CYVERSE™

Transforming Science Through Data-driven Discovery

CyVerse Overview and Tutorial

CSHL 2016 Cereal Genomics Course

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CyVerse Evolution

CyVerse 2016
Transforming Science Through Data-Driven Discovery

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

Apologies...

"I had the feeling I have been exposed to many bioinformatics tools but I would be unable to use any of them on my own."

There is help (lots)

CyVerse Workshops can come to you

- Two days covering several modular customized lessons
- Hands-on learning
- Individual consultations

Community-driven learning

software carpentry

Goal: provide basic lab skills for research computing; “get more done in less time and with less pain.”

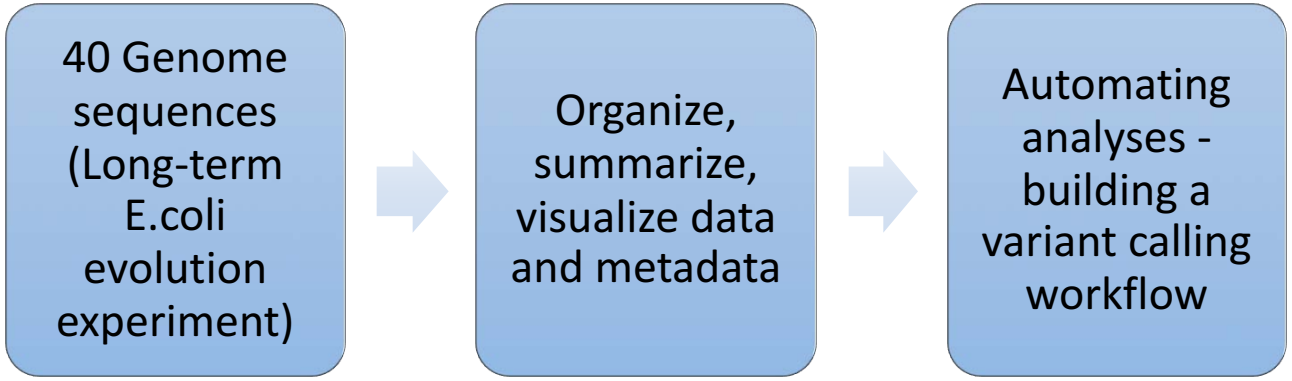
DATA CARPENTRY

MAKING DATA SCIENCE MORE EFFICIENT

Goal: provide researchers training on the fundamentals and best practices in data analysis and management.

- **Scientists teaching scientists**
- **All-volunteer Instructors (>500 world-wide)**
- **Community-maintained lessons**
- **No assumptions of knowledge for learners**

Genomics Lesson Narrative



Cover the 'unspoken' protocols make for effective, reproducible research

Hands-on lessons run from the cloud

Some learning goals

Interacting with Computers

- Could Computing
- Connecting to remote computing (SSH/PuTTY)
- File Transfer (FileZilla, other command-line tools: scp, rsynch, wget, etc.)

Automation and scripting

- R scripting
- 'For' loops
- Building automated pipelines
- Using multithreaded applications

Data Management and Organization

- Open source
- Metadata and reproducibility
- Important genomics file formats (CSV/TSV, FastQ, SAM/BAM, VCF, etc.)
- Organizing a filesystem for computational projects (Linux)
- Unix Shell (command-line: ls, cd, mkdir, cp, rm, wc, grep, cut, columns, head, tail, less etc,)
- R: Creating projects, scripts, and examining data

Data Cleaning and visualization

- R: various packages and functions
- R: dplyr
- R: ggplot
- FastQC - quality control of high-throughput sequence data
- Trimmomatic - filtering and trimming of high-throughput sequence data
- Integrated Genome Viewer

CyVerse Evolution

iPlant 2008
Empowering a New Plant Biology

iPlant 2013
Cyberinfrastructure for Life Science

CyVerse 2016
Transforming Science Through Data-Driven Discovery

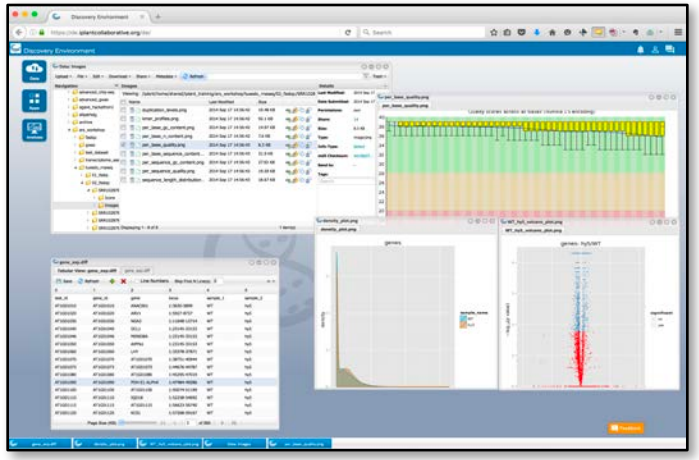
CyVerse Evolution

DBI-0735191 and DBI-1265383

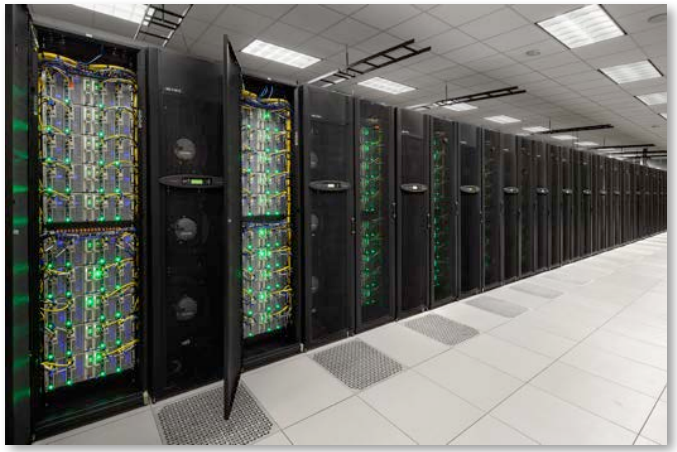
We are funded by the National Science Foundation

- 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?



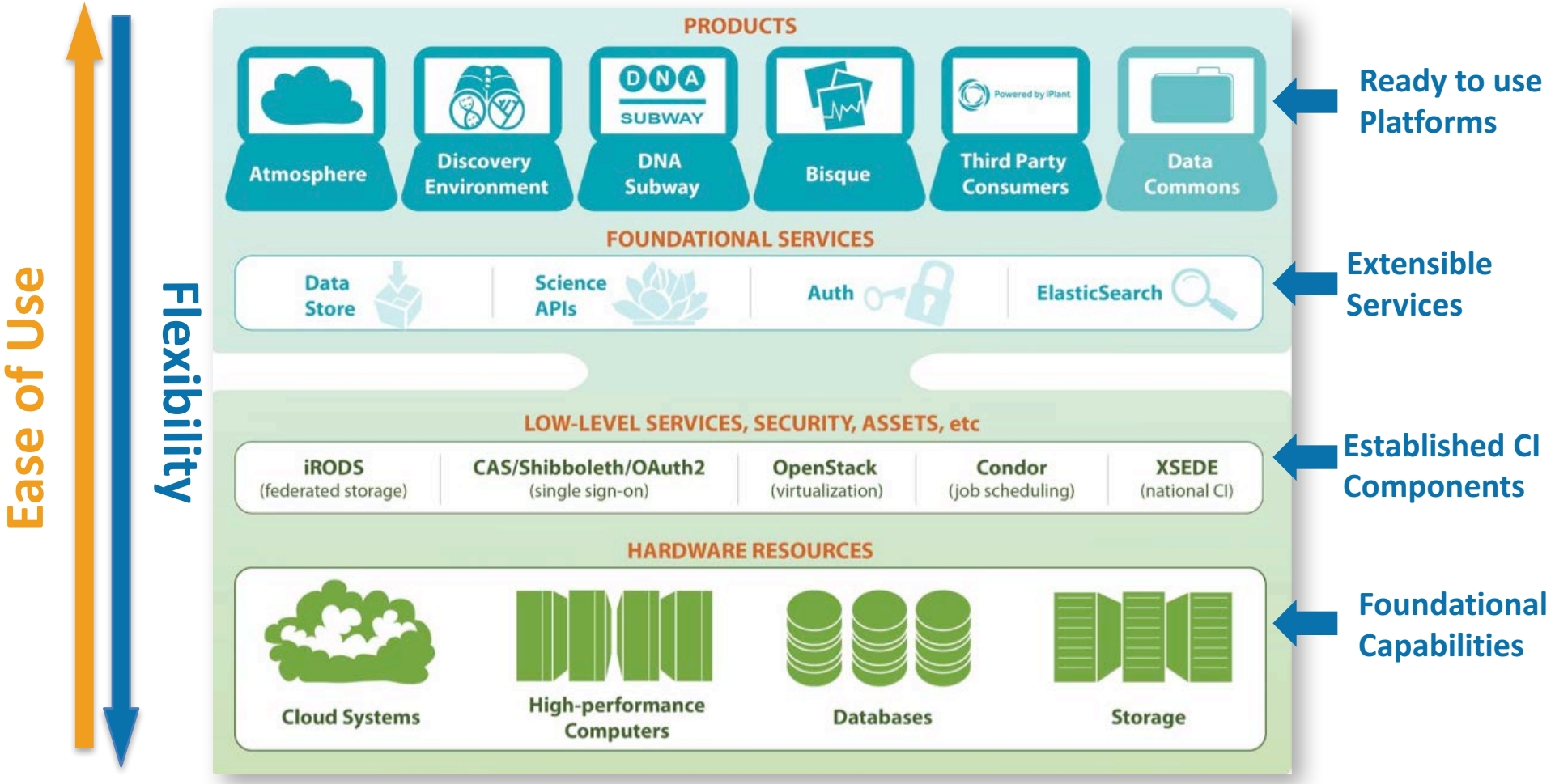
Platforms, tools, datasets



Storage and compute

Training and support

CyVerse product stack



CyVerse Institutions

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CyVerse is a collaborative virtual organization

CyVerse UK

WARWICK
THE UNIVERSITY OF WARWICK

UNIVERSITY OF LIVERPOOL

BBSRC

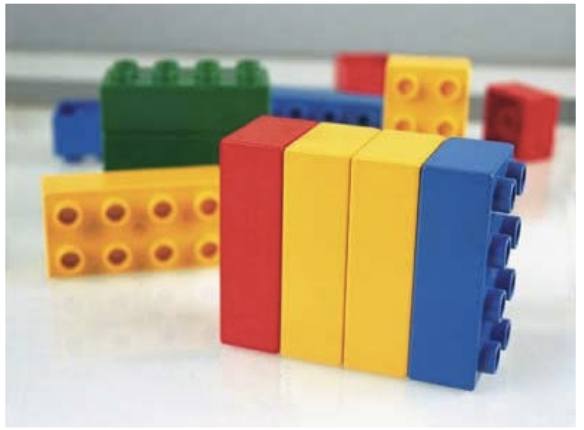
The University of Nottingham
UNITED KINGDOM · CHINA · MALAYSIA

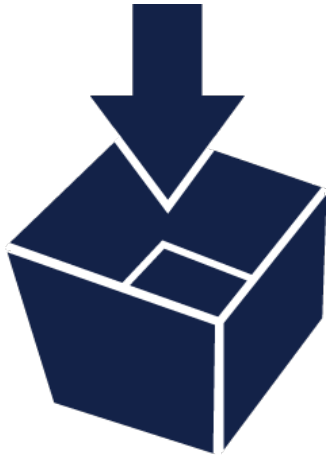
Earlham Institute

NSF

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





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: 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

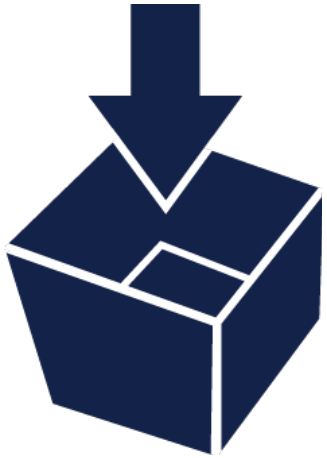
- ✓ Commonly used bioinformatics tools in streamlined workflows
- ✓ Teach important concepts in biology and bioinformatics
- ✓ Inquiry-based experiments for novel discovery and publication of data

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

Getting Data into CyVerse



CyVerse Data Store

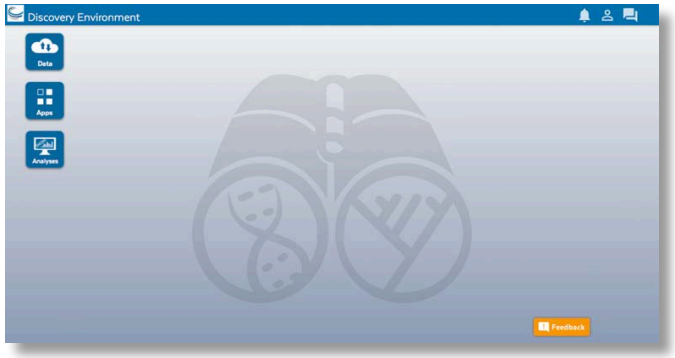
- Store any type of file related to your research
- Move files seamlessly between CyVerse platforms
- Automate file transfers
- Share files with lab members, collaborators, and communities

CyVerse Data Store

Multiple ways to access

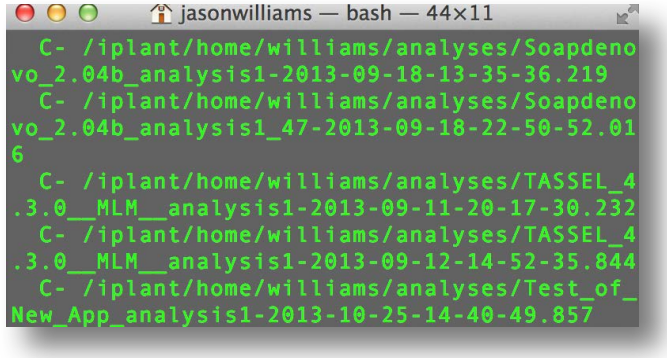
Point-and-click

Cyberduck



Discovery Environment

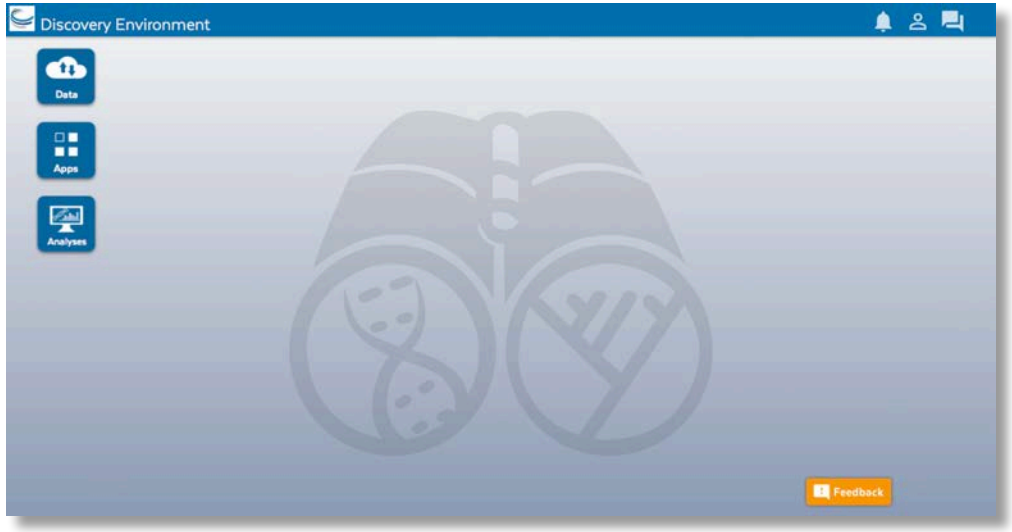
Command line



iCommands

Discovery Environment

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



Advantage +

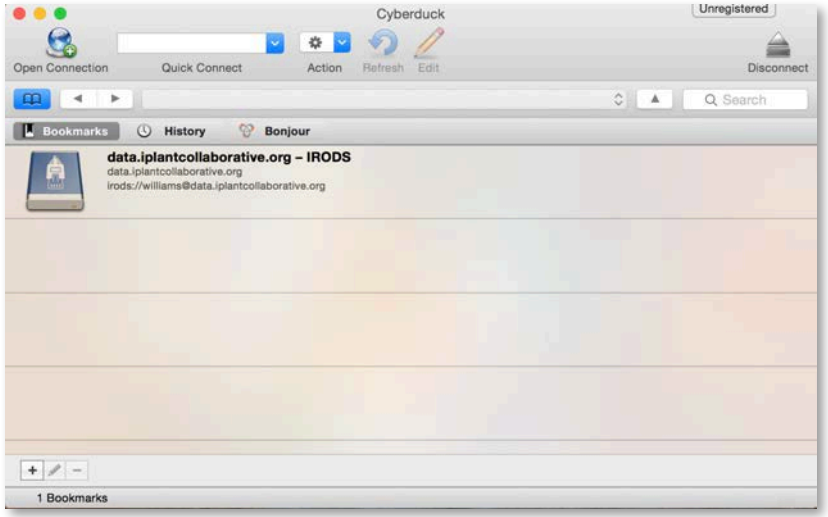
Covers most upload/download sharing needs

Disadvantage -

Some size/speed limitations

Cyberduck

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



Advantage +

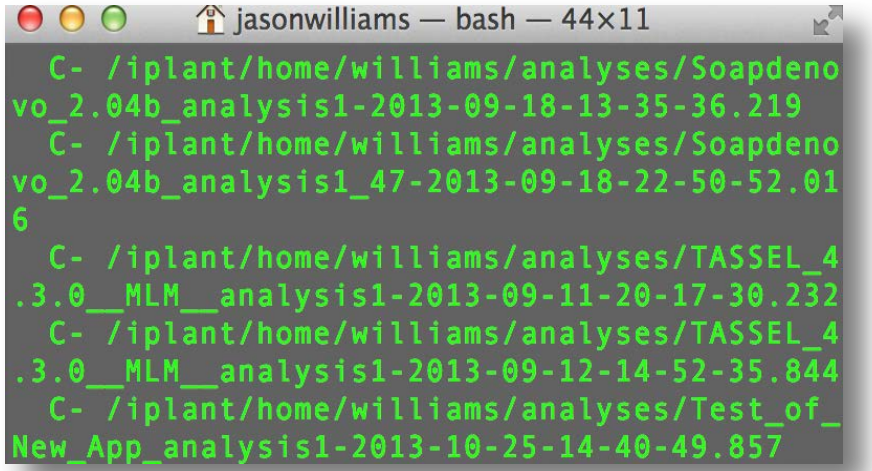
More like desktop file systems

Disadvantage -

No permissions/metadata control

iCommands

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



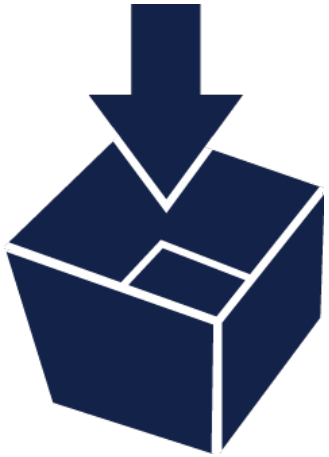
Advantage +

Customizability

Disadvantage -

Requires some command line expertise

Cyberduck and iCommands Demo



Discovery Environment

Discovery Environment

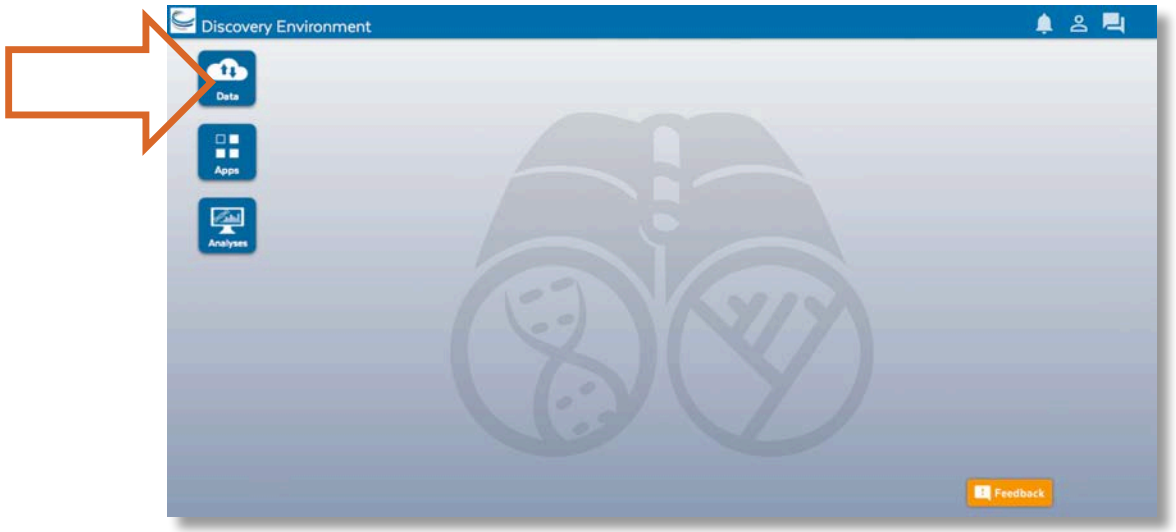
- ✓ A platform that can run almost any bioinformatics application
- ✓ Seamlessly integrated with data and high performance computing
- ✓ User extensible – add your own applications

Discovery Environment Overview

Manage data

Data

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

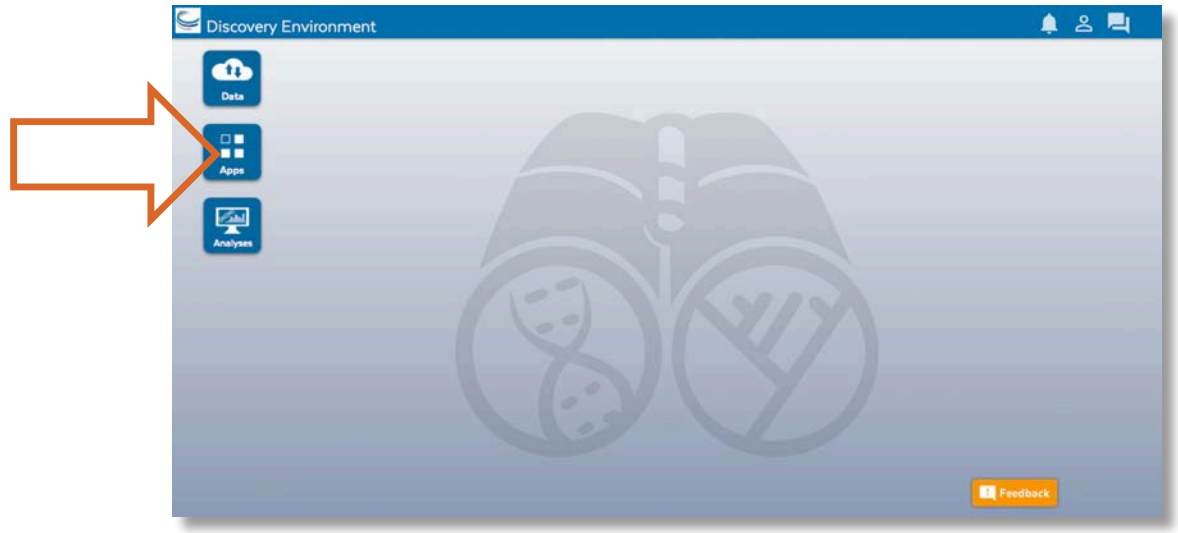


Discovery Environment Overview

Analyze data and customize Applications

Apps

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

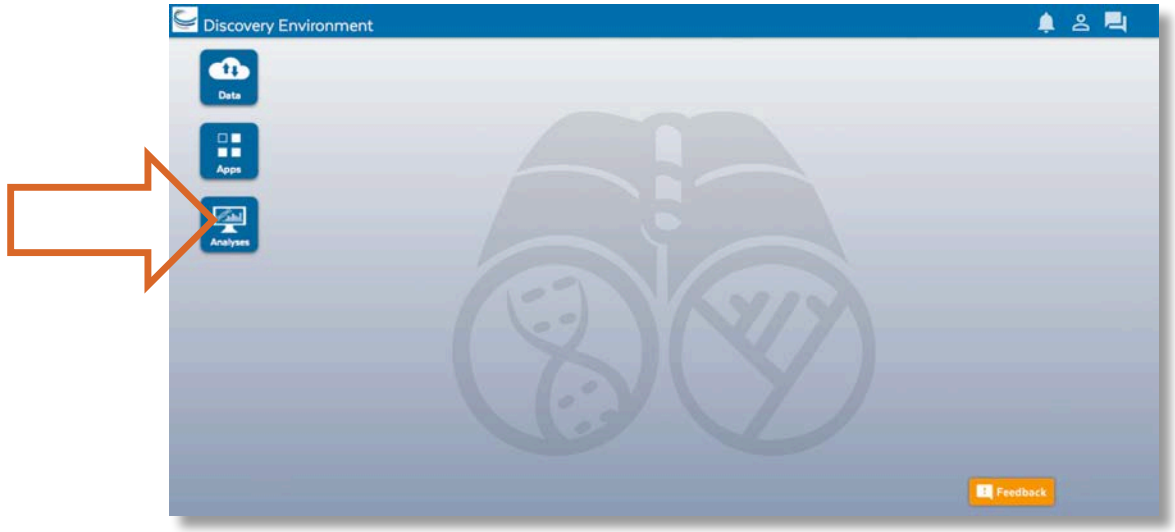


Discovery Environment Overview

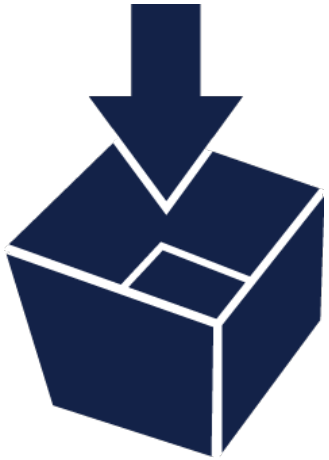
View history, find results, reproduce analyses, optimize parameters

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 Data Store
- ✓ Launch a job using the MUSCLE sequence alignment app
- ✓ Monitor the job progress and view results

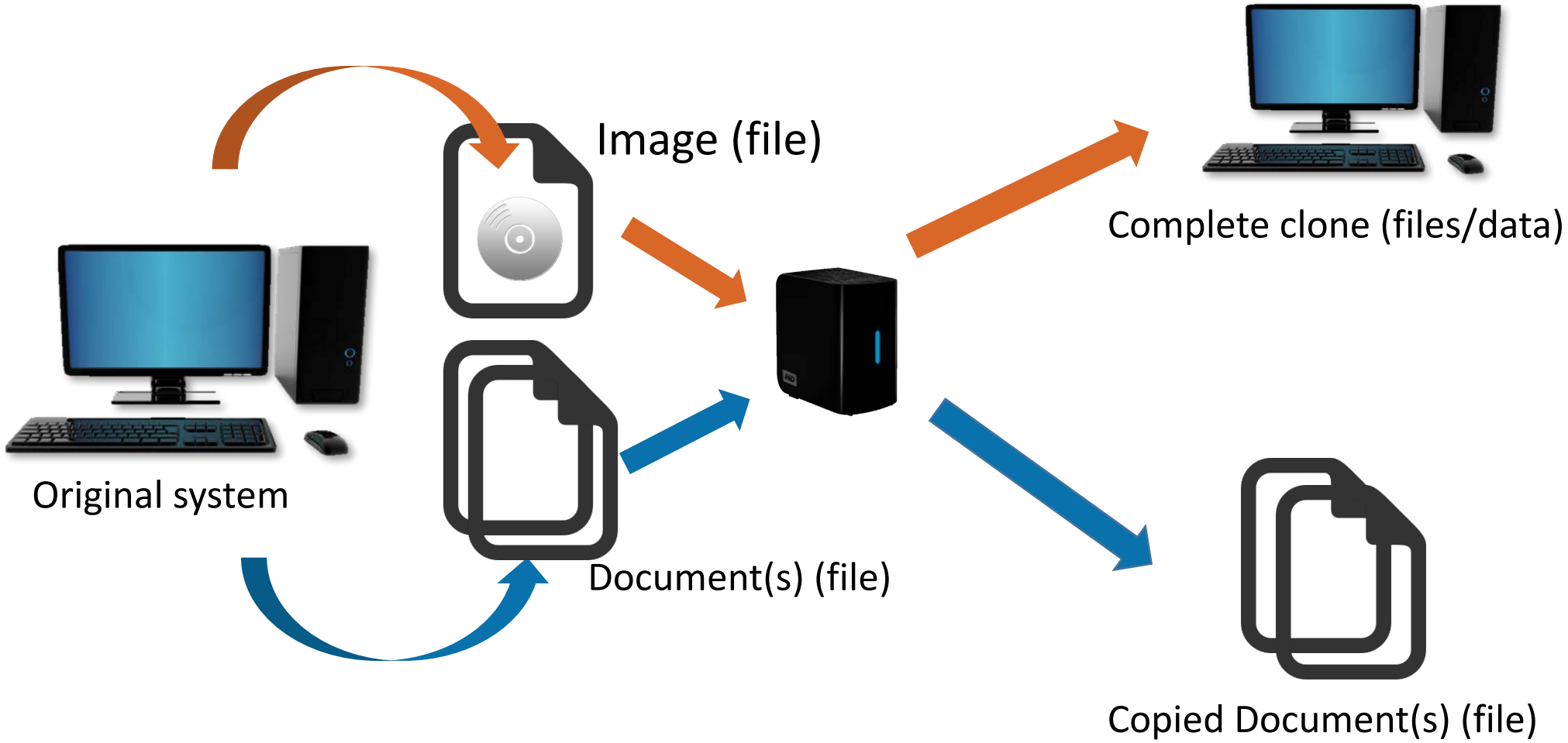
Atmosphere

Atmosphere

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

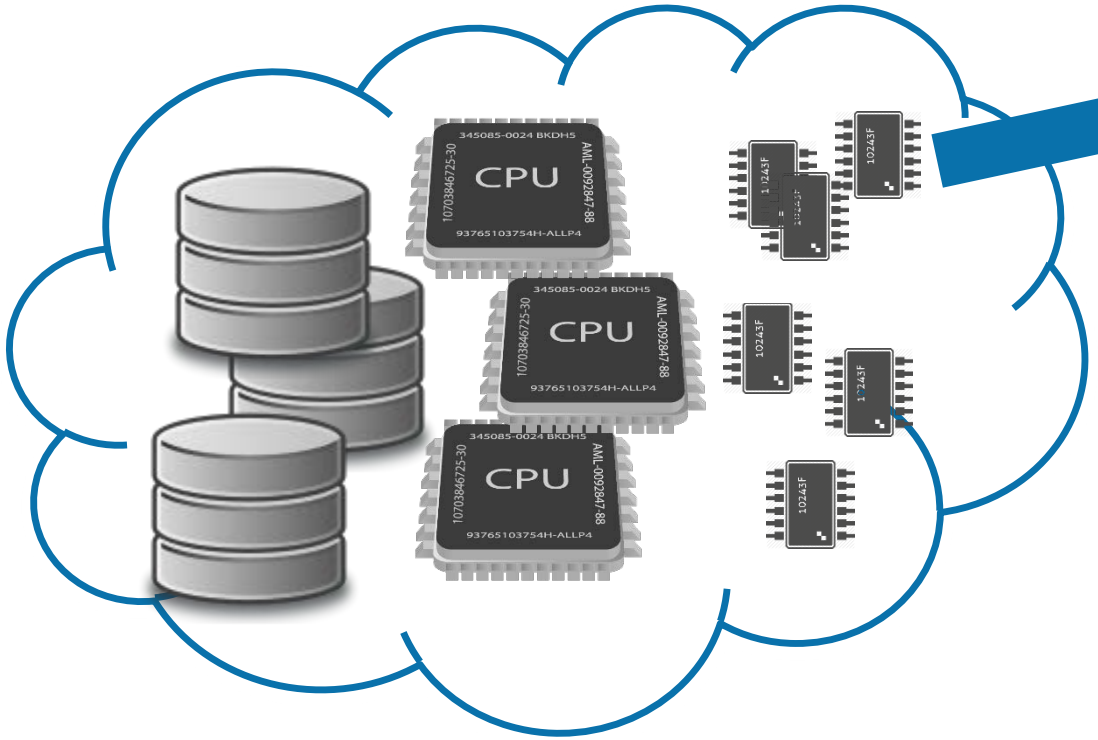
What is Cloud Computing?

Important concepts: Image

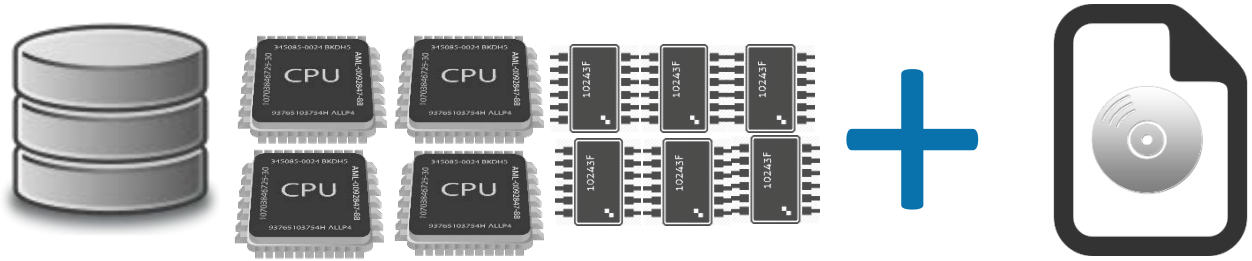


What is Cloud Computing?

Important concepts: Instance

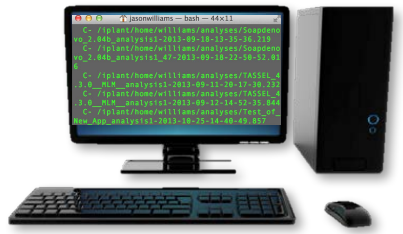


CyVerse Cloud



(Disk + CPU + Memory) + (Image)

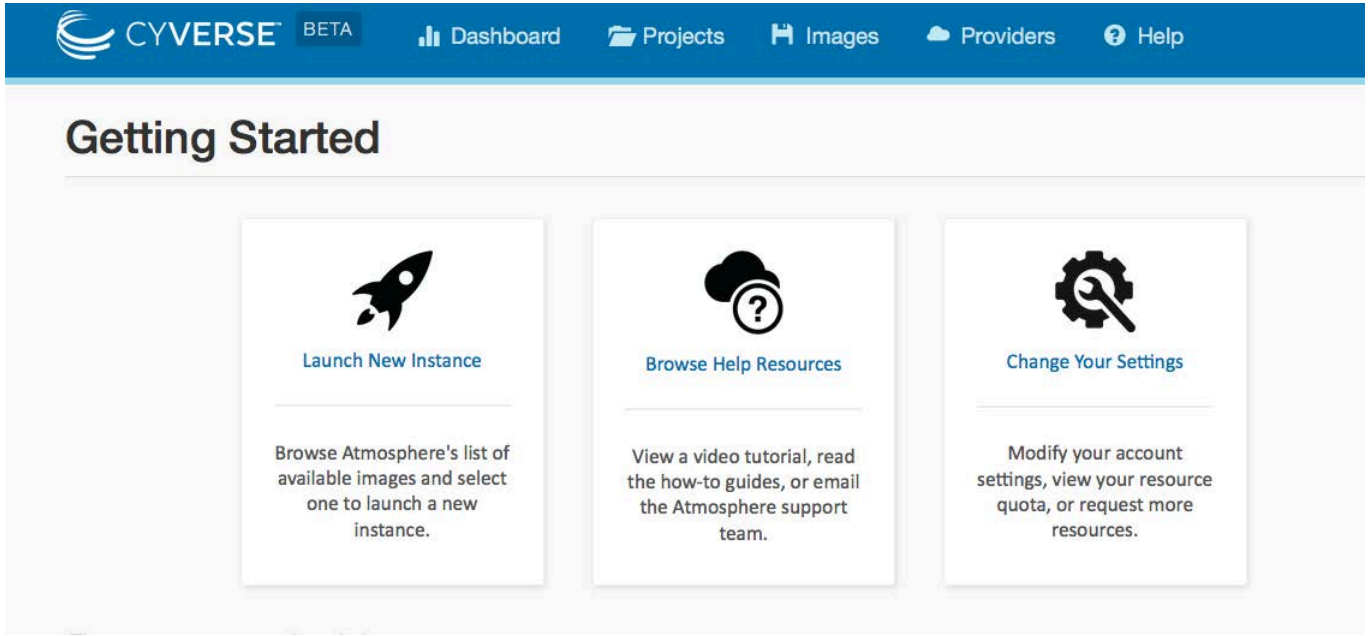
128.196.34.158



Atmosphere Instance
(virtual machine)

Atmosphere Overview

Largest, easiest to use cloud for Life Sciences



- 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

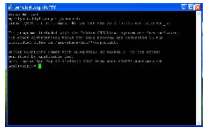
Atmosphere Demo

Atmosphere

Cloud computing for life sciences

Windows

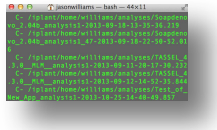
VNC Viewer



PuTTY

Mac

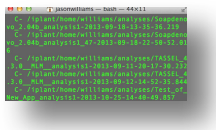
VNC Viewer



Shell/terminal

Linux

VNC Viewer

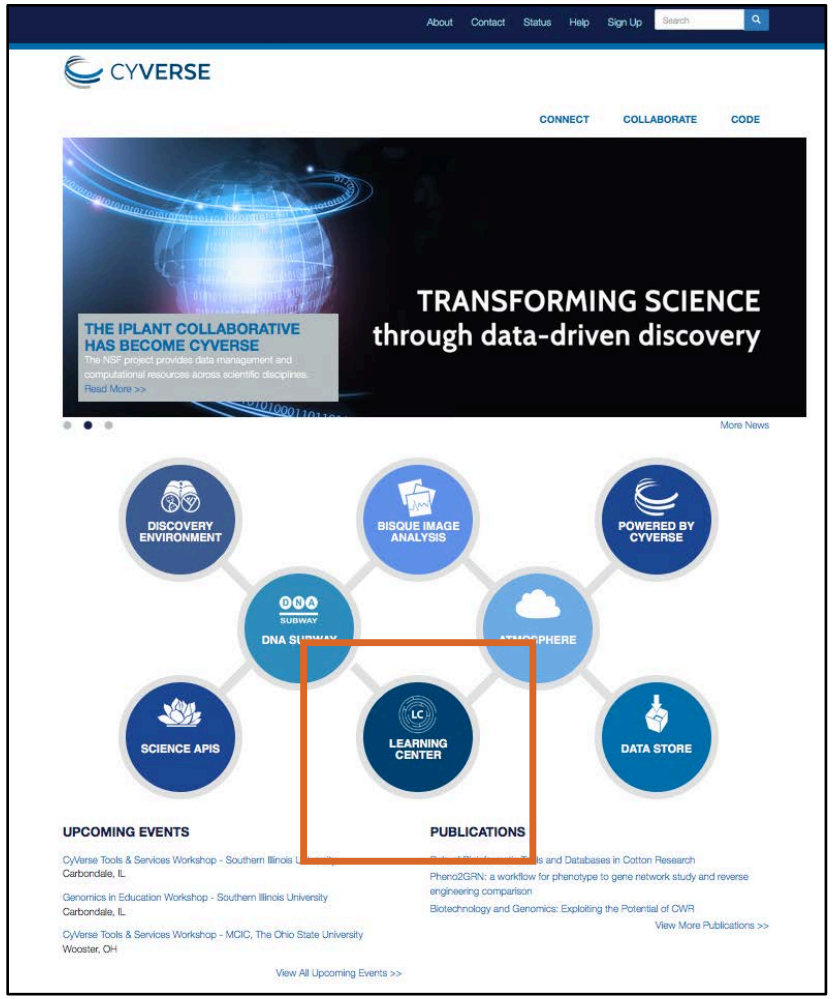


Shell/terminal

VNC Viewer: www.realvnc.com/download/viewer

PuTTy: www.putty.org

Where to go from here:



Learning Center

- Get Started Guide
- Tutorials and Videos
- Documentation

Upcoming Events

- Workshops
- Webinars

CYVERSE

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Executive Team

THE UNIVERSITY OF ARIZONA

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