

Big process for big data

Process automation for data-driven science

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Computation Institute

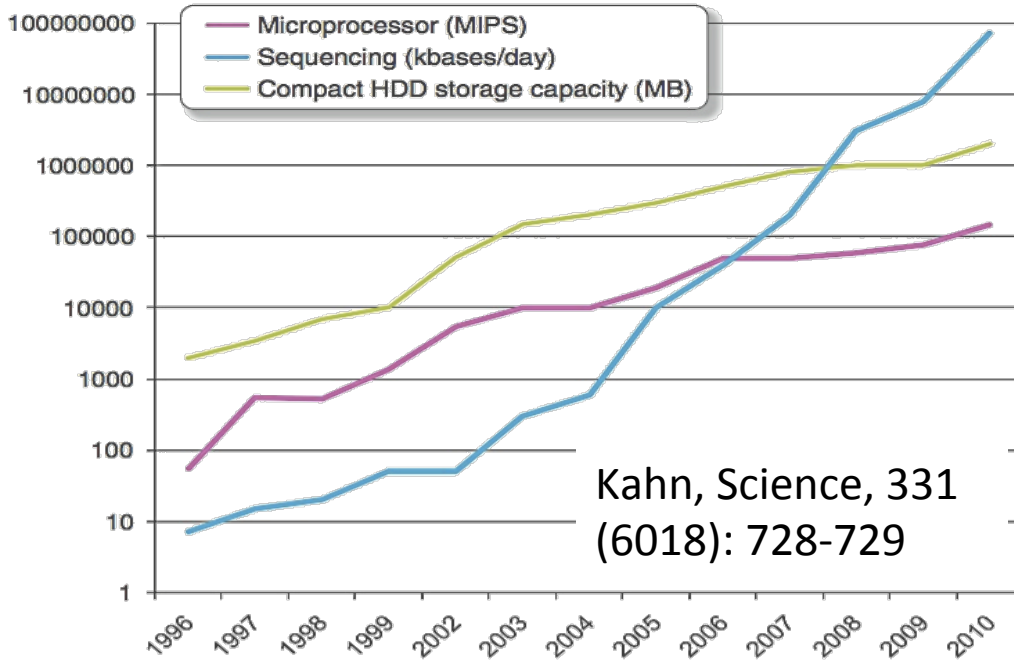
Mathematics and Computer Science Division

Department of Computer Science

Argonne National Laboratory & The University of Chicago

Talk at University of Joint Lab Workshop, Argonne, November 20, 2012

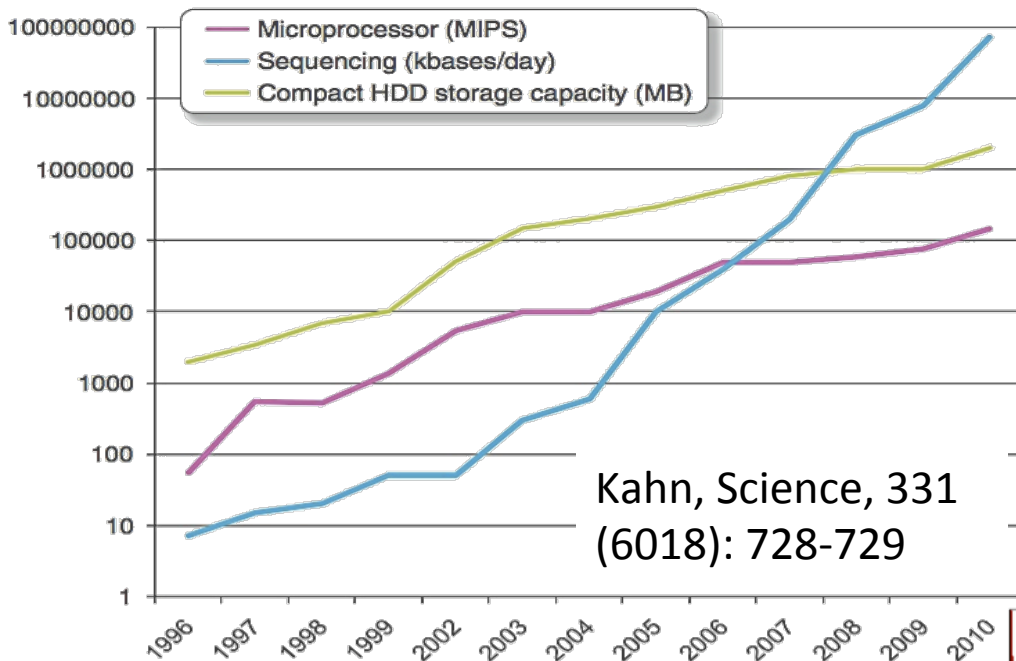
A productivity crisis in research



Data volumes
are growing
much faster than
Moore's law ...

(10,000x more over last 6
years for genome data)

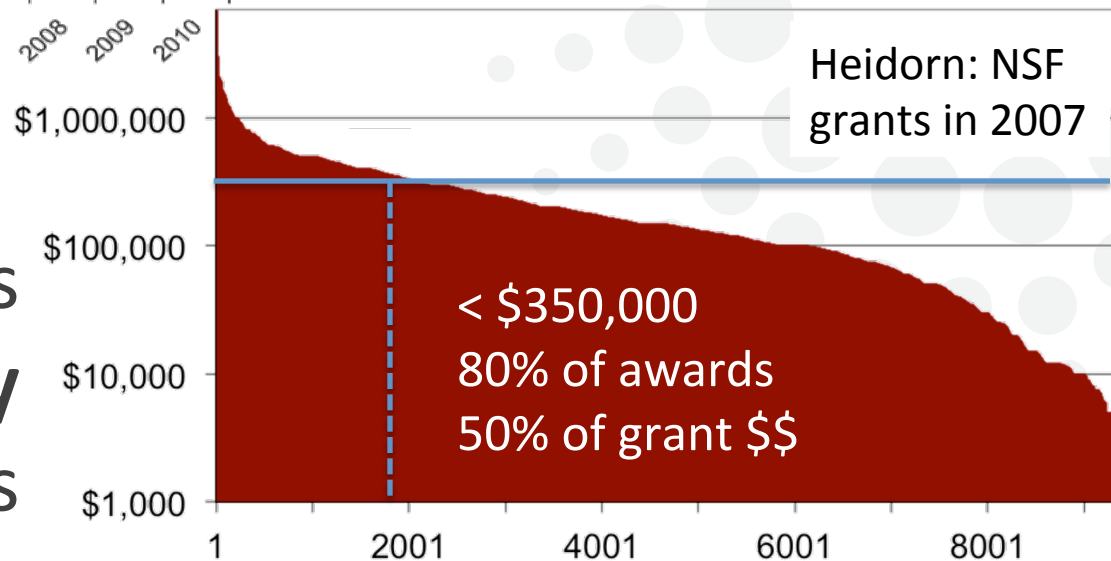
A productivity crisis in research



Data volumes are growing **much faster** than Moore's law ...

(10,000x more over last 6 years for genome data)

But most labs have **extremely limited** resources



Automation and outsourcing are key



- **Automation** is required to apply more sophisticated methods to far more data



Automation and outsourcing are key



- **Automation** is required to apply more sophisticated methods to far more data
- **Outsourcing** is needed to achieve economies of scale in the use of automated methods



They work for small and medium business



STARBUCKS COFFEE



The research data lifecycle



Simulation



Telescope



In millions of labs worldwide, researchers struggle with massive data, advanced software, complex protocols, burdensome reporting



Next-gen
genome
sequencer



Accelerate discovery and innovation by outsourcing difficult tasks

- Identify **time-consuming activity** that appears amenable to automation and outsourcing
- Implement activity as a high-quality, low-touch **SaaS solution** with high economies of scale
- Evaluate **usage and performance**
- Extract common elements as a **research automation platform**
- Repeat

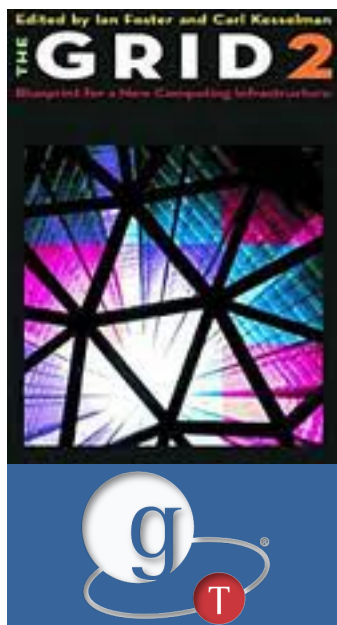
Software as a service

Platform as a service

Infrastructure as a service

Bonus question: Identify methods for delivering SaaS solutions in sustainable manner

Millions of researchers worldwide need advanced IT to tackle important and urgent problems



Characterizing big process requirements



Simulation



Telescope



In millions of labs worldwide, researchers struggle with massive data, advanced software, complex

Data movement is a frequent challenge

- Between facilities, archives, researchers
- Many files, large data volumes
- With security, reliability, performance



Next-gen
genome
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Accelerate discovery and innovation by outsourcing difficult tasks

A first step: Automated file movement

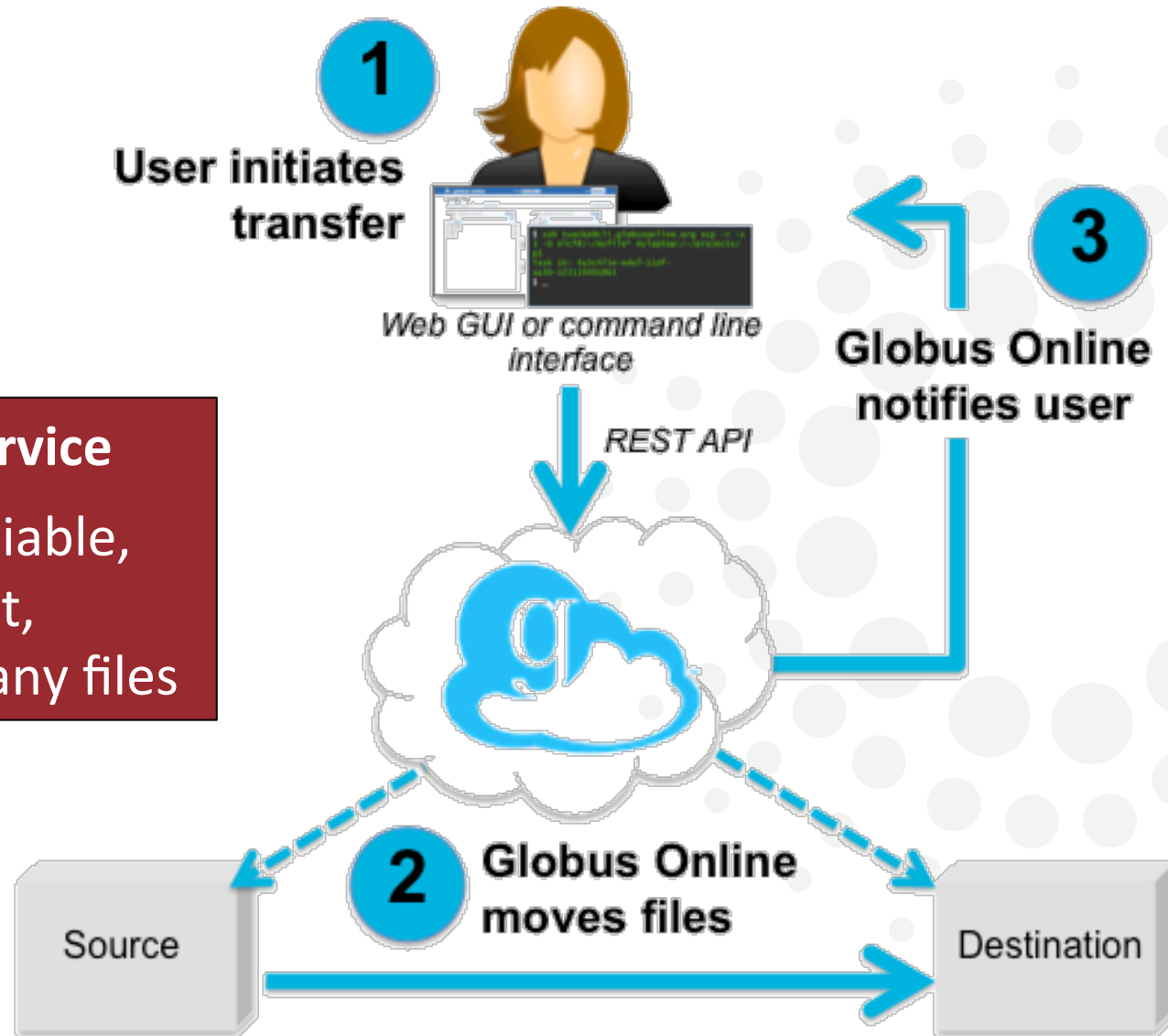


6,000 users
500 M files moved
8 PB moved
100s of endpoints
99.9% availability

File movement as a service

Secure, automated, reliable,
high-speed movement,
synchronization of many files

Biggest: 1 PB
Most files: 10M
Longest: 100 days
Furthest: Australia





Reliable, high-performance, secure file transfer by Globus Online.

Blue Waters has partnered with the Globus Online file transfer service.

You may access this service by entering your Blue Waters username and password.

NOTE - If you are accessing this file transfer service for the first time, you will be asked to link your Blue Waters account to a Globus Online account (if you don't have a Globus Online account you'll be able to create one).

Sign In

Use Your NCSA Blue Waters login

[alternate login](#)

Username

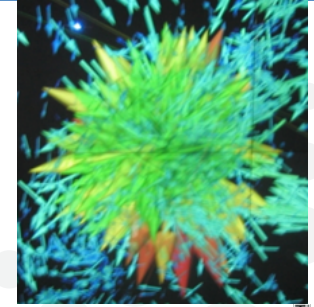
Password

Sign In

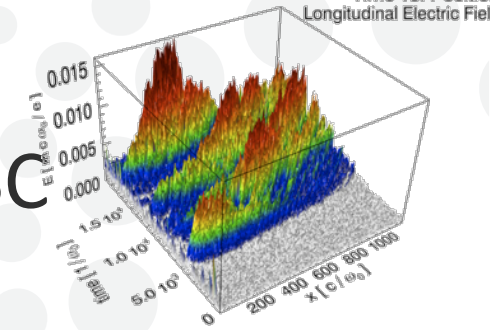
Examples of Globus Online in action



- K. Heitmann (ANL) moves 22TB **cosmology** data at 5 Gb/s LANL → ANL



- B. Winjum (UCLA) moves 900K-file **plasma physics** datasets UCLA - NERSC

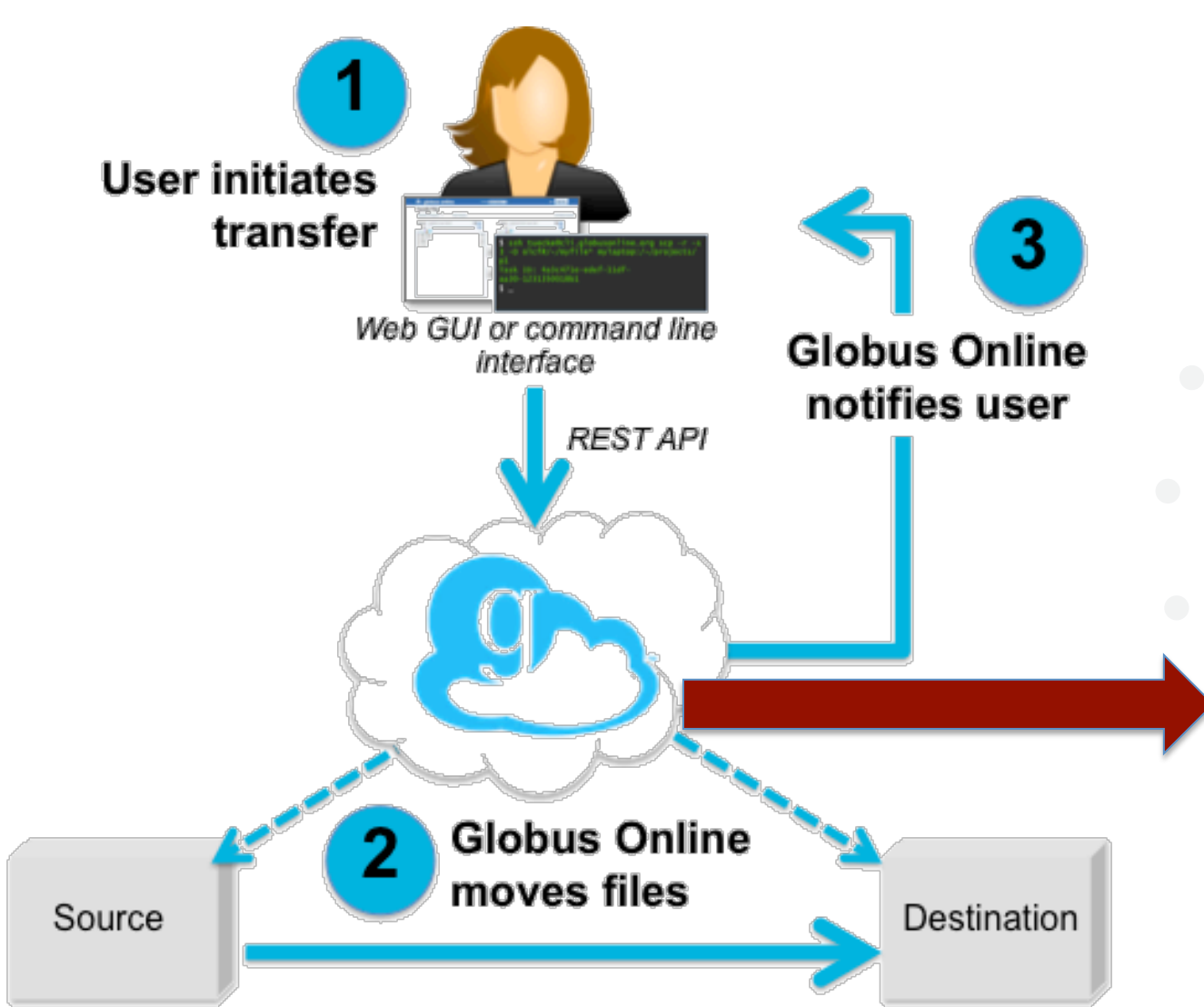



- Dan Kozak (Caltech) replicates 1 PB **LIGO** astronomy data for resilience



- Recommended by many supercomputer centers, genome facilities, light sources, universities

Globus Online under the covers



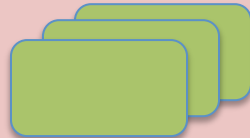
 **Nexus**

Identities, profiles, groups

Replicated


Cloud-hosted

Web servers, data movers, CLI, etc.



High availability

Transfer state

 **Transfer**

Need much more than file movement



Simulation



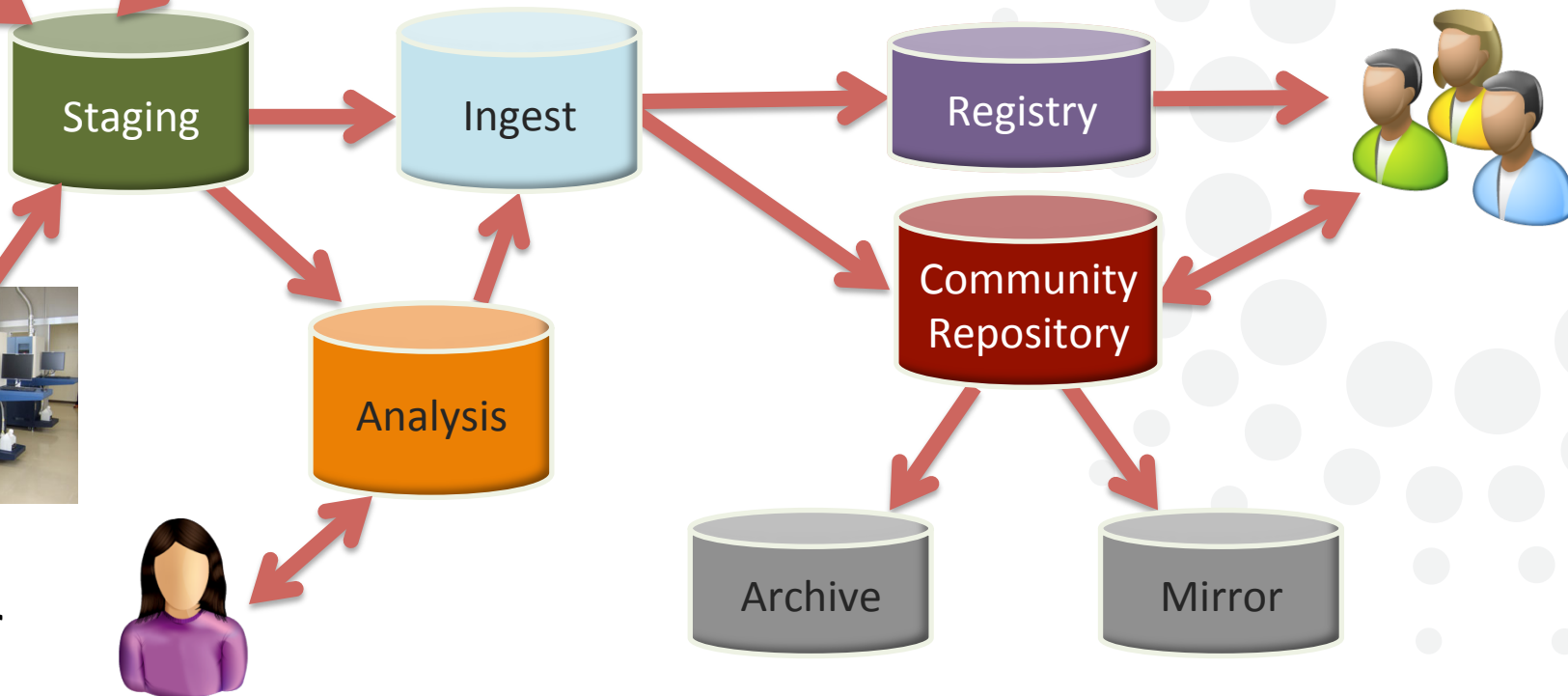
Telescope



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Next-gen
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Accelerate discovery and innovation by outsourcing difficult tasks

We are also working on other activities



- Sharing and distribution
 - User-managed sharing with individuals and groups
- Ingest and publication
 - Imagine a DropBox that not only replicates, but also extracts metadata, catalogs, converts
- Cataloging
 - Virtual views of data based on user-defined and/or automatically extracted metadata
- Computation
 - Associate computational procedures, orchestrate application, catalog results, record provenance

Endpoint



Go

Path

Go



[select all](#) | [none](#)

[up one folder](#)

[refresh list](#)



VG.pdf

kB

[new folder](#)
[show hidden files](#)
[delete selected files](#)
[share](#)



Manage Permissions For `ian#share`Source: `karlito#scdemo:/~/`

name

read

write

delegate

Path: /

Ian Foster



start typing a user account name or UUID to add to the list above

Add

Path

/

☒ read ☐ write ☐ delegate

search for users and groups »»



Close



Find Users & Groups

cvrg



- ☐ **cvrg**
 ▶ managers ▶ members
- ☐ **BIRNCommunity**
 ▶ managers ▶ members

[« Back to Permissions List](#)[Share Endpoint With Selected](#)☒ read ☐ write ☐ delegate

Find Users & Groups

cvrg

**cvrg**

▶ managers

▼ members

- ☐ Josh Bryan
- ☐ Steve Tuecke
- ☐ Lisa Childers
- ☐ Daniel Morgan

☐ **BIRNCommunity**

▶ managers

▶ members

[« Back to Permissions List](#)[Share Endpoint With Selected](#)☒ read ☐ write ☐ delegate

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**cvrg**

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- ☐ Josh Bryan
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- ☐ Daniel Morgan

**BIRNCommunity**

managers

members

[« Back to Permissions List](#)[Share Endpoint With Selected](#)

read




write



delegate

Manage Permissions For `ian#share`Source: `karlito#scdemo:/~/`

name	read	write	delegate
Path: /			
Ian Foster	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
 cvrg	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

✔ cvrg added successfully.

start typing a user account name or UUID to add to the list above

Add

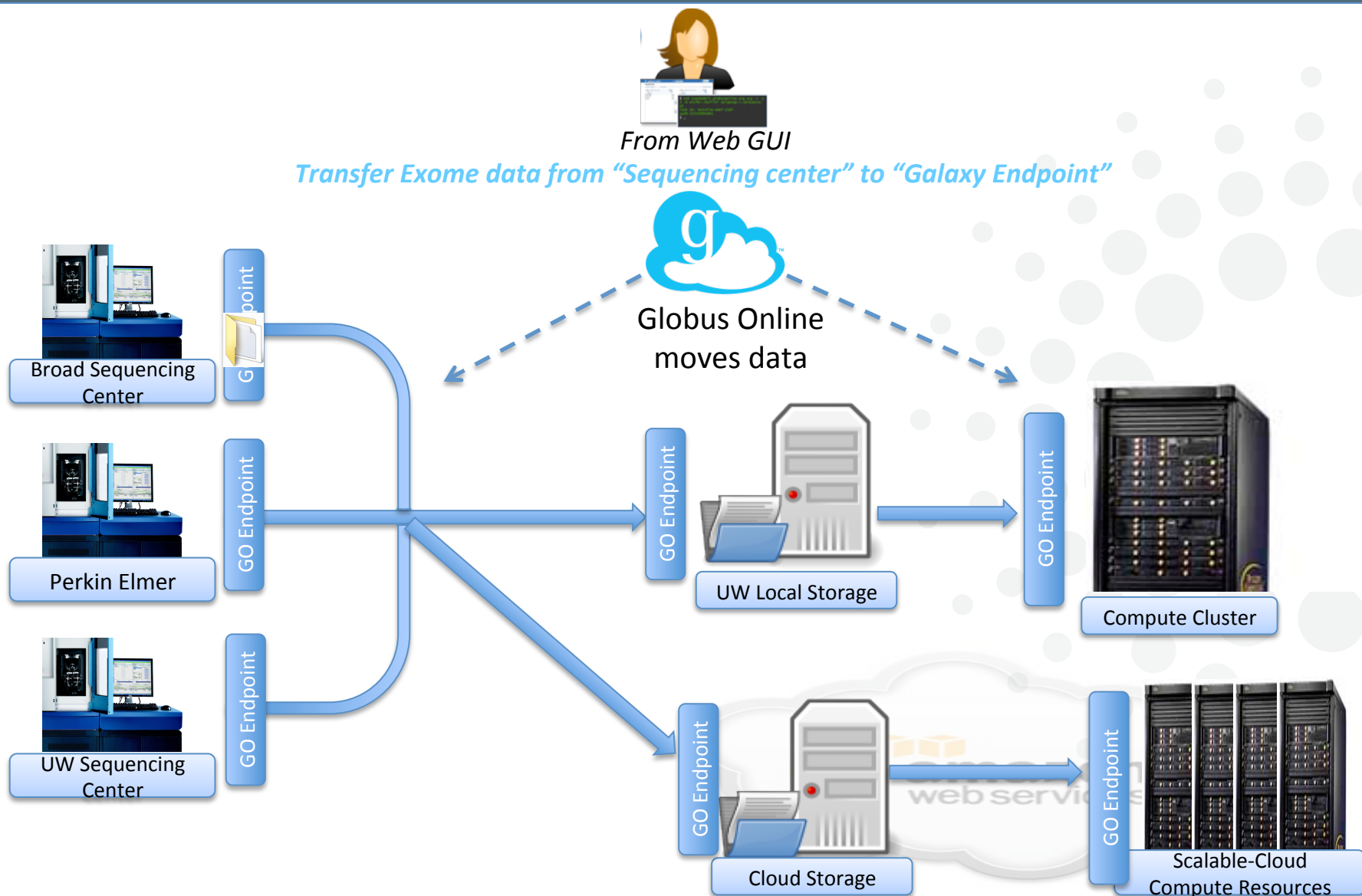
Path

/

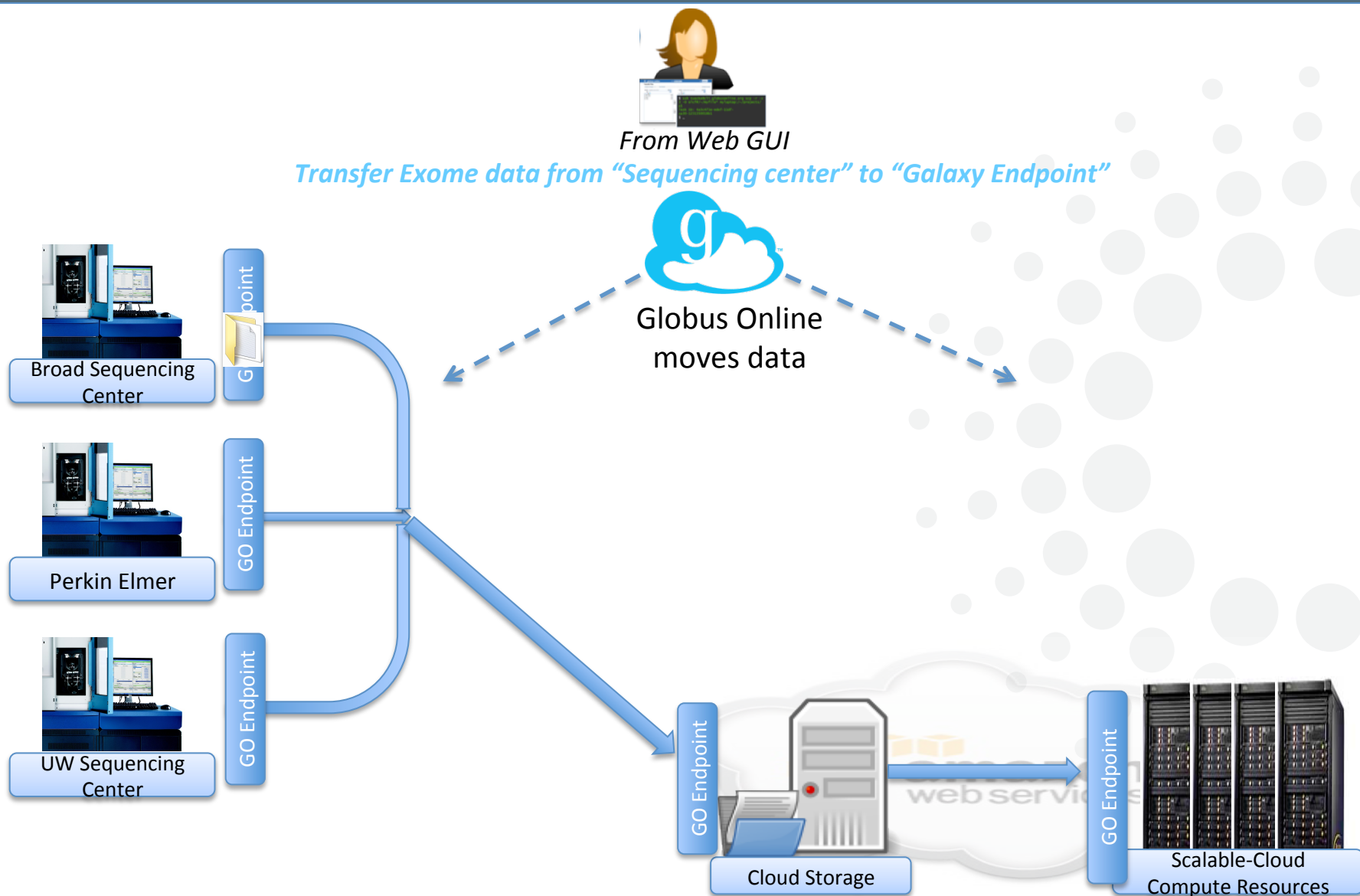
☒ read ☐ write ☐ delegate

search for users and groups »»

Cloud-based data analysis



Cloud-based data analysis



- We need **active data repositories** providing for:
 - Integration and maintenance of large, diverse data
 - Not just access to individual elements but demanding user-defined computations over entire datasets
 - Linking of diverse computational results produced by different methods and people
 - Maintenance in the face of diverse updates
- Observations and questions
 - Architecture TBD. Surely HDFS is inadequate?
 - ADRs will surely be heterogeneous
 - Integration with investigator research platforms

A research data management platform



Platform: “technology that enables the creation of products and processes”

- File, catalog, analysis management
- **Identity hub:** Manage user profiles, identities, delegated credentials
- **Group hub:** Manage group membership information

Software as a service

Platform as a service

Infrastructure as a service

All accessible via REST APIs (and CLI), allowing user or team services to offload these functions

Kbase: Identity, group, file movement

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The new Systems Biology Knowledgebase (KBase) is a collaborative effort designed to accelerate our understanding of microbes, microbial communities, and plants. It will be a community-driven, extensible and scalable open-source software framework and application system. KBase will offer free and open access to data, models and simulations, enabling scientists and researchers to build new knowledge and share their findings.

For scientists

[Collaborate with us](#)

For users

[Get Started](#)

For developers

[Develop with us](#)

What can KBase do?

- ✓ Combine heterogeneous data types
- ✓ Offer standardized access to bioinformatic and modeling analyses
- ✓ Use evidence-supported annotations of genome structure and genetic function
- ✓ Discover new associations and network structures in community and molecular networks



Latest News

[August Build](#)

Posted by salazar August 09th, 2012 at 17:13pm

[Nomi Harris Joins KBase](#)

Posted by salazar July 19th, 2012 at 15:15pm

[KBase in June HPC Source](#)

Posted by salazar June 30th, 2012 at 15:38pm

[view news](#)

Upcoming Events

2012-09-27

[Mike Schatz at Beyond the Genome](#)

2012-10-21

[ASA-CSSA-SSA Conference](#)

2012-10-22

[Functional Genomics Data \(EGED\)](#)



Accelerate discovery and innovation worldwide by providing **research IT as a service**

Outsource time-consuming tasks to

- provide large numbers of researchers with unprecedented access to powerful tools;
- enable a massive shortening of cycle times in time-consuming research processes; and
- reduce research IT costs via economies of scale

Accelerate existing science; enable new science

The team includes [partial list]



At Argonne and UChicago

- Bryce Allen
- Rachana Ananthakrishnan
- Josh Bryan
- Kyle Chard
- Lisa Childers
- Vytas Cuplinskas
- Paul Davé
- Raj Kettimuthu
- Jack Kordas
- Lukasz Lacinski
- Mattias Lidman
- Ravi Madduri
- Stuart Martin

- Dan Morgan
- JP Navarro
- Gigi Rohder
- Steve Tuecke
- Vas Vasiliadis

Collaborators

- Carl Kesselman
- Karl Czajkowski
- Dean Williams
- Francesco de Carlo
- Jim Basney
- Martin Swany
- David Skinner

“Research IT as a service: designing and creating the research cloud.” For example:

- End-to-end understanding and optimization of local and wide area file transfers
- Identifying research data management activities suitable for outsourcing
- Data-intensive applications involving simulation and/or experimental data
- Architecture and implementation of active data repositories

Thank you!

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www.mcs.anl.gov

www.globusonline.org, [@globusonline](#)