Galaxy Australasia Workshop 2014

Galaxy in the wild

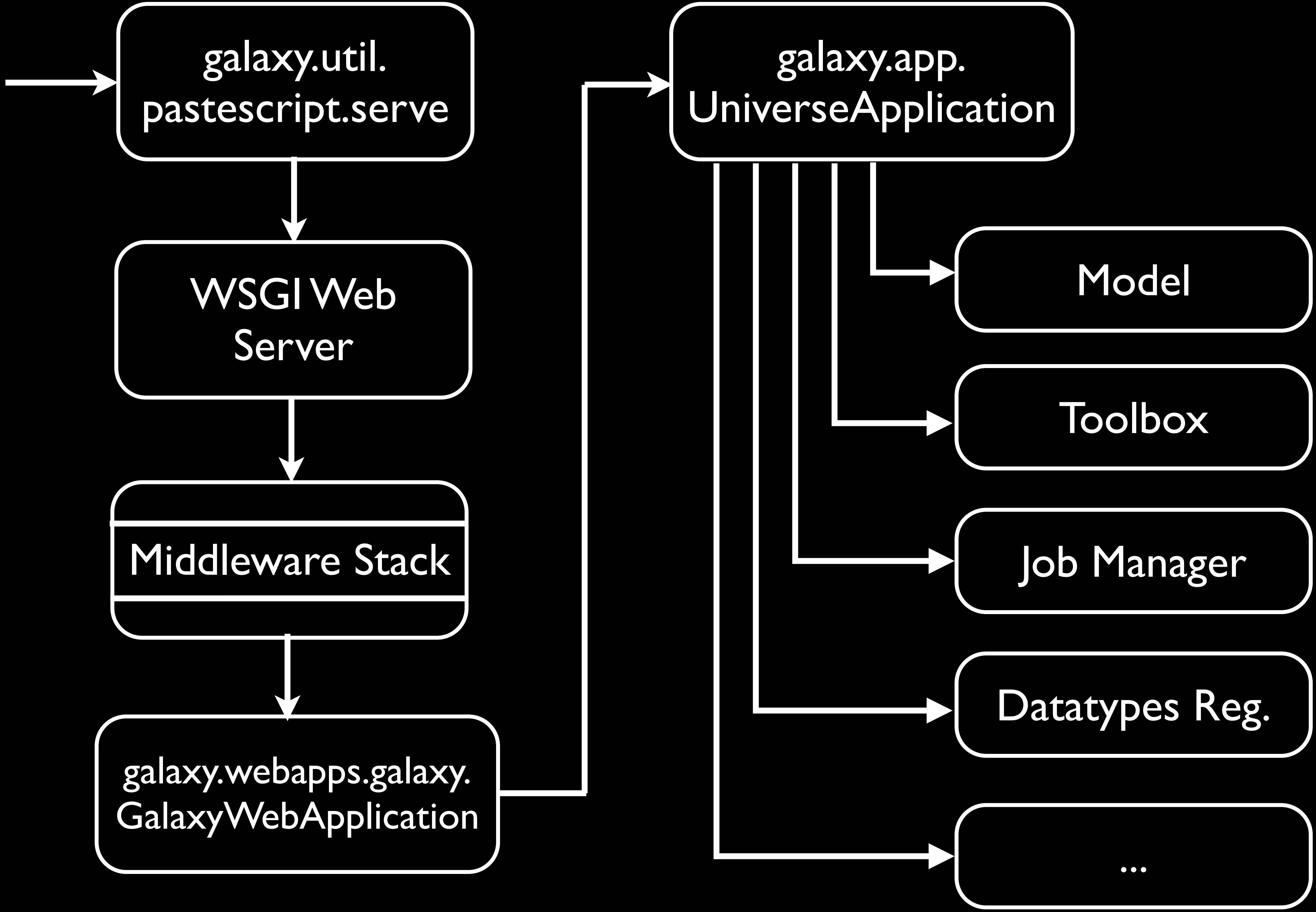
Galaxy Architecture and Supporting Production Level Genomics

Nate Coraor
The Galaxy Team
Penn State University

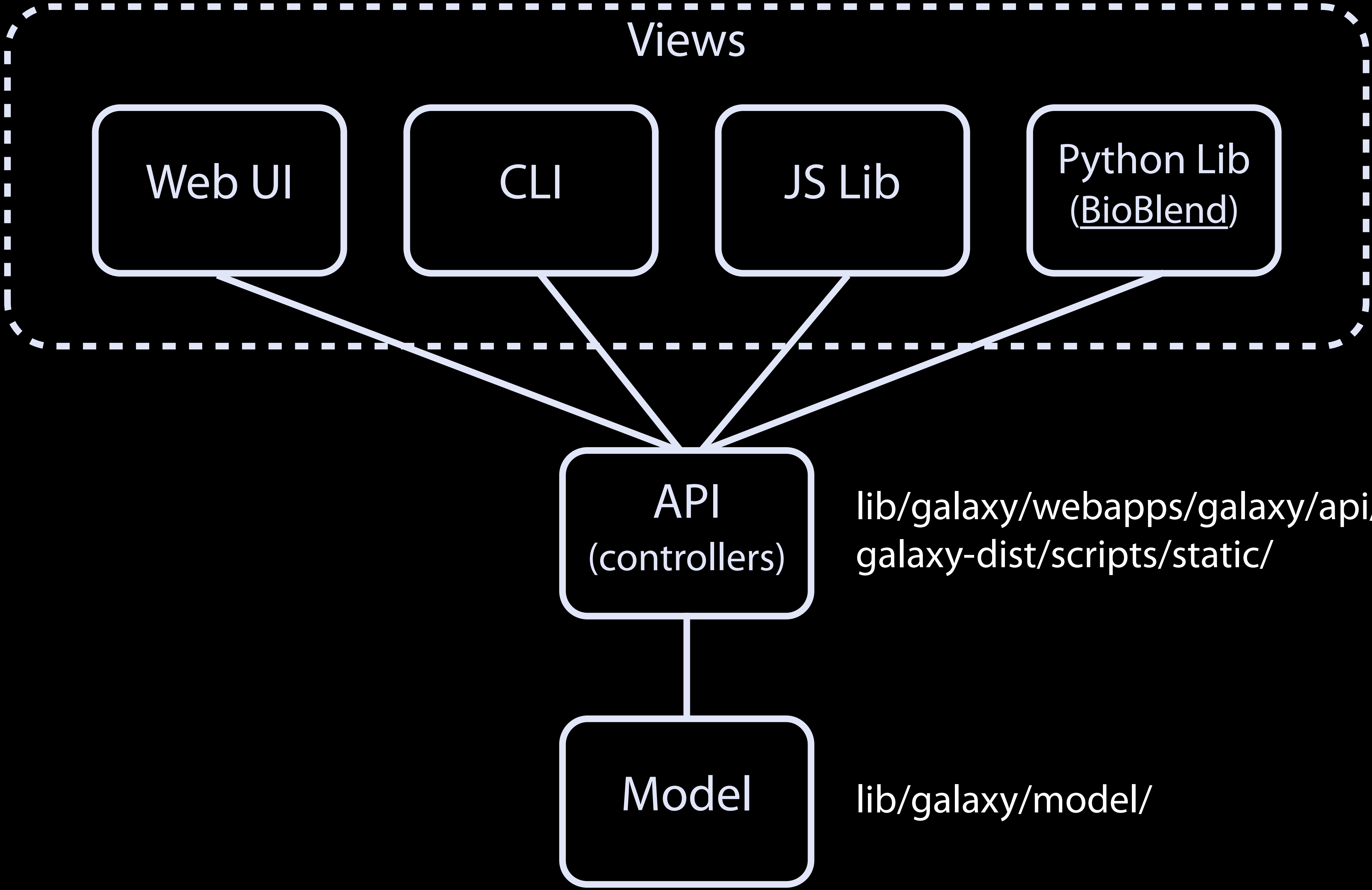
Ask questions (please!)

- Who is this for?
  - People who want to hack on Galaxy
  - People who want to run a Galaxy server
- Who isn’t this for?
  - People who just want to use Galaxy (sorry)

- Code architecture
- Running a server


galaxy.util.
pastescript.serve
WSGI Web Server
Middleware Stack
galaxy.webapps.galaxy.
GalaxyWebApplication
galaxy.app.
UniverseApplication
Model
Toolbox
Job Manager
Datatypes Reg.
...

UI Architecture



lib/galaxy/webapps/galaxy/api/
galaxy-dist/scripts/static/

lib/galaxy/model/

Coding standards

- Galaxy mostly follows PEP-8 (but not entirely)
- Comment lines should be under 79 characters, code lines can be up to 200 characters if it improves readability
- Whitespace: whatever is most readable, both for blank lines and space around operators

Modularity and Reusability

- Datatypes: subclasses of more general datatypes
- Job runners: plugins, and subclasses of existing plugins
- API: standardized layout, framework
- Javascript: modeled data representation

- Code architecture
- Running a server

usegalaxy.org/production

Development/Production

- Galaxy is easy to start using:

```
% sh run.sh
```

- Galaxy is not as easy to set up for a big lab, University, research org, etc.

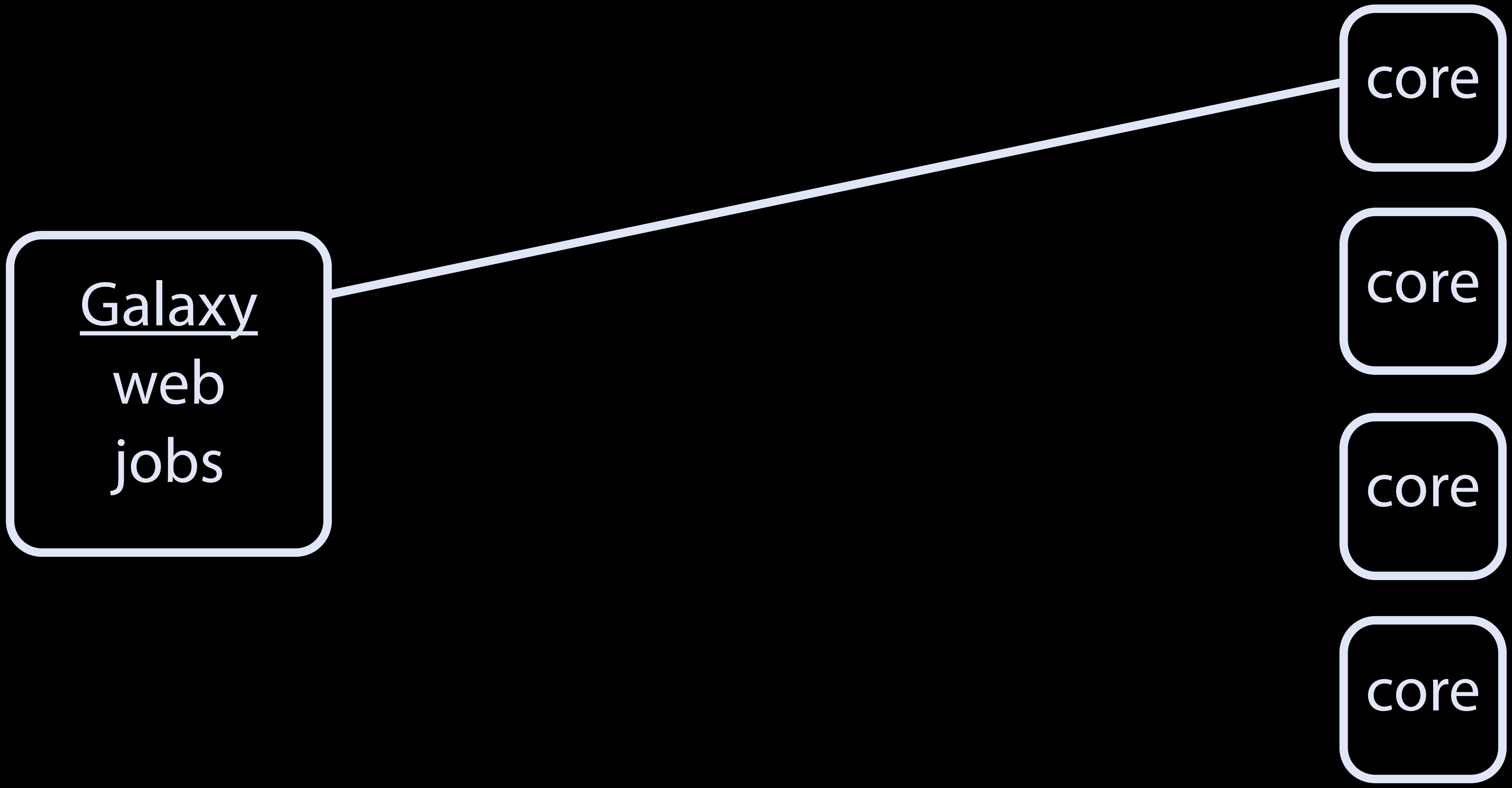
Look at universe_wsgi.ini

Database

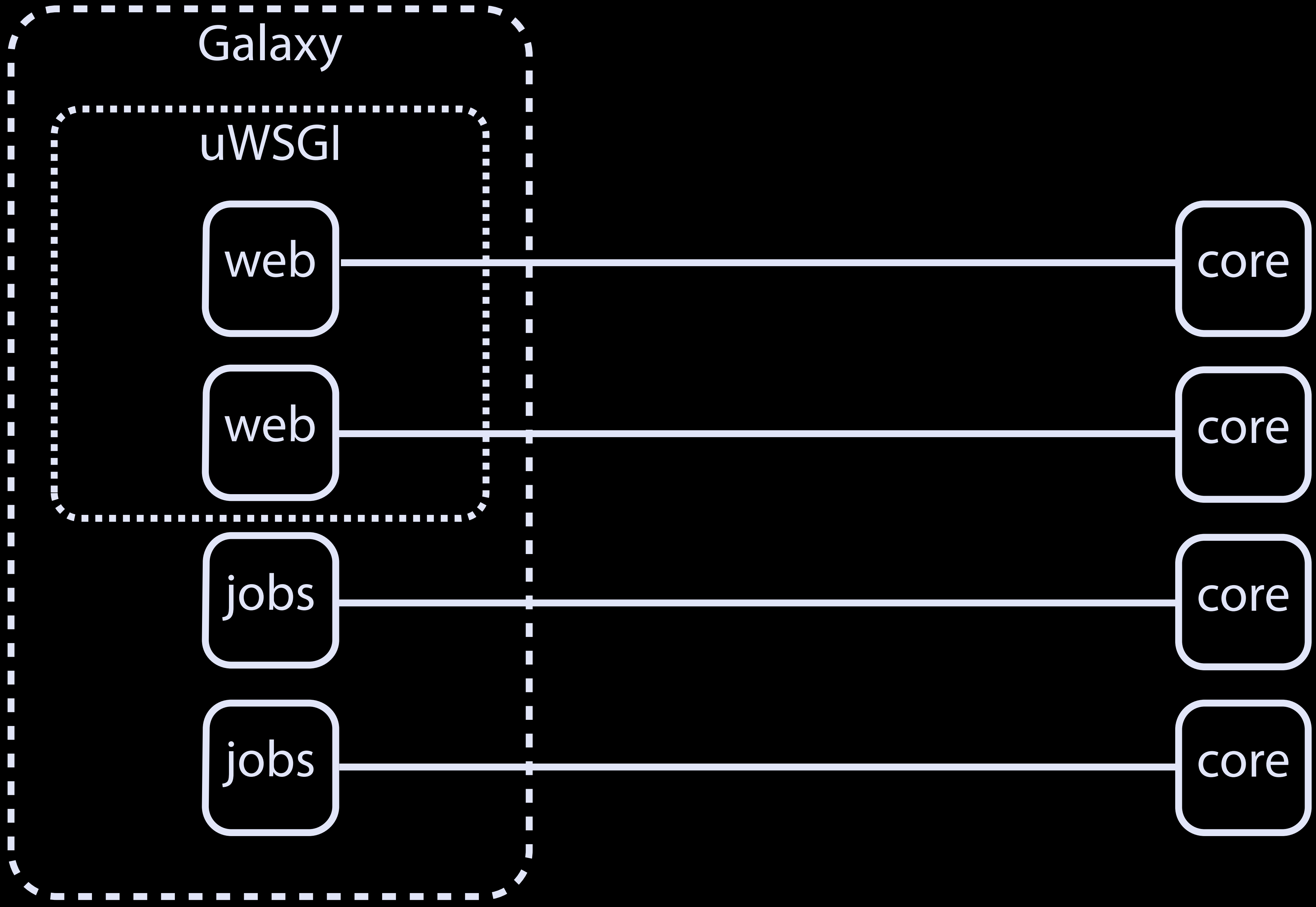
~~SQLite~~

PostgreSQL

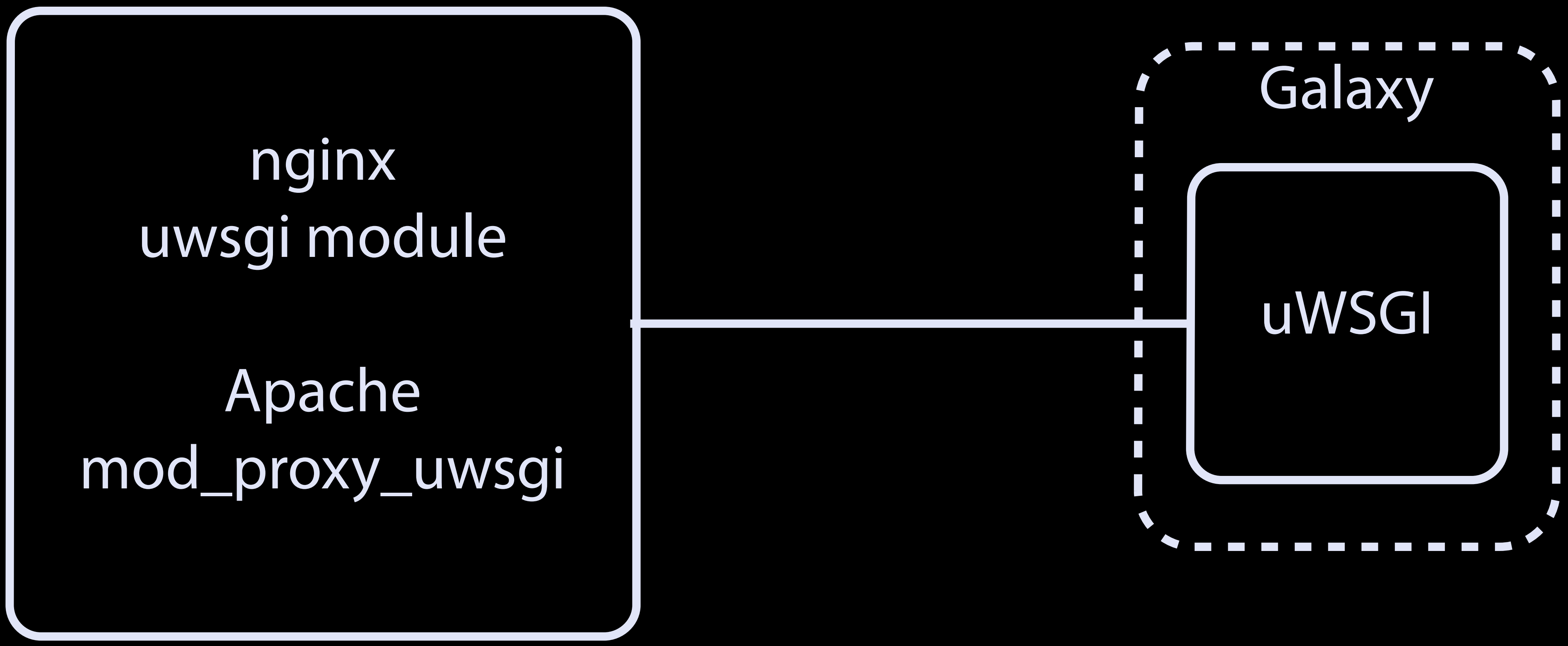
Galaxy process model



Galaxy multiprocess model



Galaxy multiprocess model



Bonus: upload and download via proxy

Cluster

CLUSTER RESOURCES INC.
TORQUE

Condor
High Throughput Computing

slurm
workload manager

PBS Works™

GRID ENGINE

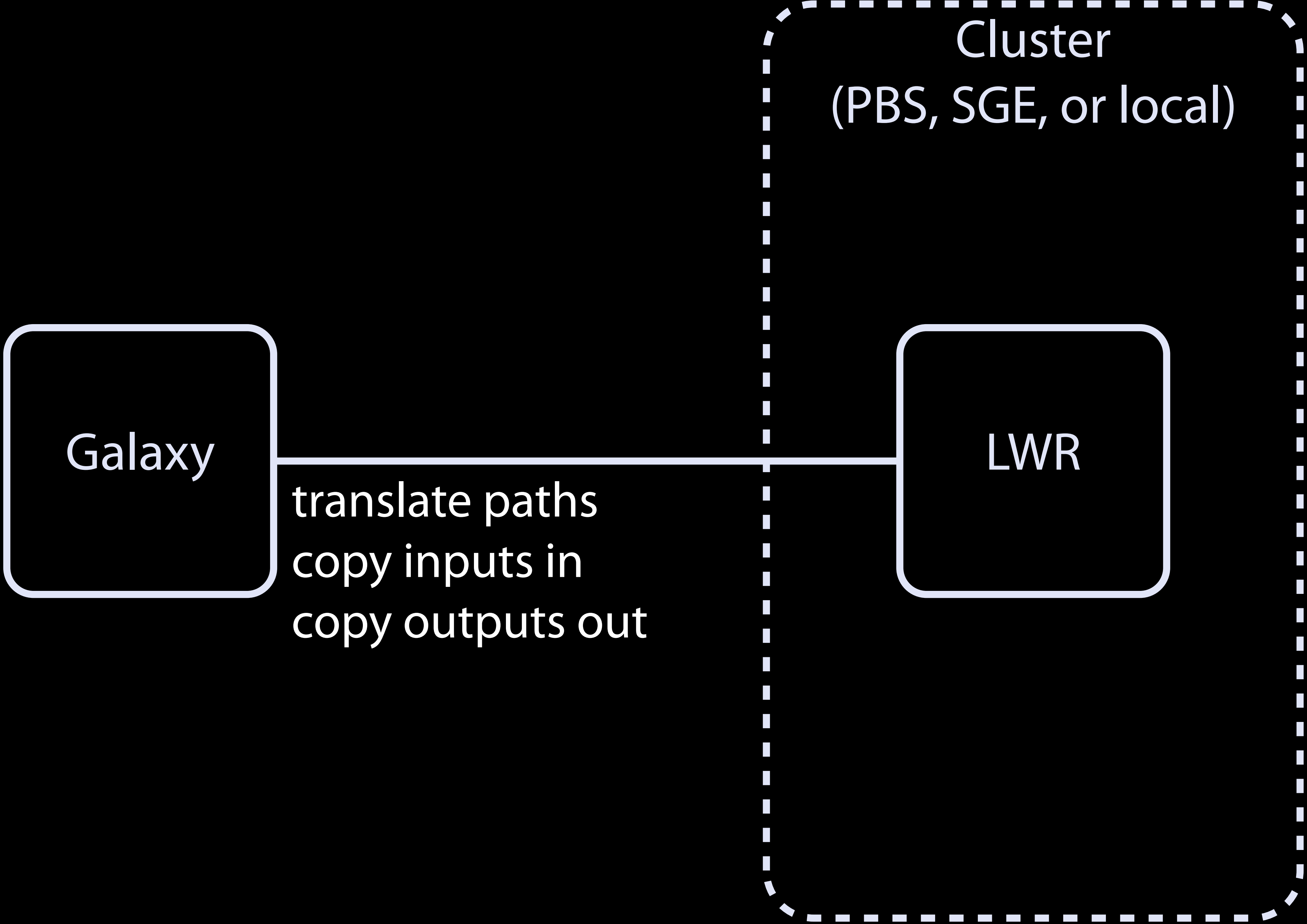
Platform Computing

DRMAA
Distributed Resource Management Application API — www.drmaa.org

requires common filesystem

Cluster with LWR

John Chilton



Job Execution Features

- All cluster DRM options available
  - walltime
  - number of cores, amount of memory
  - queue selection
- Dynamically choose the above based on
  - User
  - Tool
  - Tool parameters
  - Tool inputs
- Limit users' concurrent jobs

Controlling Data

- Quotas
- Use Data Libraries for common data
  - Can upload from filesystem!
- Data removal
  - Allow users to “purge” unwanted data
  - Run dataset cleanup scripts to recover space
- Transparent compression if you can get it (zfs, btrfs)

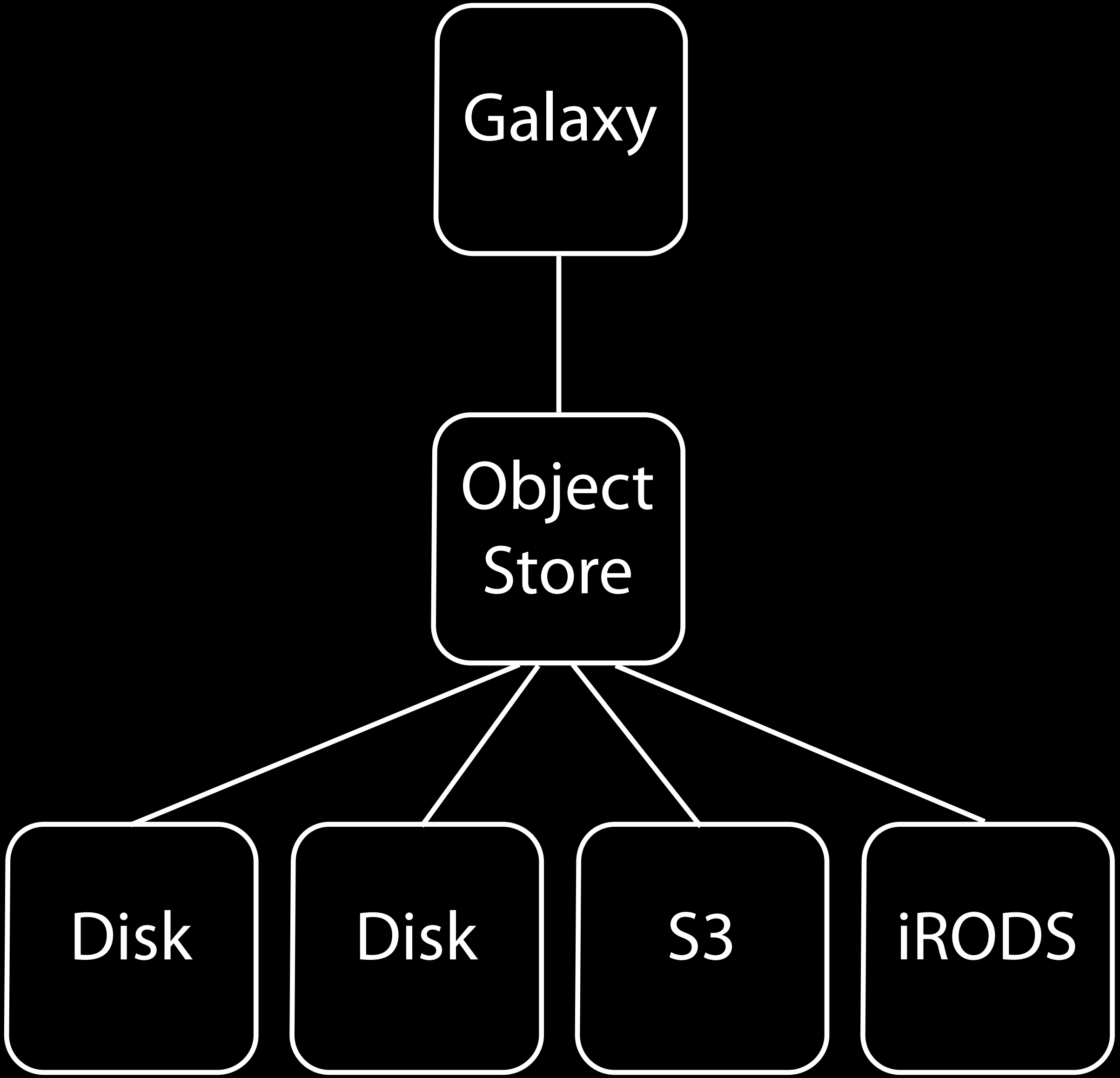
Uploading data

- nginx upload module
- S(FTP)S upload

Object Store

Enis Afgan

Dannon Baker



Reference Data

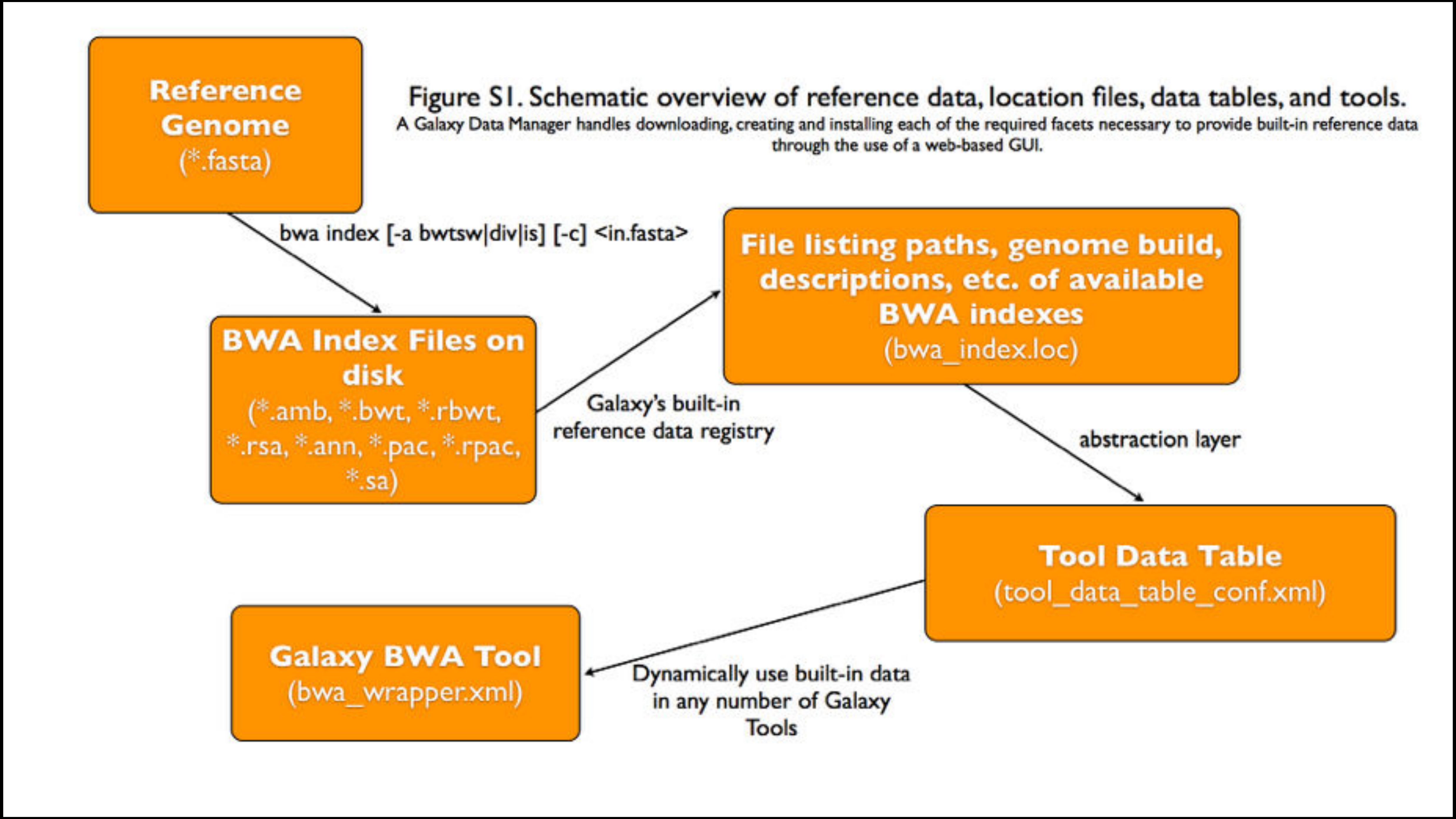

Reference Genome
(*.fasta)
bwa index [-a bwtsw|div|is] [-c] <in.fasta>
BWA Index Files on disk
(*.amb, *.bwt, *.rbwt, *.rsa, *.ann, *.pac, *.rpac, *.sa)
Galaxy's built-in reference data registry
File listing paths, genome build, descriptions, etc. of available BWA indexes
(bwa_index.loc)
abstraction layer
Tool Data Table
(tool_data_table_conf.xml)
Dynamically use built-in data in any number of Galaxy Tools
Galaxy BWA Tool
(bwa_wrapper.xml)

Figure S1. Schematic overview of reference data, location files, data tables, and tools.
A Galaxy Data Manager handles downloading, creating and installing each of the required facets necessary to provide built-in reference data through the use of a web-based GUI.

Reference Data

Dan Blankenberg

- Data tables and location files are a pain
- Use data managers
  - Versioned tools from the tool shed
  - Download data, build indexes

https://wiki.galaxyproject.org/Admin/Tools/DataManagers

Tricks and Technologies

- Run web processes from local disk to ensure network filesystem performance does not impact UI
  - Run handlers from shared filesystem
- Process management via supervisord
- Use Nagios to check individual handlers
- Use sentry to aggregate tracebacks
- Use config management

Config Management

- Formerly: CFEngine
- Now: Ansible
  - Dependencies: sshd, Python
  - No infrastructure required
  - Descriptions in YAML
  - Modules in Python

ANSIBLE

Ansible

```
- name: Update Galaxy to correct changeset
  hg: dest={{ galaxy_dir }} repo=http://bitbuck…

- name: Upgrade Galaxy database
  command: {{ galaxy_dir }}/manage_db.sh upgrade

- name: Install nginx
  apt: pkg=nginx-full
  when: ansible_os_family == “Debian”

- name: Copy nginx configs
  template: src=nginx.conf.j2 dest=/etc/nginx/…
```

usegalaxy.org/production