CYVERSE™

Transforming Science Through Data-driven Discovery

Accelerating Plant Science with CyVerse

Genomics Workflows, Data Management, and Training

Jason Williams – Lead, CyVerse – Education, Outreach, Training

Cold Spring Harbor Laboratory

williams@cshl.edu [@JasonWilliamsNY]

NSF

THE UNIVERSITY OF ARIZONA

TACC TEXAS ADVANCED COMPUTING CENTER

CSH Cold Spring Harbor Laboratory

UNCW

Slides and Tutorials

www.cyverse.org/sol2016

CyVerse Evolution

Vision:

Transforming science through data-driven discovery

Mission:

Design, develop, deploy, and expand a national cyberinfrastructure for life science research, and train scientists in its use

More than 30K users, PB of data, and hundreds of publications, courses, and discoveries

CyVerse 2016
Transforming Science Through Data-Driven Discovery

CyVerse Evolution

iPlant 2008
Empowering a New
Plant Biology

iPlant 2013
Cyberinfrastructure for
Life Science

CyVerse 2016
Transforming Science
Through Data-Driven
Discovery

CyVerse is Built for Data

Plant / Microbial

Animal

Biomedical

Ecological/Climate

CyVerse supports all domains of life science

CyVerse Evolution

We are funded by the National Science Foundation

DBI-0735191 and DBI-1265383

- We are your colleagues and collaborators!
- $100 Million in investment
- Freely available to the community
- Spur national/international collaboration
- Cite CyVerse:
  CyVerse.org/acknowledge-cite-cyverse

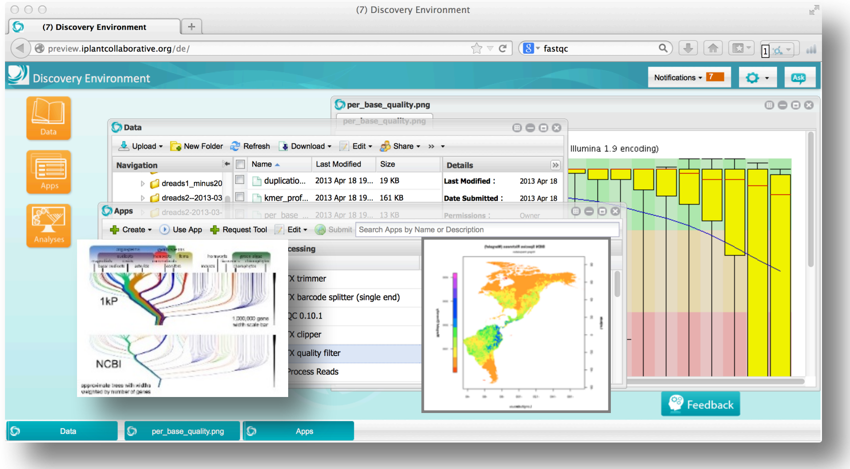
What is Cyberinfrastructure?

Cyberinfrastructure for Data-intensive Biology

- Data storage
- Software
- High-performance computing
- People

organized to solve problems of size and scope not otherwise solvable.

Cyberinfrastructure for Data-intensive Biology



Name	Last Modified	Size
duplicatio...	2013 Apr 18 19...	19 KB
kmer_prof...	2013 Apr 18 19...	161 KB

Details

Last Modified : 2013 Apr 18

Date Submitted : 2013 Apr 18

Platforms, tools, datasets

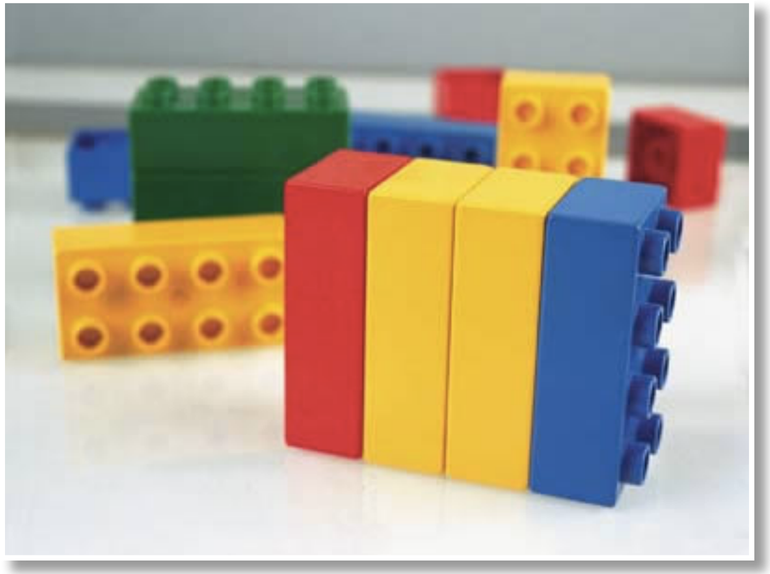
Storage and compute

Training and support

What is available in CyVerse?

CyVerse Products

- We strive to be the **CI Lego blocks**
- Danish 'leg godt' - '**play well**’
- Also translates as '**I put together**' in Latin
- If a solution is not available you can craft your own using CyVerse CI components



CyVerse Features

Get Science Done

- Ability to access and manage data
- Software to analyze data
- Computing resources
- Skills and help to use software and interpret results

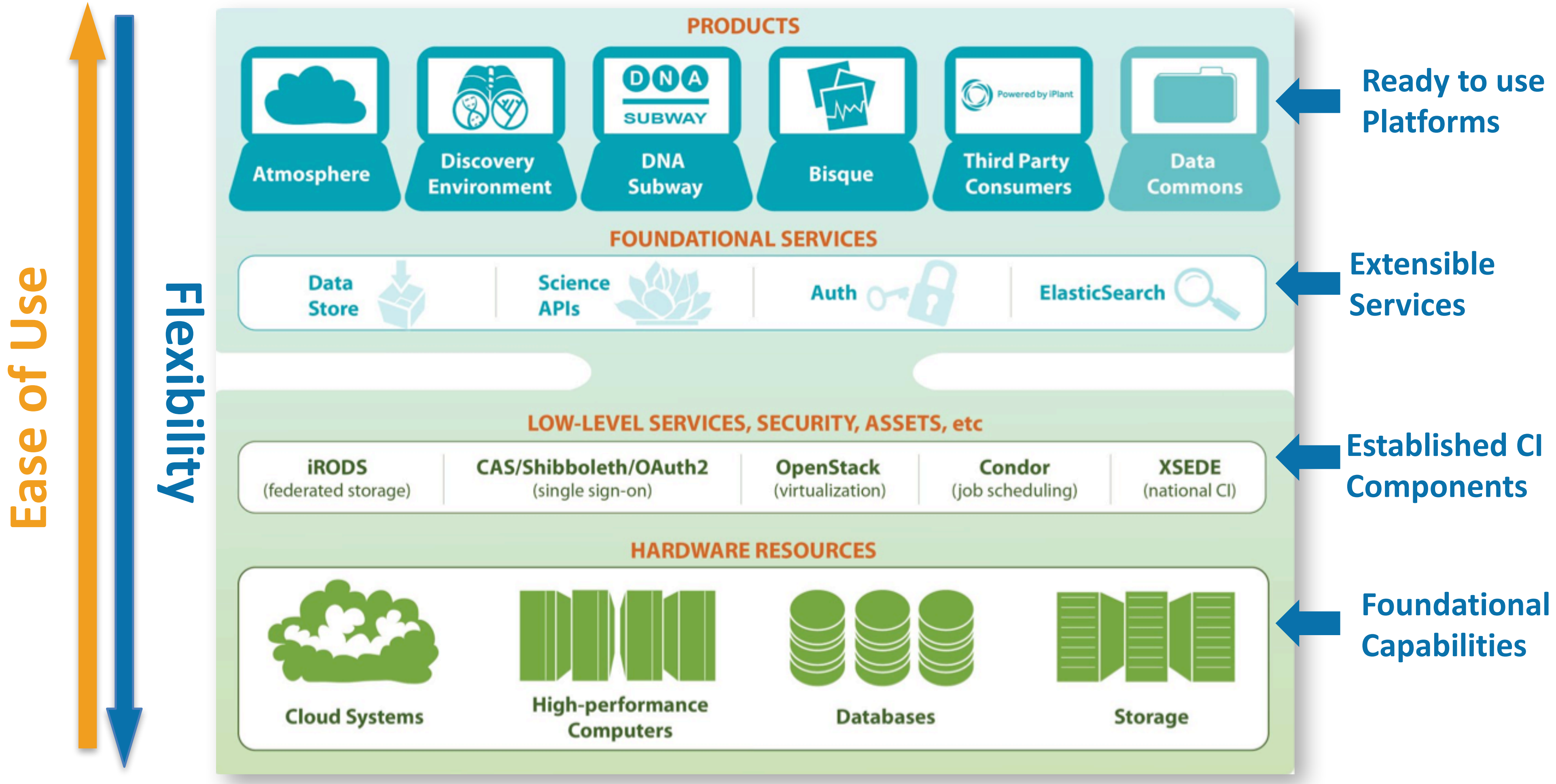
Ensure Reproducibility

- Metadata management
- Ability to share data and workflows
- Open source sustainable tools

Increase Productivity

- High-performance and scalable computing
- Ability automate and collaborate
- Funding spent on science, not software or hardware

CyVerse product stack



Ease of Use

Flexibility

PRODUCTS

- Atmosphere
- Discovery Environment
- DNA Subway
- Bisque
- Third Party Consumers
- Data Commons

FOUNDATIONAL SERVICES

- Data Store
- Science APIs
- Auth
- ElasticSearch

LOW-LEVEL SERVICES, SECURITY, ASSETS, etc

- iRODS (federated storage)
- CAS/Shibboleth/OAuth2 (single sign-on)
- OpenStack (virtualization)
- Condor (job scheduling)
- XSEDE (national CI)

HARDWARE RESOURCES

- Cloud Systems
- High-performance Computers
- Databases
- Storage

Ready to use Platforms

Extensible Services

Established CI Components

Foundational Capabilities

Data Store

The resources you need to share and manage data with your lab, colleagues and community

- ✓ Initial 100 GB allocation – TB allocations available
- ✓ Automatic data backup
- ✓ Easy upload /download and sharing

Discovery Environment

Hundreds of bioinformatics Apps in an easy-to-use interface

- ✓ A platform that can run almost any bioinformatics application
- ✓ Seamlessly integrated with data and high performance computing
- ✓ User extensible – add your own applications

Atmosphere

Cloud computing for the life sciences

✓ Simple: quick access to hundreds of virtual machine images

✓ Flexible: fully customize your software setup

✓ Powerful: integrated with CyVerse computing and data resources

Science APIs

Fully customize CyVerse resources

✓ Science-as-a-service platform

✓ Define your own compute, and storage resources (local and *CyVerse*)

✓ Build your own app store of scientific codes and workflows

DNA Subway

Educational workflows for Genomes, DNA Barcoding, RNA-Seq

- ✓ Commonly used bioinformatics tools in streamlined workflows
- ✓ Teach important concepts in biology and bioinformatics
- ✓ Inquiry-based experiments for novel discovery and publication of data

Bisque

Image analysis, management, and metadata

- ✓ Secure image storage, analysis, and data management
- ✓ Integrate existing applications or create new ones
- ✓ Custom visualization and image handling routines and APIs

How can you do science in CyVerse?

CyVerse Data Commons

Making data discoverable and reusable

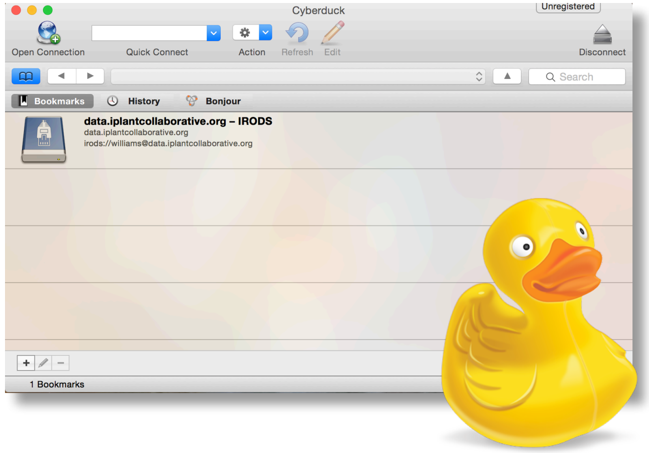
Data Store architecture is built for metadata management

- Data within CyVerse maintains provenance and can be labeled using a variety of metadata templates or using custom schemas
- Direct submission of sequencing data to NCBI Sequence Read Archive
- Request DOIs and ARKs (Archival Resource Key) for permanent data identification
- Support for elastic search, data sharing, and anonymous access

CyVerse Data Commons

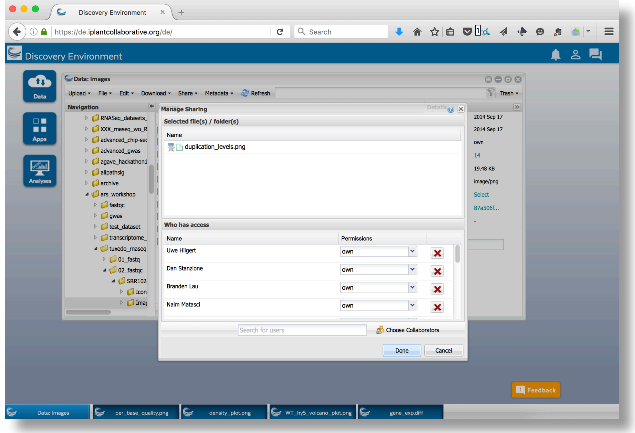
Supporting the lifecycle of data

Simple upload



data.iplantcollaborative.org – IRODS
data.iplantcollaborative.org
irods://williams@data.iplantcollaborative.org

markup, search, share



Manage Sharing

Selected file(s) / folder(s)

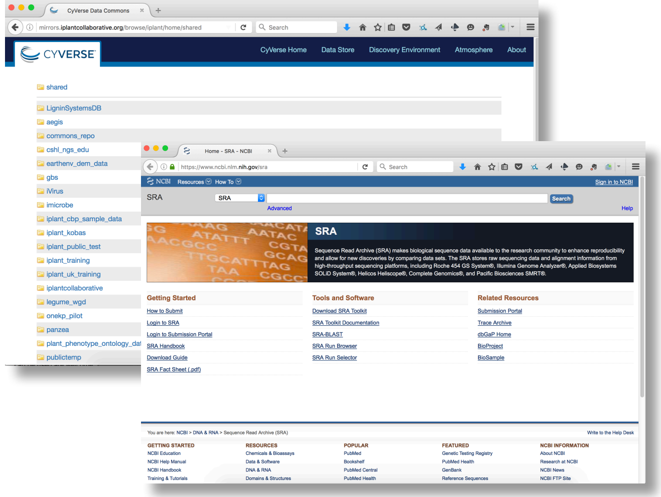
Name
duplication_levels.png

Who has access

Name	Permissions
Uwe Hilgert	own
Dan Stanzione	own
Branden Lau	own
Naim Matasci	own

Search for users · Choose Collaborators · Done · Cancel

publish



SRA

Sequence Read Archive (SRA) makes biological sequence data available to the research community to enhance reproducibility and allow for new discoveries by comparing data sets. The SRA stores raw sequencing data and alignment information from high-throughput sequencing platforms, including Roche 454 GS System®, Illumina Genome Analyzer®, Applied Biosystems SOLiD System®, Helicos Heliscope®, Complete Genomics®, and Pacific Biosciences SMRT®.

Getting Started	Tools and Software	Related Resources
How to Submit	Download SRA Toolkit	Submission Portal
Login to SRA	SRA Toolkit Documentation	Trace Archive
Login to Submission Portal	SRA-BLAST	dbGaP Home
SRA Handbook	SRA Run Browser	BioProject
Download Guide	SRA Run Selector	BioSample
SRA Fact Sheet (.pdf)		

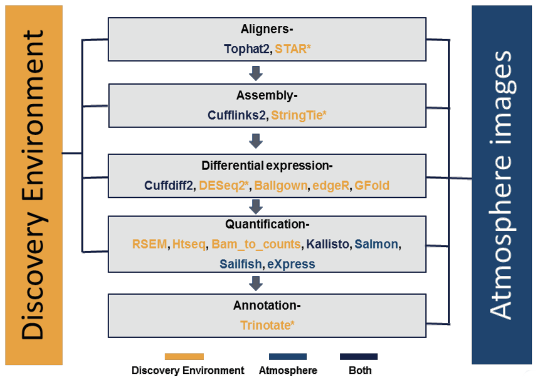
You are here: NCBI > DNA & RNA > Sequence Read Archive (SRA) · Write to the Help Desk

GETTING STARTED	RESOURCES	POPULAR	FEATURED	NCBI INFORMATION
NCBI Education	Chemicals & Bioassays	PubMed	Genetic Testing Registry	About NCBI
NCBI Help Manual	Data & Software	Bookshelf	PubMed Health	Research at NCBI
NCBI Handbook	DNA & RNA	PubMed Central	GenBank	NCBI News
Training & Tutorials	Domains & Structures	PubMed Health	Reference Sequences	NCBI FTP Site

Discovery Environment

End-to-end workflows for genomics

RNA-Seq 1: Differential Expression



Discovery Environment

Aligners-
Tophat2, STAR*

Assembly-
Cufflinks2, StringTie*

Differential expression-
Cuffdiff2, DESeq2*, Ballgown, edgeR, GFold

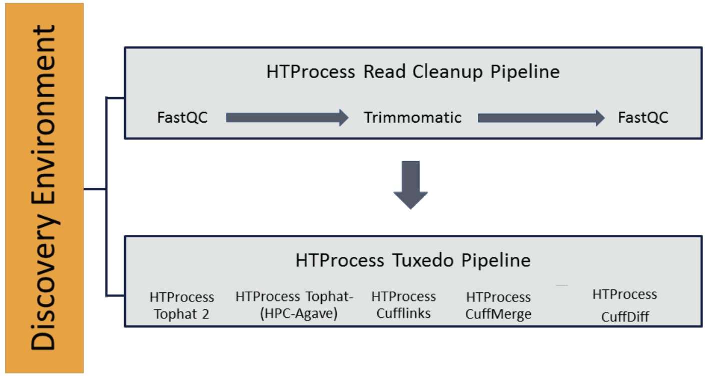
Quantification-
RSEM, Htseq, Bam_to_counts, Kallisto, Salmon, Sailfish, eXpress

Annotation-
Trinotate*

Atmosphere images

Discovery Environment
Atmosphere
Both

RNA-Seq 2: High-throughput

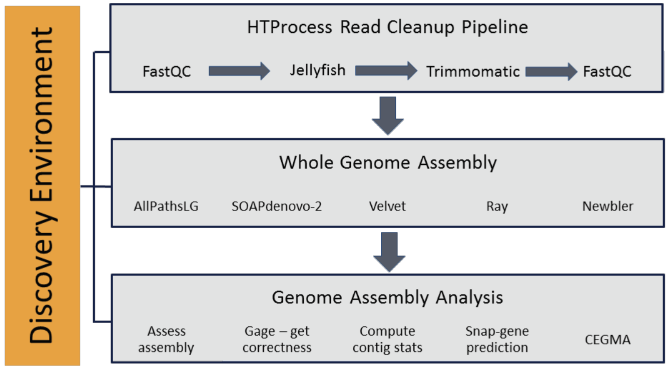


Discovery Environment

HTProcess Read Cleanup Pipeline
FastQC → Trimmomatic → FastQC

HTProcess Tuxedo Pipeline
HTProcess Tophat 2
HTProcess Tophat- (HPC-Agave)
HTProcess Cufflinks
HTProcess CuffMerge
HTProcess CuffDiff

Genome Assembly



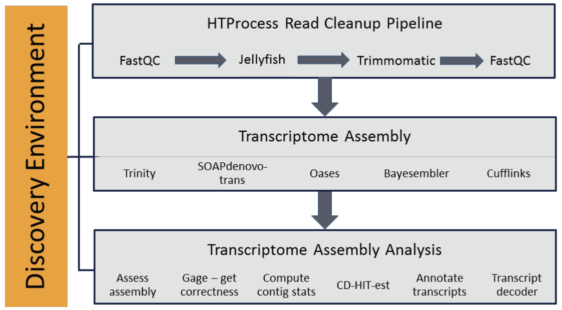
Discovery Environment

HTProcess Read Cleanup Pipeline
FastQC → Jellyfish → Trimmomatic → FastQC

Whole Genome Assembly
AllPathsLG
SOAPdenovo-2
Velvet
Ray
Newbler

Genome Assembly Analysis
Assess assembly
Gage – get correctness
Compute contig stats
Snap-gene prediction
CEGMA

Transcriptome Assembly



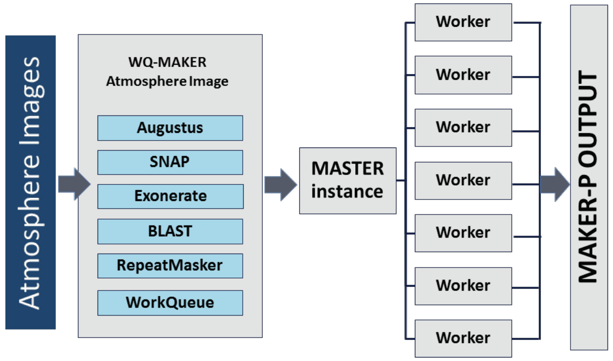
Discovery Environment

HTProcess Read Cleanup Pipeline
FastQC → Jellyfish → Trimmomatic → FastQC

Transcriptome Assembly
Trinity
SOAPdenovo-trans
Oases
Bayesembler
Cufflinks

Transcriptome Assembly Analysis
Assess assembly
Gage – get correctness
Compute contig stats
CD-HIT-est
Annotate transcripts
Transcript decoder

WQ-Maker Annotation



Atmosphere Images

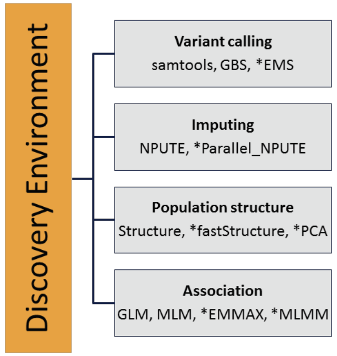
WQ-MAKER Atmosphere Image
Augustus
SNAP
Exonerate
BLAST
RepeatMasker
WorkQueue

MASTER instance

Worker
Worker
Worker
Worker
Worker
Worker
Worker

MAKER-P OUTPUT

Association Studies



Discovery Environment

Variant calling
samtools, GBS, *EMS

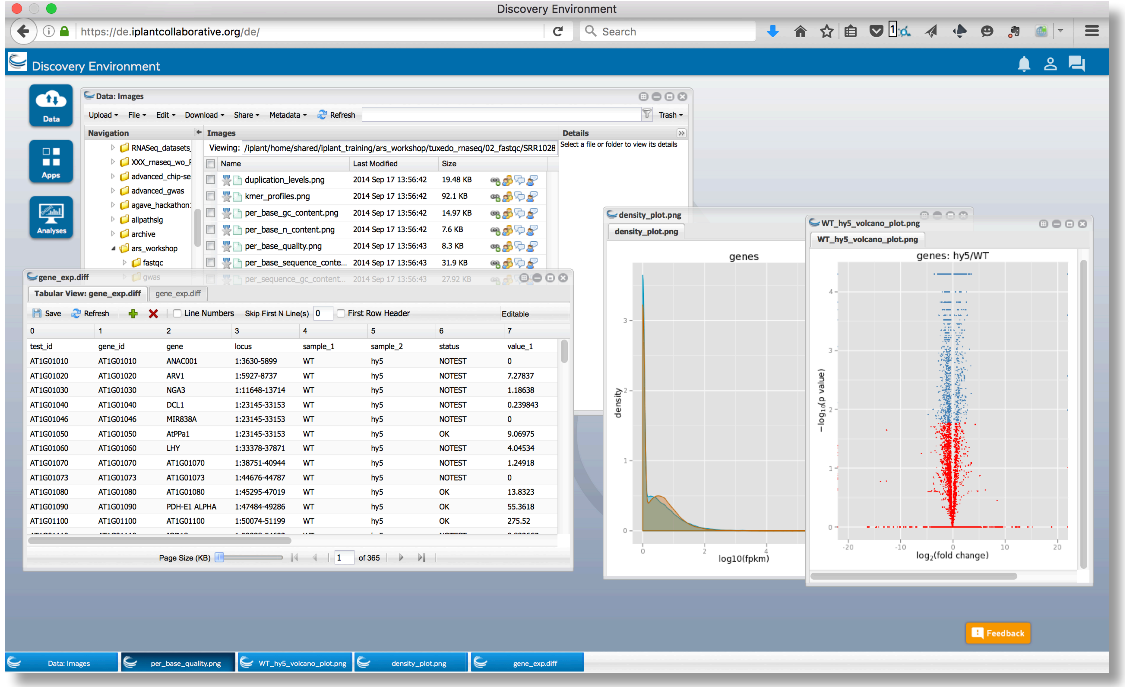
Imputing
NPUTE, *Parallel_NPUTE

Population structure
Structure, *fastStructure, *PCA

Association
GLM, MLM, *EMMAX, *MLMM

Discovery Environment

User friendly, developer friendly



Viewing: /iplant/home/shared/iplant_training/ars_workshop/tuxedo_rnaseq/02_fastqc/SRR1028

Name	Last Modified	Size
duplication_levels.png	2014 Sep 17 13:56:42	19.48 KB
kmer_profiles.png	2014 Sep 17 13:56:42	92.1 KB
per_base_gc_content.png	2014 Sep 17 13:56:42	14.97 KB
per_base_n_content.png	2014 Sep 17 13:56:42	7.6 KB
per_base_quality.png	2014 Sep 17 13:56:43	8.3 KB
per_base_sequence_conte...	2014 Sep 17 13:56:43	31.9 KB
per_sequence_gc_content...	2014 Sep 17 13:56:43	27.92 KB

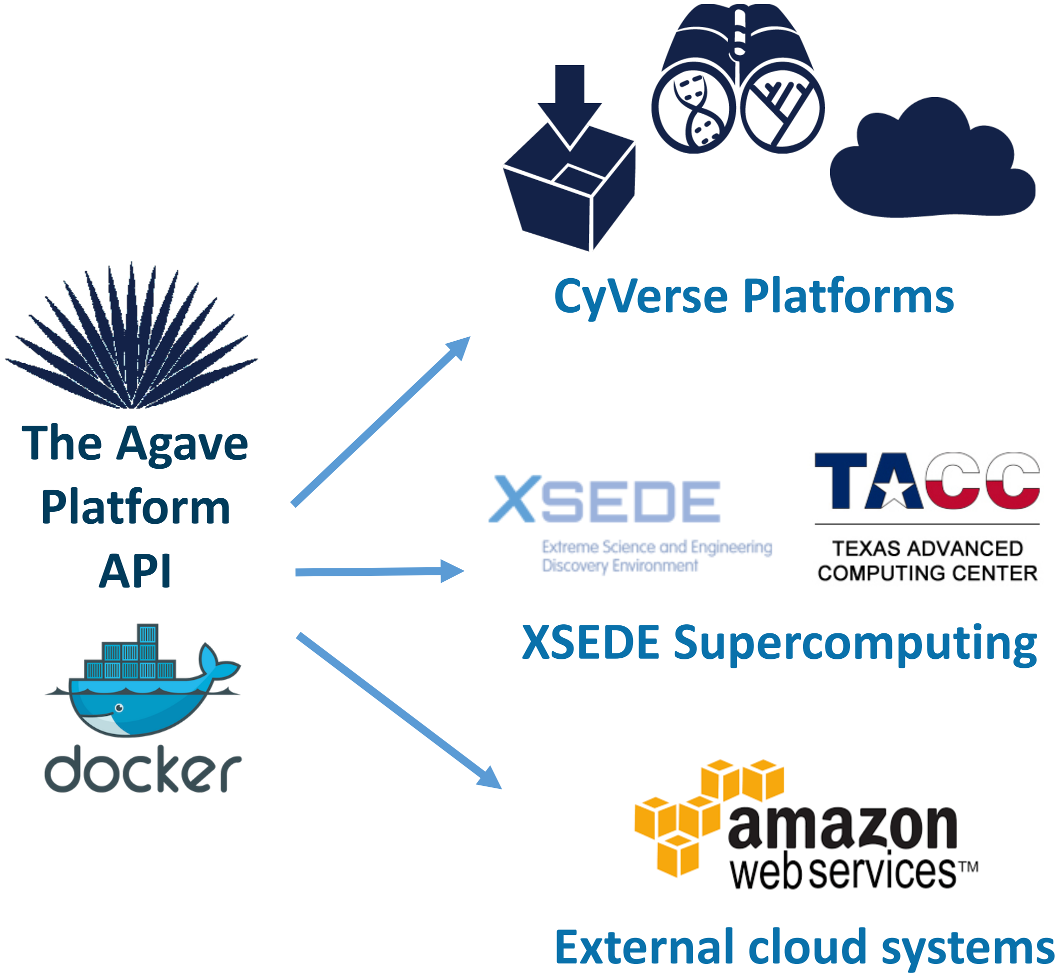
gene_exp.diff

Tabular View: gene_exp.diff | gene_exp.diff

Save | Refresh | ☐ Line Numbers | Skip First N Line(s) 0 | ☐ First Row Header | Editable

0	1	2	3	4	5	6	7
test_id	gene_id	gene	locus	sample_1	sample_2	status	value_1
AT1G01010	AT1G01010	ANAC001	1:3630-5899	WT	hy5	NOTEST	0
AT1G01020	AT1G01020	ARV1	1:5927-8737	WT	hy5	NOTEST	7.27837
AT1G01030	AT1G01030	NGA3	1:11648-13714	WT	hy5	NOTEST	1.18638
AT1G01040	AT1G01040	DCL1	1:23145-33153	WT	hy5	NOTEST	0.239843
AT1G01046	AT1G01046	MIR838A	1:23145-33153	WT	hy5	NOTEST	0
AT1G01050	AT1G01050	AtPPa1	1:23145-33153	WT	hy5	OK	9.06975
AT1G01060	AT1G01060	LHY	1:33378-37871	WT	hy5	NOTEST	4.04534
AT1G01070	AT1G01070	AT1G01070	1:38751-40944	WT	hy5	NOTEST	1.24918
AT1G01073	AT1G01073	AT1G01073	1:44676-44787	WT	hy5	NOTEST	0
AT1G01080	AT1G01080	AT1G01080	1:45295-47019	WT	hy5	OK	13.8323
AT1G01090	AT1G01090	PDH-E1 ALPHA	1:47484-49286	WT	hy5	OK	55.3618
AT1G01100	AT1G01100	AT1G01100	1:50074-51199	WT	hy5	OK	275.52

Page Size (KB) | 1 of 365



docker
TEXAS ADVANCED COMPUTING CENTER
XSEDE
Extreme Science and Engineering Discovery Environment
amazon web services™

The Agave Platform API

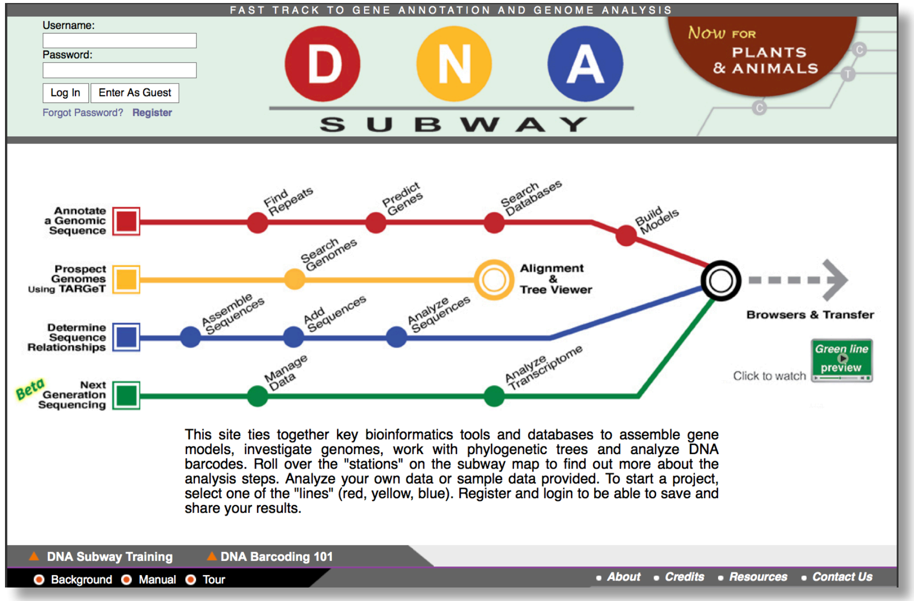
CyVerse Platforms

XSEDE Supercomputing

External cloud systems

DNA Subway

Classroom applications



This site ties together key bioinformatics tools and databases to assemble gene models, investigate genomes, work with phylogenetic trees and analyze DNA barcodes. Roll over the "stations" on the subway map to find out more about the analysis steps. Analyze your own data or sample data provided. To start a project, select one of the "lines" (red, yellow, blue). Register and login to be able to save and share your results.

RNA-Seq for the Next Generation

- Classroom-friendly RNA-Seq workflows
- More than 900Gbs Student-faculty projects analyzed in 36 genomes
- Online educational materials

NYC URBAN BARCODE PROJECT

BARCODE LONG ISLAND

- DNA Barcoding workflow
- ~10,000 student-analyzed barcodes and 125 novel NCBI submissions
- Online educational materials

How can I use CyVerse?

Hands-on training

Workshops that reach users where they are

Tools & Services

- Two days; targeted to researchers
- Hands-on learning modules tailor to interests
- Individual consultations
- 1026 participants since 2011

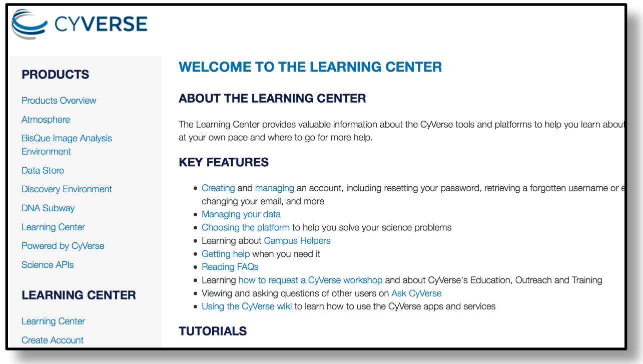
Genomics in Education

- Two days; targeted to educators
- Pair bioinformatics with classroom labs
- Help for generating lesson plans
- 748 participants since 2010

Online learning materials

Documentation, tutorials, and help

Learning Center



CYVERSE

PRODUCTS

Products Overview

Atmosphere

BisQue Image Analysis Environment

Data Store

Discovery Environment

DNA Subway

Learning Center

Powered by CyVerse

Science APIs

LEARNING CENTER

Learning Center

Create Account

WELCOME TO THE LEARNING CENTER

ABOUT THE LEARNING CENTER

The Learning Center provides valuable information about the CyVerse tools and platforms to help you learn about at your own pace and where to go for more help.

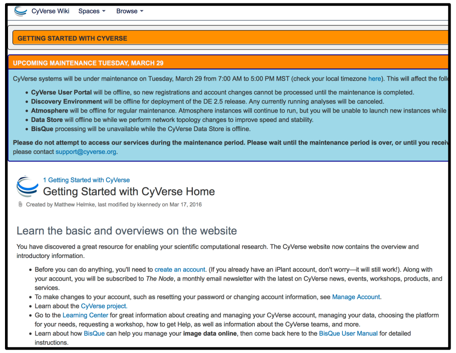
KEY FEATURES

- Creating and managing an account, including resetting your password, retrieving a forgotten username or e changing your email, and more
- Managing your data
- Choosing the platform to help you solve your science problems
- Learning about Campus Helpers
- Getting help when you need it
- Reading FAQs
- Learning how to request a CyVerse workshop and about CyVerse's Education, Outreach and Training
- Viewing and asking questions of other users on Ask CyVerse
- Using the CyVerse wiki to learn how to use the CyVerse apps and services

TUTORIALS

- cyverse.org/learning-center
- Tutorials and quick-starts

Wiki



GETTING STARTED WITH CYVERSE

UPCOMING MAINTENANCE TUESDAY, MARCH 29

CyVerse systems will be under maintenance on Tuesday, March 29 from 7:00 AM to 5:00 PM MST (check your local timezone here). This will affect the foll

- **CyVerse User Portal** will be offline, so new registrations and account changes cannot be processed until the maintenance is completed.
- **Discovery Environment** will be offline for deployment of the DE 2.5 release. Any currently running analyses will be canceled.
- **Atmosphere** will be offline for regular maintenance. Atmosphere instances will continue to run, but you will be unable to launch new instances while
- **Data Store** will offline be while we perform network topology changes to improve speed and stability.
- **BisQue** processing will be unavailable while the CyVerse Data Store is offline.

Please do not attempt to access our services during the maintenance period. Please wait until the maintenance period is over, or until you recei please contact support@cyverse.org.

1 Getting Started with CyVerse

Getting Started with CyVerse Home

Created by Matthew Helmke, last modified by kkennedy on Mar 17, 2016

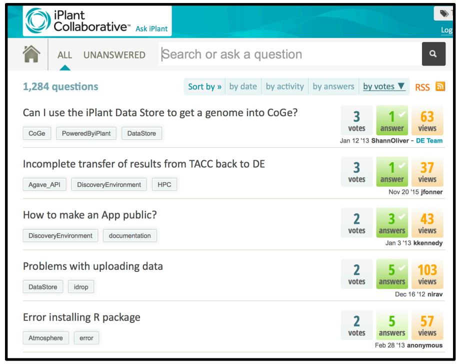
Learn the basic and overviews on the website

You have discovered a great resource for enabling your scientific computational research. The CyVerse website now contains the overview and introductory information.

- Before you can do anything, you'll need to create an account. (If you already have an iPlant account, don't worry—it will still work!). Along with your account, you will be subscribed to *The Node*, a monthly email newsletter with the latest on CyVerse news, events, workshops, products, and services.
- To make changes to your account, such as resetting your password or changing account information, see Manage Account.
- Learn about the CyVerse project.
- Go to the Learning Center for great information about creating and managing your CyVerse account, managing your data, choosing the platform for your needs, requesting a workshop, how to get Help, as well as information about the CyVerse teams, and more.
- Learn about how BisQue can help you manage your **image data online**, then come back here to the BisQue User Manual for detailed instructions.

- wiki.cyverse.org
- Documentation

Forum



1,284 questions

Can I use the iPlant Data Store to get a genome into CoGe?
CoGe · PoweredByiPlant · DataStore
3 votes · 1 answer · 63 views
Jan 12 '13 ShannOliver - DE Team

Incomplete transfer of results from TACC back to DE
Agave_API · DiscoveryEnvironment · HPC
3 votes · 1 answer · 37 views
Nov 20 '15 jfonner

How to make an App public?
DiscoveryEnvironment · documentation
2 votes · 3 answers · 43 views
Jan 3 '13 kkennedy

Problems with uploading data
DataStore · idrop
2 votes · 5 answers · 103 views
Dec 16 '12 nirav

Error installing R package
Atmosphere · error
2 votes · 5 answers · 57 views
Feb 28 '13 anonymous

- ask.iplantcollaborative.org
- Community help/Q&A

CYVERSE™

Transforming Science Through Data-driven Discovery

CyVerse Executive Team

THE UNIVERSITY OF ARIZONA®

Parker Antin
Nirav Merchant
Eric Lyons

TACC

TEXAS ADVANCED COMPUTING CENTER

Matt Vaughn

CSH

Cold Spring Harbor Laboratory

Doreen Ware
Dave Micklos

CyVerse is supported by the National Science Foundation under Grant No. DBI-0735191 and DBI-1265383.

Getting Data into CyVerse

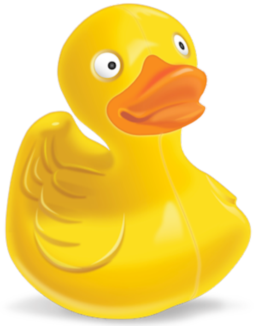
CyVerse Data Store

- Store any type of file related to your research
- Move files seamlessly between CyVerse platforms
- Automate file transfers
- Share files with lab members, collaborators, and communities

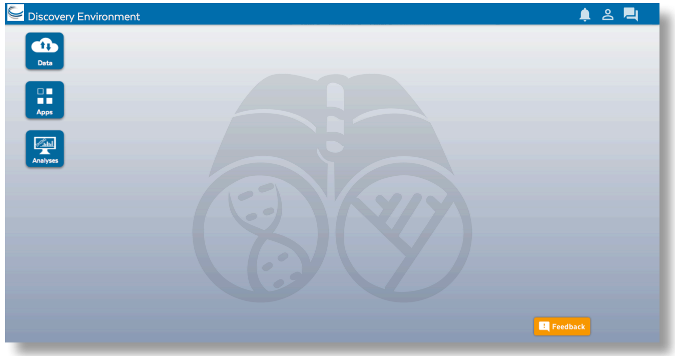
CyVerse Data Store

Multiple ways to access

Point-and-click

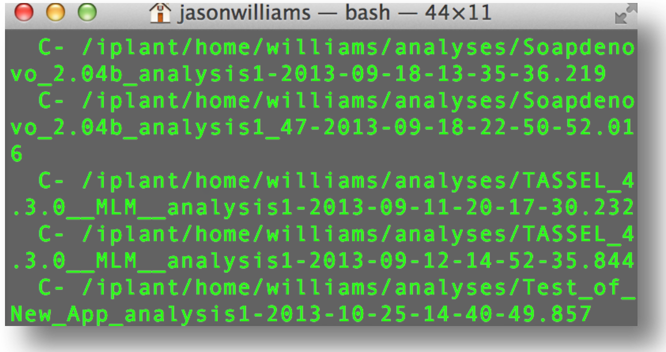


Cyberduck



Discovery Environment

Command line

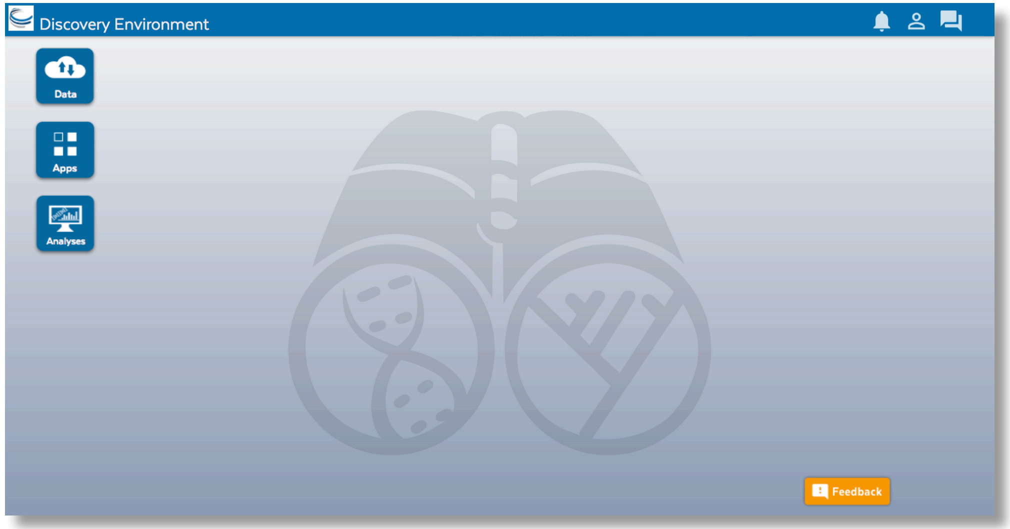


```
  C- /iplant/home/williams/analyses/Soapdeno
vo_2.04b_analysis1-2013-09-18-13-35-36.219
  C- /iplant/home/williams/analyses/Soapdeno
vo_2.04b_analysis1_47-2013-09-18-22-50-52.01
6
  C- /iplant/home/williams/analyses/TASSEL_4
.3.0__MLM__analysis1-2013-09-11-20-17-30.232
  C- /iplant/home/williams/analyses/TASSEL_4
.3.0__MLM__analysis1-2013-09-12-14-52-35.844
  C- /iplant/home/williams/analyses/Test_of_
New_App_analysis1-2013-10-25-14-40-49.857
```

iCommands

Discovery Environment

- Simple upload/download for small files
- Bulk upload files and folders (<10GB)
- Import from URL (no size limit)



Advantage +

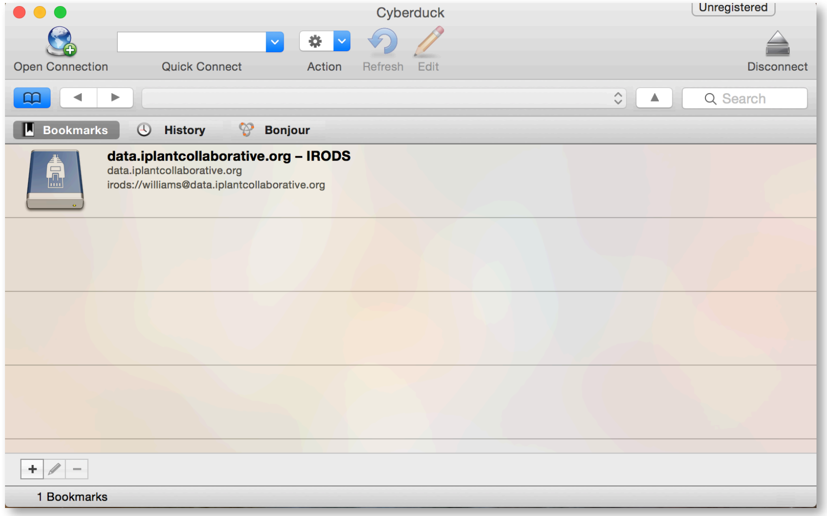
Covers most upload/download sharing needs

Disadvantage -

Some size/speed limitations

Cyberduck

- Drag and drop files and folders
- No size limit, file editing/previews
- Easy Desktop functionality



data.iplantcollaborative.org – IRODS
data.iplantcollaborative.org
irods://williams@data.iplantcollaborative.org

1 Bookmarks

Advantage +

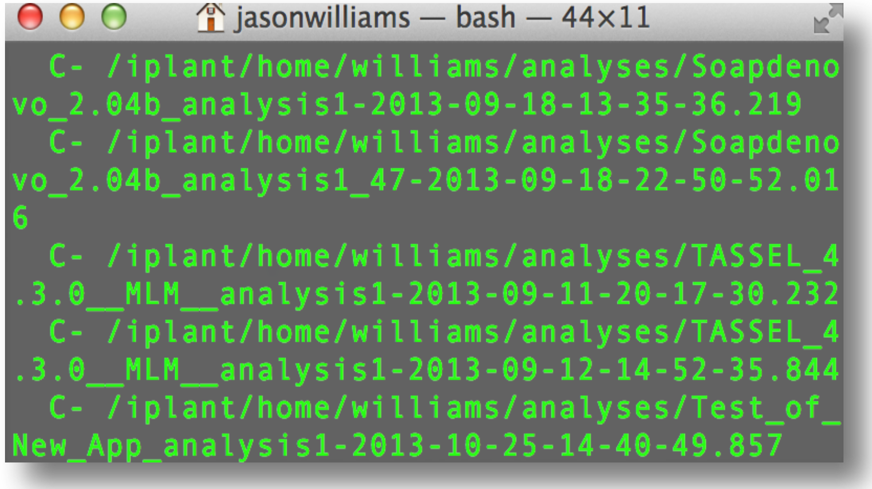
More like desktop file systems

Disadvantage -

No permissions/metadata control

iCommands

- Full flexibility
- Ability to script and automate
- Access from terminal/server



```
  C- /iplant/home/williams/analyses/Soapdeno
vo_2.04b_analysis1-2013-09-18-13-35-36.219
  C- /iplant/home/williams/analyses/Soapdeno
vo_2.04b_analysis1_47-2013-09-18-22-50-52.01
6
  C- /iplant/home/williams/analyses/TASSEL_4
.3.0__MLM__analysis1-2013-09-11-20-17-30.232
  C- /iplant/home/williams/analyses/TASSEL_4
.3.0__MLM__analysis1-2013-09-12-14-52-35.844
  C- /iplant/home/williams/analyses/Test_of_
New_App_analysis1-2013-10-25-14-40-49.857
```

Advantage +

Customizability

Disadvantage -

Requires some command line expertise

Cyberduck and iCommands Demo

Discovery Environment

Discovery Environment

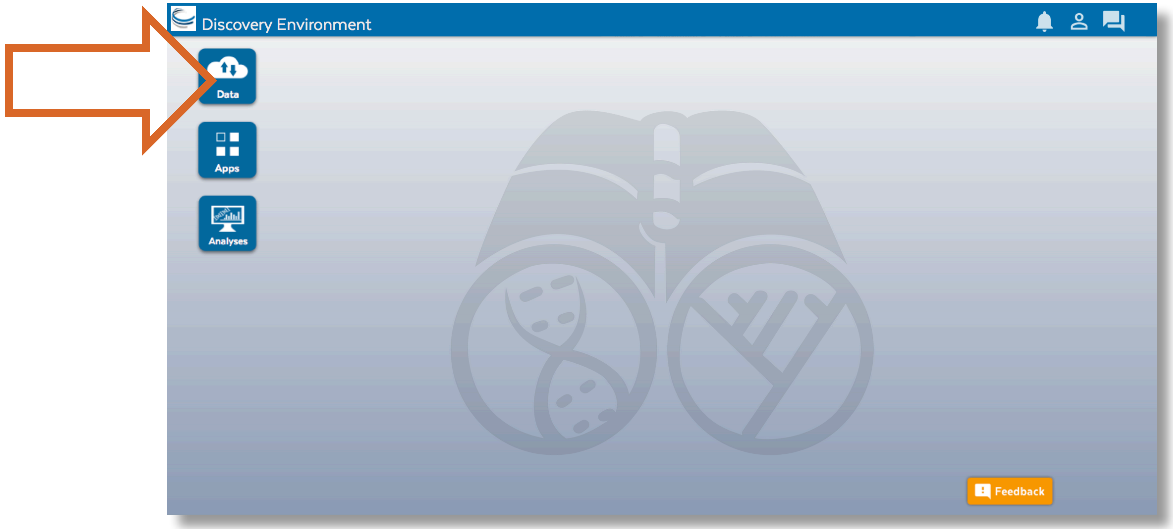
- ✓ A platform that can run almost any bioinformatics application
- ✓ Seamlessly integrated with data and high performance computing
- ✓ User extensible – add your own applications

Discovery Environment Overview

Manage data

Data

- Upload / Download files and folders
- Share files via URL (Public Links)
- Share files/folders with other users

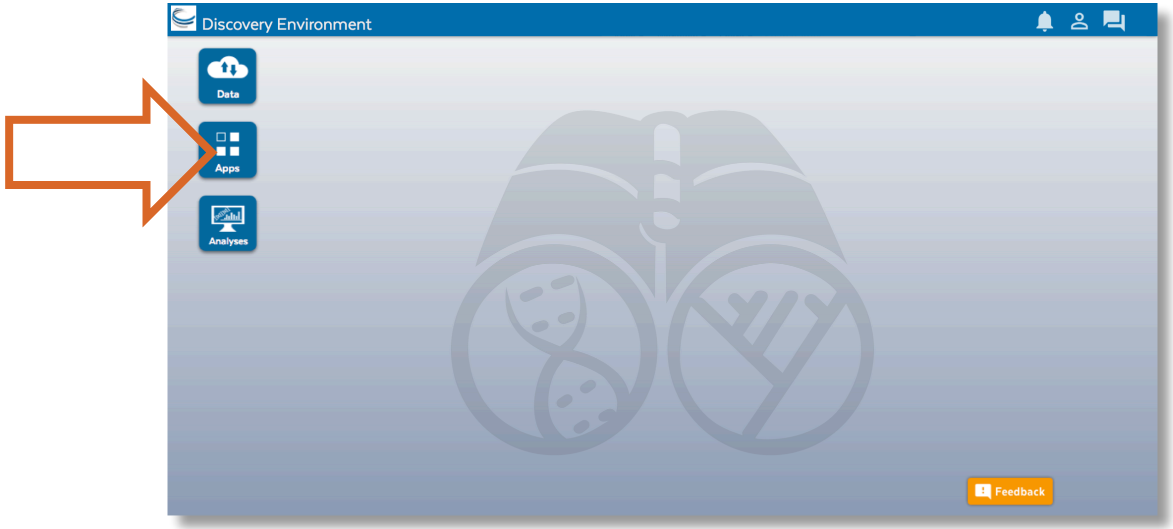


Discovery Environment Overview

Analyze data and customize Applications

Apps

- Run hundreds of bioinformatics Apps
- Build automated workflows
- Modify Apps or integrate new ones

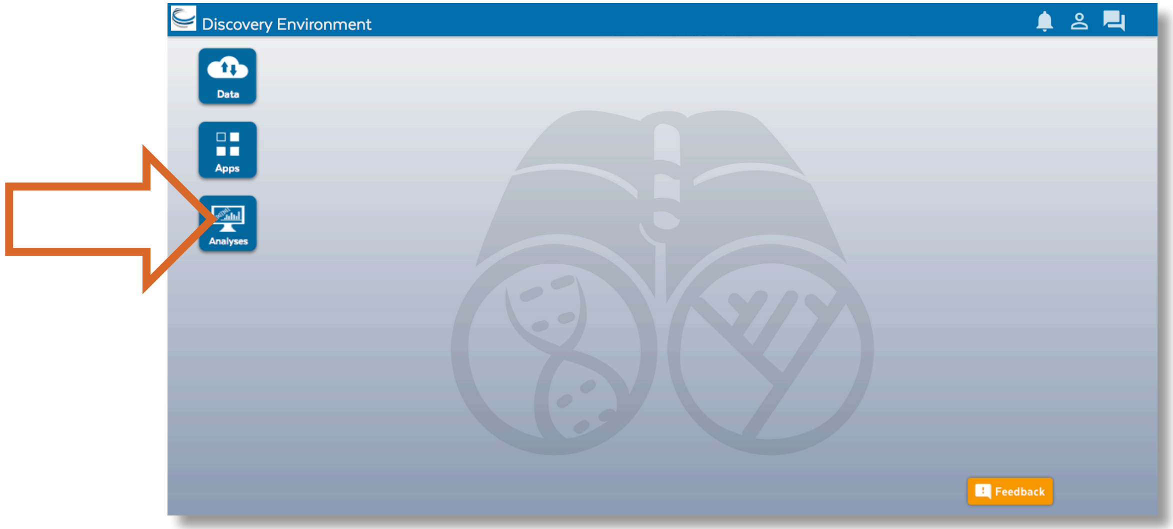


Discovery Environment Overview

View history, find results, reproduce analyses, optimize parameters

Analyses

- Monitor job status and find results
- Cancel jobs or re-launch jobs
- Detailed job history



Discovery Environment Demo

Discovery Environment

Demo analysis – sequence alignment using MUSCLE

Task: Take unaligned DNA sequences in FASTA format and create a multiple alignment

- ✓ View sample data in iPlant Data Store
- ✓ Launch a job using the MUSCLE sequence alignment app
- ✓ Monitor the job progress and view results

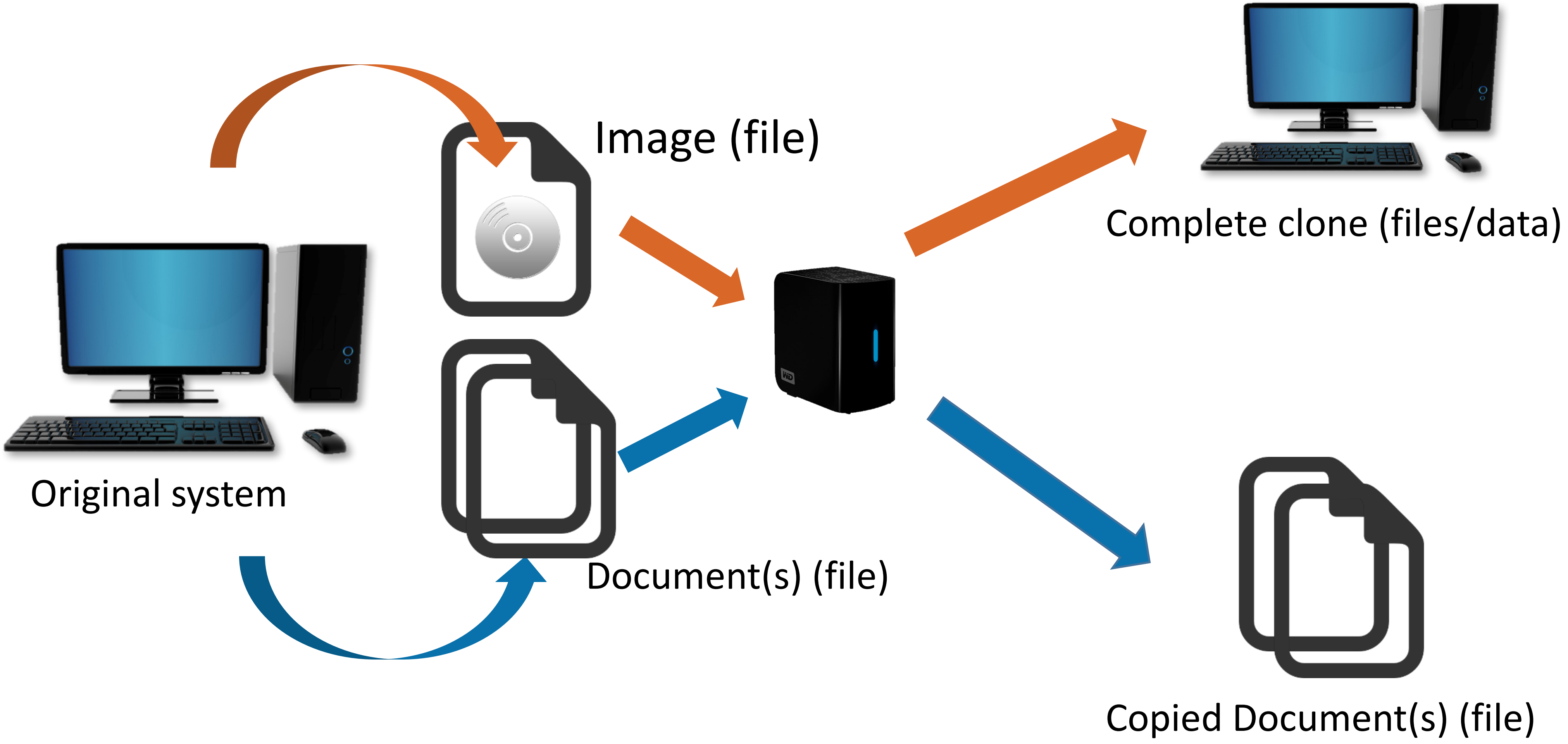
Atmosphere

Atmosphere

- ✓ Simple: 1-click access to hundreds of virtual machine images
- ✓ Flexible: Fully customize your software setup
- ✓ Powerful: Integrated with CyVerse computing and data resources

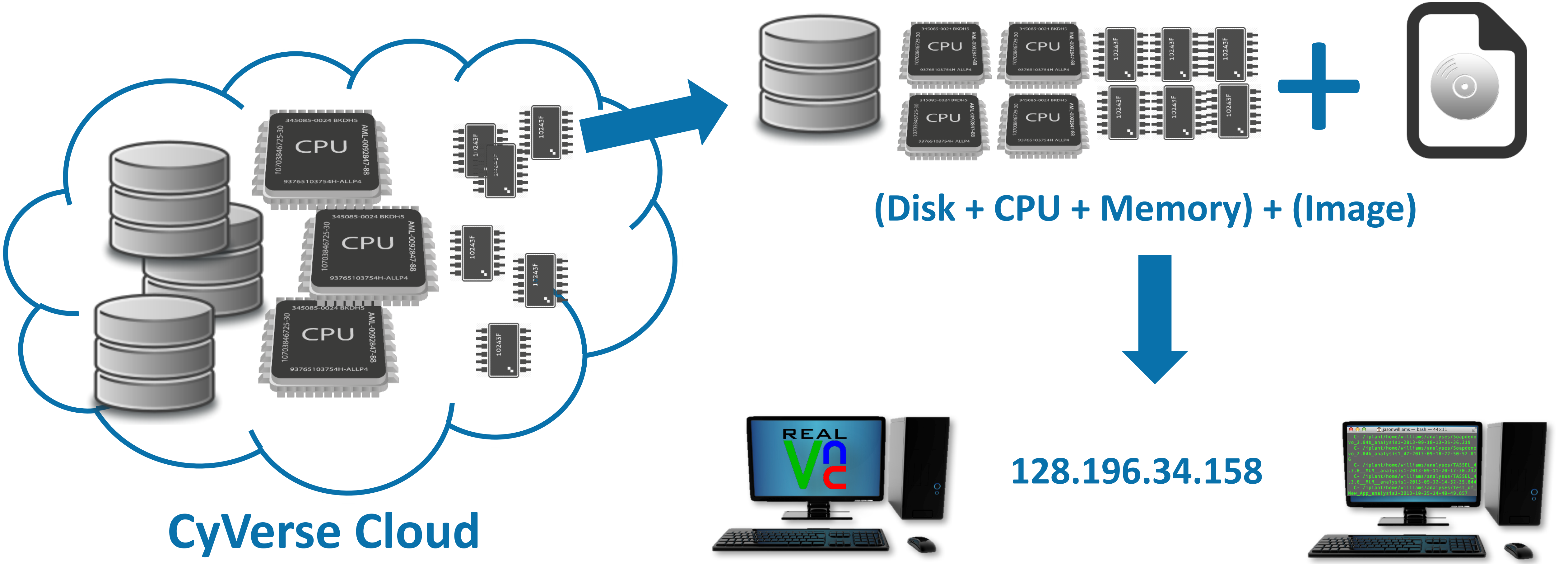
What is Cloud Computing?

Important concepts: Image



What is Cloud Computing?

Important concepts: Instance



CyVerse Cloud

(Disk + CPU + Memory) + (Image)

128.196.34.158

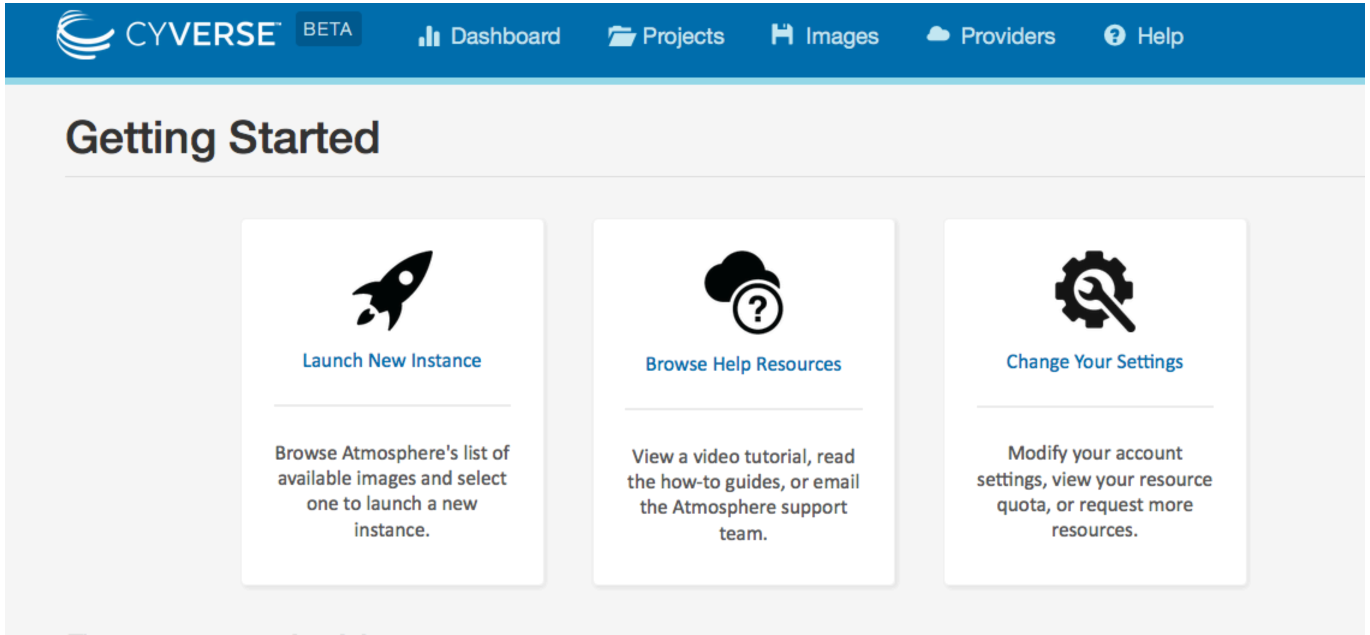
```
jasonwilliams — bash — 44×11
  C- /iplant/home/williams/analyses/Soapdeno
vo_2.04b_analysis1-2013-09-18-13-35-36.219
  C- /iplant/home/williams/analyses/Soapdeno
vo_2.04b_analysis1_47-2013-09-18-22-50-52.01
6
  C- /iplant/home/williams/analyses/TASSEL_4
.3.0__MLM__analysis1-2013-09-11-20-17-30.232
  C- /iplant/home/williams/analyses/TASSEL_4
.3.0__MLM__analysis1-2013-09-12-14-52-35.844
  C- /iplant/home/williams/analyses/Test_of_
New_App_analysis1-2013-10-25-14-40-49.857
```

Atmosphere Instance

(virtual machine)

Atmosphere Overview

Largest, easiest to use cloud for Life Sciences



Getting Started

Launch New Instance

Browse Atmosphere's list of available images and select one to launch a new instance.

Browse Help Resources

View a video tutorial, read the how-to guides, or email the Atmosphere support team.

Change Your Settings

Modify your account settings, view your resource quota, or request more resources.

- Choose an existing image or customize
- Instances up to 16-Core / 128 GB RAM
- Access via shell or VNC
- Share you image with selected users, or make them public

Atmosphere

Cloud computing for life sciences: sample use cases

- Run the software and data that are monopolizing your laptop/desktop
- Use desktop enabled images to run visually oriented programs (GUI)
- SUDO access – manage complex dependencies
- Uniform computing setups for your lab, collaborators, and students
- Make your own software available to a larger user community

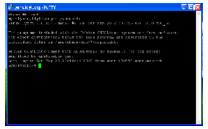
Atmosphere Demo

Atmosphere

Cloud computing for life sciences

Windows

VNC Viewer

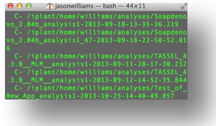


PuTTY

Mac

128.196.65.175

VNC Viewer

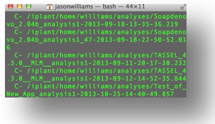


```
  C- /iplant/home/williams/analyses/Soapdeno
vo_2.04b_analysis1-2013-09-18-13-35-36.219
  C- /iplant/home/williams/analyses/Soapdeno
vo_2.04b_analysis1_47-2013-09-18-22-50-52.01
6
  C- /iplant/home/williams/analyses/TASSEL_4
.3.0__MLM__analysis1-2013-09-11-20-17-30.232
  C- /iplant/home/williams/analyses/TASSEL_4
.3.0__MLM__analysis1-2013-09-12-14-52-35.844
  C- /iplant/home/williams/analyses/Test_of_
New_App_analysis1-2013-10-25-14-40-49.857
```

Shell/terminal

Linux

VNC Viewer

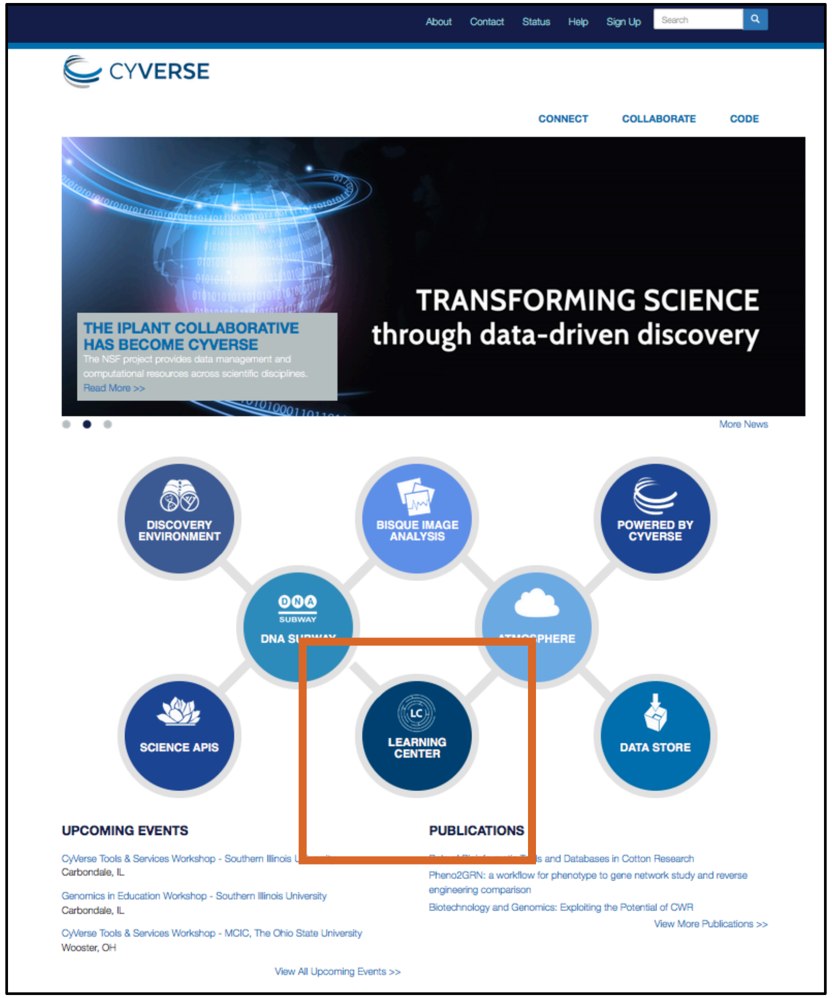


```
  C- /iplant/home/williams/analyses/Soapdeno
vo_2.04b_analysis1-2013-09-18-13-35-36.219
  C- /iplant/home/williams/analyses/Soapdeno
vo_2.04b_analysis1_47-2013-09-18-22-50-52.01
6
  C- /iplant/home/williams/analyses/TASSEL_4
.3.0__MLM__analysis1-2013-09-11-20-17-30.232
  C- /iplant/home/williams/analyses/TASSEL_4
.3.0__MLM__analysis1-2013-09-12-14-52-35.844
  C- /iplant/home/williams/analyses/Test_of_
New_App_analysis1-2013-10-25-14-40-49.857
```

Shell/terminal

VNC Viewer:	www.realvnc.com/download/viewer
PuTTy:	www.putty.org

Where to go from here:



TRANSFORMING SCIENCE
through data-driven discovery

THE IPLANT COLLABORATIVE HAS BECOME CYVERSE

The NSF project provides data management and computational resources across scientific disciplines.

Read More >>

More News

UPCOMING EVENTS

CyVerse Tools & Services Workshop - Southern Illinois University
Carbondale, IL

Genomics in Education Workshop - Southern Illinois University
Carbondale, IL

CyVerse Tools & Services Workshop - MCIC, The Ohio State University
Wooster, OH

View All Upcoming Events >>

PUBLICATIONS

Role of Bioinformatic Tools and Databases in Cotton Research

Pheno2GRN: a workflow for phenotype to gene network study and reverse engineering comparison

Biotechnology and Genomics: Exploiting the Potential of CWR

View More Publications >>

Learning Center

- Get Started Guide
- Tutorials and Videos
- Documentation

Upcoming Events

- Workshops
- Webinars

Slides and Tutorials

www.cyverse.org/sol2016

NSF

THE UNIVERSITY OF ARIZONA

TACC
TEXAS ADVANCED COMPUTING CENTER

CSH
Cold Spring Harbor Laboratory

UNCW