

Dockerized Galaxy for Tool Publishing

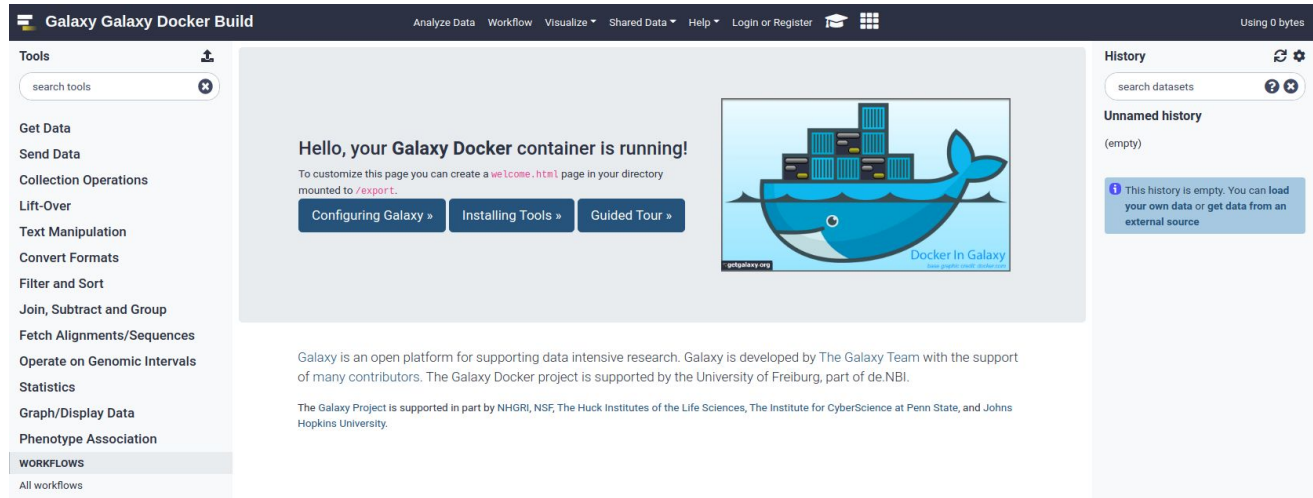
Galaxy Resources for Tools Developers
Webinar May 12th, 2021
Anthony Bretaudeau - GenOuest - Rennes, France

Galaxy Docker image

Docker image to launch Galaxy in seconds:

```
docker run -d -p 8080:80 quay.io/bgruening/galaxy:20.09
```

...then browse to <http://localhost:8080/>



The screenshot displays the Galaxy Docker Build web interface. The top navigation bar includes 'Galaxy Galaxy Docker Build', 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', 'Login or Register', and 'Using 0 bytes'. A left sidebar lists various tool categories such as 'Tools', 'Get Data', 'Send Data', 'Collection Operations', 'Lift-Over', 'Text Manipulation', 'Convert Formats', 'Filter and Sort', 'Join, Subtract and Group', 'Fetch Alignments/Sequences', 'Operate on Genomic Intervals', 'Statistics', 'Graph/Display Data', 'Phenotype Association', and 'WORKFLOWS'. The main content area features a large blue whale illustration with a stack of blue containers on its back, accompanied by the text 'Hello, your Galaxy Docker container is running!' and three buttons: 'Configuring Galaxy >', 'Installing Tools >', and 'Guided Tour >'. Below this, there is introductory text about Galaxy and the Galaxy Docker project, supported by the University of Freiburg, de.NBI, and other institutions. A right sidebar shows 'History' with a search field and a message: 'This history is empty. You can load your own data or get data from an external source'.

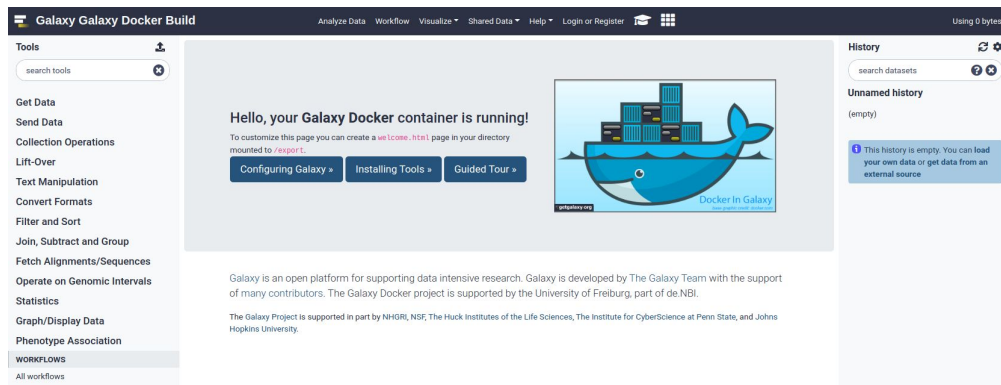
Galaxy Docker image

Image based on Ubuntu 18.04 LTS

Embeds the Galaxy web app + PostgreSQL db + ftp server + Reports web app...

Persist all data by mounting a single directory: /export/

<https://github.com/bgruening/docker-galaxy-stable>



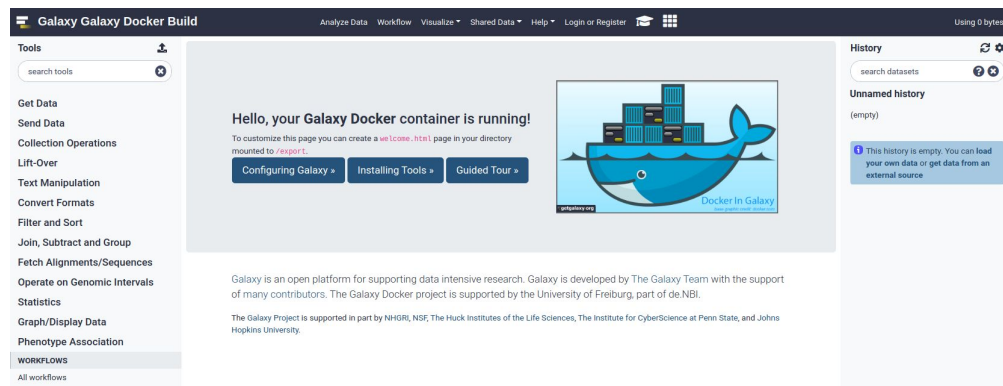
The screenshot displays the Galaxy Docker Build web interface. The header includes navigation links for 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', 'Login or Register', and a user profile icon. The main content area features a large blue whale illustration with a Docker container on its back, accompanied by the text 'Hello, your Galaxy Docker container is running!' and instructions to customize the page by creating a 'welcome.html' file in the '/export' directory. Below this, there are three buttons: 'Configuring Galaxy', 'Installing Tools', and 'Guided Tour'. The left sidebar contains a 'Tools' search bar and a list of categories such as 'Get Data', 'Send Data', 'Collection Operations', 'Lift-Over', 'Text Manipulation', 'Convert Formats', 'Filter and Sort', 'Join, Subtract and Group', 'Fetch Alignments/Sequences', 'Operate on Genomic Intervals', 'Statistics', 'Graph/Display Data', and 'Phenotype Association'. The right sidebar shows 'History' and 'Unnamed history' sections, both currently empty, with a notification that the history is empty and can be populated from an external source.

Galaxy Docker image

Configure by setting environment variables

Jobs run inside the container by default, but can be configured to run externally

Comes with default Galaxy Tools



The screenshot displays the Galaxy Docker Build interface. At the top, the title bar reads "Galaxy Galaxy Docker Build" and includes navigation links for "Analyze Data", "Workflow", "Visualize", "Shared Data", "Help", "Login or Register", and a user profile icon. The main content area features a large blue whale illustration with a city skyline on its back, representing the Docker In Galaxy project. The text "Hello, your Galaxy Docker container is running!" is prominently displayed, followed by instructions on how to customize the page. Below this, three buttons are visible: "Configuring Galaxy", "Installing Tools", and "Guided Tour". The left sidebar contains a "Tools" section with a search bar and a list of categories including "Get Data", "Send Data", "Collection Operations", "Lift-Over", "Text Manipulation", "Convert Formats", "Filter and Sort", "Join, Subtract and Group", "Fetch Alignments/Sequences", "Operate on Genomic Intervals", "Statistics", "Graph/Display Data", and "Phenotype Association". The right sidebar shows a "History" section with a search bar and a message indicating that the history is empty.

Galaxy Flavours

Docker images with preinstalled tools, workflows, data

Examples:

- RNA Workbench
- Genome Annotation
- Metagenomics
- Proteomics
- Imaging
- Workflow4Metabolomics
- HiCEXplorer
- deepTools
- ...

List on <https://github.com/bgruening/docker-galaxy-stable#list-of-galaxy-flavours--toc>

How to create your own?

Tools install

Tool list in standard YAML format

“install-tools” command inside the container

```
install-tools /path/to/tool_list.yml
```

```
api_key: admin
galaxy_instance: http://localhost:8080
install_resolver_dependencies: true
install_tool_dependencies: false
tools:

# RNA Alignment

- name: compalignp
  owner: rnateam
  tool_panel_section_label: "RNA Alignment"

- name: mafft
  owner: rnateam
  tool_panel_section_label: "RNA Alignment"

- name: suite_locarna
  owner: rnateam
  tool_panel_section_label: "RNA Alignment"

- name: locarna_multiple
  owner: rnateam
  tool_panel_section_label: "RNA Alignment"
  revisions:
    - 8414fea2a6fd
```

Workflows install

Workflows in .ga format, downloaded from a Galaxy instance

“workflow-install” command inside the container

```
workflow-install --workflow_path /path/to/workflows/ -g \  
http://localhost:8080 -u $GALAXY_DEFAULT_ADMIN_USER -p \  
$GALAXY_DEFAULT_ADMIN_PASSWORD
```

Populating data libraries

Data library content in standard YAML format

```
libraries:
  - name: "Test data"
    files:
      - url: https://raw.githubusercontent.com/eteriSokhoyan/test-data/master/cliques-high-representatives.fasta
        file_type: fasta
      - url: https://raw.githubusercontent.com/eteriSokhoyan/test-data/master/cliques-low-representatives.fasta
        file_type: fasta
      - url: https://raw.githubusercontent.com/bgruening/galaxytools/master/tools/rna_tools/vienna_rna/test-data
        file_type: rna_eps
```

“setup-data-libraries” command inside the container

```
setup-data-libraries -i /path/to/library_data.yaml -g \
http://localhost:8080 -u $GALAXY_DEFAULT_ADMIN_USER -p \
$GALAXY_DEFAULT_ADMIN_PASSWORD
```


Running Data Managers

Data manager runs in standard YAML format

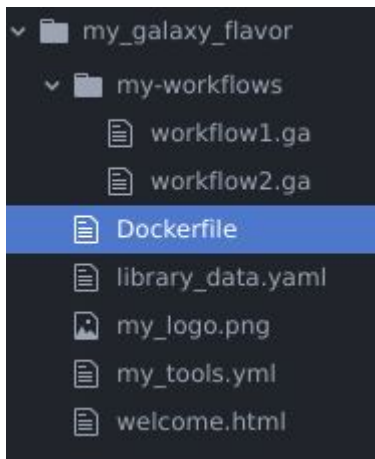
```
data_managers:
  # Data manager ID
  - id: toolshed.g2.bx.psu.edu/repos/devteam/data_manager_fetch_genome_dbkeys_all_fasta/data_manager_fetch_genome_all_fas
  # tool parameters, nested parameters should be specified using a pipe (|)
  params:
    - 'dbkey_source|dbkey': '{{ item }}'
    - 'reference_source|reference_source_selector': 'ucsc'
    - 'reference_source|requested_dbkey': '{{ item }}'
  # Items refer to a list of variables you want to run this data manager. You can use them inside the param field with
  # In case of genome for example you can run this DM with multiple genomes, or you could give multiple URLs.
  items:
    - mm10
    - dm3
  # Name of the data-tables you want to reload after your DM are finished. This can be important for subsequent data ma
  data_table_reload:
    - all_fasta
    - __dbkeys__
```

“run-data-managers” command inside the container

```
run-data-managers --config /path/to/data_manager_rna_seq.yaml -g \  
http://localhost:8080 -u $GALAXY_DEFAULT_ADMIN_USER -p \  
$GALAXY_DEFAULT_ADMIN_PASSWORD
```

Creating your own Galaxy Flavours

Create your own Docker image, based on quay.io/bgruening/galaxy



```
FROM quay.io/bgruening/galaxy:20.09

ENV GALAXY_CONFIG_BRAND="My own flavor"

# Install tools
ADD my_tools.yml $GALAXY_ROOT/tools.yaml
RUN install-tools $GALAXY_ROOT/tools.yaml

# Add data library definition file
ADD library_data.yaml $GALAXY_ROOT/library_data.yaml
RUN setup-data-libraries -i $GALAXY_ROOT/library_data.yaml -g http://localhost:8080 \
    -u $GALAXY_DEFAULT_ADMIN_USER -p $GALAXY_DEFAULT_ADMIN_PASSWORD

# Add workflows to the Docker image
ADD ./my-workflows/* $GALAXY_HOME/workflows/
RUN workflow-install --workflow_path $GALAXY_HOME/workflows/ -g http://localhost:8080 \
    -u $GALAXY_DEFAULT_ADMIN_USER -p $GALAXY_DEFAULT_ADMIN_PASSWORD

# Customize Homepage Style
ADD my_logo.png $GALAXY_CONFIG_DIR/web/welcome_image.png
ADD welcome.html $GALAXY_CONFIG_DIR/web/welcome.html
```

Creating your own Galaxy Flavours

Create your own Docker image, based on quay.io/bgruening/galaxy

Build locally (docker build)

or make it public on GitHub and have it built by hub.docker.com or quay.io

Galaxy Training Network Docker images

All tutorials in GTN have a corresponding Docker image built automatically

Galaxy instances

You can use a public Galaxy instance which has been tested for the availability of the used tools. They are listed along with the tutorials above.

You can also use the following Docker image for these tutorials:

```
docker run -p 8080:80 quay.io/galaxy/assembly-training
```

NOTE: Use the `-d` flag at the end of the command if you want to automatically download all the data-libraries into the container.

It will launch a flavored Galaxy instance available on <http://localhost:8080>. This instance will contain all the tools and workflows to follow the tutorials in this topic.

Login as **admin** with password **password** to access everything.