

# **Galaxy servers for command-line users**

Clare Sloggett, VLSCI

# We have launchable GVL images with

- Galaxy (and its workflow engine)
- SGE (with a scalable CloudMan cluster)
- CloudBioLinux bioinformatics tools
- Toolshed-installed bioinformatics tools
- Galaxy-installed reference genomes
- ...and indices of reference genomes for all sorts of tools
- NGINX and PostgreSQL

These are useful from outside Galaxy too!

# Utilities and setup scripts

[https://github.com/claresloggett/gvl\\_commandline\\_utilities](https://github.com/claresloggett/gvl_commandline_utilities)

These utilities will configure the current image;  
some of what they do will be built into future images.

# Features for command-line

What is available?

- non-sudo account(s) for ordinary use
- SGE job submission
- environment modules for toolshed tools
- symlinks to genomes
- public\_html
- ipython notebook (password-protected, encrypted)

Also...

- BioBlend ! (use on instance, or your local machine)