



# Installing and Maintaining a Local Galaxy Server - Training Day 0

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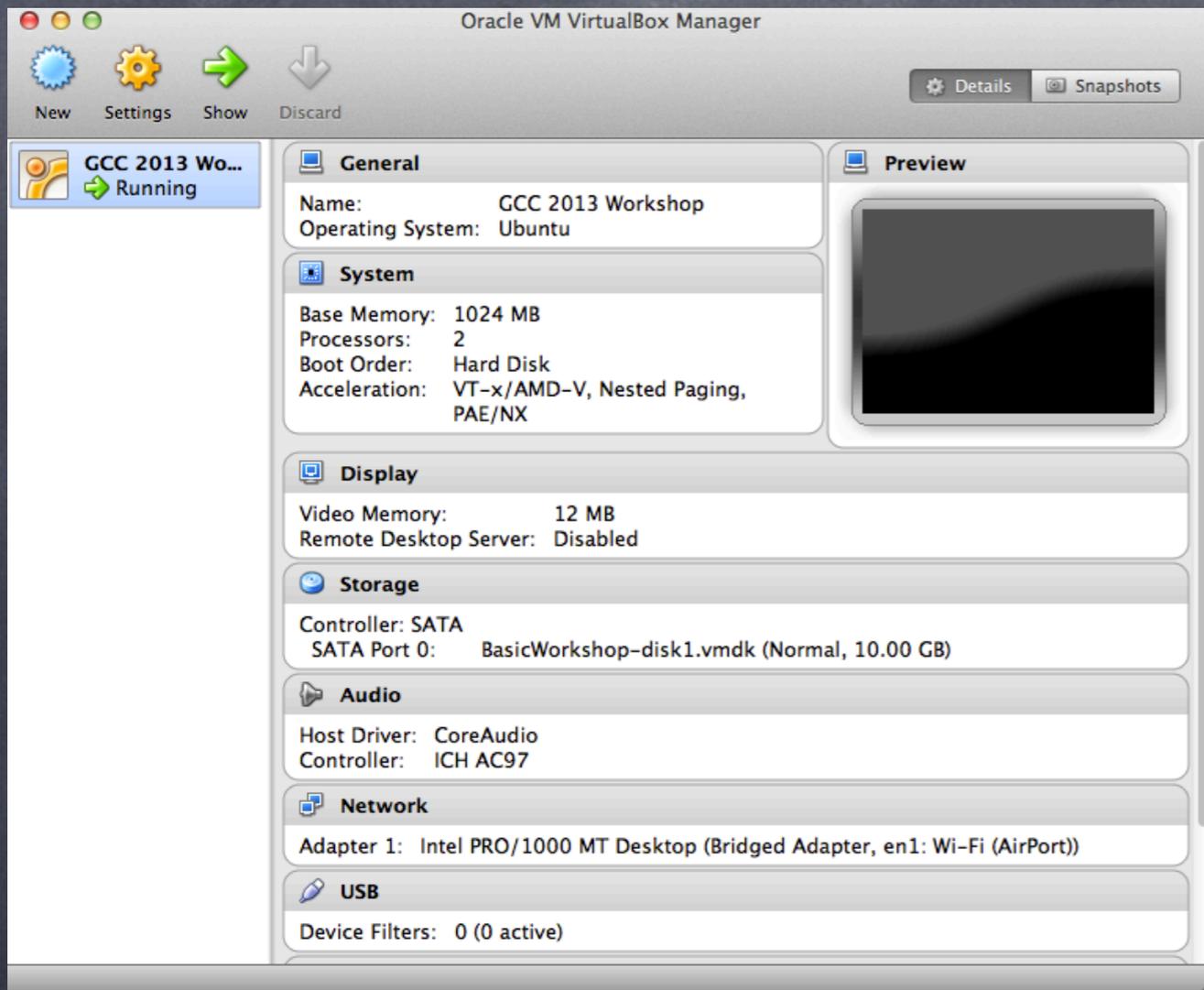
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Research Computing Services

<http://www.uio.no/english/services/it/research/hpc/abel/>

# Introduction and Agenda

- **GM:** Introduction (VM status, the galaxy environment)
- **NV:** configure Postgres, install Apache as proxy, configure and start Galaxy
- **GM:** Aspects of Galaxy administration: roles, groups, libraries and quotas
- **KM:** How do you install tools in Galaxy
- **NV:** Updating the Galaxy installation
- **GM:** A few closing words on securing your Galaxy installation

# VM installation check



VM image download:  
<ftp://ftp.no.embnet.org/galaxy/images/BasicWorkshop.ova>

Username: gcc2013

Password: 12345

Hands up if you have not:

- Downloaded the BasicWorkshop.ova image
- Installed VirtualBox and run the VM properly

# The FTP workshop repository and Wi-Fi credentials

<ftp://ftp.no.embnet.org/galaxy/>

Wi-Fi at UiO:

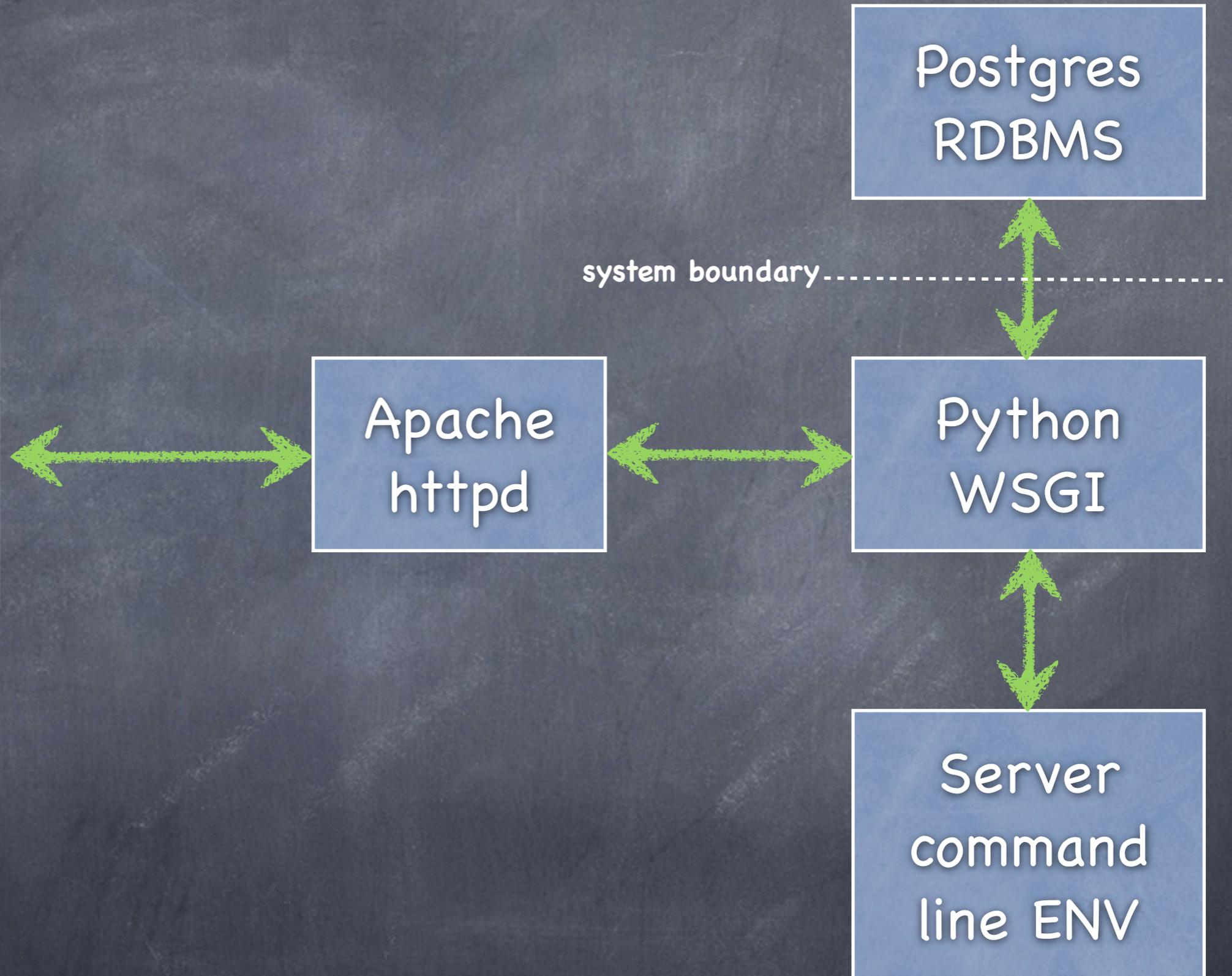
SSID: conferences

Password: uio202aar

# The Galaxy system environment (standalone)



end user



# The Galaxy system environment (HPC)

SSO gateway

Postgres RDBMS

system boundary

Apache httpd

Python WSGI



end user



supercomputer

Queue/job submission software

# The Galaxy system environment (deployment)

## -VM, cloud or in-house physical server?

-For 1-10 simultaneous users that do not need to share data or have small datasets (< 2 Tbytes), a VM option or a cloud provider (Amazon, Rackspace). RAM should be no less than 16-32 Gigs and space can easily take a few Tbytes, depending on your projects.

-If you have > 10 simultaneous users that need to share (upload, download) tenths of Tbytes of data, do invest on an in-house physical server (see next slide).

## -What kind of data will you be processing?

-Security sensitive data?

-Data streams from restricted instrument labs?

## -Expertise, manhours needed for maintenance?

-Large production installations need at least 12-18 man hours weekly.

-Unix/Linux/RDBMS skills (life science aware sysadmin or linux friendly PhD/Postdoc)

# The Galaxy system environment (hardware)



32-64 processing cores, 256-512 Gigs of RAM rack mount server with a capable RAID (6, 6+0) hardware controller (SAS/SATA)



Directly Attached Storage (DAS) SATA/SAS cabinets.

The minimum config for a good in-house server solution. Can scale to 100 Tbytes of storage. Your specs depend on your project requirements.

Beginning of the practical/fun  
fire up your VMs!



# Postgres Configuration (2)

```
Terminal - gcc2013@gcc-workshop: ~
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$ sudo apt-cache search postgresql | grep client
libpq5 - PostgreSQL C client library
postgresql-client - front-end programs for PostgreSQL (supported version)
postgresql-client-9.1 - front-end programs for PostgreSQL 9.1
postgresql-client-common - manager for multiple PostgreSQL client versions
guile-pg - Guile bindings for the PostgreSQL client library
libghc-postgresql-simple-dev - mid-level PostgreSQL client library
libghc-postgresql-simple-doc - mid-level PostgreSQL client library; documentation
libghc-postgresql-simple-prof - mid-level PostgreSQL client library; profiling libraries
libpgtcl-dev - Tcl client library binding for PostgreSQL - development files
libpgtcl1.5 - Tcl client library binding for PostgreSQL
libsphinxclient-0.0.1 - Fast standalone full-text SQL search engine - Client library
libsphinxclient-dev - Fast standalone full-text SQL search engine - Client library
ltsp-cluster-control - Web based thin-client configuration management
node-pg - PostgreSQL client library for Node
pfm - PostgreSQL graphical client using Tcl/Tk
pgstaging-client - client script for pgstaging
pgxnclient - command line client for the PostgreSQL Extension Network
postgres-xc-client - front-end programs for Postgres-XC
python3-postgresql - pgsq driver, cluster management tools, and client tools
root-plugin-sql-pgsq - PostgreSQL client plugin for ROOT
tryton-client - Tryton Application Platform (Client)
gcc2013@gcc-workshop:~$ sudo apt-get install postgresql-client-9.1 postgresql-client-common
```

Install the postgresSQL client from the package manager

# Postgres Configuration (3)

```
Terminal - gcc2013@gcc-workshop: ~
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$ ps aux | grep postgres
postgres 1014 0.1 0.7 52228 7940 ? S 09:47 0:01 /usr/lib/postgresql/9.1/bin/postgres -D /var/lib
/postgresql/9.1/main -c config_file=/etc/postgresql/9.1/main/postgresql.conf
postgres 1574 0.0 0.1 52228 1572 ? Ss 09:47 0:00 postgres: writer process
postgres 1575 0.0 0.1 52228 1332 ? Ss 09:47 0:00 postgres: wal writer process
postgres 1576 0.0 0.2 52660 2436 ? Ss 09:47 0:00 postgres: autovacuum launcher process
postgres 1577 0.0 0.1 22428 1400 ? Ss 09:47 0:00 postgres: stats collector process
gcc2013 1982 0.0 0.0 5908 864 pts/0 S+ 10:00 0:00 grep --color=auto postgres
gcc2013@gcc-workshop:~$
```

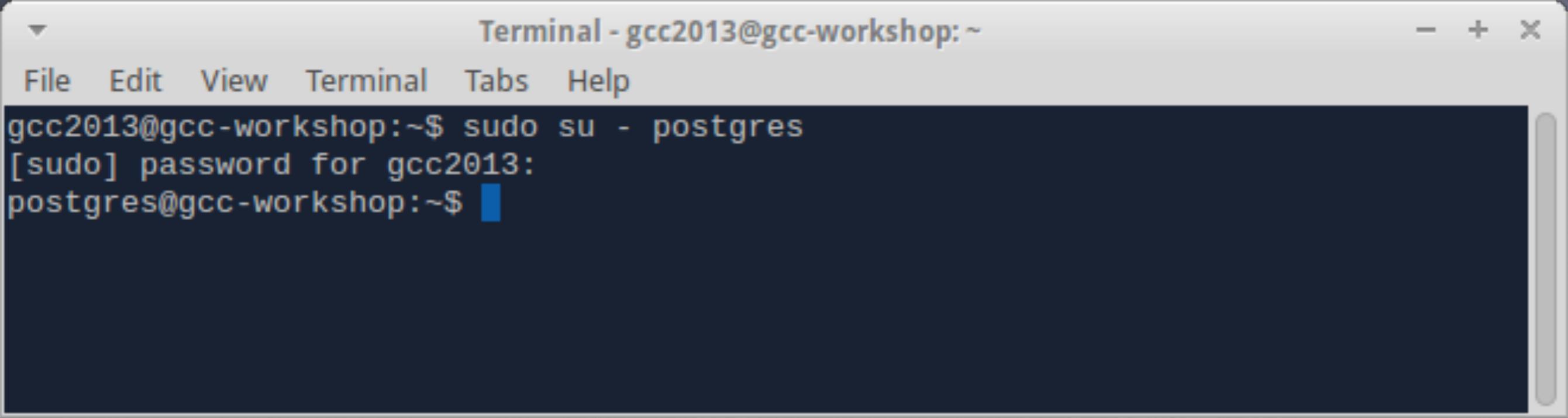
Is the PostgreSQL server running?

# Postgres Configuration (4)

```
Terminal - gcc2013@gcc-workshop: ~
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$ ps aux | grep postgres
postgres 1014 0.1 0.7 52228 7940 ? S 09:47 0:01 /usr/lib/postgresql/9.1/bin/postgres -D /var/lib
/postgresql/9.1/main -c config_file=/etc/postgresql/9.1/main/postgresql.conf
postgres 1574 0.0 0.1 52228 1572 ? Ss 09:47 0:00 postgres: writer process
postgres 1575 0.0 0.1 52228 1332 ? Ss 09:47 0:00 postgres: wal writer process
postgres 1576 0.0 0.2 52660 2436 ? Ss 09:47 0:00 postgres: autovacuum launcher process
postgres 1577 0.0 0.1 22428 1400 ? Ss 09:47 0:00 postgres: stats collector process
gcc2013 1982 0.0 0.0 5908 864 pts/0 S+ 10:00 0:00 grep --color=auto postgres
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$
gcc2013@gcc-workshop:~$ sudo /etc/init.d/postgresql stop
* Stopping PostgreSQL 9.1 database server [ OK ]
gcc2013@gcc-workshop:~$ sudo /etc/init.d/postgresql start
* Starting PostgreSQL 9.1 database server [ OK ]
gcc2013@gcc-workshop:~$ sudo /etc/init.d/postgresql status
9.1/main (port 5432): online
gcc2013@gcc-workshop:~$
```

How do I stop and start the postgresSQL server?

# Postgres Configuration (5)



```
Terminal - gcc2013@gcc-workshop: ~  
File Edit View Terminal Tabs Help  
gcc2013@gcc-workshop:~$ sudo su - postgres  
[sudo] password for gcc2013:  
postgres@gcc-workshop:~$
```

When you need to handle Postgres, sudo to username 'postgres' prior calling the Postgres client (psql)

# Postgres Configuration (6)

```
Terminal - gcc2013@gcc-workshop: ~
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$ sudo su - postgres
[sudo] password for gcc2013:
postgres@gcc-workshop:~$ psql template1
psql (9.1.9)
Type "help" for help.

template1=# CREATE USER gcc2013 WITH PASSWORD '12345';
ERROR:  role "gcc2013" already exists
template1=# CREATE DATABASE galaxy;
ERROR:  database "galaxy" already exists
template1=# GRANT ALL PRIVILEGES ON DATABASE galaxy TO gcc2013;
GRANT
template1=# \q
postgres@gcc-workshop:~$ sudo su - gcc2013
[sudo] password for postgres:
Sorry, try again.
[sudo] password for postgres:
Sorry, try again.
[sudo] password for postgres:
Sorry, try again.
sudo: 3 incorrect password attempts
postgres is not in the sudoers file.  This incident will be reported.
postgres@gcc-workshop:~$ exit
logout
gcc2013@gcc-workshop:~$ sudo su - gcc2013
gcc2013@gcc-workshop:~$ psql -d galaxy -U gcc2013
psql (9.1.9)
Type "help" for help.

galaxy=> █
```

Galaxy user creation and galaxy DB creation

# Apache Proxy config (1)

```
Terminal - gcc2013@gcc-workshop: ~
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$ sudo apt-cache search apache | grep apache2
apache2 - Apache HTTP Server metapackage
apache2-doc - Apache HTTP Server documentation
apache2-mpm-event - Apache HTTP Server - event driven model
apache2-mpm-prefork - Apache HTTP Server - traditional non-threaded model
apache2-mpm-worker - Apache HTTP Server - high speed threaded model
apache2-prefork-dev - Apache development headers - non-threaded MPM
apache2-threaded-dev - Apache development headers - threaded MPM
apache2-utils - utility programs for web servers
apache2.2-bin - Apache HTTP Server common binary files
apache2.2-common - Apache HTTP Server common files
libapache2-mod-apparmor - changehat AppArmor library as an Apache module
libapache2-mod-auth-mysql - Apache 2 module for MySQL authentication
libapache2-mod-auth-pgsql - Module for Apache2 which provides pgsql authentication
libapache2-mod-auth-plain - Module for Apache2 which provides plaintext authentication
libapache2-mod-macro - Create macros inside Apache config files
libapache2-mod-perl2 - Integration of perl with the Apache2 web server
libapache2-mod-perl2-dev - Integration of perl with the Apache2 web server - developme
nt files
libapache2-mod-perl2-doc - Integration of perl with the Apache2 web server - documenta
tion
libapache2-mod-php5 - server-side, HTML-embedded scripting language (Apache 2 module)
libapache2-mod-python - Python-embedding module for Apache 2
libapache2-mod-python-doc - Python-embedding module for Apache 2 - documentation
libapache2-mod-wsgi - Python WSGI adapter module for Apache
libapache2-reload-perl - module for reloading Perl modules when changed on disk
libapache2-mod-fastcgi - Apache 2 FastCGI module for long-running CGI scripts
apache2-mpm-itk - multiuser MPM for Apache 2.2
apache2-suexec - Standard suexec program for Apache 2 mod_suexec
apache2-suexec-custom - Configurable suexec program for Apache 2 mod_suexec
libapache-mod-jk-doc - Documentation of libapache2-mod-jk package
libapache2-authcassimple-perl - Apache2 module to authenticate trough a CAS server
libapache2-authcookie-perl - Perl Authentication and Authorization via cookies
```

What apache\* packages are available?

# Apache Proxy config (2)

```
Terminal - gcc2013@gcc-workshop: ~  
File Edit View Terminal Tabs Help  
libapache2-webkdc - Apache 2 modules for a WebAuth authentication KDC  
mahara-apache2 - Electronic portfolio, weblog, and resume builder - apache2 configuration  
rt4-apache2 - Apache 2 specific files for request-tracker4  
torrus-apache2 - Universal front-end for Round-Robin Databases (for apache 2.x) (deprecated)  
gcc2013@gcc-workshop:~$  
gcc2013@gcc-workshop:~$ sudo apt-get install apache2
```

Install the Apache web server

# Apache Proxy config (3)

```
Terminal - root@gcc-workshop:~  
File Edit View Terminal Tabs Help  
root@gcc-workshop:~# service nginx status  
* nginx is running  
root@gcc-workshop:~# service nginx stop  
* Stopping nginx nginx [ OK ]  
root@gcc-workshop:~# apt-get  
autoclean          check          dselect-upgrade  source  
autoremove        clean          install          update  
build-dep         dist-upgrade  purge           upgrade  
changelog         download      remove  
root@gcc-workshop:~# apt-get remove nginx  
Reading package lists... Done  
Building dependency tree  
Reading state information... Done  
The following packages were automatically installed and are no longer required:  
  nginx-common nginx-full  
Use 'apt-get autoremove' to remove them.  
The following packages will be REMOVED:  
  nginx  
0 upgraded, 0 newly installed, 1 to remove and 1 not upgraded.  
After this operation, 91,1 kB disk space will be freed.  
Do you want to continue [Y/n]? Y  
(Reading database ... 201572 files and directories currently installed.)  
Removing nginx ...  
root@gcc-workshop:~#
```

Our VM image comes with nginx. Make sure that you stop and remove it. nginx is a web server equivalent to Apache.

# Apache Proxy config (4)

```
Terminal - gcc2013@gcc-workshop: ~
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$ sudo /etc/init.d/apache2 start
* Starting web server apache2
[Wed Jun 26 15:45:11 2013] [warn] module alias_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module auth_basic_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module authn_file_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module authz_default_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module authz_groupfile_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module authz_host_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module authz_user_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module autoindex_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module cgid_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module deflate_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module dir_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module env_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module mime_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module negotiation_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module reqtimeout_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module setenvif_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module status_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] The Alias directive in /etc/apache2/mods-available/alias.conf at line 15 will probably never match because it overlaps an earlier Alias.
apache2: Could not reliably determine the server's fully qualified domain name, using 127.0.1.1 for ServerName
httpd (pid 1849) already running
[ OK ]
gcc2013@gcc-workshop:~$
```

Start the apache2 service and ignore the warnings.

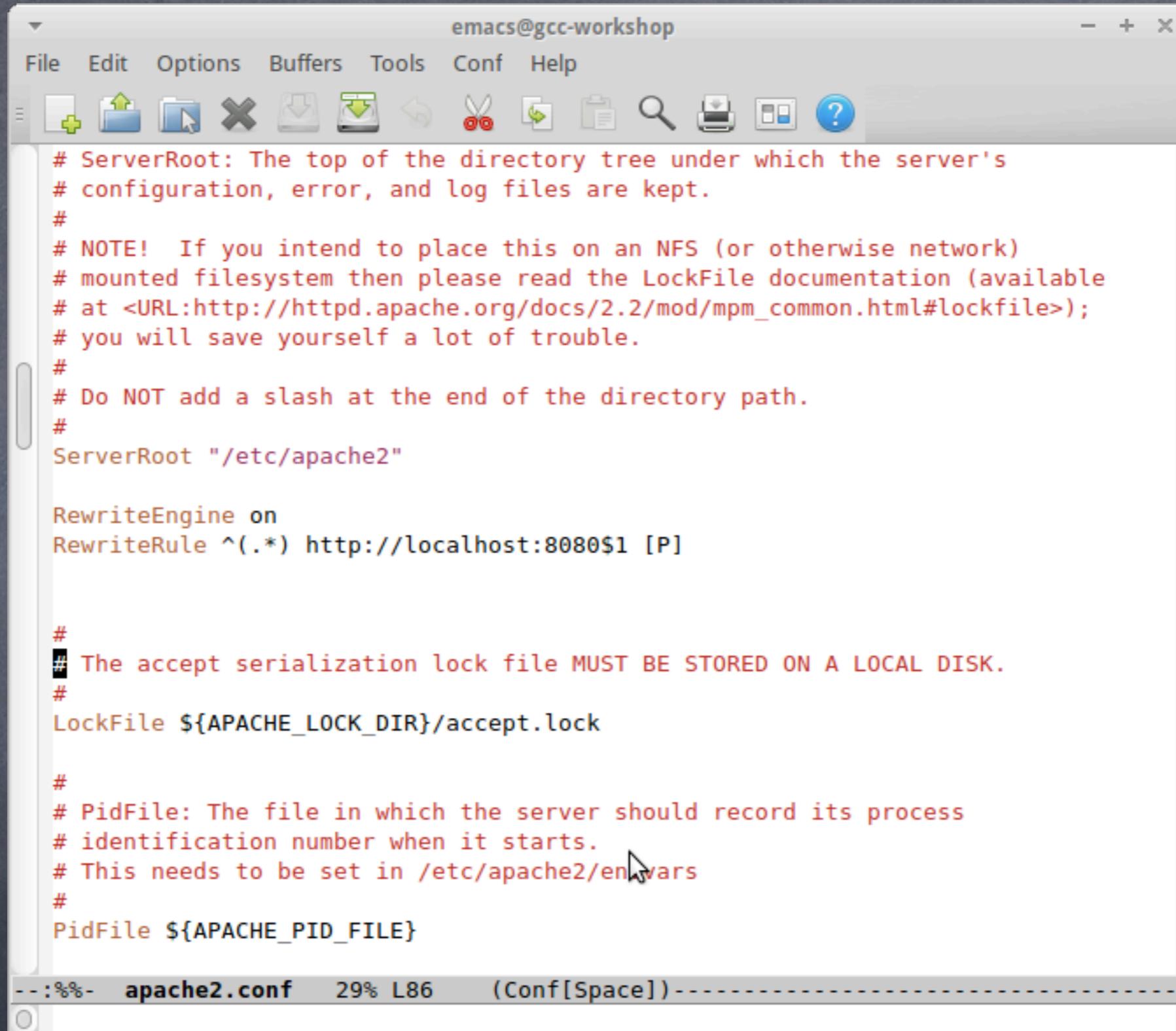
# Apache Proxy config (5)

```
Terminal - gcc2013@gcc-workshop: ~
File Edit View Terminal Tabs Help
[Wed Jun 26 15:45:11 2013] [warn] module alias_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module auth_basic_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module authn_file_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module authz_default_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module authz_groupfile_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module authz_host_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module authz_user_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module autoindex_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module cgid_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module deflate_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module dir_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module env_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module mime_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module negotiation_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module reqtimeout_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module setenvif_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module status_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] The Alias directive in /etc/apache2/mods-available/alias.conf at line 15 will probably never match because it overlaps an earlier Alias.
apache2: Could not reliably determine the server's fully qualified domain name, using 127.0.1.1 for ServerName
httpd (pid 1849) already running
[ OK ]

gcc2013@gcc-workshop:~$ apache2 -V | grep conf
-D SERVER_CONFIG_FILE="apache2.conf"
gcc2013@gcc-workshop:~$ sudo emacs /etc/apache2/apache2.conf
```

We shall need to edit the main apache2 config file.

# Apache Proxy config (6)



```
# ServerRoot: The top of the directory tree under which the server's
# configuration, error, and log files are kept.
#
# NOTE! If you intend to place this on an NFS (or otherwise network)
# mounted filesystem then please read the LockFile documentation (available
# at <URL:http://httpd.apache.org/docs/2.2/mod/mpm_common.html#lockfile>);
# you will save yourself a lot of trouble.
#
# Do NOT add a slash at the end of the directory path.
#
ServerRoot "/etc/apache2"

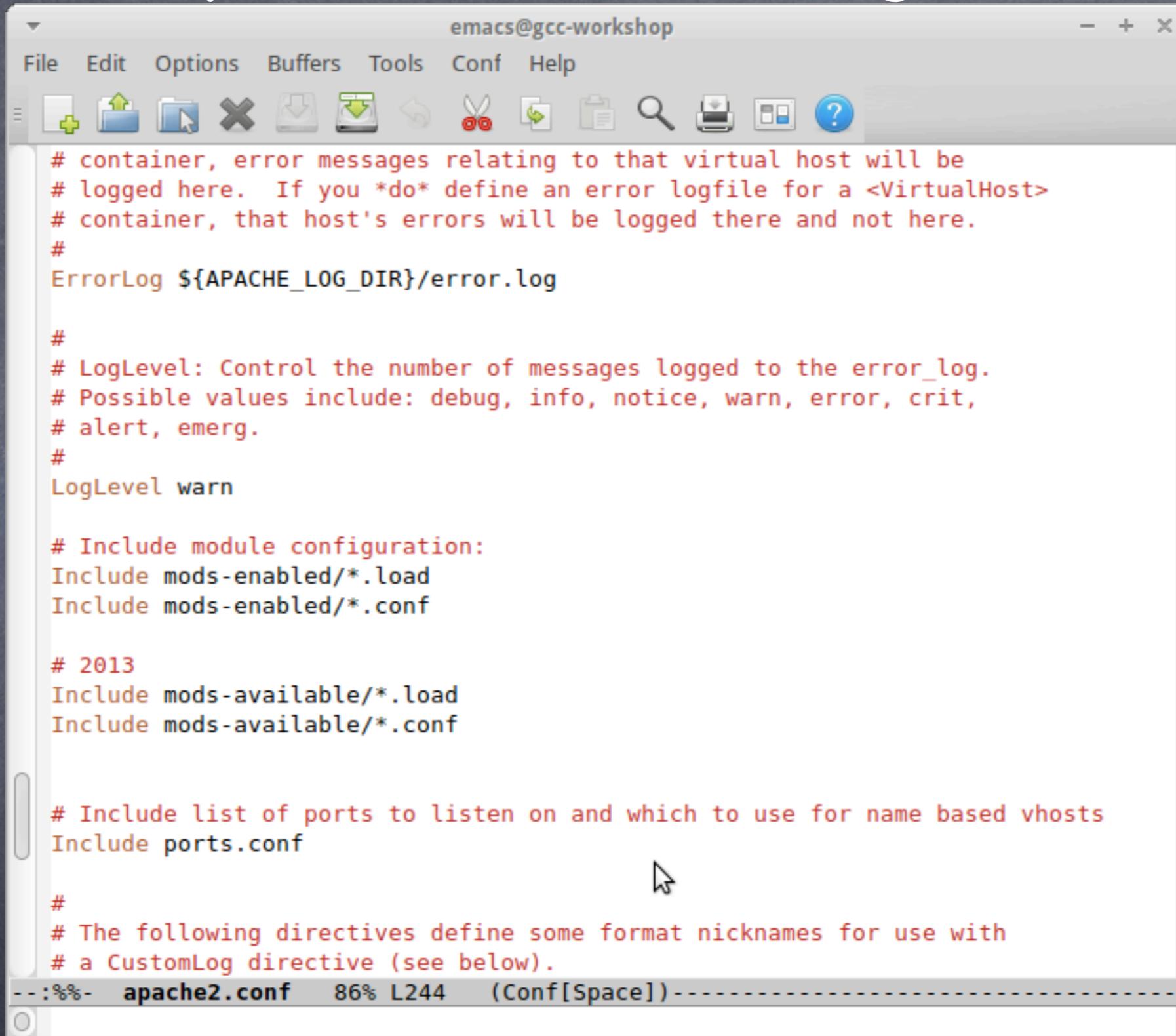
RewriteEngine on
RewriteRule ^(.*) http://localhost:8080$1 [P]

#
# The accept serialization lock file MUST BE STORED ON A LOCAL DISK.
#
LockFile ${APACHE_LOCK_DIR}/accept.lock

#
# PidFile: The file in which the server should record its process
# identification number when it starts.
# This needs to be set in /etc/apache2/envvars
#
PidFile ${APACHE_PID_FILE}
```

The re-write rule to enable the Apache proxy for Galaxy

# Apache Proxy config (7)



```
# container, error messages relating to that virtual host will be
# logged here.  If you *do* define an error logfile for a <VirtualHost>
# container, that host's errors will be logged there and not here.
#
ErrorLog ${APACHE_LOG_DIR}/error.log

#
# LogLevel: Control the number of messages logged to the error_log.
# Possible values include: debug, info, notice, warn, error, crit,
# alert, emerg.
#
LogLevel warn

# Include module configuration:
Include mods-enabled/*.load
Include mods-enabled/*.conf

# 2013
Include mods-available/*.load
Include mods-available/*.conf

# Include list of ports to listen on and which to use for name based vhosts
Include ports.conf

#
# The following directives define some format nicknames for use with
# a CustomLog directive (see below).
--:%%- apache2.conf 86% L244 (Conf[Space])-----
```

Still on the main apache2 config file. Enabling the modules.

# Galaxy config (1)

```
Terminal - gcc2013@gcc-workshop: ~/Documents/Galaxy
File Edit View Terminal Tabs Help
pping
[Wed Jun 26 15:45:11 2013] [warn] module authz_host_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module authz_user_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module autoindex_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module cgid_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module deflate_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module dir_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module env_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module mime_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module negotiation_module is already loaded, skipping
g
[Wed Jun 26 15:45:11 2013] [warn] module reqtimeout_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module setenvif_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] module status_module is already loaded, skipping
[Wed Jun 26 15:45:11 2013] [warn] The Alias directive in /etc/apache2/mods-available/a
alias.conf at line 15 will probably never match because it overlaps an earlier Alias.
apache2: Could not reliably determine the server's fully qualified domain name, using
127.0.1.1 for ServerName
httpd (pid 1849) already running

[ OK ]

gcc2013@gcc-workshop:~$ apache2 -V | grep conf
-D SERVER_CONFIG_FILE="apache2.conf"
gcc2013@gcc-workshop:~$ cd /home/gcc2013/Documents/
gcc2013@gcc-workshop:~/Documents$ ls
Galaxy
gcc2013@gcc-workshop:~/Documents$ cd Galaxy/
gcc2013@gcc-workshop:~/Documents/Galaxy$ ls
galaxy-dist
gcc2013@gcc-workshop:~/Documents/Galaxy$ sudo mkdir /home/galaxy
```

make a new directory /home/galaxy, as shown above

# Galaxy config (2)

```
Terminal - gcc2013@gcc-workshop: /home
File Edit View Terminal Tabs Help
galaxy-dist
gcc2013@gcc-workshop:~/Documents/Galaxy$ cd /home/
gcc2013@gcc-workshop:/home$ ls -ls
total 8
4 drwxr-xr-x  8 gcc2013 gcc2013 4096 juni  26 10:31 galaxy
4 drwxr-xr-x 29 gcc2013 gcc2013 4096 juni  26 14:43 gcc2013
gcc2013@gcc-workshop:/home$ chown -R gcc2013:gcc2013 galaxy/
gcc2013@gcc-workshop:/home$ cp -rf /home/gcc2013/Documents/Galaxy/galaxy-dist/ .
```

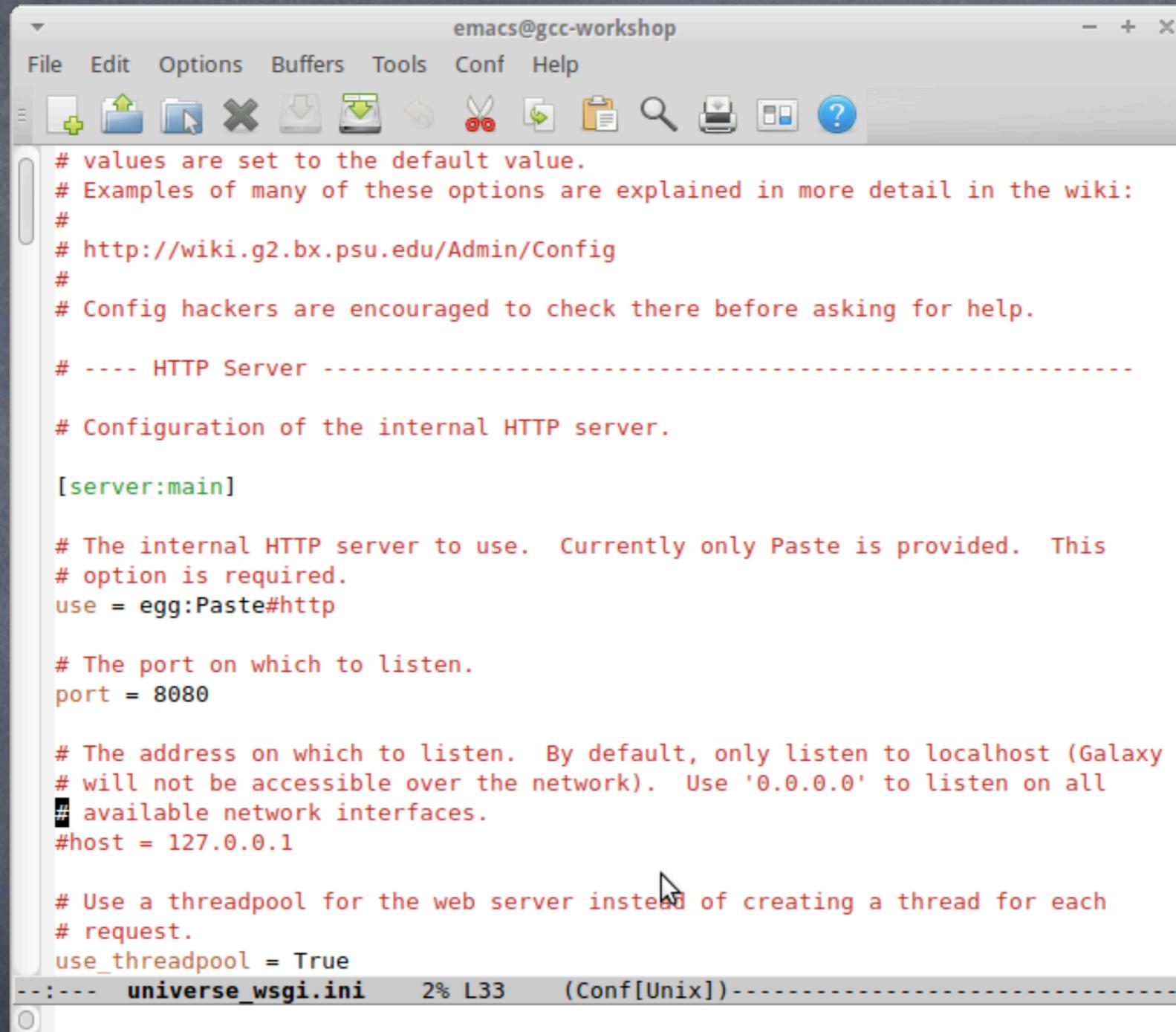
Copy the already existing code in galaxy-dist to the /home/galaxy directory. This is so we can keep the original copy in a clean state. In a real world scenario, you would do a Mercurial pull (hg pull), to get the latest and the greatest from the Galaxy repository.

# Galaxy config (3)

```
Terminal - gcc2013@gcc-workshop: /home/galaxy/galaxy-dist
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~/Documents/Galaxy$ ls
galaxy-dist
gcc2013@gcc-workshop:~/Documents/Galaxy$ cd /home/
gcc2013@gcc-workshop:/home$ ls -ls
total 8
4 drwxr-xr-x  8 gcc2013 gcc2013 4096 juni  26 10:31 galaxy
4 drwxr-xr-x 29 gcc2013 gcc2013 4096 juni  26 14:43 gcc2013
gcc2013@gcc-workshop:/home$ chown -R gcc2013:gcc2013 galaxy/
gcc2013@gcc-workshop:/home$ cd galaxy/galaxy-dist/
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$ emacs universe_wsgi.ini &
```

(almost) Everything can be controlled by the galaxy-dist/universe\_wsgi.ini file

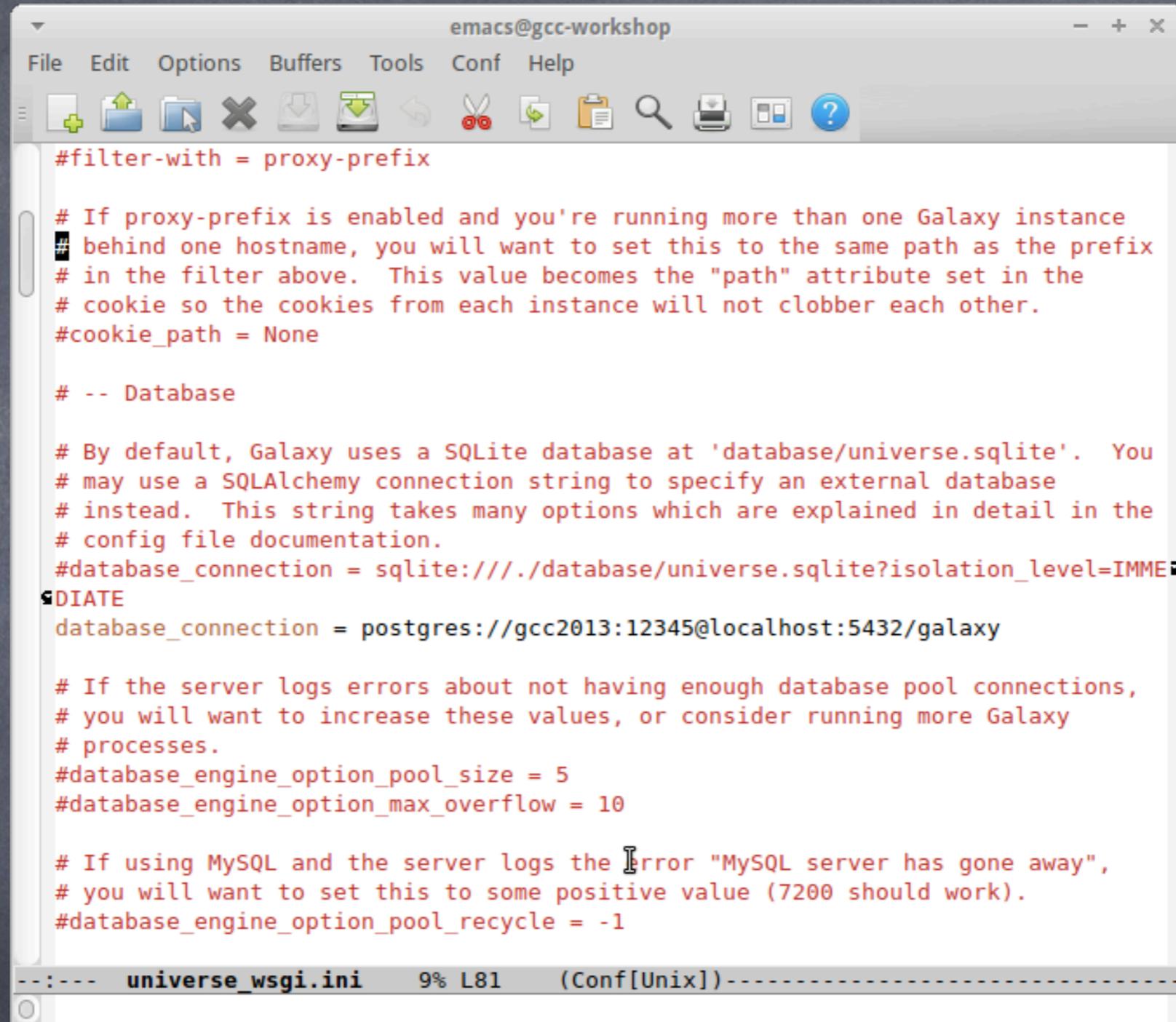
# Galaxy config (4)



```
emacs@gcc-workshop
File Edit Options Buffers Tools Conf Help
# values are set to the default value.
# Examples of many of these options are explained in more detail in the wiki:
#
# http://wiki.g2.bx.psu.edu/Admin/Config
#
# Config hackers are encouraged to check there before asking for help.
# ----- HTTP Server -----
# Configuration of the internal HTTP server.
[server:main]
# The internal HTTP server to use. Currently only Paste is provided. This
# option is required.
use = egg:Paste#http
# The port on which to listen.
port = 8080
# The address on which to listen. By default, only listen to localhost (Galaxy
# will not be accessible over the network). Use '0.0.0.0' to listen on all
# available network interfaces.
#host = 127.0.0.1
# Use a threadpool for the web server instead of creating a thread for each
# request.
use_threadpool = True
--:--- universe_wsgi.ini 2% L33 (Conf[Unix])-----
```

Specify the main port (8080) for the python WSGI. See also slide number 20. The config between the two must be consistent!

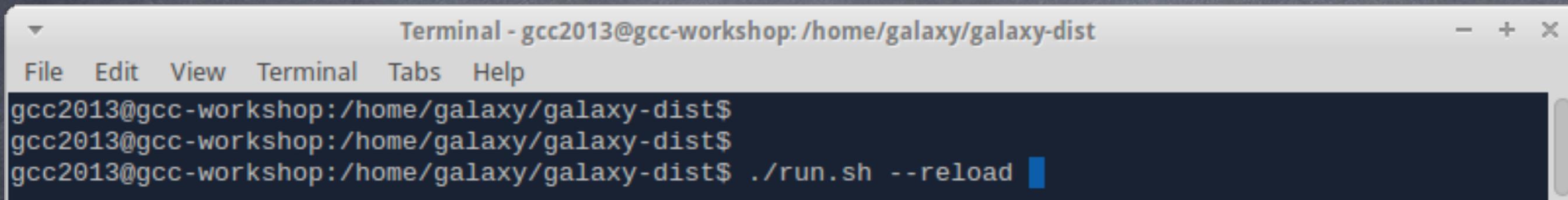
# Galaxy config (5)



```
emacs@gcc-workshop
File Edit Options Buffers Tools Conf Help
#filter-with = proxy-prefix
# If proxy-prefix is enabled and you're running more than one Galaxy instance
# behind one hostname, you will want to set this to the same path as the prefix
# in the filter above. This value becomes the "path" attribute set in the
# cookie so the cookies from each instance will not clobber each other.
#cookie_path = None
# -- Database
# By default, Galaxy uses a SQLite database at 'database/universe.sqlite'. You
# may use a SQLAlchemy connection string to specify an external database
# instead. This string takes many options which are explained in detail in the
# config file documentation.
#database_connection = sqlite:///./database/universe.sqlite?isolation_level=IMMEDIATE
database_connection = postgres://gcc2013:12345@localhost:5432/galaxy
# If the server logs errors about not having enough database pool connections,
# you will want to increase these values, or consider running more Galaxy
# processes.
#database_engine_option_pool_size = 5
#database_engine_option_max_overflow = 10
# If using MySQL and the server logs the error "MySQL server has gone away",
# you will want to set this to some positive value (7200 should work).
#database_engine_option_pool_recycle = -1
---:--- universe_wsgi.ini 9% L81 (Conf[Unix])---
```

universe\_wsgi.ini: The database\_connection line must be consistent to your Postgres config (slide 14)

# Galaxy config (6)

A terminal window titled "Terminal - gcc2013@gcc-workshop: /home/galaxy/galaxy-dist" with a menu bar containing "File", "Edit", "View", "Terminal", "Tabs", and "Help". The terminal shows three lines of text: "gcc2013@gcc-workshop:/home/galaxy/galaxy-dist\$", "gcc2013@gcc-workshop:/home/galaxy/galaxy-dist\$", and "gcc2013@gcc-workshop:/home/galaxy/galaxy-dist\$ ./run.sh --reload" with a blue cursor at the end.

```
Terminal - gcc2013@gcc-workshop: /home/galaxy/galaxy-dist
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$ ./run.sh --reload
```

If all is well, restart Galaxy and point your browser to:  
to see your newly installed Galaxy server

# Users, groups, roles, libraries and quotas (1)

**User**: A registered entity (via email and password) allowed to use the Galaxy environment.

**Group**: A group of users that can share datasets and workflow histories.

**Role**: An administrative view of a user/group over resources (datasets, quotas, etc)

**Libraries**: Data sets that can be shared amongst groups (permissions) or by everyone (public)

**Quotas**: Disk space is a valuable commodity. Set limits or have full servers and frustrated users.

# Users, groups, roles, libraries and quotas (2)

Galaxy Administration

Navigation: Analyze Data | Workflow | Shared Data | Visualization | Admin | Help | User

Left sidebar menu:

- Administration
- Security
  - Manage users
  - Manage groups
  - Manage roles
- Data
  - Manage quotas
  - Manage data libraries
  - Manage local data (beta)
- Server
  - View data types registry
  - View data tables registry
  - View tool lineage
  - Reload a tool's configuration
  - Profile memory usage
  - Manage jobs
  - Review tool migration stages
  - Reset metadata for tool shed repositories
  - Manage installed tool shed repositories
- Tool sheds
  - Search and browse tool sheds
- Form Definitions
  - Manage form definitions
- Sample Tracking
  - Manage sequencers and external services
  - Manage request types
  - Sequencing requests
  - Find samples

Username	Real Name	Quota	Groups	Roles	Created
<input type="checkbox"/> manuel.razo.m@gmail.com	manuel-razo	0	1	no	Jan 26, 2012
<input type="checkbox"/> mie231ds@gmail.com	y1wod37ho	0	1	no	Nov 02, 2012
<input type="checkbox"/> niceg.t.s.118@gmail.com	cabnuandell	0	1	no	Nov 06, 2012
<input type="checkbox"/> osalazar@lcg.unam.mx	osalazar	0	1	no	Jan 26, 2012
<input type="checkbox"/> ozono32@hotmail.com	ozono32	0	1	no	Jan 26, 2012
<input type="checkbox"/> quarkie68@yahoo.co.uk	gharisson	0	1	no	Oct 26, 2012
<input type="checkbox"/> rcappello@ecologia.unam.mx	rcappello	0	1	no	Jan 27, 2012
<input type="checkbox"/> regina_gama@hotmail.com	reginahgama	0	1	no	Jan 27, 2012
<input type="checkbox"/> roman.zapien@hotmail.com	romanzapien	0	1	no	Jan 27, 2012
<input type="checkbox"/> samendojohnss@aol.com	guaapalod	0	1	no	Oct 28, 2012
<input type="checkbox"/> scenesfromamemory4@gmail.com	benjamin-tovar	0	1	no	Jan 26, 2012
<input type="checkbox"/> skladarhm@mail.ru	skladarh	0	1	no	Dec 05, 2012
<input type="checkbox"/> slvvasquez1@gmail.com	silviabio	0	1	no	Feb 01, 2012
<input type="checkbox"/> s.p.a.r.s.elyqlo.q.x.dw@gmail.com	chmsnhlb	0	1	no	Mar 22, 2013
<input type="checkbox"/> s.p.a.rs.ely.q.lo.qxd.w@gmail.com	brwdbqwzr	0	1	no	Mar 22, 2013
<input type="checkbox"/> s.p.arse.l.yql.o.q.x.dw@gmail.com	qzmphxvai	0	1	no	Mar 21, 2013
<input type="checkbox"/> s.p.arsel.yql.o.q.x.dw@gmail.com	rpyxzbqhlq	0	1	no	Mar 21, 2013
<input type="checkbox"/> s.pa.r.sel.y.qlo.qxdw@gmail.com	duwhqqbct	0	1	no	Mar 22, 2013
<input type="checkbox"/> s.par.s.e.l.y.q.lo.q.x.dw@gmail.com	kostiqlzavx	0	1	no	Mar 23, 2013
<input type="checkbox"/> s.par.s.e.l.y.q.l.o.qxdw@gmail.com	xfjhgltwxdfe	0	1	no	Mar 23, 2013
<input type="checkbox"/> toni.hurtado@ncmm.uio.no	tonih	0	1	no	Feb 17, 2012
<input type="checkbox"/> trine.rounge@krefregisteret.no	trine-b-rounge	0	2	no	Jan 17, 2013
<input type="checkbox"/> wong2hikonrii@gmail.com	engibbono	0	1	no	Oct 26, 2012
<input type="checkbox"/> zameloon1487@gmail.com	zame1487	0	1	no	Jan 26, 2012

For 0 selected items:

# Users, groups, roles, libraries and quotas (3)

**Galaxy** Analyze Data Workflow Shared Data Visualization Admin

**Administration**

- Security
  - Manage users
  - Manage groups
  - Manage roles
- Data
  - Manage quotas
  - Manage data libraries
  - Manage local data (beta)
- Server
  - View data types registry
  - View data tables registry
  - View tool lineage
  - Reload a tool's configuration
  - Profile memory usage
  - Manage jobs

**Group 'Ian Mills Data Group'**

✔ Group Ian Mills Data Group is currently associated with 1 roles and 3 users

Roles associated with 'Ian Mills Data Group'	Roles not associated with 'Ian Mills Data Group'
Ian Mills Data Group	
>>	<<

Users associated with 'Ian Mills Data Group'	Users not associated with 'Ian Mills Data Group'
gmagklaras@gmail.com ian.mills@ncmm.uio.no i.g.mills@ncmm.uio.no	
>>	<<

Save

# Users, groups, roles, libraries and quotas (4)

Role 'Ian Mills Data Group'

**Users associated with 'Ian Mills Data Group'**

**Users not associated with 'Ian Mills Data Group'**

**Groups associated with 'Ian Mills Data Group'**

**Groups not associated with 'Ian Mills Data Group'**

Save

---

**Data library datasets associated with role 'Ian Mills Data Group'**

-  Mills Lib1
  -  Mills Lib1 / ftp://dias.uio.no/millsftp/LNCaPInpR\_GCCAAT\_L005\_R1.fastq
    - access
  -  Mills Lib1 / ftp://dias.uio.no/millsftp/VCaPInpE\_CTTGTA\_L005\_R1.fastq
    - access
  -  Mills Lib1 / ftp://dias.uio.no/millsftp/LNCaPMYCE\_ACAGTG\_L006\_R1.fastq
    - access
  -  Mills Lib1 / ftp://dias.uio.no/millsftp/VCaPMYCE\_CTTGTA\_L006\_R1.fastq
    - access
  -  Mills Lib1 / ftp://ftp.no.embnet.org/biodatabases/embl\_release/rel\_con\_env\_07\_r110.dat
    - access
  -  Mills Lib1 / ftp://dias.uio.no/millsftp/LNCaPMYCR\_GCCAAT\_L006\_R1.fastq
    - access
  -  Mills Lib1 / ftp://dias.uio.no/millsftp/VCaPMYCR\_GTGAAA\_L006\_R1.fastq
    - access
  -  Mills Lib1 / ftp://dias.uio.no/millsftp/LNCaPInpE\_ACAGTG\_L005\_R1.fastq
    - access
  -  Mills Lib1 / ftp://dias.uio.no/millsftp/VCaPInpR\_GTGAAA\_L005\_R1.fastq
    - access

# Users, groups, roles, libraries and quotas (5)

## Data Libraries



[Advanced Search](#)

<input type="checkbox"/> <u>Data library name</u>	<u>Data library description</u>	<u>Created</u>	<u>Last Updated</u>
<input type="checkbox"/> <a href="#">Escherichia coli</a>	UNAM Course Talleres 2012	Jan 21, 2012	Jan 21, 2012
<input type="checkbox"/> <a href="#">Human reads</a>	Human reads FASTQ demo	Jan 21, 2012	Jan 21, 2012
<input type="checkbox"/> <a href="#">Mills BGI</a>	BGI data for the Mills group	Jan 09, 2013	Jan 09, 2013
<input type="checkbox"/> <a href="#">Mills Lib1</a>	Lib1 Fast Chip-Seq	Jan 09, 2013	Jan 09, 2013
<input type="checkbox"/> <a href="#">Reference Genomes</a>		Jan 09, 2013	Jan 09, 2013
<input type="checkbox"/> <a href="#">test4</a>		Jan 26, 2012	Jan 26, 2012
<input type="checkbox"/> <a href="#">trine01</a>	Methylation analysis for Trine Rounge	Jan 14, 2013	Jan 14, 2013
<input type="checkbox"/> <a href="#">Uniprot Fasta</a>		Oct 25, 2012	Oct 25, 2012
<input type="checkbox"/> <a href="#">Viral influenza</a>		Jan 22, 2012	Jan 22, 2012

For 0 selected libraries:

## Data Library "Escherichia coli"

Containing the E. Coli reference genome

<input type="checkbox"/> <u>Name</u>	<u>Message</u>	<u>Data type</u>	<u>Date uploaded</u>
<input type="checkbox"/> <a href="#">AP012306.fasta</a>		fasta	2012-01-21
<input type="checkbox"/> <a href="#">SRR001666_1.fastq</a>		fastq	2012-01-21

For selected datasets:

**i** TIP: You can download individual library datasets by selecting "Download this dataset" from the context menu (triangle) next to each dataset's name.

**i** TIP: Several compression options are available for downloading multiple library datasets simultaneously:

- gzip: Recommended for fast network connections
- bzip2: Recommended for slower network connections (smaller size but takes longer to compress)
- zip: Not recommended but is provided as an option for those who cannot open the above formats

# Users, groups, roles, libraries and quotas (6)

## Create quota

**Name:****Description:****Amount**

Examples: "10000MB", "99 gb", "0.2T", "unlimited"

**Assign, increase by amount, or decrease by amount?** **Is this quota a default for a class of users (if yes, what type)?** 

Warning: Any user or group associations selected below will be ignored if this quota is used as a default.

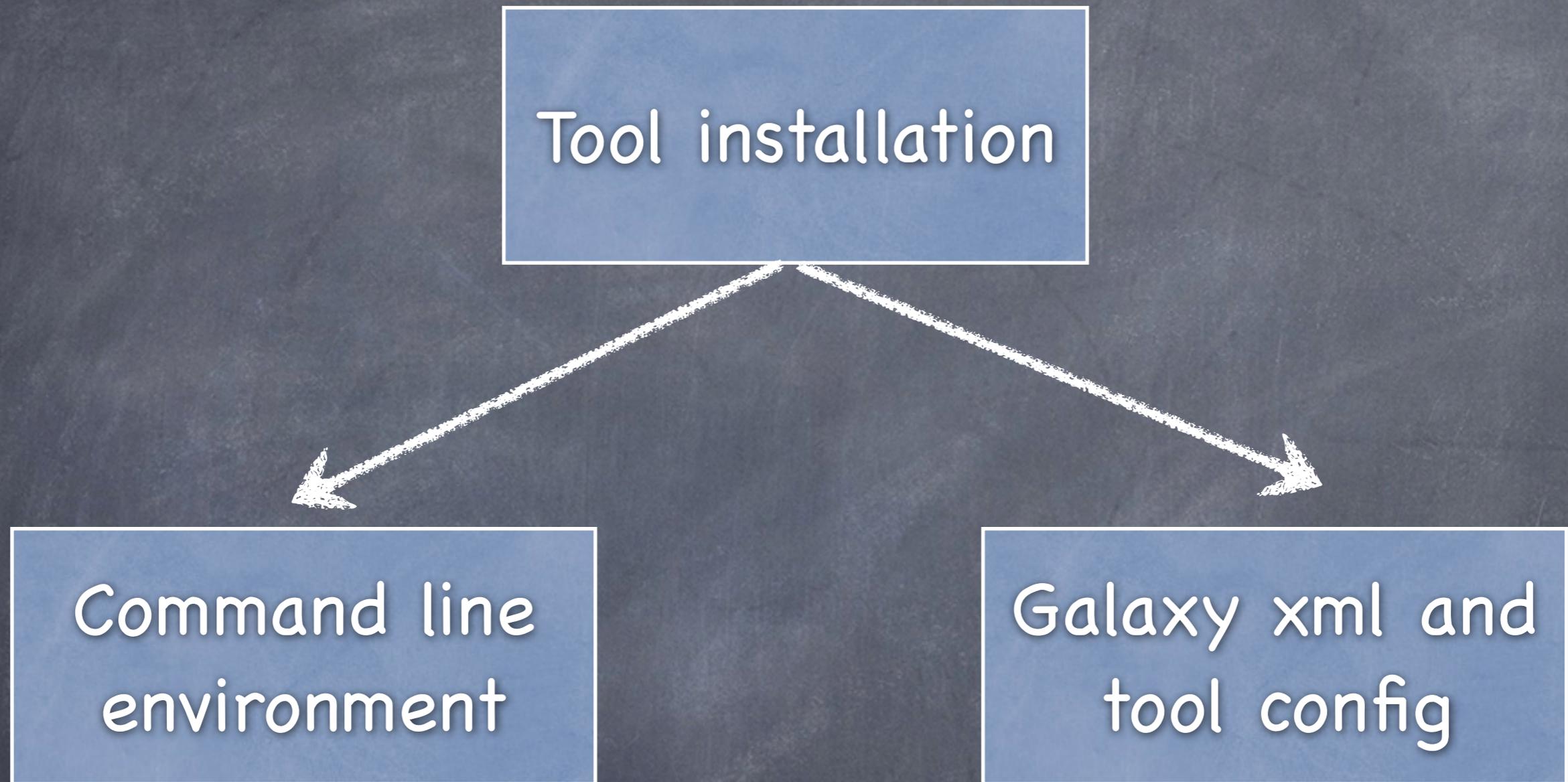
**Users associated with new quota**  
  
**Users not associated with new quota****Groups associated with new quota****Groups not associated with new quota**

# Installing Galaxy tools

i) NCBI BLAST+

ii) write your own tool and install it

# Installing Galaxy tools (1)



# Installing Galaxy tools (2)

```
Terminal - gcc2013@gcc-workshop: ~/Downloads/blastfiles
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$ cd
gcc2013@gcc-workshop:~$ cd Downloads/
gcc2013@gcc-workshop:~/Downloads$ mkdir blastfiles
gcc2013@gcc-workshop:~/Downloads$ cd blastfiles
gcc2013@gcc-workshop:~/Downloads/blastfiles$ wget ftp://ftp.no.embnet.org/galaxy/ncbi-blast-2.2.28+-ia32-linux.tar.gz
--2013-06-28 08:40:13-- ftp://ftp.no.embnet.org/galaxy/ncbi-blast-2.2.28+-ia32-linux.tar.gz
      => 'ncbi-blast-2.2.28+-ia32-linux.tar.gz'
Resolving ftp.no.embnet.org (ftp.no.embnet.org)... 129.240.235.130
Connecting to ftp.no.embnet.org (ftp.no.embnet.org)|129.240.235.130|:21... connected.
Logging in as anonymous ... Logged in!
==> SYST ... done.      ==> PWD ... done.
==> TYPE I ... done.   ==> CWD (1) /galaxy ... done.
==> SIZE ncbi-blast-2.2.28+-ia32-linux.tar.gz ... 167568023
==> PASV ... done.     ==> RETR ncbi-blast-2.2.28+-ia32-linux.tar.gz ... done.
Length: 167568023 (160M) (unauthoritative)

100%[=====>] 167 568 023 2,24MB/s   in 72s

2013-06-28 08:41:25 (2,22 MB/s) - 'ncbi-blast-2.2.28+-ia32-linux.tar.gz' saved [167568023]

gcc2013@gcc-workshop:~/Downloads/blastfiles$
```

Fetch the blast 32-bit binaries by FTP

# Installing Galaxy tools (3)

Fetch  
the BLAST  
database and  
tool tarballs  
by  
FTP

```
Terminal - gcc2013@gcc-workshop: ~/Downloads/blastfiles
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~/Downloads/blastfiles$ wget ftp://ftp.no.embnet.org/galaxy/pataasmall.tar.gz
--2013-06-28 08:42:39-- ftp://ftp.no.embnet.org/galaxy/pataasmall.tar.gz
      => 'pataasmall.tar.gz'
Resolving ftp.no.embnet.org (ftp.no.embnet.org)... 129.240.235.130
Connecting to ftp.no.embnet.org (ftp.no.embnet.org)|129.240.235.130|:21... connected.
Logging in as anonymous ... Logged in!
==> SYST ... done.      ==> PWD ... done.
==> TYPE I ... done.   ==> CWD (1) /galaxy ... done.
==> SIZE pataasmall.tar.gz ... 4735073
==> PASV ... done.     ==> RETR pataasmall.tar.gz ... done.
Length: 4735073 (4,5M) (unauthoritative)

100%[=====>] 4 735 073    2,25MB/s   in 2,0s

2013-06-28 08:42:42 (2,25 MB/s) - 'pataasmall.tar.gz' saved [4735073]

gcc2013@gcc-workshop:~/Downloads/blastfiles$ wget ftp://ftp.no.embnet.org/galaxy/blast_tool.tar.gz
--2013-06-28 08:43:18-- ftp://ftp.no.embnet.org/galaxy/blast_tool.tar.gz
      => 'blast_tool.tar.gz'
Resolving ftp.no.embnet.org (ftp.no.embnet.org)... 129.240.235.130
Connecting to ftp.no.embnet.org (ftp.no.embnet.org)|129.240.235.130|:21... connected.
Logging in as anonymous ... Logged in!
==> SYST ... done.      ==> PWD ... done.
==> TYPE I ... done.   ==> CWD (1) /galaxy ... done.
==> SIZE blast_tool.tar.gz ... 4822
==> PASV ... done.     ==> RETR blast_tool.tar.gz ... done.
Length: 4822 (4,7K) (unauthoritative)

100%[=====>] 4 822      --.-K/s   in 0,002s

2013-06-28 08:43:18 (1,90 MB/s) - 'blast_tool.tar.gz' saved [4822]

gcc2013@gcc-workshop:~/Downloads/blastfiles$
```

# Installing Galaxy tools (4)

```
Terminal - gcc2013@gcc-workshop: ~/db
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$ cd
gcc2013@gcc-workshop:~$ mkdir db
gcc2013@gcc-workshop:~$ cd db
gcc2013@gcc-workshop:~/db$ mv ~/Downloads/blastfiles/pataasmall.tar.gz .
gcc2013@gcc-workshop:~/db$ tar xvzf pataasmall.tar.gz
pataasmall.phr
pataasmall.pin
pataasmall.psq
gcc2013@gcc-workshop:~/db$
```

Install the sample BLAST database

# Installing Galaxy tools (5)

```
Terminal - gcc2013@gcc-workshop: /home/galaxy/galaxy-dist/tools/ncbi_blast_plus
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$ cd
gcc2013@gcc-workshop:~$ cd Downloads/blastfiles
gcc2013@gcc-workshop:~/Downloads/blastfiles$ tar xvzf blast_tool.tar.gz
hide_stderr.py
ncbi_blastp_wrapper.xml
query.fa
tool_conf_section.xml
gcc2013@gcc-workshop:~/Downloads/blastfiles$ cd /home/galaxy/galaxy-dist/tools
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tools$ mkdir ncbi_blast_plus
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tools$ cd ncbi_blast_plus
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tools/ncbi_blast_plus$ cp ~/Downlo
ads/blastfiles/ncbi_blastp_wrapper.xml .
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tools/ncbi_blast_plus$ cp ~/Downlo
ads/blastfiles/hide_stderr.py .
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tools/ncbi_blast_plus$ ls -l
total 20
-rwxr-xr-x 1 gcc2013 gcc2013 1803 juni 28 08:56 hide_stderr.py
-rw-r--r-- 1 gcc2013 gcc2013 14060 juni 28 08:55 ncbi_blastp_wrapper.xml
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tools/ncbi_blast_plus$
```

Navigate to the galaxy-dist/tools directory and make the tool directory entry

# Installing Galaxy tools (5)

```
emacs@gcc-workshop
File Edit Options Buffers Tools Help
#This is a sample file distributed with Galaxy that is used to define a
#list of protein BLAST databases, using three columns tab separated
#(longer whitespace are TAB characters):
#
#<unique_id>    <database_caption>    <base_name_path>
#
#The captions typically contain spaces and might end with the build date.
#It is important that the actual database name does not have a space in it,
#and that the first tab that appears in the line is right before the path.
#
#So, for example, if your database is NR and the path to your base name
#is /data/blastdb/nr, then the blastdb_p.loc entry would look like this:
#
#nr            NCBI NR (non redundant)    /data/blastdb/nr
pataasmall    custom pataa /home/gcc2013/db
#
#and your /data/blastdb directory would contain all of the files associated
#with the database, /data/blastdb/nr.*.
#
#Your blastdb_p.loc file should include an entry per line for each "base name"
#you have stored. For example:
#
#nr_05Jun2010  NCBI NR (non redundant) 05 Jun 2010    /data/blastdb/05
Jun2010/nr
#nr_15Aug2010  NCBI NR (non redundant) 15 Aug 2010    /data/blastdb/15
Aug2010/nr
#...etc...
--:--- blastdb_p.loc Top L1 (Fundamental)-----
Welcome to GNU Emacs, one component of the GNU/Linux operating system.
Emacs Tutorial Learn basic keystroke commands
Emacs Guided Tour Overview of Emacs features at gnu.org
-U:%%- *GNU Emacs* Top L3 (Fundamental)-----
```

Here you define the available databases that can be used from the Galaxy environment.

# Installing Galaxy tools (6)

```
Terminal - gcc2013@gcc-workshop: /home/galaxy/galaxy-dist/tool-data
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tools/ncbi_blast_plus$ cd ../../
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$ cd tool-data/
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tool-data$ ls -l blastdb_p.loc
-rw-rw-r-- 1 gcc2013 gcc2013 1124 juni 25 08:59 blastdb_p.loc
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tool-data$ emacs blastdb_p.loc
```

Navigate to the galaxy-dist/tool-data dir and check out the blastdb\_p.loc file

# Installing Galaxy tools (7)

The image shows two overlapping windows. The top window is a terminal titled 'Terminal - gcc2013@gcc-workshop: /home/galaxy/galaxy-dist'. It shows the following commands and output:

```
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tool-data$ cd ..
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$ emacs tool_conf.xml
```

The bottom window is an Emacs editor titled 'emacs@gcc-workshop'. It shows the content of the 'tool\_conf.xml' file being edited:

```
<?xml version="1.0"?>
<toolbox>
  <section name="NCBI BLAST+" id="ncbi_blast_plus_tools">
    <tool file="ncbi_blast_plus/ncbi_blastp_wrapper.xml"/>
  </section>

  <section name="MyTools" id="myTools">
    <tool file="myTools/helloVM.xml" />
  </section>

  <section name="Get Data" id="gettext">
    <tool file="data_source/upload.xml"/>
    <tool file="data_source/ucsc_tablebrowser.xml" />
  </section>
</toolbox>
```

Below the code, Emacs displays status bars and a welcome message:

```
-U:**-  tool_conf.xml  Top L3      (nXML Valid)-----
Welcome to GNU Emacs, one component of the GNU/Linux operating system.
Emacs Tutorial          Learn basic keystroke commands
-U:%%-  *GNU Emacs*    Top L3      (Fundamental)-----
```

In the galaxy-dist/tool-data dir, you also need to edit the tool\_conf.xml file.

# Installing Galaxy tools (8)

```
Terminal - gcc2013@gcc-workshop: /home/galaxy/galaxy-dist
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$ export PATH=$PATH:/home/gcc2013/src/ncbi-blast-2.2.28+/bin
```

```
Terminal - gcc2013@gcc-workshop: /home/galaxy/galaxy-dist
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$ ./run.sh --reload
```

Make sure that the newly installed NCBI BLAST+ binaries are in your PATH environment and then restart Galaxy to make the new PATH effective.

# Installing Galaxy tools (9)

The screenshot shows the Galaxy web interface. The main content area is titled "Upload File (version 1.1.3)". It features several input fields and buttons:

- File Format:** A dropdown menu set to "fasta". Below it, the text "Which format? See help below" is displayed.
- File:** A text input field containing "/home/gcc2013/Downloads" and a "Browse..." button.
- URL/Text:** A large empty text area for pasting URLs or file contents.
- Convert spaces to tabs:** A checkbox labeled "Yes" which is currently unchecked. Below it, the text "Use this option if you are entering intervals by hand." is shown.
- Genome:** A dropdown menu set to "unspecified (?)".
- Execute:** A blue button at the bottom of the form.

On the left side, there is a "Tools" panel with a search bar and a list of tools under categories like "NCBI BLAST+", "MyTools", and "Get Data".

On the right side, there is a "History" panel showing a list of jobs. The top job is "2: demo script on infile.txt" with a status of "1 line" and "format: text, database: ?". Below it is "1: infile.txt".

Fire up your VM's web browser on <http://127.0.0.1/> and upload the query.fa file

# Installing Galaxy tools (10)

**Galaxy** Analyze Data Workflow Shared Data Visualization Help User Using 287 bytes

**Tools**

search tools

**NCBI BLAST+**

- NCBI BLAST+ blastp Search protein database with protein query sequence(s)

**MyTools**

**Get Data**

- Upload File from your computer
- UCSC Main table browser
- UCSC Test table browser
- UCSC Archaea table browser
- BX table browser
- EBI SRA ENA SRA
- Get Microbial Data
- BioMart Central server
- BioMart Test server
- CBI Rice Mart rice mart
- GrameneMart Central server
- modENCODE fly server
- Flymine server

**NCBI BLAST+ blastp (version 0.0.10)**

**Protein query sequence(s):**  
4: query.fa

**Subject database/sequences:**  
BLAST Database

**Protein BLAST database:**  
custom pataa db

**Type of BLAST:**  
 blastp  
 blastp-short

**Set expectation value cutoff:**  
0.001

**Output format:**  
Tabular (standard 12 columns)

**Advanced Options:**  
Hide Advanced Options

**Execute**

**History**

Unnamed history  
287 bytes

4: query.fa  
1 line  
format: text, database: ?  
Hello tutorial participant! This Galax

1: infile.txt

**Note.** Database searches may take a substantial amount of time. For large input datasets it is advisable to allow overnight processing.

Now run your BLAST+ query!

# Installing Galaxy tools (11)

Galaxy

Analyze Data Workflow Shared Data Visualization Help User Using 433 bytes

Tools

search tools

**NCBI BLAST+**

- NCBI BLAST+ blastp Search protein database with protein query sequence(s)

MyTools

Get Data

Send Data

ENCODE Tools

Lift-Over

Text Manipulation

Filter and Sort

Join, Subtract and Group

Convert Formats

Extract Features

Fetch Sequences

Fetch Alignments

Get Genomic Scores

Operate on Genomic Intervals

Statistics

Wavelet Analysis

unnamed gi|91146441|gb|ABE22103.1| 100.00 80 0 0 1 80 161

History

Unnamed history  
433 bytes

9: blastp on db

4: query.fa

2: demo script on infile.txt  
1 line  
format text, database: ?

1: infile.txt

Find: ubuntu

Previous Next Highlight all Match case Phrase not found

If you get this result, congratulations, you just installed your first tool in Galaxy!

# Installing Galaxy tools (12)

```
Terminal - gcc2013@gcc-workshop: ~/Downloads
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$ cd
gcc2013@gcc-workshop:~$ cd Downloads
gcc2013@gcc-workshop:~/Downloads$ wget ftp://ftp.no.embnet.org/galaxy/toolfiles.tar.gz
--2013-06-28 08:34:55-- ftp://ftp.no.embnet.org/galaxy/toolfiles.tar.gz
=> 'toolfiles.tar.gz'
Resolving ftp.no.embnet.org (ftp.no.embnet.org)... 129.240.235.130
Connecting to ftp.no.embnet.org (ftp.no.embnet.org)|129.240.235.130|:21... connected.
Logging in as anonymous ... Logged in!
==> SYST ... done.      ==> PWD ... done.
==> TYPE I ... done.   ==> CWD (1) /galaxy ... done.
==> SIZE toolfiles.tar.gz ... 757
==> PASV ... done.     ==> RETR toolfiles.tar.gz ... done.
Length: 757 (unauthoritative)

100%[=====>] 757          --.-K/s   in 0s

2013-06-28 08:34:55 (1,66 MB/s) - 'toolfiles.tar.gz' saved [757]

gcc2013@gcc-workshop:~/Downloads$ tar xvzf toolfiles.tar.gz
toolfiles/
toolfiles/helloVM.pl
toolfiles/tool_conf.xml
toolfiles/infile.txt
toolfiles/helloVM.xml
gcc2013@gcc-workshop:~/Downloads$
```

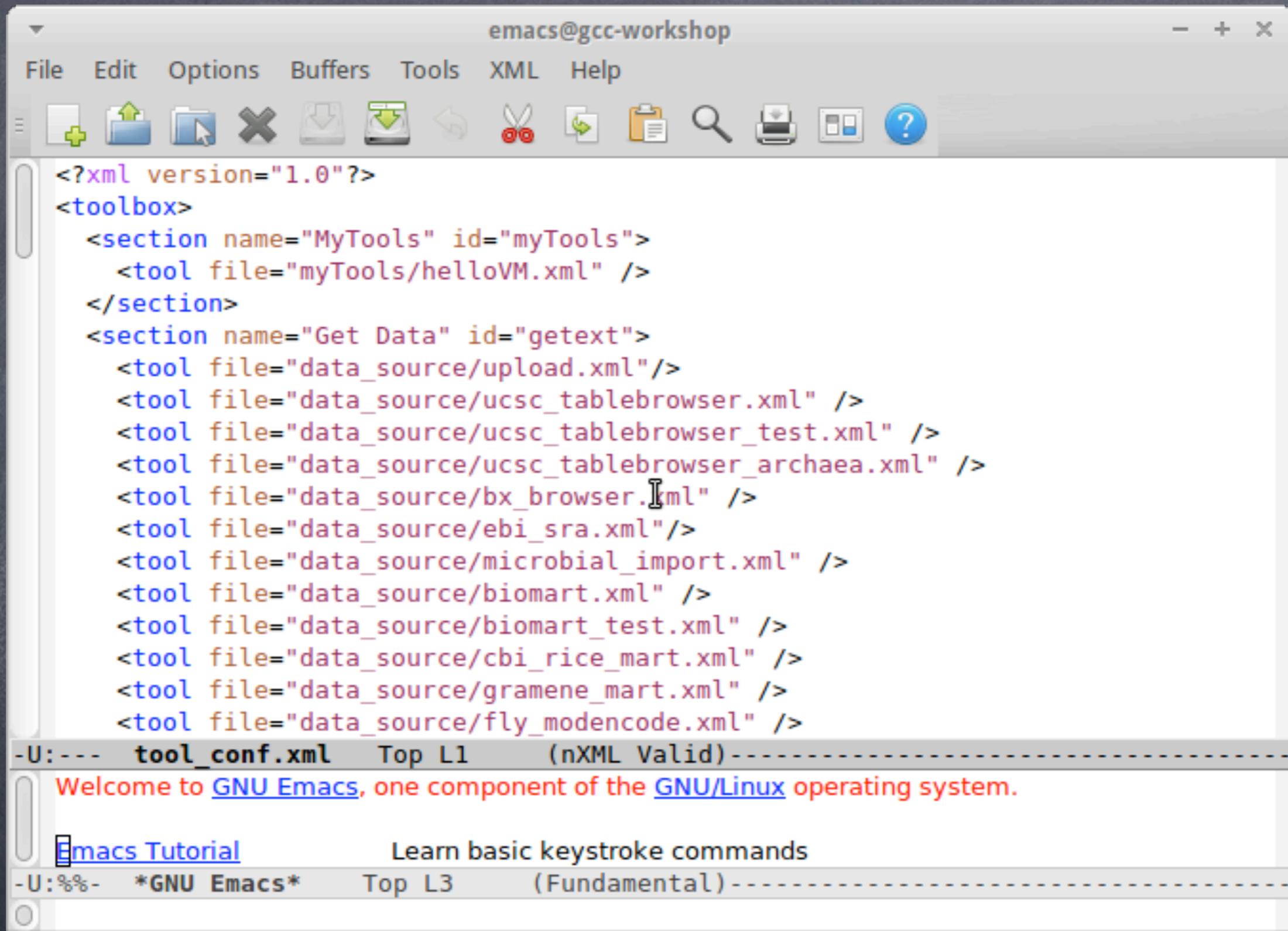
What about writing your own tool and enabling it in Galaxy? Just fetch the files as shown above.

# Installing Galaxy tools (13)

```
Terminal - gcc2013@gcc-workshop: /home/galaxy/galaxy-dist/tools/myTools
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$ cd tools
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tools$ mkdir myTools
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tools$ cd myTools/
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tools/myTools$ cp ~/Downloads/toolfiles/helloVM.* .
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tools/myTools$ chmod a+x helloVM.pl
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tools/myTools$ ls -l
total 8
-rwxrwxr-x 1 gcc2013 gcc2013 366 juni 25 10:50 helloVM.pl
-rw-rw-r-- 1 gcc2013 gcc2013 453 juni 25 10:50 helloVM.xml
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tools/myTools$
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist/tools/myTools$ cd /home/galaxy/galaxy-dist/
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$ more ~/Downloads/toolfiles/tool_conf.xml
<section name="MyTools" id="myTools">
  <tool file="myTools/helloVM.xml" />
</section>
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$ emacs tool_conf.xml
```

The procedure is the same to the one we followed with NCBI BLAST+. Here you have a simple Perl script.

# Installing Galaxy tools (14)



The image shows a screenshot of the Emacs editor window titled "emacs@gcc-workshop". The window contains XML code for a Galaxy tool configuration file. The code is as follows:

```
<?xml version="1.0"?>
<toolbox>
  <section name="MyTools" id="myTools">
    <tool file="myTools/helloVM.xml" />
  </section>
  <section name="Get Data" id="gettext">
    <tool file="data_source/upload.xml"/>
    <tool file="data_source/ucsc_tablebrowser.xml" />
    <tool file="data_source/ucsc_tablebrowser_test.xml" />
    <tool file="data_source/ucsc_tablebrowser_archaea.xml" />
    <tool file="data_source/bx_browser.xml" />
    <tool file="data_source/ebi_sra.xml"/>
    <tool file="data_source/microbial_import.xml" />
    <tool file="data_source/biomart.xml" />
    <tool file="data_source/biomart_test.xml" />
    <tool file="data_source/cbi_rice_mart.xml" />
    <tool file="data_source/gramene_mart.xml" />
    <tool file="data_source/fly_modencode.xml" />
  </section>
</toolbox>
```

Below the code, the Emacs status bar shows the file name "tool\_conf.xml" and the mode "Top L1 (nXML Valid)". A message box displays the text: "Welcome to GNU Emacs, one component of the GNU/Linux operating system." Below this, there is a link to "Emacs Tutorial" and the text "Learn basic keystroke commands". The status bar at the bottom shows "\*GNU Emacs\*" and "Top L3 (Fundamental)".

Editing galaxy-dist/tool-data/tool\_conf.xml file.

# Installing Galaxy tools (15)

The screenshot shows the Galaxy web interface. At the top, the navigation bar includes 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The top right corner shows 'Using 0 bytes'. On the left, the 'Tools' panel is visible with a search bar and a list of tool categories: MyTools, Get Data, Send Data, ENCODE Tools, Lift-Over, Text Manipulation, Filter and Sort, Join, Subtract and Group, Convert Formats, Extract Features, Fetch Sequences, Fetch Alignments, Get Genomic Scores, Operate on Genomic Intervals, Statistics, Wavelet Analysis, Graph/Display Data, Regional Variation, Multiple regression, Multivariate Analysis, and Evolution. The main workspace displays a green notification box with a checkmark: 'Hello world! It's running... To customize this page edit static/welcome.html'. Below this is a workflow diagram titled 'WWFSMD? grow noodly appendages...' with the URL 'usegalaxy.org'. The workflow consists of several tools: two 'Input dataset' tools, a 'Filter' tool, a 'Join' tool (highlighted with a blue box), a 'Group' tool, a 'Sort' tool, a 'Join two Queries' tool, and a 'Select first' tool. The right-hand 'History' panel shows 'Unnamed history' with '0 bytes' and a message: 'Your history is empty. Click 'Get Data' on the left pane to start'.

Restart Galaxy.

Can you spot the new tool on the left?

# Installing Galaxy tools (16)

The screenshot displays the Galaxy web interface. At the top, the navigation bar includes 'Galaxy' and menu items: 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The top right corner shows 'Using 21 bytes'. On the left, the 'Tools' sidebar contains a search bar and lists 'MyTools' (including 'demo script for Galaxy tutorial') and 'Get Data' (including 'Upload File from your computer', 'UCSC Main table browser', etc.). The main workspace shows a tool titled 'demo script (version 1.0.0)'. Under 'Source file:', there is a dropdown menu with '1: infile.txt' selected. A blue 'Execute' button is visible. Below the button, a text box contains the message: 'This tool is to illustrate a simple XML tool definition file.' On the right, the 'History' panel shows 'Unnamed history' with '21 bytes' and a single entry '1: infile.txt' which is highlighted in green and has an eye icon.

Upload the infile.txt into your history and Execute.

# Installing Galaxy tools (17)

The screenshot displays the Galaxy web interface. At the top, the navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The top right corner shows 'Using 125 bytes'. On the left, the 'Tools' panel is visible with a search bar and a list of tools under 'MyTools' and 'Get Data'. The central workspace features a green notification box with a checkmark icon, stating: 'The following job has been successfully added to the queue: 2: demo script on infile.txt'. Below this, it provides instructions: 'You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.' On the right, the 'History' panel shows 'Unnamed history' with '125 bytes'. Below this, the job '2: demo script on infile.txt' is listed with '1 line' of output: 'Hello tutorial participant! This Galax'. The input file '1: infile.txt' is also visible in the history list.

The execution of the demo script tool.

# Keeping Galaxy up-to-date

Galaxy uses Mercurial for software distribution

<http://mercurial.selenic.com/>

and

<http://mercurial.selenic.com/wiki/Tutorial>

# Galaxy upgrade (1)

```
Terminal - gcc2013@gcc-workshop: /home/galaxy_upgrade_howto
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$ pwd
/home/gcc2013
gcc2013@gcc-workshop:~$ sudo mkdir /home/galaxy_upgrade_howto
[sudo] password for gcc2013:
gcc2013@gcc-workshop:~$ ls -ls /home/
total 12
4 drwxr-xr-x  3 gcc2013 gcc2013 4096 juni  27 10:05 galaxy
4 drwxr-xr-x  2 root    root    4096 juni  27 10:24 galaxy_upgrade_howto
4 drwxr-xr-x 29 gcc2013 gcc2013 4096 juni  27 10:03 gcc2013
gcc2013@gcc-workshop:~$ sudo chown -R gcc2013:gcc2013 /home/galaxy_upgrade_howto/
gcc2013@gcc-workshop:~$ cd /home/galaxy_upgrade_howto/
gcc2013@gcc-workshop:/home/galaxy_upgrade_howto$
```

Make a new dir and ensure it has the right ownership/permissions

# Galaxy upgrade (2)

```
Terminal - gcc2013@gcc-workshop: /home/galaxy_upgrade_howto
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$ pwd
/home/gcc2013
gcc2013@gcc-workshop:~$ sudo mkdir /home/galaxy_upgrade_howto
[sudo] password for gcc2013:
gcc2013@gcc-workshop:~$ ls -ls /home/
total 12
4 drwxr-xr-x  3 gcc2013 gcc2013 4096 juni  27 10:05 galaxy
4 drwxr-xr-x  2 root    root    4096 juni  27 10:24 galaxy_upgrade_howto
4 drwxr-xr-x 29 gcc2013 gcc2013 4096 juni  27 10:03 gcc2013
gcc2013@gcc-workshop:~$ sudo chown -R gcc2013:gcc2013 /home/galaxy_upgrade_howto/
gcc2013@gcc-workshop:~$ cd /home/galaxy_upgrade_howto/
gcc2013@gcc-workshop:/home/galaxy_upgrade_howto$ hg clone -r release_2013.01.13 http://bitbucket.org/galaxy/galaxy-dist
real URL is https://bitbucket.org/galaxy/galaxy-dist
destination directory: galaxy-dist
adding changesets
adding manifests
adding file changes
█
```

Perform the Mercurial hg clone operation.  
This gets a specific galaxy release.

# Galaxy upgrade (3)

```
Terminal - gcc2013@gcc-workshop: /home/galaxy_upgrade_howto/galaxy-dist
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$ cd /home/galaxy_upgrade_howto/
gcc2013@gcc-workshop:/home/galaxy_upgrade_howto$ cd galaxy-dist/
gcc2013@gcc-workshop:/home/galaxy_upgrade_howto/galaxy-dist$ hg incoming
real URL is https://bitbucket.org/galaxy/galaxy-dist
comparing with http://bitbucket.org/galaxy/galaxy-dist
searching for changes
█
```

Search for changes in the Mercurial Galaxy repository.

# Galaxy upgrade (4)

```
Terminal - gcc2013@gcc-workshop: /home/galaxy_upgrade_howto/galaxy-dist
File Edit View Terminal Tabs Help
ry/session corruption.

changeset: 10002:9d42f1e32efb
branch:    stable
parent:    9996:e79a60e7c67a
user:      Dannon Baker <dannonbaker@me.com>
date:      Wed Jun 12 10:39:09 2013 -0400
summary:   For user impersonation, fully log the admin out prior to assuming user persona to avoid any histo
ry/session corruption.

changeset: 10003:b4a373d86c51
tag:       tip
parent:    10001:471484ff8be6
user:      greg
date:      Wed Jun 12 11:48:09 2013 -0400
summary:   Add targets to Repository Actions menu items.

gcc2013@gcc-workshop:/home/galaxy_upgrade_howto/galaxy-dist$ hg pull
real URL is https://bitbucket.org/galaxy/galaxy-dist
pulling from http://bitbucket.org/galaxy/galaxy-dist
searching for changes
adding changesets
adding manifests
adding file changes
added 1478 changesets with 3964 changes to 1264 files (+1 heads)
(run 'hg heads' to see heads)
gcc2013@gcc-workshop:/home/galaxy_upgrade_howto/galaxy-dist$ hg update release_2013.06.03
1179 files updated, 0 files merged, 452 files removed, 0 files unresolved
gcc2013@gcc-workshop:/home/galaxy_upgrade_howto/galaxy-dist$
```

When you 'pull', Mercurial will fetch all the latest changes since your last 'hg clone' operation.

# Galaxy upgrade (5)

```
Terminal - gcc2013@gcc-workshop: /home/galaxy_upgrade_howto/galaxy-dist
File Edit View Terminal Tabs Help
migrate.versioning.script.base DEBUG 2013-06-27 11:03:30,172 Loading script lib/galaxy/model/migrate/versions/0114_update_migrate_tools_table_again.py...
migrate.versioning.script.base DEBUG 2013-06-27 11:03:30,172 Script lib/galaxy/model/migrate/versions/0114_update_migrate_tools_table_again.py loaded successfully
migrate.versioning.script.base DEBUG 2013-06-27 11:03:30,172 Loading script lib/galaxy/model/migrate/versions/0115_longer_user_password_field.py...
migrate.versioning.script.base DEBUG 2013-06-27 11:03:30,173 Script lib/galaxy/model/migrate/versions/0115_longer_user_password_field.py loaded successfully
migrate.versioning.repository DEBUG 2013-06-27 11:03:30,173 Repository lib/galaxy/model/migrate loaded successfully
migrate.versioning.repository DEBUG 2013-06-27 11:03:30,173 Config: OrderedDict([('db_settings', OrderedDict([('__name__', 'db_settings'), ('repository_id', 'Galaxy'), ('version_table', 'migrate_version'), ('required_dbs', '[]')]))])
galaxy.model.migrate.check DEBUG 2013-06-27 11:03:30,177 psycopg2 egg successfully loaded for postgres dialect /home/galaxy_upgrade_howto/galaxy-dist/eggs/SQLAlchemy-0.7.9-py2.7-linux-i686-ucs4.egg/sqlalchemy/engine/url.py:105: SADeprecationWarning: The SQLAlchemy PostgreSQL dialect has been renamed from 'postgres' to 'postgresql'. The new URL format is postgresql[+driver]://<user>:<pass>@<host>/<dbname>
Traceback (most recent call last):
  File "/home/galaxy_upgrade_howto/galaxy-dist/lib/galaxy/webapps/galaxy/buildapp.py", line 35, in app_factory
    app = UniverseApplication( global_conf = global_conf, **kwargs )
  File "/home/galaxy_upgrade_howto/galaxy-dist/lib/galaxy/app.py", line 52, in __init__
    create_or_verify_database( db_url, kwargs.get( 'global_conf', {} ).get( '__file__', None ), self.config.database_engine_options, app=self )
  File "/home/galaxy_upgrade_howto/galaxy-dist/lib/galaxy/model/migrate/check.py", line 107, in create_or_verify_database
    % ( db_schema.version, migrate_repository.versions.latest, config_arg ) )
Exception: Your database has version '109' but this code expects version '115'. Please backup your database and then migrate the schema by running 'sh manage_db.sh upgrade'.
gcc2013@gcc-workshop:/home/galaxy_upgrade_howto/galaxy-dist$
```

After the 'hg pull', when restarting Galaxy and Postgres, you will see this problem. So, you will need to run:

**sh manage\_db.sh upgrade**

# Galaxy upgrade (6)

```
Terminal - gcc2013@gcc-workshop: /home/galaxy/galaxy-dist
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$ cd /home/galaxy/galaxy-dist/
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$ ./manage_db.sh upgrade
/home/galaxy_upgrade_howto/galaxy-dist/eggs/SQLAlchemy-0.7.9-py2.7-linux-i686-uc
s4.egg/sqlalchemy/engine/url.py:105: SADeprecationWarning: The SQLAlchemy Postgr
eSQL dialect has been renamed from 'postgres' to 'postgresql'. The new URL forma
t is postgresql[+driver]://<user>:<pass>@<host>/<dbname>
109 -> 110...

Add UUID column to dataset table

█
```

Running the `manage_db.sh` script updates the Galaxy Postgres SQL schema

# Galaxy upgrade (7)

```
Terminal - gcc2013@gcc-workshop: /home/galaxy/galaxy-dist
File Edit View Terminal Tabs Help
0112_add_data_manager_history_association_and_data_manager_job_association_tables DEBUG 2013-06-27 15:35:00,089 Created data_manager_history_association table
Created data_manager_history_association table
0112_add_data_manager_history_association_and_data_manager_job_association_tables DEBUG 2013-06-27 15:35:01,118 Created data_manager_job_association table
0112_add_data_manager_history_association_and_data_manager_job_association_tables DEBUG 2013-06-27 15:35:01,118 Created data_manager_job_association table
Created data_manager_job_association table
done
112 -> 113...

Migration script to update the migrate_tools.repository_path column to point to
the new location lib/tool_shed/galaxy_install/migrate.

done
113 -> 114...

Migration script to update the migrate_tools.repository_path column to point to
the new location lib/tool_shed/galaxy_install/migrate.

done
114 -> 115...
done
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$ ./run.sh --reload
```

After the Postgres SQL schema update,  
restart Galaxy.

# Galaxy upgrade (7)

```
Terminal - gcc2013@gcc-workshop: /home/galaxy/galaxy-dist
File Edit View Terminal Tabs Help
gcc2013@gcc-workshop:~$ cd /home/galaxy/galaxy-dist/
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$ ./run.sh --daemon
Entering daemon mode
gcc2013@gcc-workshop:/home/galaxy/galaxy-dist$ tail -f paster.log
galaxy.web.framework.base DEBUG 2013-06-27 15:43:37,613 Enabling 'request_types'
API controller, class: RequestTypeAPIController
galaxy.webapps.galaxy.buildapp DEBUG 2013-06-27 15:43:37,613 app.config.api_fold
ers: False
galaxy.webapps.galaxy.buildapp DEBUG 2013-06-27 15:43:37,830 Enabling 'httpexcep
tions' middleware
galaxy.webapps.galaxy.buildapp DEBUG 2013-06-27 15:43:37,831 Enabling 'recursive
' middleware
galaxy.webapps.galaxy.buildapp DEBUG 2013-06-27 15:43:37,861 Enabling 'eval exce
ptions' middleware
galaxy.webapps.galaxy.buildapp DEBUG 2013-06-27 15:43:37,861 Enabling 'trans log
ger' middleware
galaxy.webapps.galaxy.buildapp DEBUG 2013-06-27 15:43:37,861 Enabling 'x-forward
ed-host' middleware
galaxy.webapps.galaxy.buildapp DEBUG 2013-06-27 15:43:37,862 Enabling 'Request I
D' middleware
Starting server in PID 4088.
serving on http://127.0.0.1:8080
```

The `paster.log` file is your troubleshooting friend.

# Securing your Galaxy server

- Keep up with your Linux distro updates
- Keep up with the Galaxy updates (hg pull)
- VPN the Galaxy environment



Questions:

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