
galaxy-upload

Release 1.0.1

The Galaxy Project

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CONTENTS:

1	galaxy-upload - Galaxy Command-Line Upload Utility	1
1.1	Installation	1
1.2	Usage	2
2	History	5
2.1	1.0.1	5
2.2	1.0.0	5
2.3	0.0.1	5
2.4	Indices and tables	5

GALAXY-UPLOAD - GALAXY COMMAND-LINE UPLOAD UTILITY

A utility for uploading files to a Galaxy server from the command line. `galaxy-upload` supports [Galaxy](#) servers 22.01+, which include support for resumable uploads with the [tus](#) protocol.

1.1 Installation

1.1.1 Using pip

Python 3.7 or later is required.

To install:

```
$ pip install galaxy-upload
```

This installs two commands: `galaxy-upload`, used to upload file(s) to a Galaxy server, and `galaxy-history-search`, a helper utility for finding Galaxy histories to pass to the `galaxy-upload` command.

To make your life easier, you are encouraged to install into a Python virtual environment. The easiest way to do this is with Python's built-in [venv](#) module:

```
$ python3 -m venv ~/galaxy-upload
$ . ~/galaxy-upload/bin/activate
$ pip install galaxy-upload
```

1.1.2 Using Conda

Alternatively, `galaxy-upload` can be installed using the [Conda](#) package manager. The `galaxy-upload` Conda package can be found on the [bioconda](#) channel and installed like so:

```
$ conda create -n galaxy-upload -c conda-forge -c bioconda galaxy-upload
$ conda activate galaxy-upload
```

1.1.3 Using Containers

It is also possible to run galaxy-upload in either a [Docker](#) or [Singularity/Apptainer](#) container. The galaxy-upload BioContainer is automatically built and maintained by the [BioContainers](#) project.

To use the Docker container:

```
$ docker run -it --rm -v "$(pwd):$(pwd)" -w "$(pwd)" -u "$(id -u):$(id -g)" \
  quay.io/biocontainers/galaxy-upload:1.0.0--pyhdfd78af_0 /bin/bash
```

Or as a single command without entering an interactive shell:

```
$ docker run --rm -v "$(pwd):$(pwd)" -w "$(pwd)" -u "$(id -u):$(id -g)" \
  quay.io/biocontainers/galaxy-upload:1.0.0--pyhdfd78af_0 galaxy-upload
```

Adjust the values of -v and -w according to where the data you want to upload are located. In the example above, it is assumed they are in the current working directory.

To use the Singularity container:

```
$ singularity run https://depot.galaxyproject.org/singularity/galaxy-upload:1.0.0--
↳pyhdfd78af_0
```

Or as a single command without entering an interactive shell:

```
$ singularity run https://depot.galaxyproject.org/singularity/galaxy-upload:1.0.0--
↳pyhdfd78af_0 galaxy-upload
```

Additional (newer) versions of the container may be available, BioContainers does not use the latest tag, but you can find all tags (which are valid for the Singularity images hosted on depot.galaxyproject.org as well as the Docker images) at the [galaxy-upload quay.io](#) page

1.2 Usage

Upload a pair of fastq.gz files:

```
$ galaxy-upload --url https://usegalaxy.org \
  --api-key 70ffec0ffea11e1eaccede1337loaf --history-name 'Run 2' \
  RUN2_F_001.fastq.gz RUN2_R_001.fastq.gz
RUN2_F_001.fastq.gz 100/100 mB ? eta 0:00:00
RUN2_R_001.fastq.gz 100/100 mB ? eta 0:00:00
```

Required arguments are the Galaxy server URL and API key, and a history ID or name. Your API key can be found in the Galaxy UI after logging in, by navigating to **User Preferences Manage API Key**.

You can set the URL and API key options as environment variables to avoid retyping and prevent the key from being visible to other users in ps(1) output:

```
$ export GALAXY_URL=https://usegalaxy.org
$ export GALAXY_API_KEY=70ffec0ffea11e1eaccede1337loaf
$ galaxy-upload --history-name stuff reads.bam
```

When selecting a history by name, regular expression matching is used. If the name matches multiple histories, galaxy-upload will exit will output details about the matched histories and then exit with an error. You can then select the correct history ID using the --history-id option:

```
$ galaxy-upload --history-name stuff reads.bam
Active Histories
```

ID	Name	Last Modified
70ffeec0ffeed07	Newer stuff	Mon Jul 11 15:54:05 2022
alleleaccedeble8	Older stuff	Wed May 25 18:03:46 2022

ERROR: Multiple histories matching stuff found! Use --history-id to select one.

```
$ galaxy-upload --history-id 70ffeec0ffeed07 reads.bam
reads.bam 3.6/3.6 gB ? eta 0:00:00
```

If you want to find the correct history without attempting an upload, use the `galaxy-history-search` command. The `--ignore-case` option can be used to perform a case-insensitive search:

```
$ galaxy-history-search --ignore-case trinity
Active Histories
```

ID	Name	Last Modified
084649feb42d4295	: test trinity inputs	Wed Dec 9 10:02:35 2020
f697f94ca47080cf	automate_trinity	Mon Dec 21 17:40:24 2015
c79278c7a37e619e	TrinityRun	Fri Mar 10 14:21:56 2017
ee31286b26ff3352	trinity	Wed Sep 30 09:04:03 2020

Regular expressions are supported, for example, to find only the histories with names *ending* with `trinity`:

```
$ galaxy-history-search --ignore-case 'trinity$'
Active Histories
```

ID	Name	Last Modified
f697f94ca47080cf	automate_trinity	Mon Dec 21 17:40:24 2015
ee31286b26ff3352	trinity	Wed Sep 30 09:04:03 2020

Multiple options mirror those of the Galaxy UI's upload dialog, including `--file-type`, `--dbkey`, and `--space-to-tab`. The `--file-name` option can be used when uploading single files to control the file name in the history (by default it will be the same as the name on the local filesystem).

To support resuming interrupted uploads, use the `--storage` option to point to a state file (it will be created if it does not exist):

```
$ galaxy-upload --file-type bam --file-name Reads --storage /data/upload.txt /data/reads.
↪bam
```

If the upload is interrupted, simply repeat the same command to resume uploading from the point of interruption.

Note that if you are trying to re-upload (not resume) a file that you have already uploaded once before, you will need to remove it from the storage file or use a different storage file.

HISTORY

2.1 1.0.1

- Document installation/usage with conda and containers by @natefoo in <https://github.com/galaxyproject/galaxy-upload/pull/7>
- Use click to require file arg to exist by @natefoo in <https://github.com/galaxyproject/galaxy-upload/pull/9>
- Pin tuspny to !=1.0.1 due to issue with upload_chunk(). by @natefoo in <https://github.com/galaxyproject/galaxy-upload/pull/10>

2.2 1.0.0

- Initial release

2.3 0.0.1

- Initial prerelease for comment and testing

2.4 Indices and tables

- [genindex](#)
- [search](#)