



1. New genotoul-bioinfo Galaxy infrastructure

1.1. Old Galaxy server

Our previous Galaxy server was available through the following URL:

<https://vm-galaxy-prod.toulouse.inra.fr>

This URL is still valid, but points to a web page that describes the new Galaxy infrastructure.

A link on this page points to the real location of the old Galaxy server:

<https://vm-galaxy-prod.toulouse.inra.fr/galaxy/>

This server will be shut down no later than the end of spring. In the meantime, you can use it to export your workflows as “.ga” text files. You can’t submit jobs anymore (your storage quota is 0, thus “100% quota consumed” displayed).

Because of changes in tool names or versions between old and new Galaxy servers, these “.ga” text files **have to be edited before upload** to on the new Galaxy server. Tool naming/version must be edited in such a way it will be possible to import the associated workflows without problem. We can help you to find the correct editing.

To export your history, a dedicated Galaxy server has been setup.

1.2. Export Galaxy server

The URL of this server is: https://vm-galaxy-prod.toulouse.inrae.fr/galaxy_export/

As explained on its welcome page, datasets are stored as files, but also as records in a database.

The structure of the database has changed between the old and new version of Galaxy, resulting on a poor compatibility of exports made with the old Galaxy server.

An upgrade of old Galaxy server 16.05 to version 21.05 would have correct its database structure, but also its software part, and would have led to it no longer being functional at all.

The galaxy_export server is a 21.05 Galaxy server (same version as our new Galaxy main server). It has a copy of old Galaxy server database, and an upgrade of its structure has been made. This upgrade doesn’t modify old Galaxy data: the upgrade modify the copy of the database, and old dataset files are mounted read only. Only three new tools are provided to help history exports, and will be described later.

WARNING : Since the database of the export server is a copy of that of the old one at a given time, if in the meantime files are deleted and purged on the old server, they will not be seen as such on the export server which will attempt to create an archive with files that no longer exist, and export will fail! It is therefore important to have the same history contents between the old and export servers, and therefore to delete on the export server the datasets deleted from the old one.

1.3. New Galaxy main server

This server is a 21.05 Galaxy server too, as the Export one. Histories exported from this latter can be uploaded to the new server without error.

However, still because of changes in tool naming/version, some datasets require database updates to be displayed/rerun correctly. If you have such a problem, contact us to make these updates.

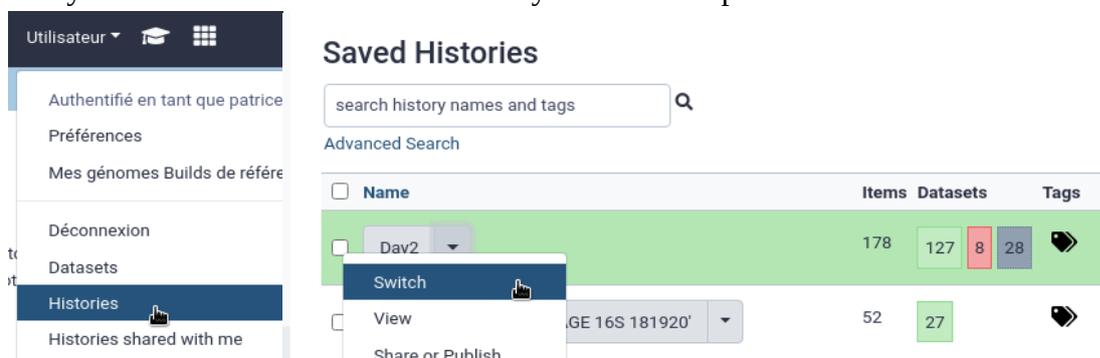
2. History export from Galaxy Export

To authenticate on Galaxy Export, use your genotoul-bioinfo LDAP credential id.

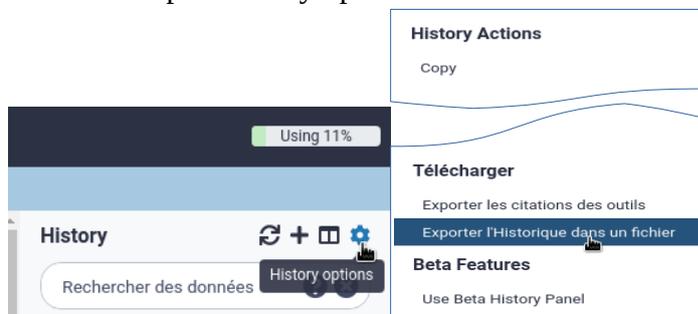
You will all find your data as it was at the end of December on the old server.

2.1. Generate export link

1. List your histories and switch to the one you want to export



2. Go to the export history option



3. Generate the export link (if not already available)

Export history archive

No link for history export ready, no history export ever initiated for this history.

[Click here to generate a new archive for this history.](#)

then wait until the link is displayed (you can leave you web page, close your browser, even shut down your computer, and check link availability later following the same process)

Export history archive

Galaxy server is preparing history for download, this will likely take a while....

Export history archive

Link for download ready http://vm-galaxy-prod.toulouse.inrae.fr/galaxy_export/history/exj_details . Use this link to download the archive or import it on another Galaxy server.

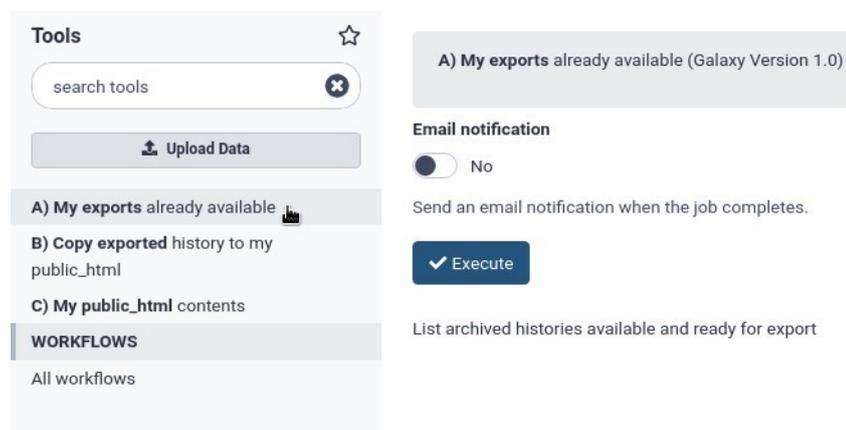
You can use the displayed link to download you history on you own computer as a compressed

archive (.tgz). Otherwise follow the next steps to save it on one of your genotoul-bioinfo storage volumes.

2.2. Check available exports

Another way to check if an export is ready, is to list all your histories that are ready.

A dedicated tool, with no parameter, just a report output, is provided:



The screenshot shows the Galaxy web interface. On the left, the 'Tools' sidebar is visible with a search bar and an 'Upload Data' button. The main panel displays the tool 'A) My exports already available (Galaxy Version 1.0)'. Below the tool name, there is a section for 'Email notification' with a toggle set to 'No' and a description: 'Send an email notification when the job completes.' A blue 'Execute' button is present. Below the button, it says 'List archived histories available and ready for export'. The tool's output area shows a list of export-ready histories:

- A) My exports already available
- B) Copy exported history to my public_html
- C) My public_html contents

WORKFLOWS

- All workflows

The report is a simple text:

```
Hereunder are your available exported histories:
Copy of 'imported: MILAGE 16S 181920'
    2,7G    dataset_722479.dat
Day1
    162M    dataset_722474.dat
Day2
    2,9G    dataset_722475.dat
Day3
    2,4G    dataset_722476.dat
Lefse
    66M     dataset_722787.dat
```

It gives for all export ready histories, its name on a first line, and then the internal dataset file corresponding to the compress archive file generated and its size.

2.3. Copy export archive file to your public_html

This tool will take as parameters an history name that is ready for export, and the name of the archive that will be copied in your public_html folder on genotoul-bioinfo platform. This copy is really faster than a download on your own computer because our Galaxy servers are in the genotoul-bioinfo “local” network. And if your purpose is to copy your histories from old to new Galaxy server, it’s a waste of time to detour through your computer.

First a few explanations:

- every user on genotoul-bioinfo platform have at least three storage volumes:
 - your “home” folder; small but secure (backup each night): /home/username
 - your “save” folder, 250GB and secure too: /save/username, which is also available in your home folder as a symbolic link /home/username/save

- your “work” folder, 1TB (no backup): /work/username, which is also available in your home folder as a symbolic link /home/username/work
- you can access to these folder via an ssh connection (ssh username@genologin.toulouse.inrae.fr), or via an sftp or sshfs file transfer client (like FileZilla, WinSCP, or MobaXterm)
- if you have a folder (or a link to a folder) named public_html in your home folder, its contents will also be available for download via an URL. Suppose you have a file my_archive.tgz in your /home/username/public_html, it can be downloaded via the following URL:
http://genoweb.toulouse.inra.fr/~username/my_archive.tgz
- This URL will work only if:
 - each folder which compose the path to the archive file as the “x” (pass through) right set for everybody
 - the archive file has its “r” (read) right set

How to prepare your public_html ?

First choose the right place where to put it. As mentioned above, the natural place is in your home folder.

You have to check that your home folder has the required rights:

```
# ls -ld /home/john
drwx--- 2 root root 4096 21 janv. 22:13 /home/john
```

The rights can be divided in 3 groups rwx (read/write/pass through), one for the **owner**, one for the **group**, and one for **others**. If the “x” right is missing for others, add it:

```
# chmod o+x /home/john
# ls -ld /home/john
drwx--x 2 root root 4096 21 janv. 22:13 /home/john
```

Create the public_folder if it doesn't already exist:

```
# mkdir /home/john/public_html
```

Check again that the “x” right for others is set for this folder.

Copy a file in this folder, check that it has the “r” right for others set, and that's it: it can be retrieved via URL.

Now, your home folder is tiny. To have more space, use a symbolic link:

- check that your save (or work) folder has “x” right set for others
- create the public_html folder in it, check its rights
- create a symbolic link in your home folder (no folder/file public_html must be there)

```
# ln -s /save/username/public_html /home/username
```
- Check the rights of your home folder

Now the tool:

The screenshot shows a web interface for a tool. On the left, there is a sidebar with a menu. The menu items are: "A) My exports already available", "B) Copy exported history to my public_html", "C) My public_html contents", "WORKFLOWS", and "All workflows". The "WORKFLOWS" section is currently selected. On the right, there are configuration options: "History name" with an empty text input field, "Output archive name" with an empty text input field, and a note "extension and path added automatically". Below that is an "Email notification" section with a toggle switch set to "No" and the text "Send an email notification when the job completes.". At the bottom right, there is a blue button with a checkmark and the text "Execute".

The history name is one the your ready for export histories. The name must contain a quote “ ’ ”. This history name must be unique, no other history can have it. If one of these rules is not fulfilled, change the history name before launching the tool.

The tool will perform several controls, and will fail if something is wrong.

The normal output of this tool looks like this:

You can retrieve your exported history archive at:

`http://genoweb.toulouse.inra.fr/~username/my_archive.tgz`

You can use this link on the new Galaxy server(1) to import your exported history
(1) https://vm-galaxy-prod.toulouse.inra.fr/galaxy_main

2.4. List archives in your public_html

The third tool proposed (no parameter), just lists the archives present in your public_html folder.

The screenshot shows a web interface for a tool. On the left, there is a sidebar with a menu. The menu items are: "A) My exports already available", "B) Copy exported history to my public_html", "C) My public_html contents", "WORKFLOWS", and "All workflows". The "WORKFLOWS" section is currently selected. On the right, there are configuration options: "Email notification" with a toggle switch set to "No" and the text "Send an email notification when the job completes.". At the bottom right, there is a blue button with a checkmark and the text "Execute".

and the output is:

```
/save/username/public_html
Your archives in your /home/username/public_html:
-rw-r--r-- 1 username my_group 141M 12 janv. 10:54 archive1.tgz
http://genoweb.toulouse.inra.fr/~username/archive1.tgz
-rw-r--r-- 1 username my_group 41M 13 janv. 15:55 archive2.tgz
http://genoweb.toulouse.inra.fr/~username/archive2.tgz
```

3. Import history to Galaxy Main

Once you have the genoweb URL, you can import the associated history to the new Galaxy server https://vm-galaxy-prod.toulouse.inrae.fr/galaxy_main

- go to your histories list as shown previously
- click on the “Import from file” button

- keep the selected option “Export URL from another Galaxy instance”
- paste the genoweb URL
- click on the “Import history” button

Saved Histories

search history names and tags

[Advanced Search](#)

Import a history from an archive

How would you like to specify the history archive?

Export URL from another Galaxy instance

Upload local file from your computer

Archived History URL

Import a history from an archive

Waiting on history import job, this may take a while....

The history, depending on its size, can take a long time to be imported. You can leave this web page. When the history will be imported, it will be displayed in your histories list.

If you wait, you will have a a link to display your histories list.

Import a history from an archive

Done!

History imported, check out [your histories](#).

Now, you have your history imported and your datasets ready to be used as input for tools.

Some datasets that have “dynamic” display, like html pages , and require some updates (tool name/version) in the Galaxy database to be displayed correctly.

To be rerun, it’s the same, updates are necessary.

In such case, contact us to make these changes.