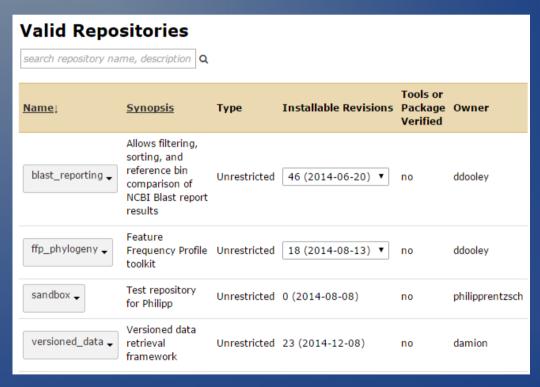
Sharing your Galaxy tool with the world

This involves uploading the tool files into a Galaxy "toolshed" where a Galaxy admin can select it for installation at their own location.



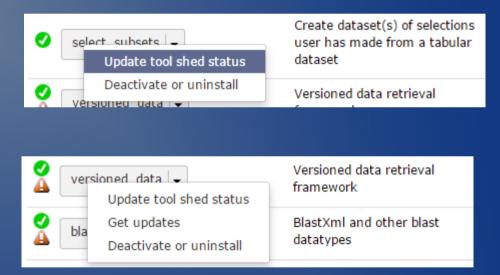
Created by Hsiao lab, BC Public Health Microbiology & Reference Laboratory, BC Centre for Disease Control, https://github.com/Public-Health-Bioinformatics

Galaxy Tool – Versioning

Every tool should have a version number.

<tool id="blast_reporting" name="BLAST Reporting" version="1.0.5">

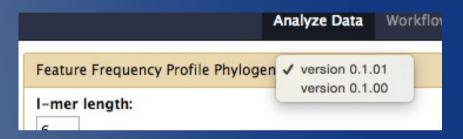
Incrementing the version number causes a toolshed (and Galaxy) to treat the uploaded tool version as its own entity, like a new model of a car that can be taken out for a drive.





Galaxy Tool – Versioning

With a few tool version installed on a Galaxy server, a user will have a choice of which to run.



If version number stays the same: the upload becomes an update to the existing toolshed version (same car). If a Galaxy admin downloads your changes they will be applied to their currently loaded tool (if same version).

Uploads to main Galaxy toolshed should include a version number increment, i.e. try to limit uploads to significant changes.



Mask of Yul Brynner, Westworld (1973)

Galaxy Tool – Version Id

Note: The Galaxy toolshed "Revisions" list is a bit odd in that it lists off its own item record id and upload date, but doesn't list the tool's version id. (View its record to see this).

<u>Name</u> ↓	<u>Synopsis</u>	Туре	Metadata Revisions
blast reporting	Allows filtering, sorting, and reference bin comparison of NCBI Blast report results	Unrestricted	46 (2014-06-20) ▼ 46 (2014-06-20) 32 (2014-05-08) 21 (2014-01-21) 19 (2014-01-21) 18 (2014-01-20)
ffp_phylogeny	Feature Frequency Profile toolkit	Unrestricted	

Preparing a Toolshed Update

Make a tar archive of the tool folder contents for upload to a toolshed.

Select which files or subfolders to include or exclude in the archive. E.g. include all files **except** text editor backups, compiled python templates, and planemo output reports:

```
tar -zcvf [tool name].tar.gz * --exclude "*~" --exclude "*.pyc" --exclude "tool_test_output*" --exclude "*.gz"
```

Download to your local computer so that it can be uploaded to a Galaxy toolshed. The last "./" places the file in your current folder.

scp [your user name]@[your server name]:\
/usr/local/galaxy/galaxytest/galaxy-dist/tools/TESTING/[folder]/[tool name].tar.gz ./

Links

https://wiki.galaxyproject.org/ToolShed/PublishTool