, it takes precedence.

Value

data.frame with columns: invocation_id, workflow_id, history_id, state, create_time, update_time, stringsAsFactors

---

`galaxy_list_tools` *List tools installed on a Galaxy instance*

Description

List tools installed on a Galaxy instance

Usage

```
galaxy_list_tools(
  galaxy_url = "https://usegalaxy.eu",
  in_panel = FALSE,
  panel_id = NULL
)
```

Arguments

`galaxy_url`	Character. Base URL of the Galaxy instance (for example `"https://usegalaxy.eu"`). If the environment variable `GALAXY_URL` is set, it takes precedence.
`in_panel`	Logical. If `TRUE`, return the tool panel structure (sections/categories). If `FALSE`, return the flat list of all tools as supplied by Galaxy. Default: `FALSE`.
`panel_id`	Optional character. When supplied, only tools from the matching panel (section/category) are returned. The value is matched against both the panel `id` and `name`. Supplying `panel_id` automatically requests the panelized structure, regardless of the value of `in_panel`.

Value

A list corresponding to the parsed JSON returned by Galaxy. If `panel_id` is provided, a list of tool entries belonging to the requested panel is returned (each entry is the raw tool metadata as provided by Galaxy).

Examples

```
# All tools (flat list)
tools_list <- galaxy_list_tools()
length(tools_list)

# Panel structure
panel_list <- galaxy_list_tools(in_panel = TRUE)
length(panel_list)

# Tools from a specific panel (match by id or name)
tools_list <- galaxy_list_tools(panel_id = "Get Data")
length(tools_list)
```

`galaxy_list_workflows` *List workflows available to the user*

Description

Retrieves workflows accessible to the authenticated user from a Galaxy instance. Optionally includes public (published) workflows if supported by the Galaxy server.

Usage

```
galaxy_list_workflows(
  include_public = FALSE,
  galaxy_url = "https://usegalaxy.eu"
)
```

Arguments

`include_public`	Logical. If `TRUE`, attempt to also include published public workflows. Default: `FALSE`.
`galaxy_url`	Character. Base URL of the Galaxy instance (for example `"https://usegalaxy.eu"`). If the environment variable `GALAXY_URL` is set, it takes precedence.

Details

By default, only workflows owned by or shared with the current user are returned. When `include_public = TRUE`, the function will attempt to request published workflows as well. Availability of public workflows depends on the Galaxy instance and version.

Value

A data.frame with one row per workflow and columns including: `id`, `name`, `published`, `owner`.

Examples

```
workflows <- galaxy_list_workflows(TRUE)
head(workflows)
```

`galaxy_poll_tool` *Generic for galaxy_poll_tool*

Description

Generic for galaxy_poll_tool

Wait for a Galaxy job to complete

S4 method to poll the status of a tool invocation

Usage

```
galaxy_poll_tool(
  x,
  galaxy_url = "https://usegalaxy.eu",
  poll_interval = 3,
  timeout = 600
)

## S4 method for signature 'character'
galaxy_poll_tool(
  x,
  galaxy_url = "https://usegalaxy.eu",
  poll_interval = 3,
  timeout = 600
```

```
)

## S4 method for signature 'Galaxy'
galaxy_poll_tool(x, poll_interval = 3, timeout = 600)
```

Arguments

`x`	A job ID (`character`) or a `Galaxy` object.
`galaxy_url`	Base URL of the Galaxy instance, used by the character method.
`poll_interval`	Seconds between status checks.
`timeout`	Maximum time to wait in seconds.

Value

For the character method, the final job object; for the `Galaxy` method, the modified `Galaxy` object.

`galaxy_poll_workflow` *Generic for polling workflows*

Description

`galaxy_poll_workflow()` is an S4 generic. With `x` as a character vector it is treated as a workflow invocation ID; the invocation is polled until it completes and a list of output dataset IDs is returned. With `x` as a `Galaxy` object, the `invocation_id` and `galaxy_url` are taken from the object, and the object is updated with the resulting `output_dataset_ids` and state.

Usage

```
galaxy_poll_workflow(
  x,
  galaxy_url = "https://usegalaxy.eu",
  poll_interval = 30,
  ...
)

## S4 method for signature 'character'
galaxy_poll_workflow(
  x,
  galaxy_url = "https://usegalaxy.eu",
  poll_interval = 30,
  ...
)

## S4 method for signature 'Galaxy'
galaxy_poll_workflow(
  x,
```

```
  galaxy_url = "https://usegalaxy.eu",
  poll_interval = 30,
  ...
)
```

Arguments

`x`	A workflow invocation ID (`character`) or a `Galaxy` object.
`galaxy_url`	Base URL of the Galaxy instance, used by the character method. If `GALAXY_URL` is set it takes precedence.
`poll_interval`	Time in seconds between polling attempts.
`...`	not in use

Value

For the character method, a list with elements `success` and `output_ids`. For the `Galaxy` method, the modified `Galaxy` object.

Examples

```
invocation_id <- "abc123"
galaxy_poll_workflow(invocation_id)
```

`galaxy_run_tool` *Generic run tool*

Description

`galaxy_run_tool()` is an S4 generic. With `x` as a character vector it is treated as a history ID; the specified tool is invoked in that history and the job ID is returned. With `x` as a `Galaxy` object, the history ID and URL are taken from the object and the object is updated with the job ID.

Usage

```
galaxy_run_tool(
  x,
  tool_id,
  inputs = NULL,
  dataset_id = NULL,
  galaxy_url = "https://usegalaxy.eu"
)

## S4 method for signature 'character'
galaxy_run_tool(
  x,
  tool_id,
```

```
  inputs = NULL,
  dataset_id = NULL,
  galaxy_url = "https://usegalaxy.eu"
)

## S4 method for signature 'Galaxy'
galaxy_run_tool(x, tool_id, inputs = NULL, dataset_id = NULL)
```

Arguments

`x`	A history ID (`character`) or a `Galaxy` object.
`tool_id`	Tool identifier to execute.
`inputs`	Named list of tool inputs.
`dataset_id`	ID of the input dataset (HDA).
`galaxy_url`	Base URL of the Galaxy instance, used by the character method.

Value

For the character method, a job ID; for the `Galaxy` method, the modified `Galaxy` object.

`galaxy_set_credentials` *Set Galaxy connection parameters for the current R session*

Description

Set Galaxy connection parameters for the current R session

Usage

```
galaxy_set_credentials(
  api_key = NULL,
  username = NULL,
  password = NULL,
  galaxy_url = "https://usegalaxy.eu",
  overwrite = TRUE
)
```

Arguments

`api_key`	Character. Galaxy API key.
`username`	Character. Galaxy username (only required for FTP uploads).
`password`	Character. Galaxy password (only required for FTP uploads).
`galaxy_url`	Character. Base URL of the Galaxy instance (e.g. `"https://usegalaxy.eu"`). If set all galaxy_url arguments of functions will be ignored.
`overwrite`	Logical. Whether to overwrite existing environment variables. Default: `TRUE`.

Details

This helper is intended for interactive sessions. It sets the following environment variables using `Sys.setenv()`:

- `GALAXY_API_KEY`
- `GALAXY_URL`
- `GALAXY_USERNAME`
- `GALAXY_PASSWORD`

Only arguments that are provided (non-NULL) are set.

Value

Invisibly returns a named list of values that were set.

Examples

```
# This requires valid credentials to your galaxy instance
## Not run:
galaxy_set_credentials(
  api_key = "your-secret-key",
  username = "your-username",
  password = "your-password",
  galaxy_url = "https://usegalaxy.eu"
)

## End(Not run)
```

`galaxy_start_workflow` *Generic start workflow*

Description

`galaxy_start_workflow()` is an S4 generic. With `x` as a character vector it is treated as a history ID: the given workflow is invoked in that history and the invocation ID is returned. With `x` as a `Galaxy` object, the history ID and URL are taken from the object; the workflow is started and the object is updated with the resulting `invocation_id`.

Usage

```
galaxy_start_workflow(
  x,
  workflow_id,
  inputs = NULL,
  dataset_id = NULL,
  galaxy_url = "https://usegalaxy.eu"
```

```
)

## S4 method for signature 'character'
galaxy_start_workflow(
  x,
  workflow_id,
  inputs = NULL,
  dataset_id = NULL,
  galaxy_url = "https://usegalaxy.eu"
)

## S4 method for signature 'Galaxy'
galaxy_start_workflow(x, workflow_id, inputs = NULL, dataset_id = NULL)
```

Arguments

`x`	A `Galaxy` object, or a history ID (`character`) to use the default method.
`workflow_id`	Character. Galaxy workflow ID.
`inputs`	Named list. Optional workflow input mapping; keys are workflow input step IDs, values are lists describing datasets/parameters.
`dataset_id`	Character. ID of the input dataset (HDA). Ignored if `inputs` is supplied. When `x` is a `Galaxy` and `dataset_id` is missing, `x@input_dataset_id` is used.
`galaxy_url`	Base URL of the Galaxy instance, used by the character method. If `GALAXY_URL` is set it takes precedence.

Value

For the character method, a character scalar invocation ID. For the `Galaxy` method, the modified `Galaxy` object.

`galaxy_upload_ftp` *Generic upload ftp*

Description

`galaxy_upload_ftp()` is an S4 generic. With no `x` supplied it uploads a local file via FTP and registers it in the specified history, returning the encoded dataset ID. When called with a `Galaxy` object it uses the object's `history_id` and `galaxy_url` and updates the object with the new `input_dataset_id`.

Usage

```
galaxy_upload_ftp(
  x,
  input_file,
  galaxy_ftp = "ftp.usegalaxy.eu",
  galaxy_url = "https://usegalaxy.eu",
```

```
  ...
)

## S4 method for signature 'character'
galaxy_upload_ftp(
  x,
  input_file,
  galaxy_ftp = "ftp.usegalaxy.eu",
  galaxy_url = "https://usegalaxy.eu",
  ...
)

## S4 method for signature 'Galaxy'
galaxy_upload_ftp(
  x,
  input_file,
  galaxy_ftp = "ftp.usegalaxy.eu",
  galaxy_url = "https://usegalaxy.eu",
  ...
)
```

Arguments

`x`	A `Galaxy` object, or a `history_id` to use the default method.
`input_file`	Path to the local file to upload.
`galaxy_ftp`	FTP server address of the Galaxy instance.
`galaxy_url`	Base URL of the Galaxy instance, used by the default method. If `GALAXY_URL` is set it takes precedence.
`...`	not in use

Details

A valid API key (`GALAXY_API_KEY`) and FTP credentials (`GALAXY_USERNAME`, `GALAXY_PASSWORD`) must be available in the environment.

Value

For the default method, a character scalar dataset ID. For the `Galaxy` method, the modified `Galaxy` object.

Examples

```
galaxy_ftp <- "ftp.usegalaxy.eu"
input_file <- tempfile(fileext = ".txt")
writeLines("Example", input_file)
hid <- galaxy_initialize("test upload")
did <- galaxy_upload_ftp(input_file, hid, galaxy_ftp)
g <- galaxy()
g <- galaxy_initialize(g)
```

```
g <- galaxy_upload_ftp(g, input_file, galaxy_ftp = galaxy_ftp)
```

`galaxy_upload_https` *Generic upload file with https*

Description

`galaxy_upload_https()` is an S4 generic. With no `x` supplied it uploads a local file via HTTPS to the specified history and returns the encoded dataset ID. When called with a `Galaxy` object it uses the object's `history_id` and `galaxy_url`, uploads the file, and updates the object with the new `input_dataset_id`.

Usage

```
galaxy_upload_https(
  x,
  input_file,
  wait = FALSE,
  wait_timeout = 600,
  galaxy_url = "https://usegalaxy.eu",
  file_type = "auto",
  dbkey = "?",
  ...
)

## S4 method for signature 'character'
galaxy_upload_https(
  x,
  input_file,
  wait = FALSE,
  wait_timeout = 600,
  galaxy_url = "https://usegalaxy.eu",
  file_type = "auto",
  dbkey = "?",
  ...
)

## S4 method for signature 'Galaxy'
galaxy_upload_https(
  x,
  input_file,
  wait = FALSE,
  wait_timeout = 600,
  galaxy_url = "https://usegalaxy.eu",
  file_type = "auto",
  dbkey = "?",
```

```
  ...
)
```

Arguments

`x`	A `Galaxy` object, or a `history_id` to use the default method.
`input_file`	Path to the local file to upload.
`wait`	Logical. Whether to wait for Galaxy to finish processing.
`wait_timeout`	Time in seconds until `wait` times out with an error.
`galaxy_url`	Base URL of the Galaxy instance, used by the default method. If `GALAXY_URL` is set it takes precedence.
`file_type`	Galaxy datatype identifier (e.g. `"auto"`, `"fastq"`, `"bam"`).
`dbkey`	Reference genome identifier (e.g. `"?"` or `"hg38"`).
`...`	not in use

Details

This uses Galaxy's built-in `upload1` tool and performs a multipart form POST. Large files may still require FTP depending on server configuration. A valid API key (`GALAXY_API_KEY`) must be available in the environment.

Value

For the default method, a character scalar dataset ID. For the `Galaxy` method, the modified `Galaxy` object.

Examples

```
hid <- galaxy_initialize("test upload")
test_file <- tempfile(fileext = ".txt")
writeLines("This is an example test file.", test_file)
file_id <- galaxy_upload_https(hid, test_file)
g <- galaxy()
g <- galaxy_initialize(g)
g <- galaxy_upload_https(g, test_file)
```

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