

Package ‘GalaxyR’

May 7, 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 htr, jsonlite, methods

RoxygenNote 7.3.3

Depends R (>= 4.1.0)

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-02-17 13:30:02 UTC

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galaxy	<i>Create a Galaxy session object</i>
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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

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

Value

A Galaxy object in state "new".

Galaxy-class	<i>Galaxy session object</i>
--------------	------------------------------

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	<i>Delete a Galaxy dataset by ID</i>
-----------------------	--------------------------------------

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 <code>purge=true</code> 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("test upload")
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

<code>x</code>	A history ID (character), or a Galaxy object.
<code>dest_file</code>	Path to save the downloaded RO-Crate (defaults to a temporary .zip file).
<code>galaxy_url</code>	Base URL of the Galaxy instance, used by the character method. If GALAXY_URL is set it takes precedence.
<code>format</code>	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'.
<code>poll_interval</code>	Seconds between status checks.
<code>timeout</code>	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.

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	<i>Retrieve detailed metadata for a Galaxy tool</i>
-----------------	-----------------------------------------------------

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 identifier (for example "toolshed.g2.bx.psu.edu/repos/devteam/fastqc").
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	<i>Retrieve Galaxy tool IDs by name</i>
--------------------	-----------------------------------------

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 <code>galaxy_list_tools</code> . If NULL, the function will fetch tools on the fly by calling <code>galaxy_list_tools</code> .
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 <code>galaxy_list_tools</code> 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(\emptyset) 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	<i>Check whether a Galaxy API key is available</i>
----------------	----------------------------------------------------

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	<i>Galaxy history size Get the disk usage / size of a Galaxy history</i>
---------------------	--------------------------------------------------------------------------

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 (required)

`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: 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

```
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	<i>Generic run tool</i>
-----------------	-------------------------

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

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

Value

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

<code>galaxy_upload_ftp</code>	<i>Generic upload ftp</i>
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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

<code>x</code>	A Galaxy object, or a <code>history_id</code> to use the default method.
<code>input_file</code>	Path to the local file to upload.
<code>galaxy_ftp</code>	FTP server address of the Galaxy instance.
<code>galaxy_url</code>	Base URL of the Galaxy instance, used by the default method. If <code>GALAXY_URL</code> is set it takes precedence.
<code>...</code>	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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