CyVerse Discovery Environment



Web-based bioinformatics and data













Download Slides and Follow Along

mcbios.readthedocs.org





Welcome to the Discovery Environment

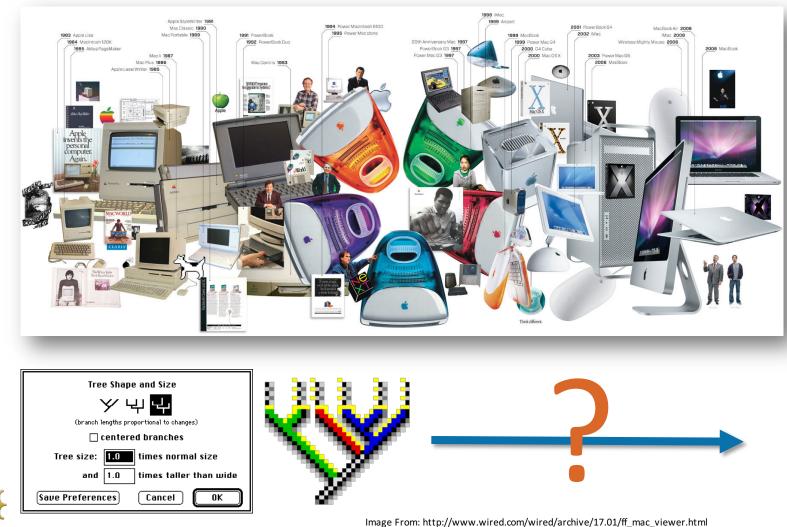


A Simple Interface to Hundreds of Bioinformatics Apps, Powerful Computing, and Data

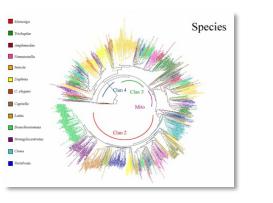








- It can be difficult to keep up!
 - Investing in newer 'better' tools and resources is expensive.







NSF



Access your computational science through a single portal

Ciscovery Environment	🌲 🛎 💐
Data	
Apps	
Analyses	
	Feedback





Get Science Done



- Use hundreds of bioinformatics Apps without the command line
- Add your own applications an extensible, scalable platform

Reproducibility

- Create and publish Apps and workflows so anyone can use them
- Analysis history and provenance "avoid forensic bioinformatics"

Productivity

• High-performance computing – not dependent on your hardware



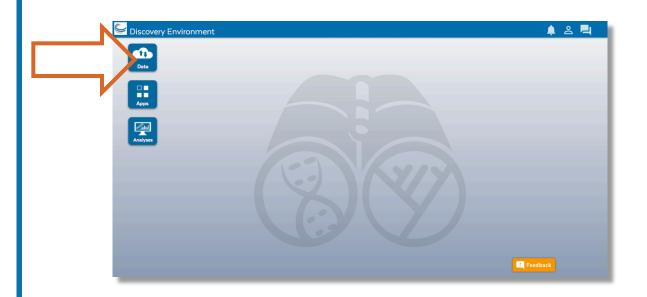
• Manage a secure data repository and share data easily







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











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



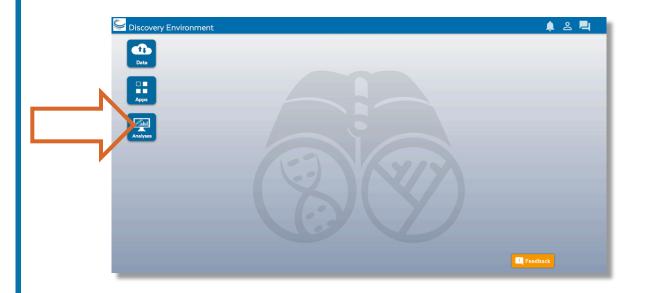




View history, find results, reproduce analyses, optimize parameters



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









By the end of this demo you should be able to:

- Navigate the components of the DE
- Access and manipulate data (upload, download, move, etc.)
- Run an analysis
- Track your analysis and see your results





Discovery Environment Overview Hands-on demo: Create a multiple alignment

Find a file in the Community Data folder
Download a small file of unaligned DNA sequences
Upload a small file



Data

- 4. Use the MUSCLE App to align the sequences
- 5. Monitor the job status and export its parameters

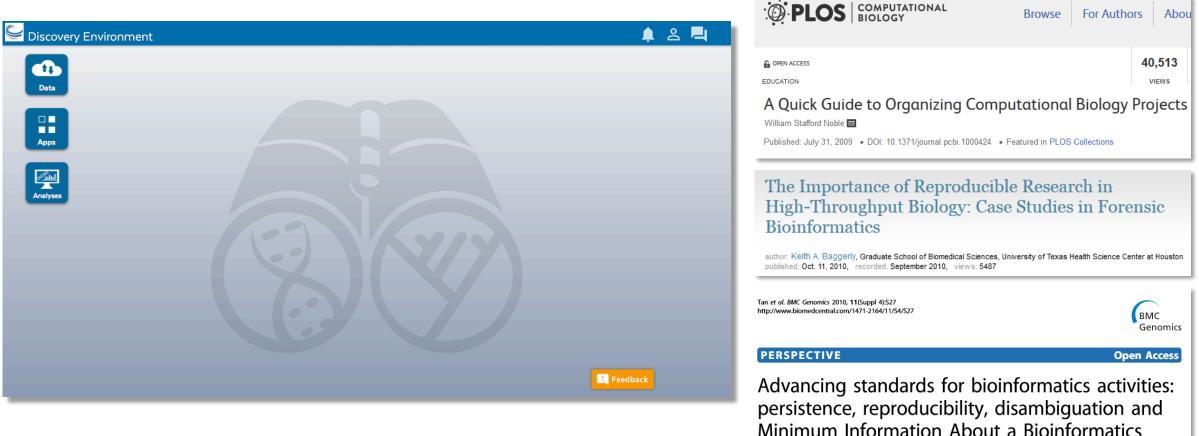


6. View results





Built for bioinformatics best practices: data stewardship, reproducibility, reliability



investigation (MIABi)

An extensible platform that scales with your science

User perspectives and possible applications



Bioinformatician

Core Facilities



- Does most of his data uploads/downloads/sharing here
- He pushes results from his lab's workflow into a common folder



- Installed an HPC application here so that anyone can use it
- Creates custom applications with default parameters exposed



- Developed a workflow to QC and Filter reads for his users
- Teaches about genome assembly with examples in the DE





- Detailed instructions with videos, manuals, documentation in
- Keep asking: ask.iplantcollabortive.org

