



Clouds and VM showcase from Australia: The GVL as a training platform

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Australia != Austria



The problem

“Bioinformatics analysis typically involves a large number of software and reference data, making the installation process a time-consuming task.”

“This problem is aggravated in a course setting, where every participant needs to have an identical installation, sufficient hardware to run it, and, ideally, access to an identical set-up after the course.”

Genomics on the cloud

What do you need?

Configurable **linux** server/cluster +

- Many analysis **tools**
- Large storage
- Analysis platforms
 - **Workflow** (eg Galaxy)
 - **Statistical** (RStudio)
 - **Computational** (iPython)
- Access to **reference data**

The cloud for training

Training is:

- Transient & bursty
- developed centrally, distributed & delivered locally
- aimed at range of expertise -> accessibility is key

all running on

- complex, ideally online, controlled best practice tool and data environments



The Genomics Virtual Lab

ANDREW

GVL drivers

- *Accessible* → Web, cloud
- *Scalable* → Cloud
- *Flexible* → multiple services, user managed
- *Reproducible* → launchable by user + resource agnostic
- *Useful!* → many tools, reference data, tutorials

A genomics cloud platform

<http://genome.edu.au>

The screenshot shows a PLOS ONE article page. At the top left is the PLOS ONE logo. Below it are links for 'OPEN ACCESS' and 'PEER-REVIEWED'. Underneath is the heading 'RESEARCH ARTICLE'. The main title of the article is 'Genomics Virtual Laboratory: A Practical Bioinformatics Workbench for the Cloud'. Below the title is a list of authors: Enis Afgan, Clare Sloggett, Nuwan Goonasekera, Igor Makunin, Derek Benson, Mark Crowe, Simon Gladman, Yousef Kowsar, Michael Pheasant, Ron Horst, Andrew Lonie. A small envelope icon is next to the name Andrew Lonie. At the bottom of the article summary is the text 'Published: October 26, 2015 • <http://dx.doi.org/10.1371/journal.pone.0140829>'.

The screenshot displays the 'Genomics Virtual Lab' website and a 'Galaxy' interface. The website header includes a logo, a search bar, and navigation links for 'Use', 'Get', 'Learn', 'Help', and 'About'. The main content area features a heading 'Genomics Virtual Lab' and a subtext 'A virtual laboratory for genomics research and training.' Below this are three call-to-action boxes: 'USE' (with text 'Use our Galaxy servers and genome browser.'), 'GET' (with text 'Get your own private server in the cloud with Galaxy, command-line bioinformatics, RStudio Server and IPython Notebook.'), and 'LEARN' (with text 'Learn genomics methods using our tutorials.'). To the right of the website is a screenshot of the 'Galaxy / mGVL 3.05' interface, showing a list of available tools and datasets. A 'Screenshot Added' notification is visible in the bottom right corner of the Galaxy interface.

<http://genome.edu.au>

A screenshot of a web browser window titled "Genomics Virtual Lab - GV". The address bar shows "genome.edu.au". The page content includes a navigation bar with links for "Use", "Get", "Learn", "Help", and "About". A search bar is located at the top right. The main content area displays a screenshot of a virtual desktop environment. The desktop shows an RStudio interface with an R console window displaying the R version 3.0.2 welcome message. To the right of the RStudio window is a file browser showing a folder named "Home" containing files "Arenis", "Desktop", "Documents", "Downloads", "galaxy", and "galaxy-fuse.py".

Genomics Virtual Lab

A virtual laboratory for genomics research and training.

USE

Use our Galaxy servers and genome browser.

GET

Get your own private server in the cloud with Galaxy, command-line bioinformatics, RStudio Server and IPython Notebook.

LEARN

Learn genomics methods using our tutorials.

https://launch.genome.edu.au

GVL Launcher Andrew Restore Down

https://launch.genome.edu.au/launch

GVL Launcher

Easily launch your own cloud servers for use with [Galaxy](#) and [CloudMan](#). See [this page](#) for detailed instructions on how to get started.

Cloud Choose from the available clouds. The credentials you provide below must match (ie, exist on) the chosen cloud.

Access key Your cloud account API access key. For the Amazon cloud, available from the [security credentials page](#).

Secret key Your cloud account API secret key. For the Amazon cloud, also available from the [security credentials page](#).

Institutional email Your institutional email. For grant-reporting purposes only.

Cluster name or Name of your cluster used for identification and restarting. If creating a new cluster, type any name you like.

Password Your choice of password, for the CloudMan web interface and accessing the server via ssh.

Instance type Type (ie, virtual hardware configuration) of the server to start.

Cluster type

Cluster with Galaxy
 Cluster only
 Do not set cluster type now

The cluster type determines the initial startup template used by CloudMan. See [this page](#) for details on cluster types.

GVL services

Screenshot of the GVL Dashboard showing Instance Services for ajl-gvl4.0.0-29sep1706.

Service Name	Description	Status	Access Link
 Galaxy	Galaxy is an open, web-based platform for accessible, reproducible, and transparent computational biomedical research.		http://43.240.97.4/galaxy Username: manual sign up Password: <custom password>
 Cloudman	CloudMan is a cloud manager that orchestrates the steps required to provision and manage compute clusters on cloud infrastructure. Use Cloudman to start and manage your Galaxy service and to add additional nodes to your compute cluster.		http://43.240.97.4/cloud Username: ubuntu Password: <cluster password>
 Lubuntu Desktop	Lubuntu is a lightweight desktop environment through which you can run desktop applications on your virtual machine. You can also access the GVL commandline utilities through the desktop.		http://43.240.97.4/vnc Username: ubuntu Password: <cluster password>
 SSH	You can login to your virtual machine remotely through an SSH client.		<code>ssh ubuntu@43.240.97.4</code> Username: ubuntu Password: <cluster password>
 JupyterHub	JupyterHub can be used to access your personal IPython Notebook. IPython Notebook is a web-based interactive computational environment where you can combine code execution, text, mathematics, plots and rich media into a single document.		http://43.240.97.4/jupyter Username: researcher Password: <cluster password>
 RStudio	RStudio IDE is a powerful and productive user interface for R.		http://43.240.97.4/rstudio Username: researcher

GVL services

Galaxy / GVL 4.0.0 43.240.97.4/galaxy Andrew Using 0 bytes

Galaxy / GVL 4.0.0

- Analyze Data
- Workflow
- Shared Data
- Visualization
- Help
- User

Tools

search tools

BASIC TOOLS

- Get Data
- Lift-Over
- Text Manipulation
- Filter and Sort
- Join, Subtract and Group
- Convert Formats
- Operate on Genomic Intervals
- Extract Features

STATISTICS AND VISUALISATION

- Fetch Sequences
- Fetch Alignments
- Statistics

Graph

File Edit Code View Plots Session Build Debug Tools Help

Go to file/function

R version 3.2.2 (2015-08-14) -- "Fire Safety"
 Copyright (C) 2015 The R Foundation for Statistical Computing
 Platform: x86_64-pc-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
 You are welcome to redistribute it under certain conditions.
 Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.
 Type 'contributors()' for more information and
 'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
 'help.start()' for an HTML browser interface to help.

WARNING: Your CRAN mirror is set to "http://cran.r-project.org" which has an insecure (non-HTTPS) URL. The repository was likely specified in .Rprofile or Rprofile.site so if you wish to change it you may need to edit one of those files. You should either switch to a repository that supports HTTPS or change your Rstudio options to not require HTTPS downloads.

To learn more and/or disable this warning message see the "Use secure download method for HTTP" option in Tools -> Global Options -> Packages.

Ubuntu@server-0ab1c9f3-a3dd-4e41-8d57-b874733b1c0c:~\$ stty cols 120
 Ubuntu@server-0ab1c9f3-a3dd-4e41-8d57-b874733b1c0c:~\$ module avail

Please set Wrench->Zoom to 100%

History

search datasets

Unnamed history

0 bytes

This history is empty. You can load your own data and run scripts here.

vcftools/0.1.11
 velvet/1.2.10
 velvetoptimiser/2.2.5
 weblogo/3.3
 zlib/1.2.8

atlas/3.10.2
 barrnap/0.7
 biocbasics/2.14
 bioc_qvalue/1.34.0
 blast+/2.2.28
 bowtie/0.12.7
 bowtie2/2.2.4
 bowtie2/2.2.5
 bwa/0.7.10.039ea20639
 bx-python/0.7.1
 clustalw2/2.1
 cufflinks/2.2.1
 cummeRbund/2.8.2
 dot
 emboss/5.0.0
 environment_settings/CUFFDIFF_SCRIPT_PATH
 environment_settings/GATK2_PATH
 environment_settings/GATK2_SITE_OPTIONS
 express/1.1.1
 fastqc_dist_0_10_1/0.10.1
 fastx_toolkit/0.0.13
 freebayes/0.9.18_0059bdf
 freetype/2.4.11
 galaxy-ops/1.0.0
 galaxy_sequence_utils/1.0.0
 gatk/1.4
 ggplot2/0.9.3
 ghostscript/9.10
 graphicsmagick/1.3.18
 htseq/0.5.4p3
 imaging/1.1.7
 lastz/1.02.00
 libcurl/7.35
 libpng/1.6.7
 Mako/0.7.2
 Ubuntu@server-0ab1c9f3-a3dd-4e41-8d57-b874733b1c0c:~\$

Environment History

Global Environment

Environment is empty

Files Plots Packages Help Viewer

New Folder Upload Delete Rename More

Home

Name	Size	Mod
Desktop		
Documents		
Downloads		
galaxy	8.3 KB	Sep
galaxy-fuse.py		
galaxy.genomes		
monthly.ao.index.b50.current.ascii	19.3 KB	Jan
Mus		
Pictures		
Public		
public_html		
README.txt		
Templates		
Untitled Document	2.7 KB	Sep

GVL management: Cloudman

CloudMan: elixir-allhand

115.146.88.168/cloud

Andrew

Initializing 'Galaxy' cluster type with storage type 'transient'. Please wait... (2016-03-09 06:26:28)
All cluster services started; the cluster is ready for use. (2016-03-09 06:32:15)

the cluster configuration has been completed (indicated by a notification popup), you can start using the cluster and the services that were started. For more information on the system features, see the [wiki](#).

Cluster controls

Shut down... Add worker nodes ▾ Remove worker nodes ▾ Access Galaxy

Cluster status

Cluster name: elixir-allhand

Disk status: 17G / 118G (15%)

Worker status: Requested: 2 Available: 2 Idle: 2

Service status: Applications ● Data ●

Autoscaling is off.
Turn [on](#)?

Cluster info log ▾

Collapse

```
06:26:28 - Initializing 'Galaxy' cluster type with storage type 'transient'. Please wait...
06:26:29 - Completed the initial cluster startup process. Configuring a predefined cluster of type Galaxy.
06:26:34 - Extracting archive url https://swift.rc.nectar.org.au:8888/v1/AUTH_377/cloudman-gvl-400/gvl-indices-tutorial-4.0.0.tar.gz to /mnt/galaxyIndices. This could take a while...
06:29:39 - MD5 checksum for archive https://swift.rc.nectar.org.au:8888/v1/AUTH_377/cloudman-gvl-400/gvl-indices-tutorial-4.0.0.tar.gz is OK:
4b360787af3672a2f20ab0ce961912bc == 4b360787af3672a2f20ab0ce961912bc
06:29:42 - Supervisor service prerequisites OK; starting the service.
06:29:42 - Extracting archive url https://swift.rc.nectar.org.au:8888/v1/AUTH_377/cloudman-gvl-400/gvl-galaxyfs-4.0.0.tar.gz to /mnt/galaxy. This could take a while...
06:31:06 - MD5 checksum for archive https://swift.rc.nectar.org.au:8888/v1/AUTH_377/cloudman-gvl-400/gvl-galaxyfs-4.0.0.tar.gz is OK:
b1c822cc2101fc20810d0d127d7b6722 == b1c822cc2101fc20810d0d127d7b6722
```



How does GVL work?

SIMON

https://launch.genome.edu.au

GVL Launcher Andrew Restore Down

https://launch.genome.edu.au/launch

GVL Launcher

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Cluster name or Name of your cluster used for identification and restarting. If creating a new cluster, type any name you like.

Password Your choice of password, for the CloudMan web interface and accessing the server via ssh.

Instance type Type (ie, virtual hardware configuration) of the server to start.

Cluster type

Cluster with Galaxy
 Cluster only
 Do not set cluster type now

The cluster type determines the initial startup template used by CloudMan. See [this page](#) for details on cluster types.

Or: Command-line launch

Use Python launch script to launch multiple GVLs

```
python launch_gvl.py \
    -a access_key \
    -s secret_key \
    -t instance_size \
    -i image_name \
    -z cloud_zone \
    -n number_of_instances \
    -u user_data \
    -p password
```

Genomics Virtual Lab: Architecture

GVL Workbench

- Ubuntu Linux



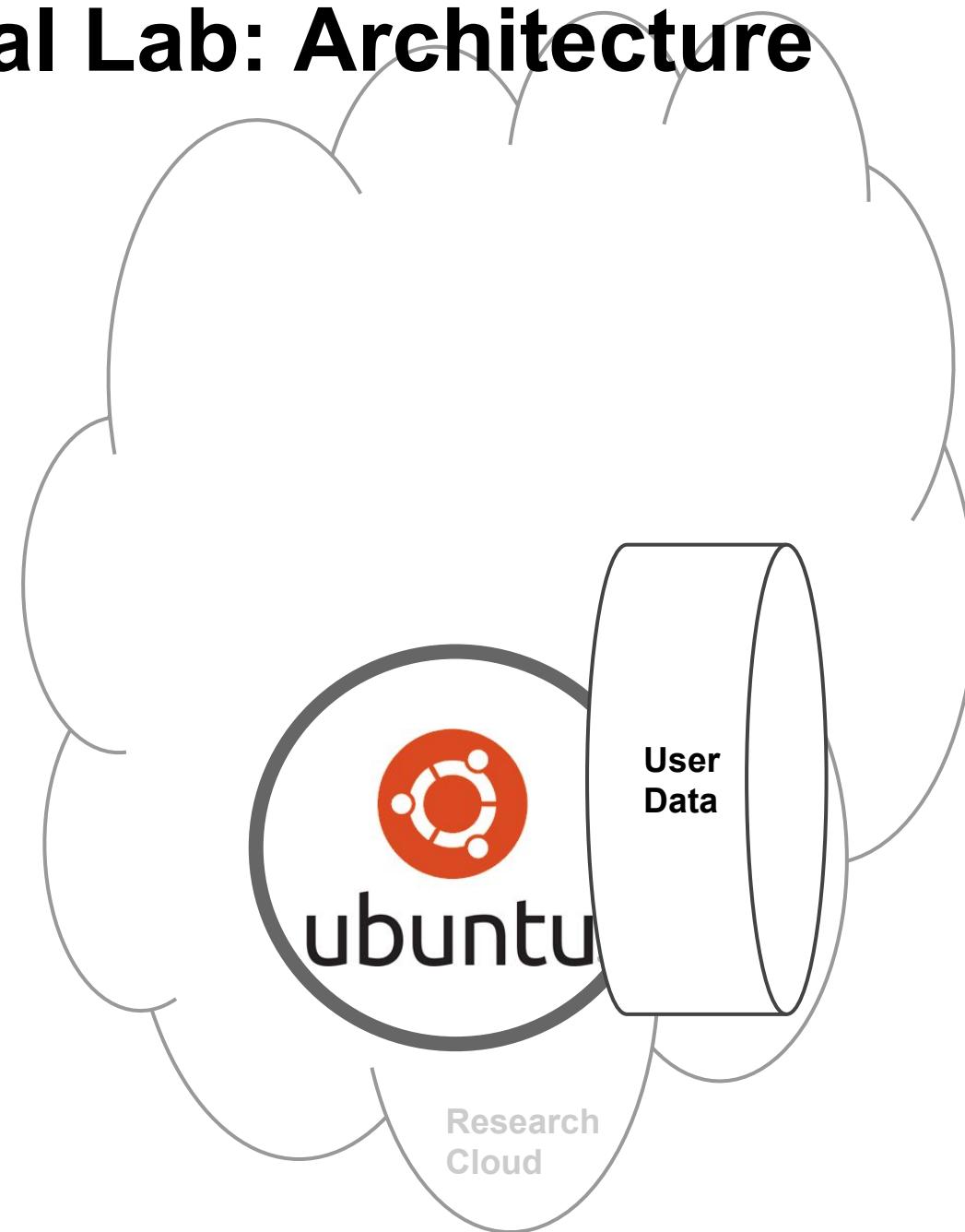
ubuntu

Research
Cloud

Genomics Virtual Lab: Architecture

GVL Workbench

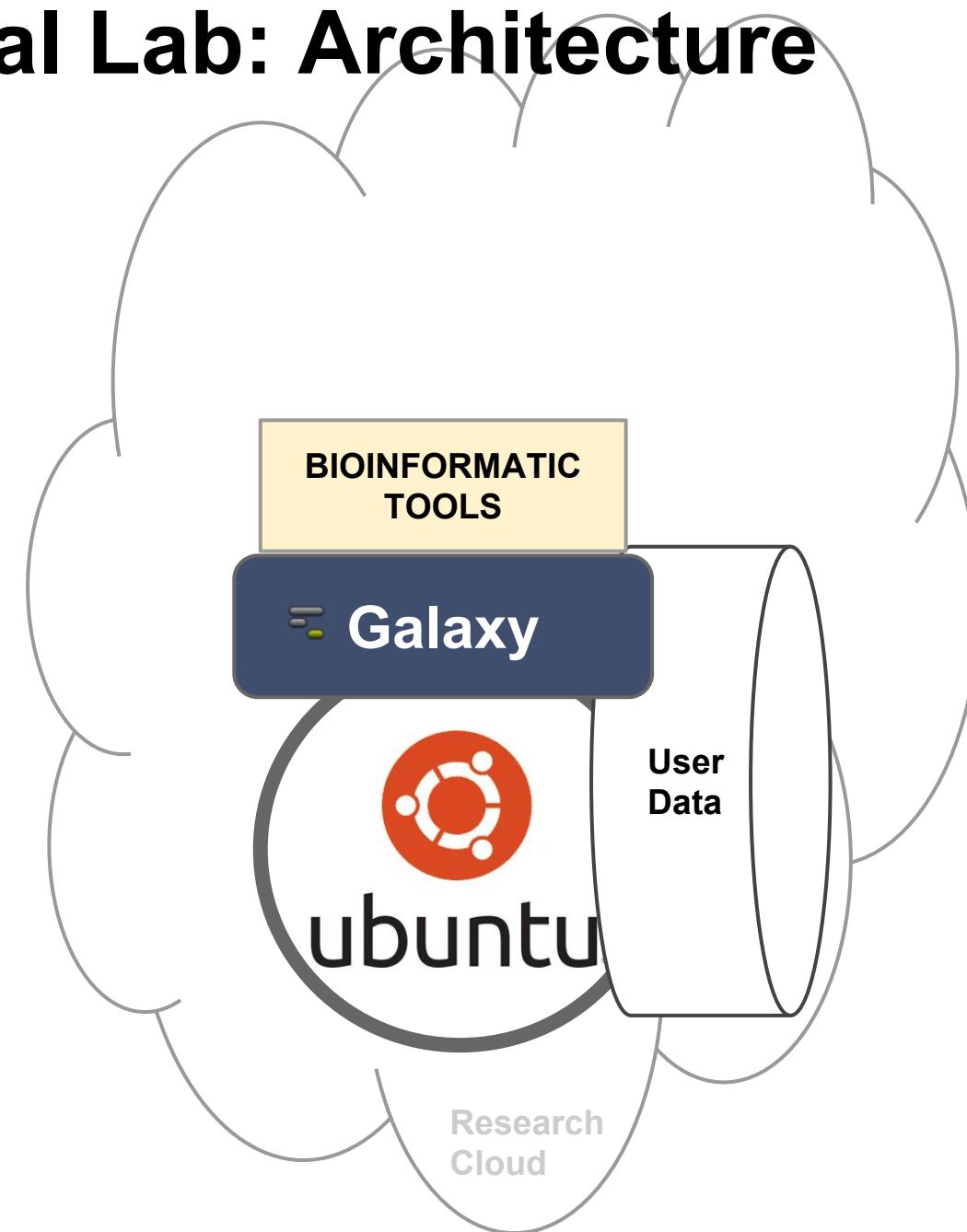
- Ubuntu Linux
- User Data



Genomics Virtual Lab: Architecture

GVL Workbench

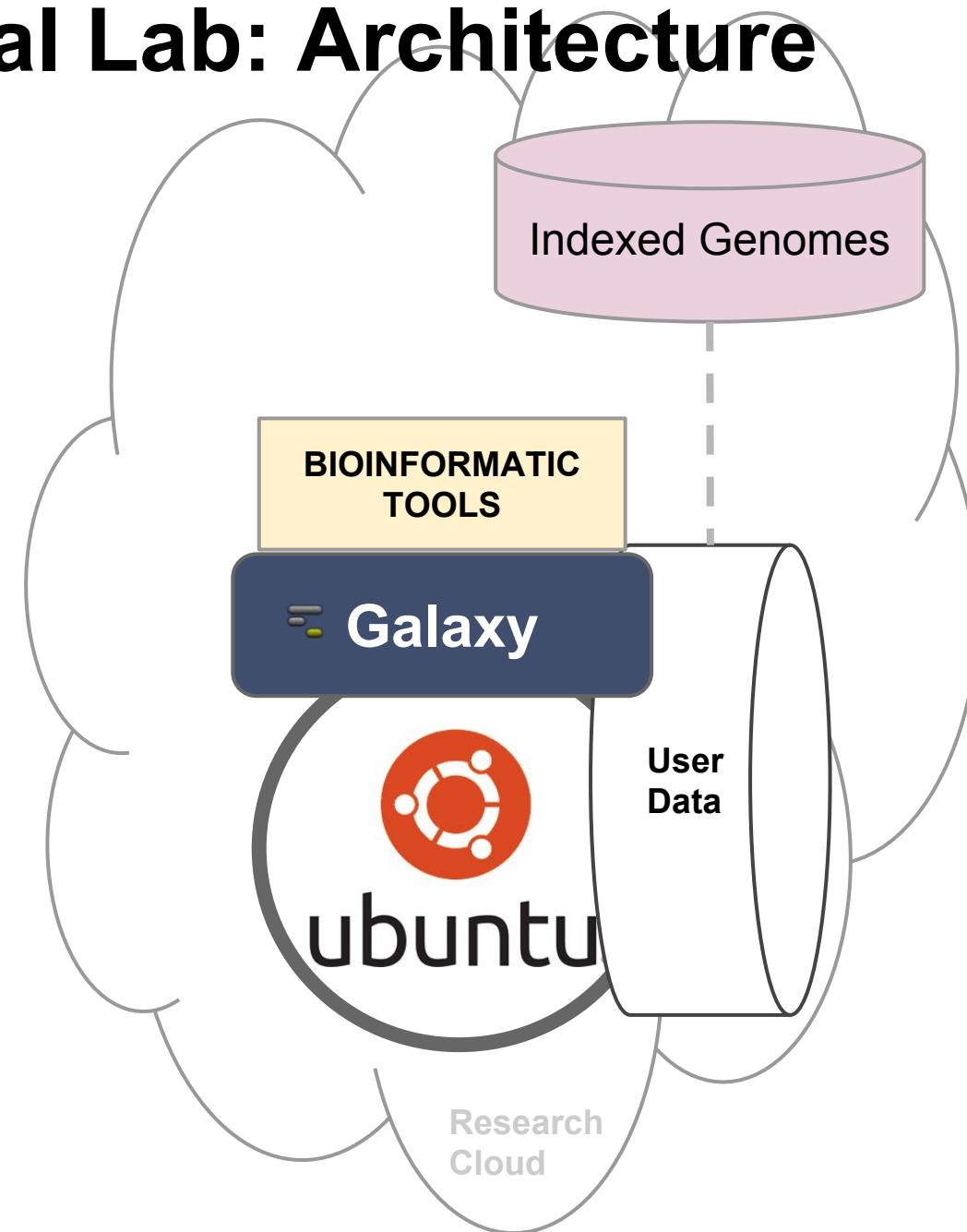
- Ubuntu Linux
- User Data
- Analysis Platforms & Tools



Genomics Virtual Lab: Architecture

GVL Workbench

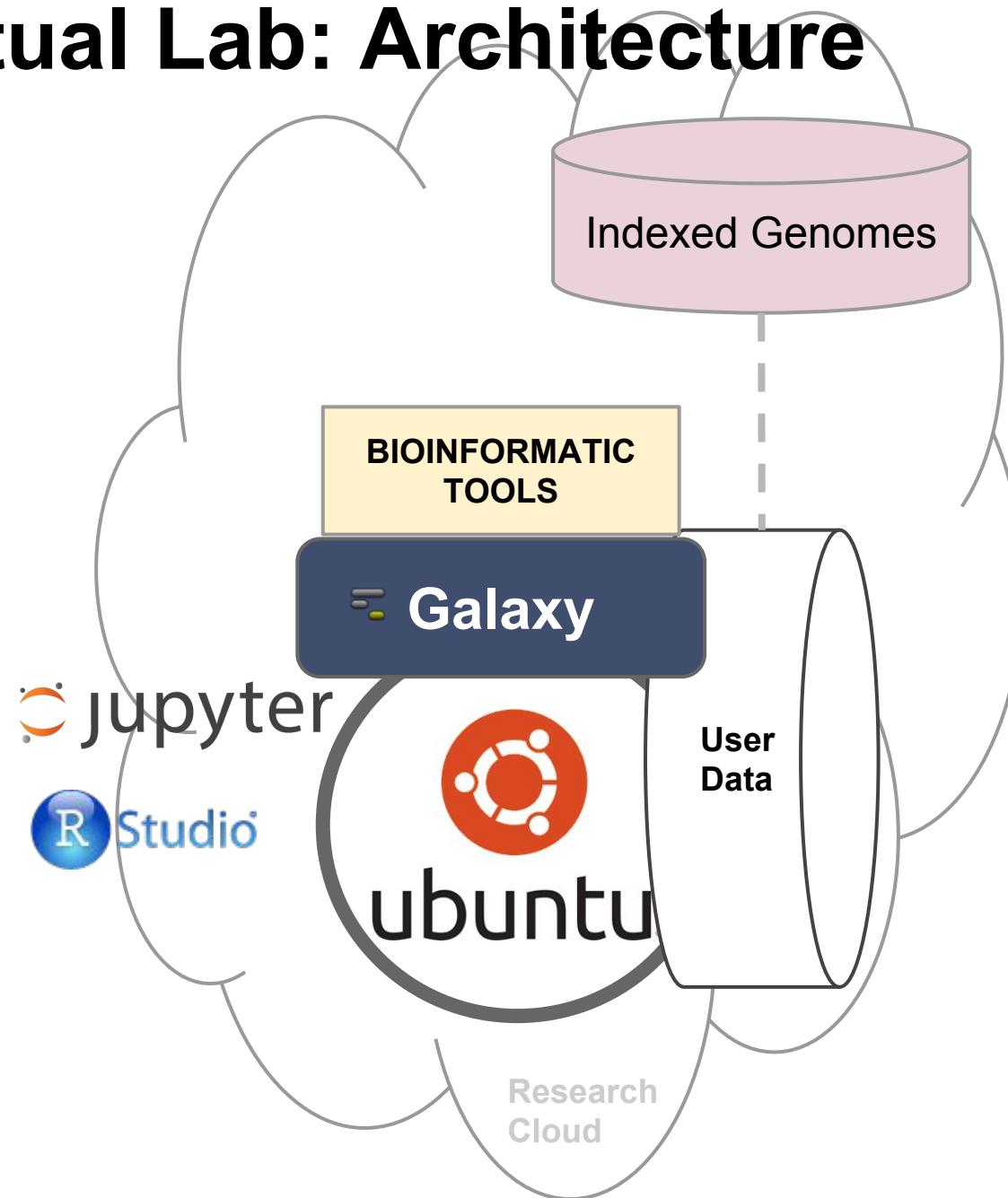
- Ubuntu Linux
- User Data
- Analysis Platforms & Tools
- Fast Reference Data



Genomics Virtual Lab: Architecture

GVL Workbench

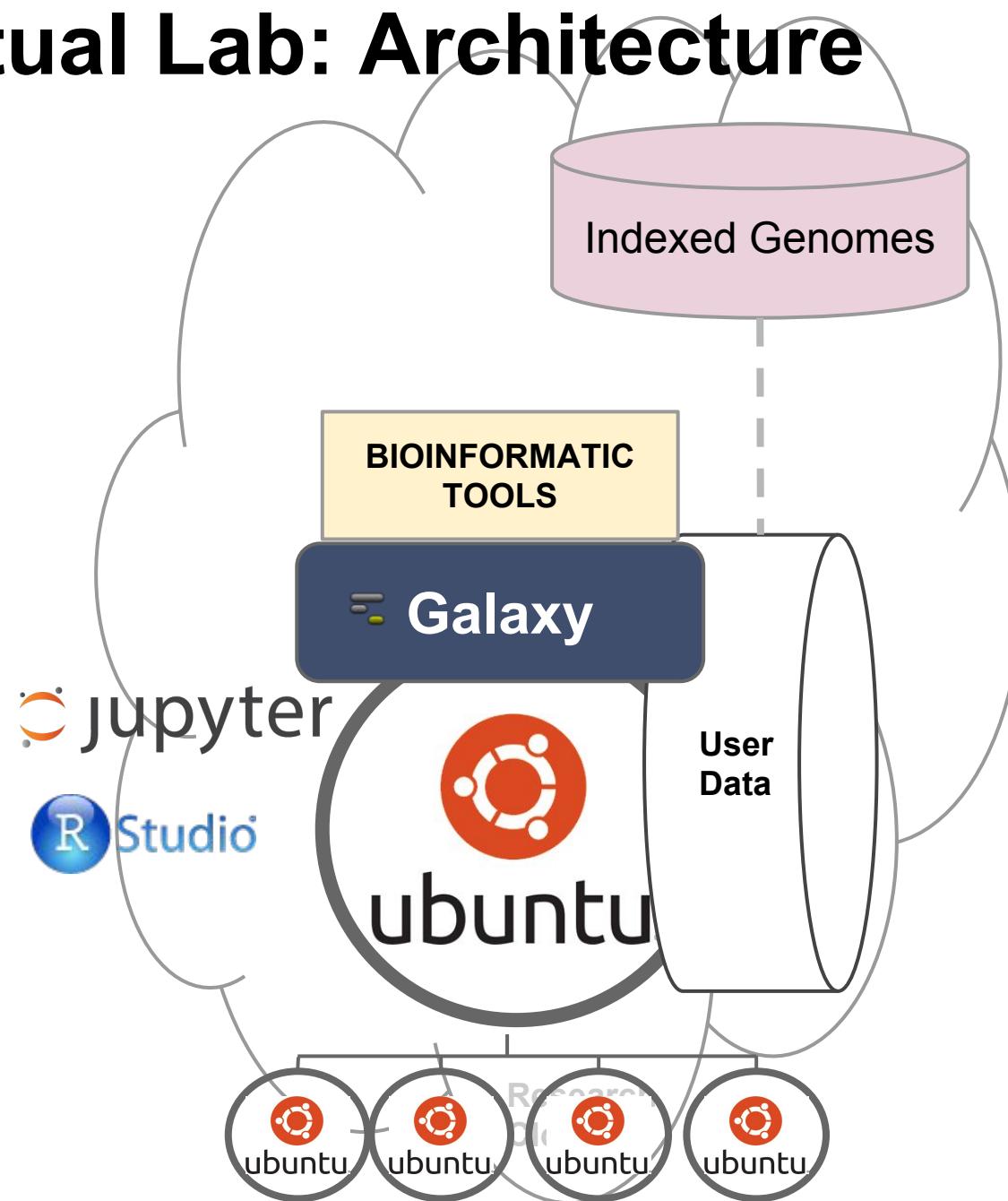
- Ubuntu Linux
- User Data
- Analysis Platforms & Tools
- Fast Reference Data
- Interactive Analysis
- Statistical Analysis



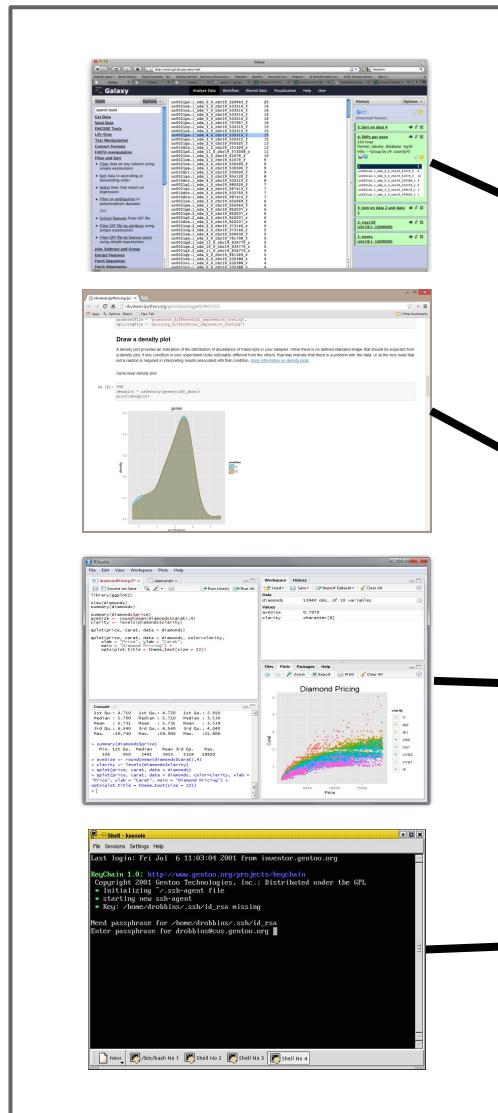
Genomics Virtual Lab: Architecture

GVL Workbench

- Ubuntu Linux
- User Data
- Analysis Platforms & Tools
- Fast Reference Data
- Interactive Analysis
- Statistical Analysis
- **Scalable Compute**



Genomics Virtual Lab: Architecture



The Genomics Virtual Lab

43.240.97.4 GVL Dashboard Home Admin About

GVL 4.0.0

Welcome to the GVL Dashboard! The GVL Dashboard is a portal through which you can access all services on your GVL instance.

Instance Services
for ajl-gvl4.0.0-29sep1706

Service Name	Description
Galaxy	Galaxy is an open, web-based platform for accessible, reproducible, and transparent computational biomedical research.
CloudMan	CloudMan is a cloud manager that orchestrates the steps required to provision and manage compute clusters on cloud infrastructure. Use Cloudman to start and manage Galaxy service and to add additional nodes to your compute cluster.
Lubuntu Desktop	Lubuntu is a lightweight desktop environment through which you can run desktop applications on your virtual machine. You can also access the GVL commandline through the desktop.
SSH	You can login to your virtual machine remotely through an SSH client.
JupyterHub	JupyterHub can be used to access your personal IPython Notebook. IPython Notebooks are web-based interactive computational environment where you can combine code and text, mathematics, plots and rich media into a single document.
RStudio	RStudio IDE is a powerful and productive user interface for R.

https://gsui.genomespace.org/jsui/gsui.html

Welcome to GenomeSpace

File | Launch | View | Connect | Manage | Recipes | Help

Cistrome Galaxy GenePattern Genomica IGV InSilicoDB UCSC Table Browser Gitools ISACreator MSigDB

Home Up to: Home

- alone
- Shared to alone
- Public
- s3:gvl-genomespace

Tags Owner Size Last Modified

Waiting for gsui.genomespace.org...

©2016 The Broad Institute of MIT and Harvard

Unnamed history 0 bytes

This history is empty. You can load your own data or get data from an external source

Welcome to Galaxy Melbourne

The GVL paper has recently been published.

Afgan E, Sloggett C, Goonasekera N, Makunin I, Benson D, Crowe M, Gladman S, Kowars Y, Pheasant M, Horst R, Lomie A., Genomics Virtual Laboratory: A Practical Bioinformatics Workbench for the Cloud., PLoS One, 2015 Oct 26;10(10):e0140829. doi:

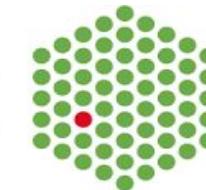
Training breadth



IP[y]: Notebook



EMBL-EB



Genome Browser

Building a microGVL tool suite



GitHub - gvlproject/microgvl.ansible.filesystem

microgvl.ansible.filesystem

This is the ansible playbook for the **Microbial Genomics Virtual Laboratory (mGVL)** filesystems. It is an extension of the normal GVL filesystem ansible script. It is located at <https://github.com/gvlproject/microgvl.ansible.filesystem>

This role creates two filesystem objects for later use with the GVL launch system (one automatically, second one manually.)

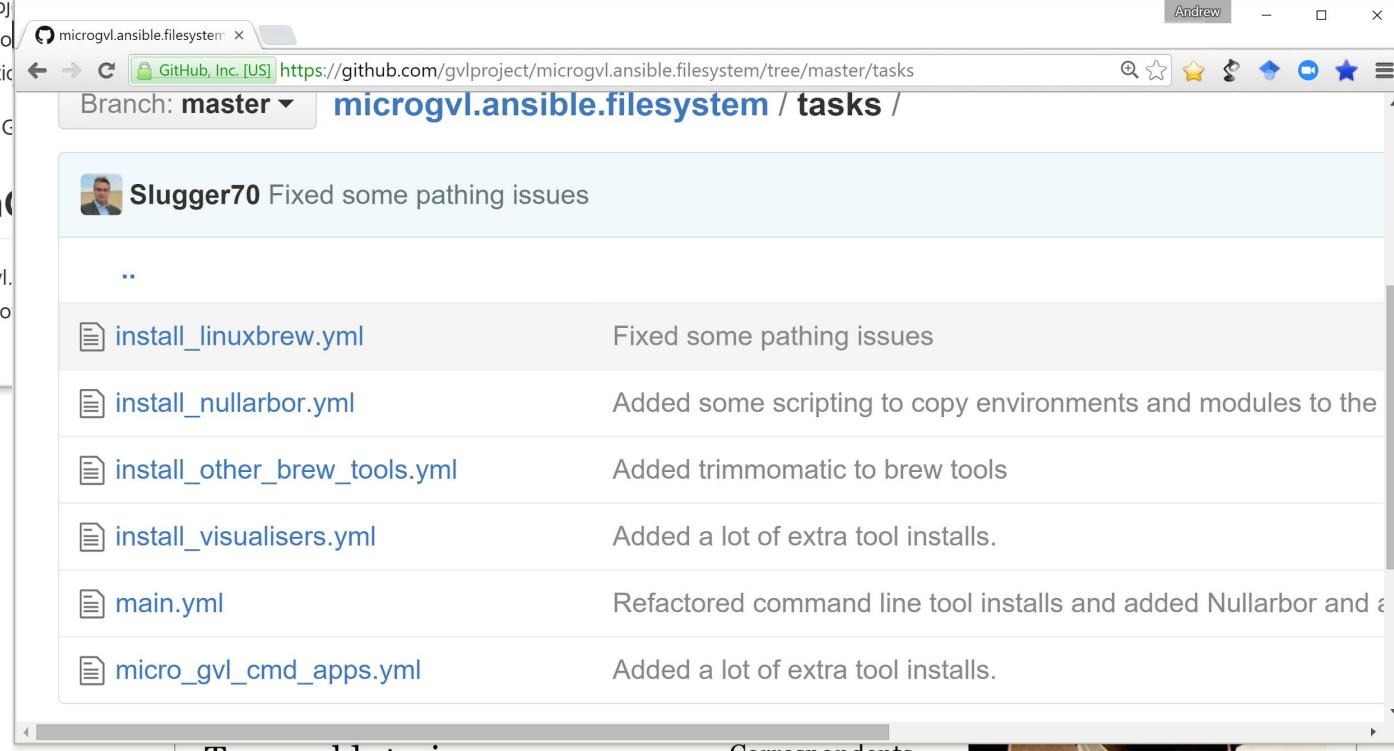
1. The mGVL galaxy filesystem object - **microgvl-fs-< version## >.tar.gz**
 - o Contains Galaxy, all of the installed Galaxy tools, the poststart.d script directory and the ftp upload store.
2. The mGVL application filesystem object
 - o Contains installations of all of core tools
 - o Contains the linuxbrew installation

These two tarballs are then used by the GVL launch system.

Usage/Building the mGVL tool suite

To use the role you need to clone the gvl.ansible.filesystem repository. Then follow the instructions in it's readme to do the build.

Then to run the build process:



Branch: master / [microgvl.ansible.filesystem](#) / [tasks](#) /

 Slugger70 Fixed some pathing issues

..

File	Description
install_linuxbrew.yml	Fixed some pathing issues
install_nullarbor.yml	Added some scripting to copy environments and modules to the Nullarbor
install_other_brew_tools.yml	Added trimmomatic to brew tools
install_visualisers.yml	Added a lot of extra tool installs.
main.yml	Refactored command line tool installs and added Nullarbor and a few other tools
micro_gvl_cmd_apps.yml	Added a lot of extra tool installs.

microbialGVL

The screenshot shows the Galaxy web interface running on a cloud instance. The main title is "Welcome to Galaxy on the Cloud" managed by CloudMan. Below it, a large banner reads "Microbial Genomics Virtual Lab Galaxy". On the left, a sidebar lists various tool categories: BASIC TOOLS, STATISTICS AND VISUALISATION, NGS COMMON TOOLSETS, and NGS ANALYSIS. A terminal window at the bottom displays a list of available modules and their versions.

Welcome to Galaxy on the Cloud
managed by CloudMan

Microbial Genomics Virtual Lab Galaxy

- To learn how to use Galaxy please see the [Galaxy tutorial](#).
- To install new tools to your Galaxy follow the [CloudMan documentation](#).
- To manage this cloud instance, use [CloudMan](#).

Thank you for using Galaxy and the Genomics Virtual Laboratory!

0 packages can be updated.
0 updates are security updates.

```
module ubuntu@server-693f14ae-7225-4005-a35e-518c248fcacf:~$ module avail
```

The Genomics Virtual Laboratory takes the form of a web-based suite of genomics analysis tools that can be used to analyze genomic data. Refer to [workbench services](#) for full details.

Galaxy is an open, web-based platform for biological data analysis.

```
aragorn/1.2.36
atlas/3.10.2
barnap/0.7
bioc_qvalue/1.34.0
blast/2.2.28
blast/2.2.31
bowtie/0.12.7
bowtie/2/2.2.5
bowtie2/2.2.6
bwa/0.7.10_039ea20639
bwa/0.7.12
bx-python/0.7.1
clustalw2/2.1
cufflinks/2.2.1
dot
emboss/5.0.0
environment_settings/GATK2_PATH
environment_settings/GATK2_SITE_OPTIONS
express/1.1.1
FastQC/0.11.4
galaxy/3.2.10
galaxy-ops/1.0.0
galaxy_sequence_utils/1.0.0
galaxy_sequence_utils/1.0.1
gatk/1.4
ggplot2/0.9.3
ghostscript/9.10
gnu_coreutils/8.22
gnu_parallel/20131122
hmmer/3.1b2
infernal/1.1
kmergenie/1.6715
lastz/1.02.00
libcurl/7.35
libpng/1.6.7
linuxbrew_module
express/1.1.1
Mako/0.7.2
ubuntu@server-693f14ae-7225-4005-a35e-518c248fcacf:~$
```

Please set Wrench->Zoom to 100%

GVL: BUILD

Ansible build system:

<https://github.com/gvlproject/gvl.ansible.playbook>

1. Build base Ubuntu image with all dependencies
2. Build Galaxy file system with all tools

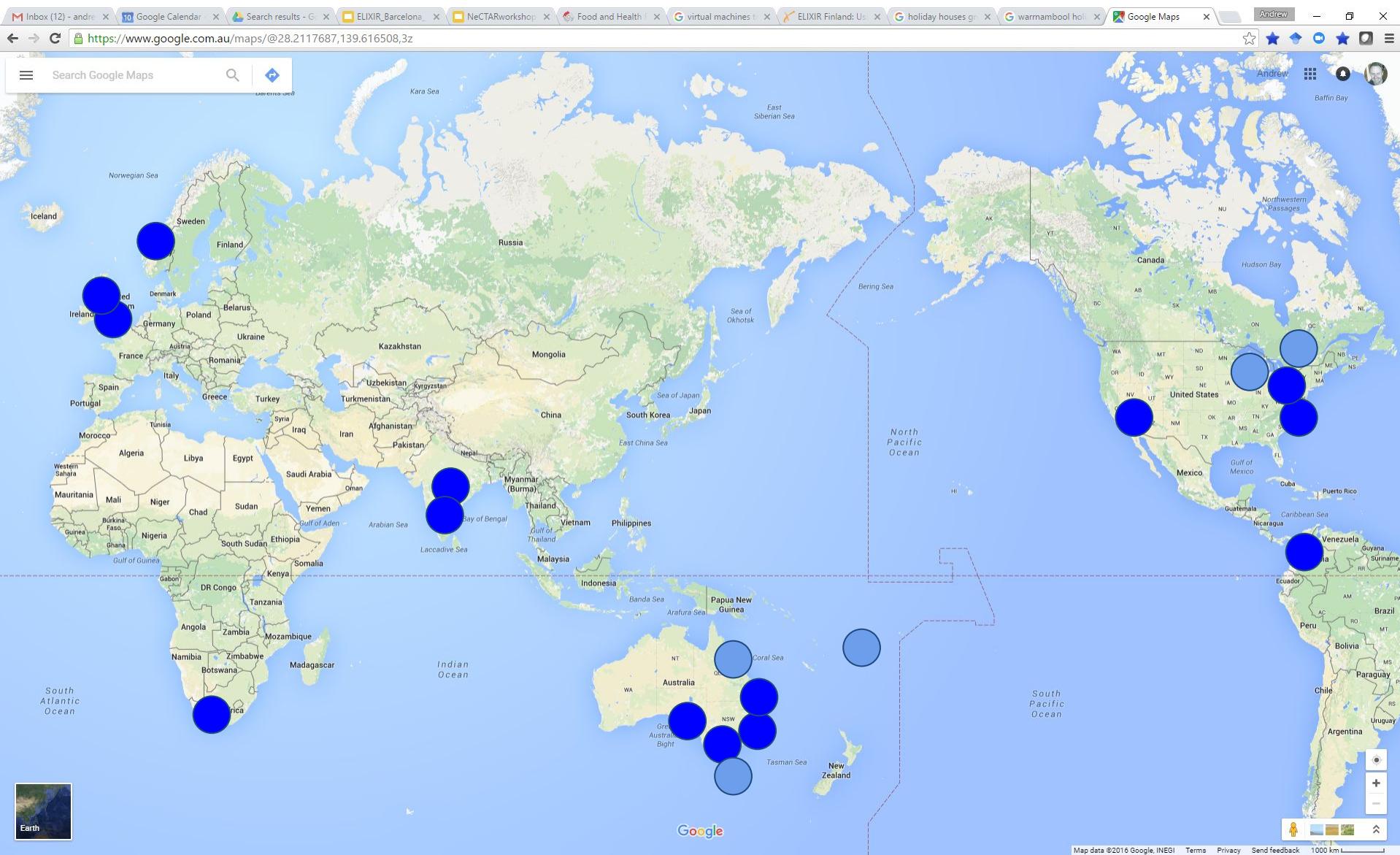
→ These all get combined at runtime



How is it being used in practice?

ANDREW + SIMON

Building global training resources



Building global training resources

mGVL r

“...the GVL is a brilliant resource, and Australia is really leading the way in this area. I am really pleased we will be able to run it on CLIMB. Think it is going to become critical for many in the UK through the research community”

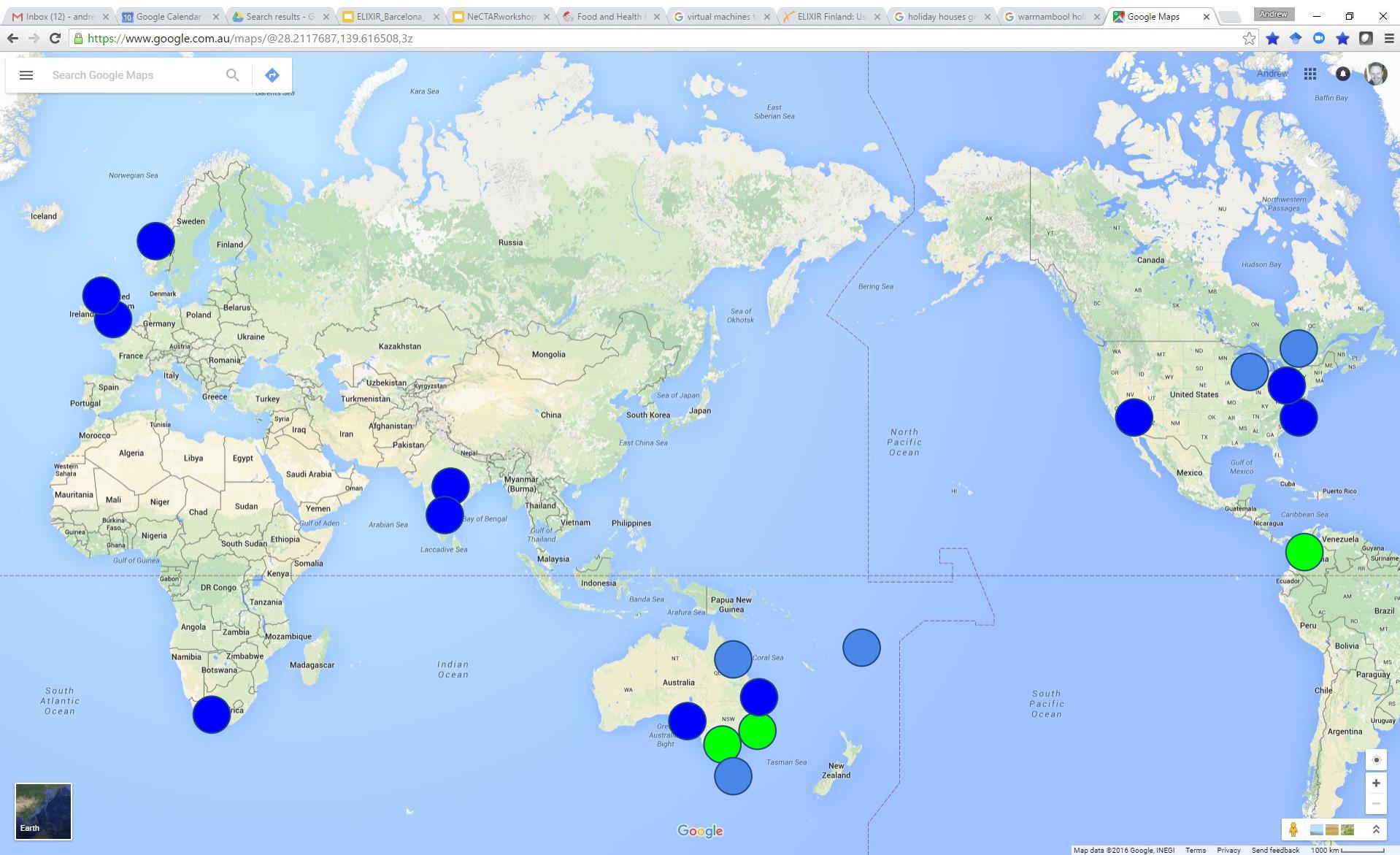
Tom Connor, Cardiff U (12.42pm 9th March!)

<http://www.climb.ac.uk>



UNIVERSITY OF
BIRMINGHAM

Microbial genomics workshop



Intro to Microbial Bioinformatics

- 1 day workshop
- 40 students
- 40 GVL instances
- Hands on!
- Only need web browser and internet connection.

Bioinformatics Workshop - The Genomics Virtual Laboratory & An Introduction to Microbial Genomics

TOAST/JAMS Sydney
Monday 14th March 2016

URL: <http://tinyurl.com/TOAST2016-Day1>

Dieter Bulach, Simon Gladman, Aaron Darling

www.vlsci.org.au, UTS weblink

Program

Time	Topic	Workshop materials	Other resources
9:00 - 9:15	Welcome, Introduction and Outline Slides		
9:15 - 9:45	The NeCTAR Cloud and the GVL Slides	List of GVL instances	
9:45 - 11:00	Intro to Galaxy Slides (Including morning tea)	Introduction to Galaxy Tutorial	The GVL website www.genome.edu.au Galaxy wiki wiki.galaxyproject.org
11:00 - 12:30	NGS data Slides Microbial Genome Assembly	Genome assembly and annotation tutorial	SPADEs website http://bioinf.spbau.ru/spades GVL Assembly protocol www.genome.edu.au/learn/learn#assembly - Uses Velvet instead of Spades.
12:30 - 13:30	Lunch		
13:30 - 14:15	Microbial Genome Annotation Microbial Variation Slides	Variant calling tutorial	Prokka website https://github.com/tseemann/prokka
14:30 - 15:30	Read Mapping Variant Calling Slides		Information on BWA http://bio-bwa.sourceforge.net/ Freebayes website https://github.com/ekg/freebayes
15:45 - 17:00	Comparative Genomics with Mauve	Comparative genomics tutorial	Mauve website http://darlinglab.org/mauve/mauve.html
17:00	Close	Workshop evaluation	

After the workshop

All materials/training data are available on web at:

<http://genome.edu.au>

The screenshot shows a sidebar with a light gray background and a main content area with a white background. The sidebar contains a list of sections and their durations:

- RNA-Seq Differential Gene Expression: Advanced Tutorial
- Tutorial Overview
- Background [15 min]
- Section 1: Preparation [15 min]
- Section 2: Alignment [30 mins]
- Section 3. Cuffdiff [40 min]
- Section 4. Count reads in features [30 min]
- Section 5: edgeR [30 min]
- Section 6. DESeq2 [30 min]
- Section 7: How much concordance is there between methods?
- Section 8: Gene set enrichment analysis
- Optional extension: Degust



RNA-Seq Differential Gene Expression: Advanced Tutorial

Authors: Mahtab Mirmomeni, Andrew Lonie, Jessica Chung

Tutorial Overview

In this tutorial we compare the performance of three statistically-based expression analysis tools:

- CuffDiff
- EdgeR
- DESeq2

This tutorial builds on top of the [basic RNA-seq DGE tutorial](#). It is recommended to have some familiarity of RNA-seq before beginning this tutorial.

Background [15 min]

Where does the data in this tutorial come from?

The data for this tutorial is from the paper, *A comprehensive comparison of RNA-Seq-based transcriptome analysis from reads to differential gene expression and cross-comparison with microarrays: a case study in Saccharomyces*

After the workshop

Andrew

Restore Down

genome.edu.au

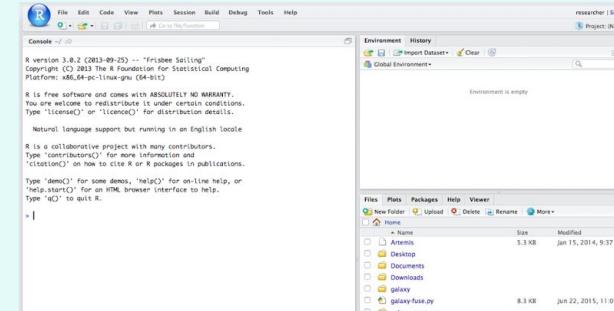
Genomics Virtual Lab

Use Get Learn Help About

Search

Genomics Virtual Lab

A virtual laboratory for genomics research and training.



USE

Use our Galaxy servers and genome browser.

GET

Get your own private server in the cloud with Galaxy, command-line bioinformatics, RStudio Server and IPython Notebook.

LEARN

Learn genomics methods using our tutorials.

After the workshop

Students can launch an identical GVL bioinformatics platform all over the world

- For more training
- For real research/project work

GVL Launcher

Easily launch your bioinformatics platform.

Cloud

Access key

Secret key

Institutional email

Amazon US West - N. California (AWS EC2)
Amazon AP - Sydney (AWS EC2)
Amazon EU - Frankfurt (AWS EC2)
Amazon US East - N. Virginia (AWS EC2)

✓ NeCTAR (OpenStack)
CLIMB-UK (OpenStack)
NeCTAR Melbourne Dev (OpenStack)
Climb-Cardiff (OpenStack)

Your cloud account API access key. For the Amazon cloud, available from the [security credentials page](#).

Your cloud account API secret key. For the Amazon cloud, also available from the [security credentials page](#).

Your institutional email. For grant-reporting purposes only.

1. See [this page](#) for detailed instructions on how to set up your cloud account.

The provider below must match (ie, exist on) the chosen cloud.



Thanks!



THE UNIVERSITY
OF QUEENSLAND
AUSTRALIA



R D S I
Research Data Storage
Infrastructure



Genomics Virtual Lab

