Dockerized Galaxy for Tool Publishing

Galaxy Resources for Tools Developers
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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/](http://localhost:8080/)
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
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
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

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

```yaml
libraries:
  - name: "Test data"
    files:
      - url: https://raw.githubusercontent.com/eteriSokhoyan/test-data/master/cliques-high-representatives.fa
        file_type: fasta
      - url: https://raw.githubusercontent.com/eteriSokhoyan/test-data/master/cliques-low-representatives.fa
        file_type: fasta
        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|required_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.