

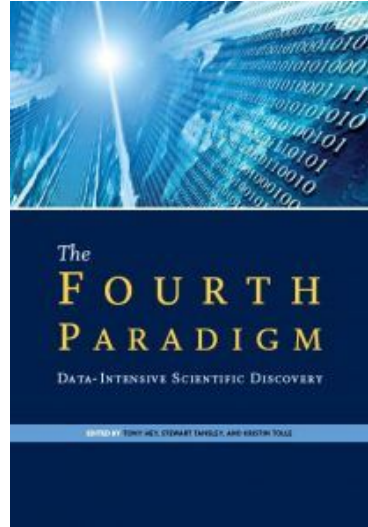
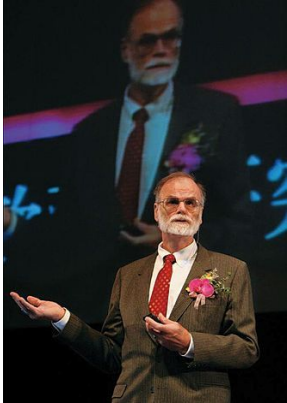
SciServer

A Collaborative Science Platform developed by IDIES

Outline

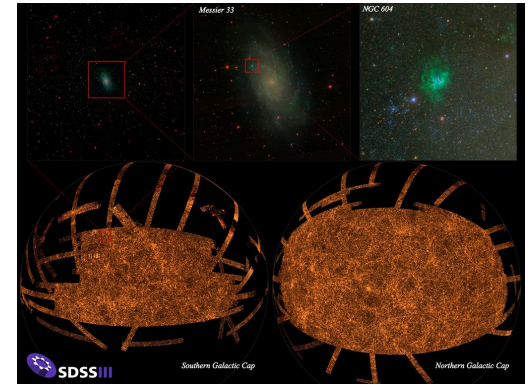
- Background
- SciServer overview
- Use case highlights
- Architecture & Deployments
- New/hidden features/accelerated computing
- Future directions
- Questions

Beginnings



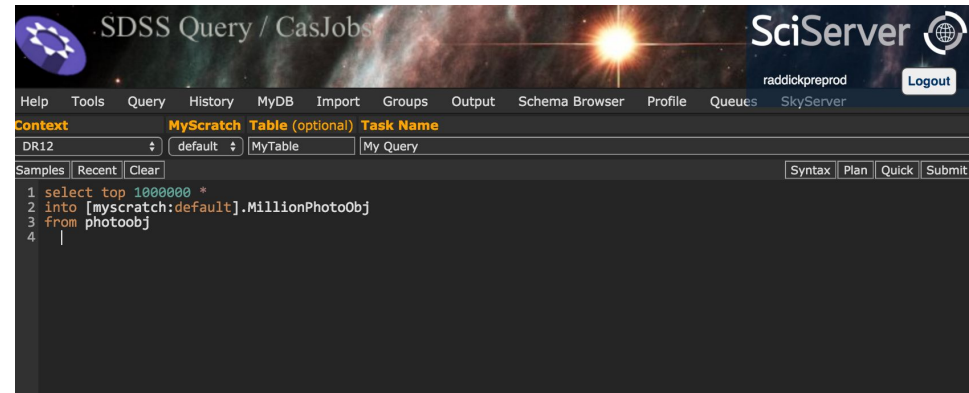
The fourth paradigm: **Data exploration.**

More data being produced than can be analyzed, increasing dependence on tools and machine learning to help make sense.



SDSS / CasJobs

- SQL interface to large catalog of object data
- Server-side execution, download small result-set of interest
- Personal DB space
- Sharing features

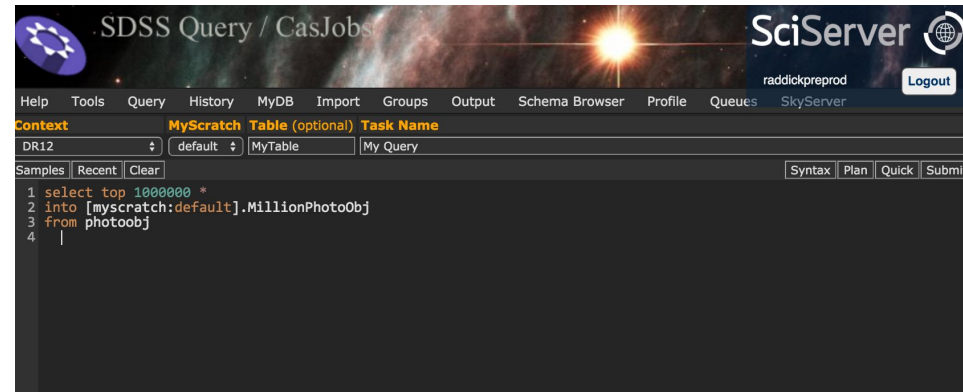


The screenshot shows the SDSS Query / CasJobs interface. The page title is "SDSS Query / CasJobs" and the SciServer logo is in the top right corner. The user is logged in as "raddickpreprod". The interface includes a navigation menu with options: Help, Tools, Query, History, MyDB, Import, Groups, Output, Schema Browser, Profile, Queues, and SkyServer. Below the menu, there is a "Context" section with a dropdown menu showing "DR12". To the right of the context, there are fields for "MyScratch Table (optional)" with "default" selected and "MyTable" entered, and "Task Name" with "My Query" entered. Below these fields, there are buttons for "Samples", "Recent", and "Clear". On the right side of the interface, there are buttons for "Syntax", "Plan", "Quick", and "Submit". The main area contains a SQL query editor with the following code:

```
1 select top 1000000 *
2 into [myscratch:default].MillionPhotoObj
3 from photoobj
4 |
```

SDSS / CasJobs

- SQL interface to large catalog of object data
 - Server-side execution, download small result-set of interest
 - Personal DB space
 - Sharing features
-
- Still need to download
 - No solution for file-based data
 - limited/no visualization support



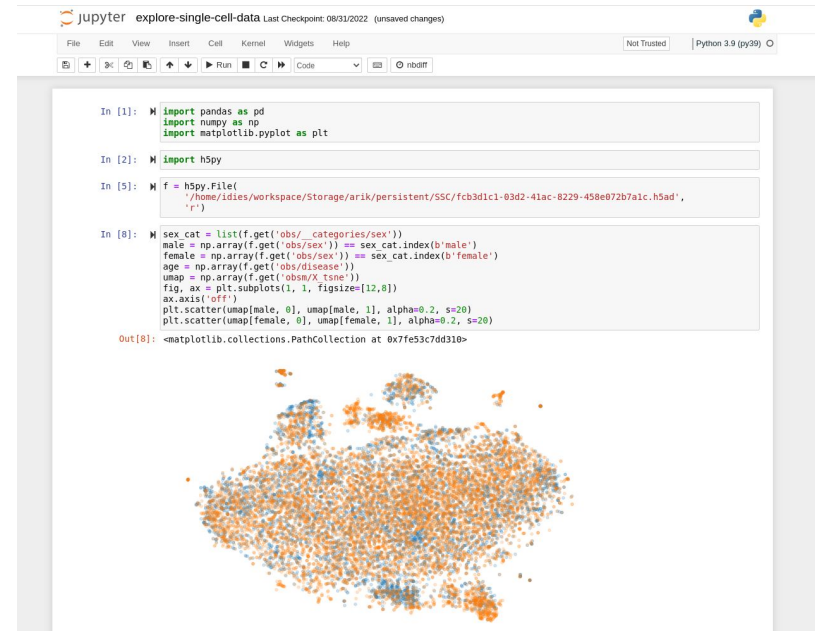
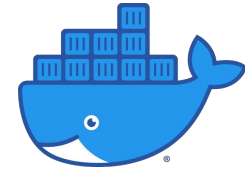
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```
1 select top 1000000 *
2 into [myscratch:default].MillionPhotoObj
3 from photoobj
4 |
```

Buttons for "Syntax", "Plan", "Quick", and "Submit" are visible at the bottom right of the query editor.

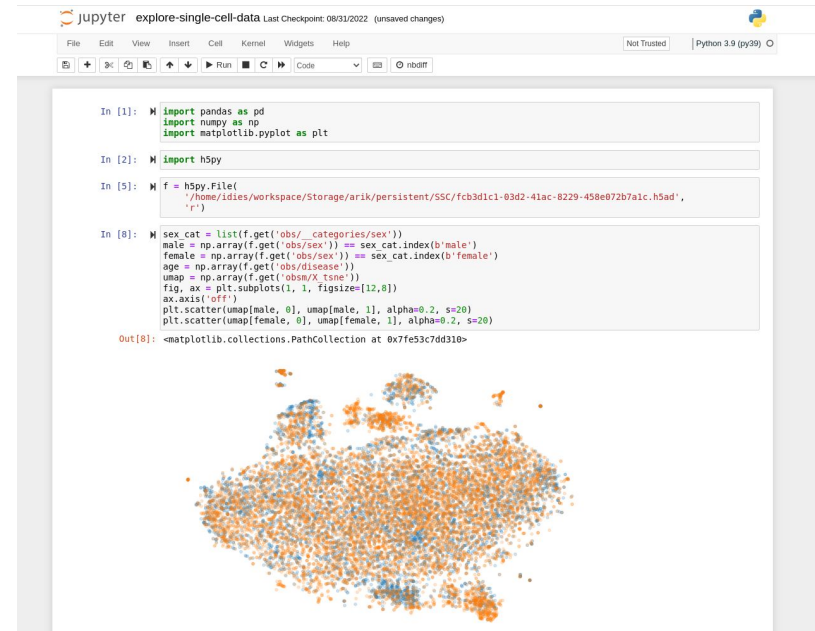
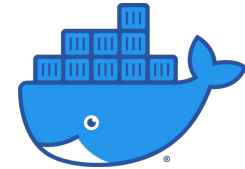
Beyond SQL

- Add Jupyter
- Docker makes scheduling simple
- Jupyter can run arbitrary codes
- Inline visualization
- Common dependencies included
- SDK for CasJobs (get a pandas DF)



Beyond SQL

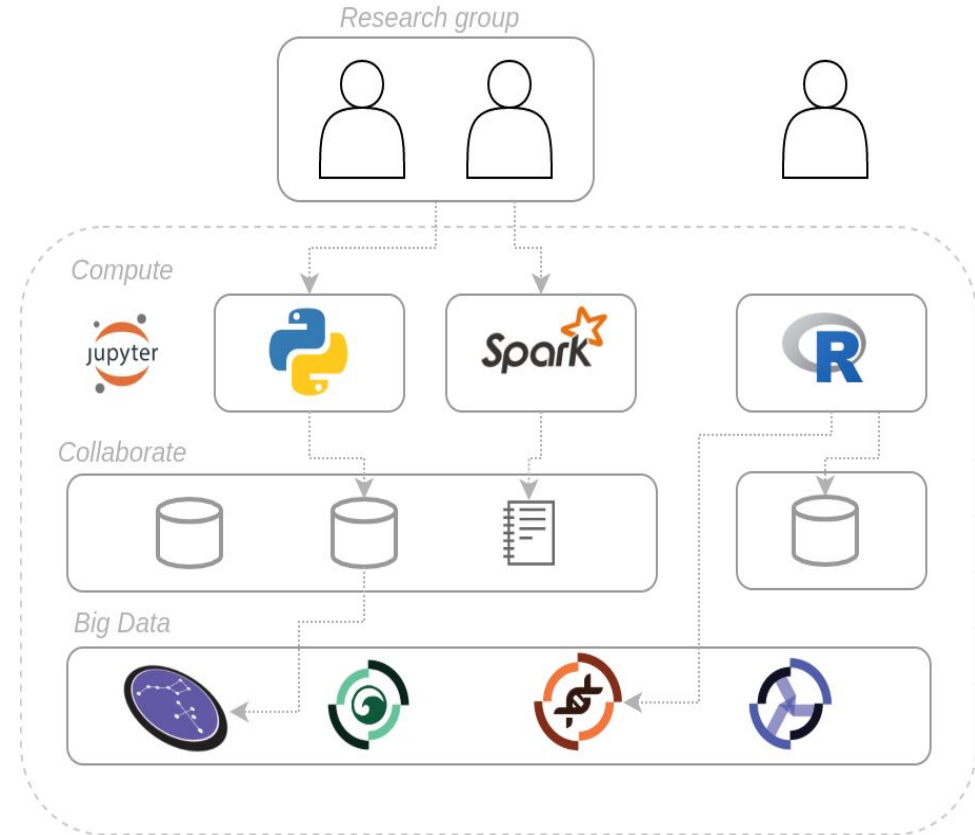
- Add Jupyter
 - Docker makes scheduling simple
 - Jupyter can run arbitrary codes
 - Inline visualization
 - Common dependencies included
 - SDK for CasJobs (get a pandas DF)
-
- Server-side collaboration?
 - Expanding scope?



SciServer

- Add in an ecosystem
- Sharing/resource access control
- Web based portals
- Curated data
 - Astronomy
 - Genomics
 - Earth Science
 - Simulation data,...

A Science Platform



Basic Usage

- Go to <https://apps.sciserver.org>
- Create an account
 - You can sign in with your institution via globus, your google account or orcid by using “sign in with Globus”



Login with SciServer

User name

Password

[Sign in](#)

[Create a new account](#)

[Forgot your password?](#)

Login with Globus

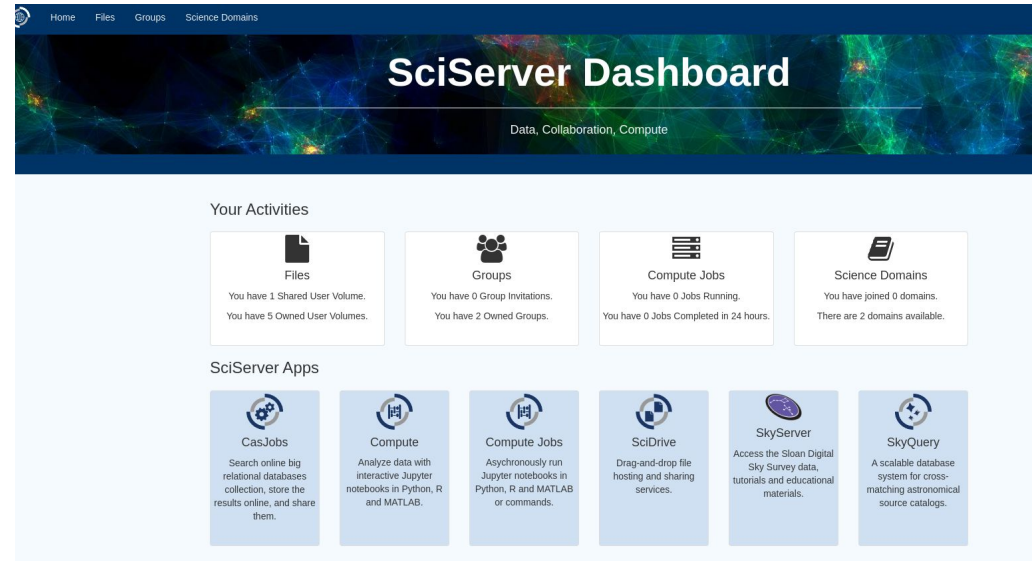
Globus allows you to use your educational institution or Google login to authenticate with SciServer.

[Sign in with Globus](#)

[Sign out of Globus](#)

Basic Usage

- Arrive at dashboard
- A number of links to services
 - Files
 - Groups
 - Compute
 - Casjobs



The screenshot shows the SciServer Dashboard interface. At the top, there is a navigation bar with links for Home, Files, Groups, and Science Domains. The main header features the SciServer logo and the tagline "Data, Collaboration, Compute". Below this, the dashboard is divided into two main sections: "Your Activities" and "SciServer Apps".

Your Activities

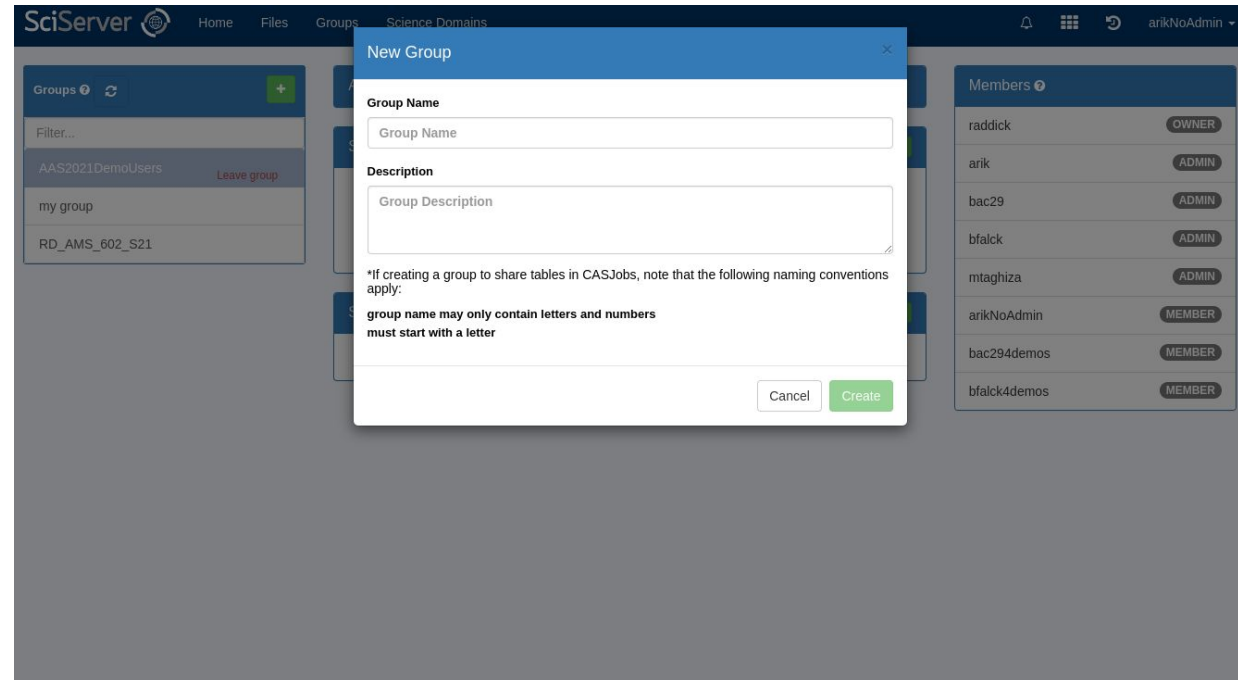
- Files:** You have 1 Shared User Volume. You have 5 Owned User Volumes.
- Groups:** You have 0 Group Invitations. You have 2 Owned Groups.
- Compute Jobs:** You have 0 Jobs Running. You have 0 Jobs Completed in 24 hours.
- Science Domains:** You have joined 0 domains. There are 2 domains available.

SciServer Apps

- CasJobs:** Search online big relational databases collection, store the results online, and share them.
- Compute:** Analyze data with interactive Jupyter notebooks in Python, R and MATLAB.
- Compute Jobs:** Asynchronously run Jupyter notebooks in Python, R and MATLAB or commands.
- SciDrive:** Drag-and-drop file hosting and sharing services.
- SkyServer:** Access the Sloan Digital Sky Survey data, tutorials and educational materials.
- SkyQuery:** A scalable database system for cross-matching astronomical source catalogs.

Basic Usage - Groups

- Create groups
- Groups are a unit of sharing
- Invite other users



The screenshot displays the SciServer interface with a 'New Group' dialog box open. The dialog box contains the following elements:

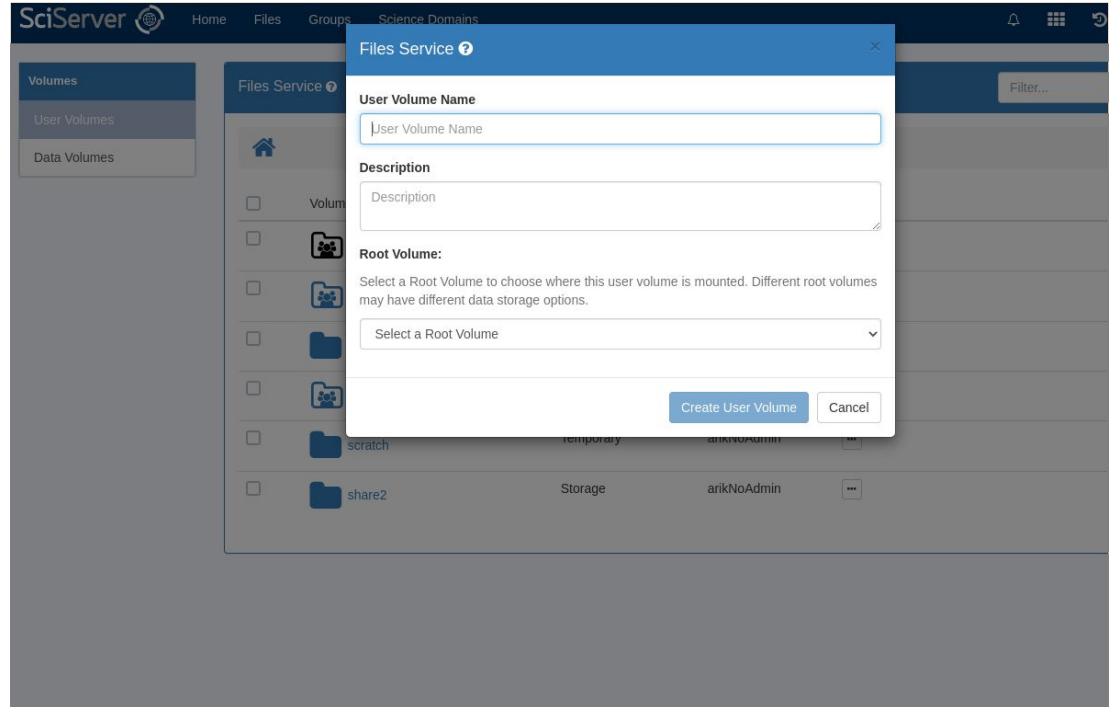
- Group Name:** A text input field.
- Description:** A text area for entering a description.
- Instructions:** A note stating: "*If creating a group to share tables in CASJobs, note that the following naming conventions apply: group name may only contain letters and numbers must start with a letter".
- Buttons:** 'Cancel' and 'Create' buttons at the bottom right.

The background interface shows a 'Groups' panel on the left with a list of groups: 'AAS2021DemoUsers' (with a 'Leave group' button), 'my group', and 'RD_AMS_602_S21'. On the right, a 'Members' panel shows a list of users and their roles:

Member	Role
raddick	OWNER
arik	ADMIN
bac29	ADMIN
bfalck	ADMIN
mtaghiza	ADMIN
arikNoAdmin	MEMBER
bac294demos	MEMBER
bfalck4demos	MEMBER

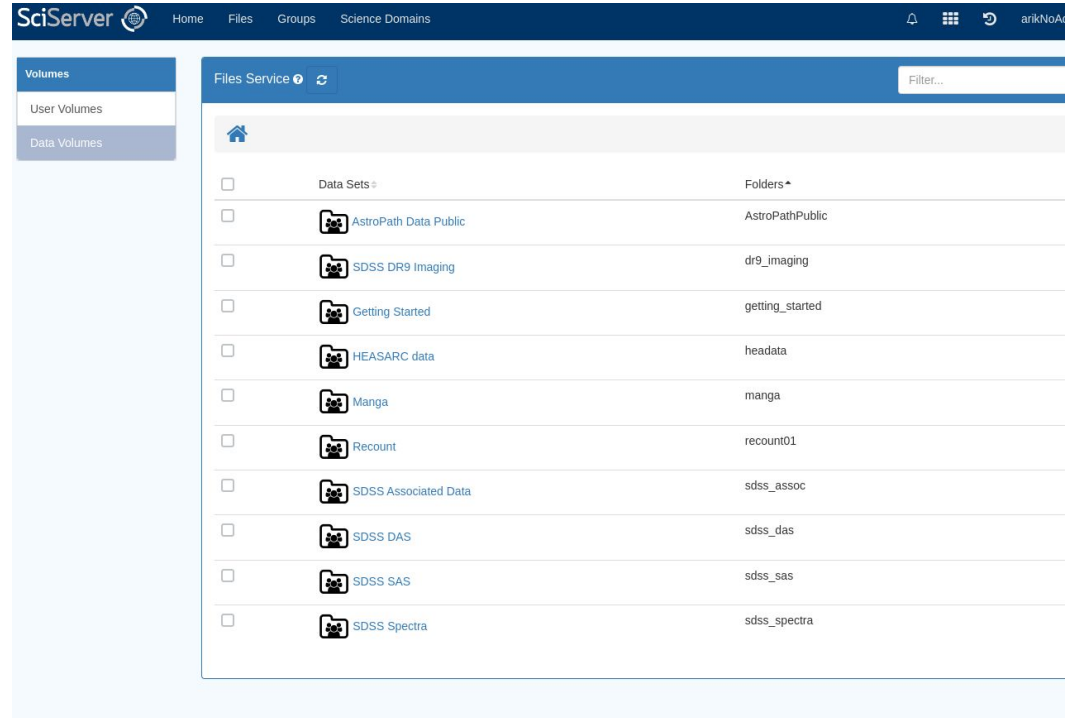
Basic Usage - User Volumes

- Create “User Volumes”
- Volumes can be shared
- Store your own data
- Default limited space
- Temporary space:
 - For intermediate results
 - “Unlimited”
 - time-to-live













Basic Usage - Data Volumes

- “Data Volumes”
- Read-only
- Curated data (typically)
- Shared by “admins”



The screenshot displays the SciServer web interface. The top navigation bar includes 'Home', 'Files', 'Groups', and 'Science Domains'. A left sidebar shows 'Volumes' with sub-options for 'User Volumes' and 'Data Volumes'. The main content area, titled 'Files Service', shows a list of data volumes. Each volume is represented by a folder icon, a name, and a corresponding folder name. A search filter is visible in the top right of the main area.

<input type="checkbox"/>	Data Sets	Folders
<input type="checkbox"/>	 AstroPath Data Public	AstroPathPublic
<input type="checkbox"/>	 SDSS DR9 Imaging	dr9_imaging
<input type="checkbox"/>	 Getting Started	getting_started
<input type="checkbox"/>	 HEASARC data	headata
<input type="checkbox"/>	 Manga	manga
<input type="checkbox"/>	 Recount	recount01
<input type="checkbox"/>	 SDSS Associated Data	sdss_assoc
<input type="checkbox"/>	 SDSS DAS	sdss_das
<input type="checkbox"/>	 SDSS SAS	sdss_sas
<input type="checkbox"/>	 SDSS Spectra	sdss_spectra

Basic Usage - Compute

- Create a “container”
- Backed by docker
- Web service listening at specific port (Jupyter)
- Mount volumes needed

The screenshot displays the 'Create a new container' dialog in the SciServer interface. The dialog includes the following sections:

- Container name:** A text input field with the placeholder 'Please enter a name...'.
- Domain:** A dropdown menu currently set to 'Interactive Docker Compute Domain'. Below it, a note states: 'Shared Intel Xeon E7 systems. All containers are limited to 100GIB of RAM. Unused containers are shut down after 3 days.'
- Compute Image:** A dropdown menu set to 'SciServer Essentials 2.0'. Below it, the image details are listed: 'Python 3.8 (Anaconda 2020.11), R 4.0.3, TensorFlow 2.3.0, PyTorch 1.7.1'.
- User volumes:** A section with a 'All' checkbox and several checked items:
 - AAS2021Demos, Storage Volume created by gerard
 - RD_AMS_602_S21, Storage Volume created by arikNoAdmin
 - my group uw, Storage Volume created by arikNoAdmin
 - persistent, Storage Volume created by arikNoAdmin
 - scratch, Temporary Volume created by arikNoAdmin
 - share2, Storage Volume created by arikNoAdmin
- Data volumes:** A section with an 'All' checkbox and several unchecked items:
 - AstroPath Data Public
 - Getting Started
 - HEASARC data
 - Manga
 - Ocean Circulation
 - Poseidon
 - Recount
 - SDSS Associated Data
 - SDSS DAS
 - SDSS DR9 Imaging
 - SDSS SAS
 - SDSS Spectra

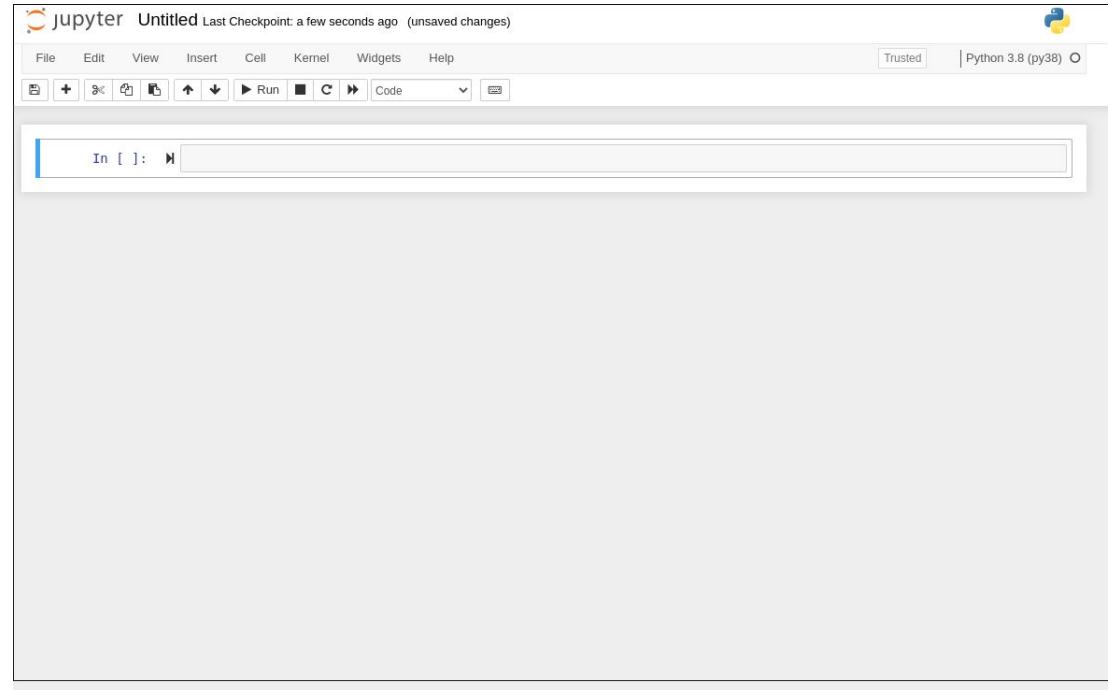
The background interface shows a 'Containers' table with the following data:

Created At
2022-04-25 13:01:00.0
2022-04-25 12:53:43.0
2022-04-25 12:27:50.0

At the bottom of the dialog, there is a 'Create' button. The SciServer footer indicates 'SciServer SciServer 2.1.0 Compute 2.4.1-181-g55efec3'.

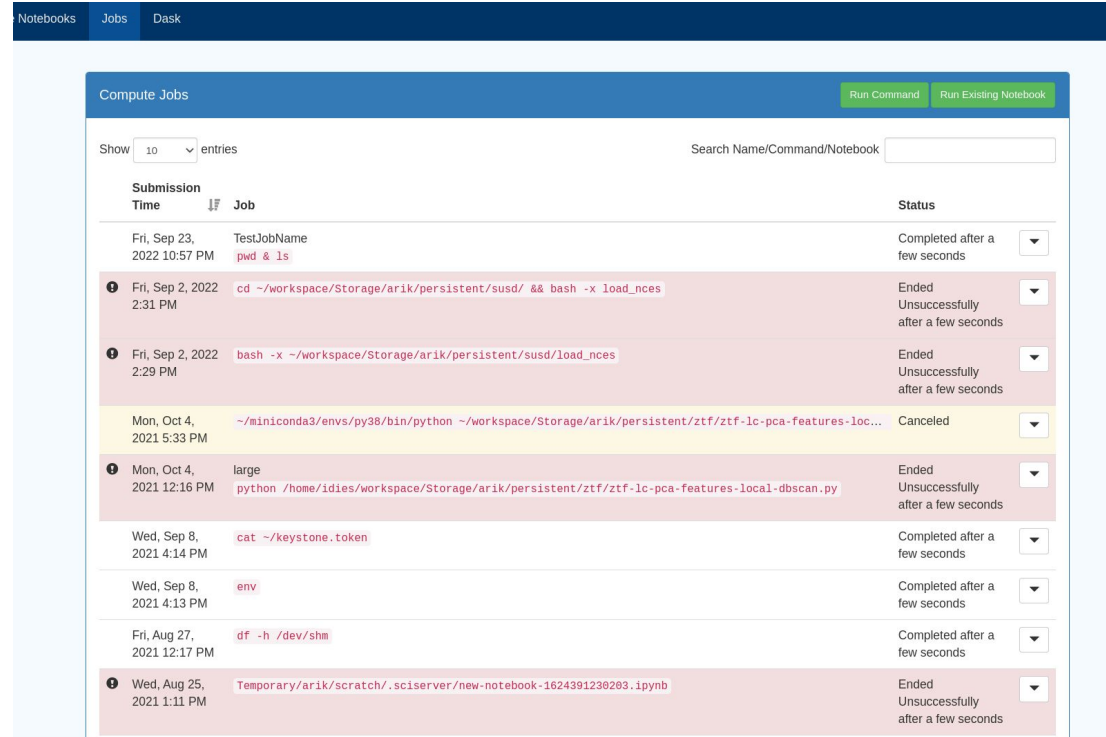
Basic Usage - Compute

- Do analysis
- Volumes are mounted
 - Posix access to regular files
- Lots of software already included
- Token “injected” for API access to SciServer and CasJobs



Basic Usage - Jobs

- Asynchronous Jobs
- Time-limited
- Large/specialized resources
- Queued, fair scheduling
- Clearer provenance



The screenshot displays the 'Compute Jobs' interface. At the top, there are tabs for 'Notebooks', 'Jobs', and 'Dask'. Below the tabs, there are two buttons: 'Run Command' and 'Run Existing Notebook'. The main area shows a list of jobs with the following columns: 'Submission Time', 'Job', and 'Status'. The 'Show' dropdown is set to '10' entries, and there is a search bar for 'Name/Command/Notebook'.

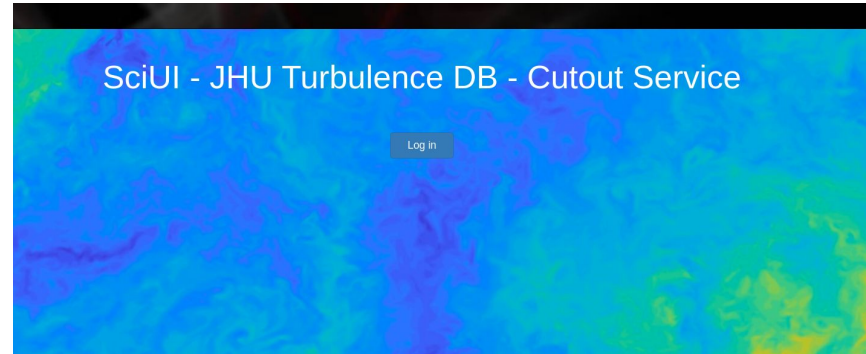
Submission Time	Job	Status
Fri, Sep 23, 2022 10:57 PM	TestJobName <code>pwd & ls</code>	Completed after a few seconds
Fri, Sep 2, 2022 2:31 PM	<code>cd ~/workspace/Storage/arik/persistent/susd/ && bash -x load_nces</code>	Ended Unsuccessfully after a few seconds
Fri, Sep 2, 2022 2:29 PM	<code>bash -x ~/workspace/Storage/arik/persistent/susd/load_nces</code>	Ended Unsuccessfully after a few seconds
Mon, Oct 4, 2021 5:33 PM	<code>~/miniconda3/envs/py38/bin/python ~/workspace/Storage/arik/persistent/ztf/ztf-1c-pca-features-loc...</code>	Canceled
Mon, Oct 4, 2021 12:16 PM	large <code>python /home/idies/workspace/Storage/arik/persistent/ztf/ztf-1c-pca-features-local-dbscan.py</code>	Ended Unsuccessfully after a few seconds
Wed, Sep 8, 2021 4:14 PM	<code>cat ~/keystone.token</code>	Completed after a few seconds
Wed, Sep 8, 2021 4:13 PM	<code>env</code>	Completed after a few seconds
Fri, Aug 27, 2021 12:17 PM	<code>df -h /dev/shm</code>	Completed after a few seconds
Wed, Aug 25, 2021 1:11 PM	Temporary/arik/scratch/.sciserver/new-notebook-1624391238283.ipynb	Ended Unsuccessfully after a few seconds

Use Case Highlights

Use Case: Turbulence

- Get cutouts of a large-scale turbulence simulation ($\sim 1/2$ PB)
- Web interface, actions backed by SciServer jobs
- Use notebooks to analyze results

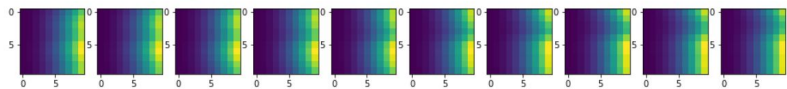
<http://turbulence.pha.jhu.edu/>



```
In [2]: M import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import h5py

n [21]: M f = h5py.File('/home/idies/workspace/Temporary/arik/scratch/jobs/__turbcutout_/20221013/20221013120636-195226/channel.h5', 'r')

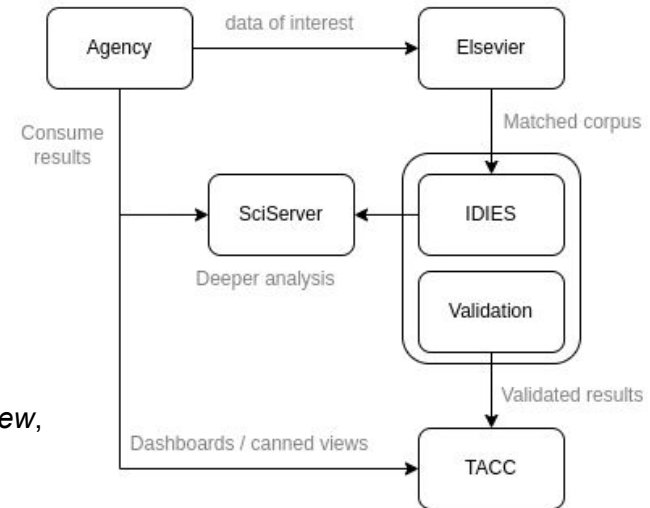
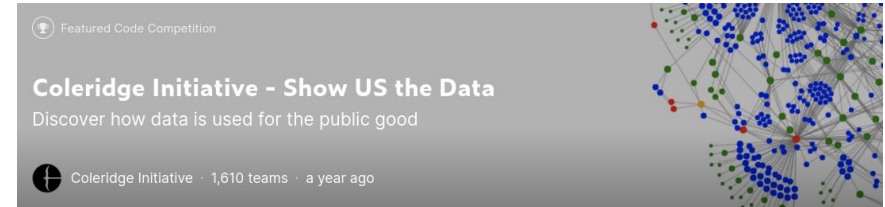
n [27]: M fig, a = plt.subplots(1, 10, figsize=[16,4])
for i in range(10):
    plt.sca(a[i])
    plt.imshow(f['Velocity_0001'][:, :, i, 0])
```



```
In [ ]: M
```

Use Case: Democratizing Data (Show Us The Data)

- Context: track dataset usage for gov agencies
- Rich data model, SQL backed
- Simple APIs for Tableau (hosted at TACC), but...
- SciServer enables deeper dive for those interested



See also: Potok, N. (2022). Show US the Data. *Harvard Data Science Review*, 4(2). <https://doi.org/10.1162/99608f92.9d13ba15>

Use Case: Teaching

- Focus on course materials, not setup
- Share examples with students
- Immediate feedback and experimentation
- Collect materials via share

Biotechnology: RNA-Seq



Get Help

Welcome

What is RNA-seq?

In vivo - Eukaryotic Gene Expression

In vitro - RNA sequencing

In silico - Computational Analysis

Summary

Start Over

← → ↻ apps.sciserver.org/dockervm30/1d5631ed-4e40-11ed-82c5-5254001d4703/?

C-MOOR Tutorials

Introduction to Model Organisms and Biological Databases

1. [Introduction to Model Organisms](#)
2. [Model Organisms: *Drosophila melanogaster* \(fruit fly\)](#)
3. [Introduction to Biological Databases](#)
4. [Biological Databases: FlyBase](#)
5. [Biological Databases: Human Protein Atlas](#)

A taste of RNA-seq

1. [Biotechnology: Next-Gen Sequencing](#)
2. [Biotechnology: RNA-seq](#)

In vitro - RNA sequencing

Before transcriptome samples can be sequenced, scientists must (1) change the mRNA into DNA, and (2) purify the mRNA (i.e. remove other cellular RNAs).

We cannot sequence RNA directly. Instead, scientists recode the information in the mRNA back into DNA, using an enzyme called **Reverse Transcriptase**. Reverse transcriptase can make a DNA copy, called cDNA, of all the mRNAs in a sample. The cDNA can then be sequenced using Next-generation Sequencing.

It would be disadvantageous, however, to sequence all the RNA in a sample. Approximately 80% of the RNA in a eukaryotic cell is rRNA and another 15% is tRNA. Only a small fraction of the RNA is actually mRNA. Scientists can purify the mRNAs from the total RNA using an **Oligo-dT primer**. This method focuses on a feature that is unique to mRNAs: the Poly-A tail. An Oligo-dT primer is made of a string of thymine nucleotides that can base pair with the Poly A tails. This will target the reverse transcriptase enzyme directly to the mRNAs. Once the cDNA has been synthesized, the samples are prepared for sequencing.

RNA sequencing

Which feature of the mRNA allows scientists to specifically sequence the mRNAs?

- Poly-A Tail
- Exons
- 5'-cap
- Introns

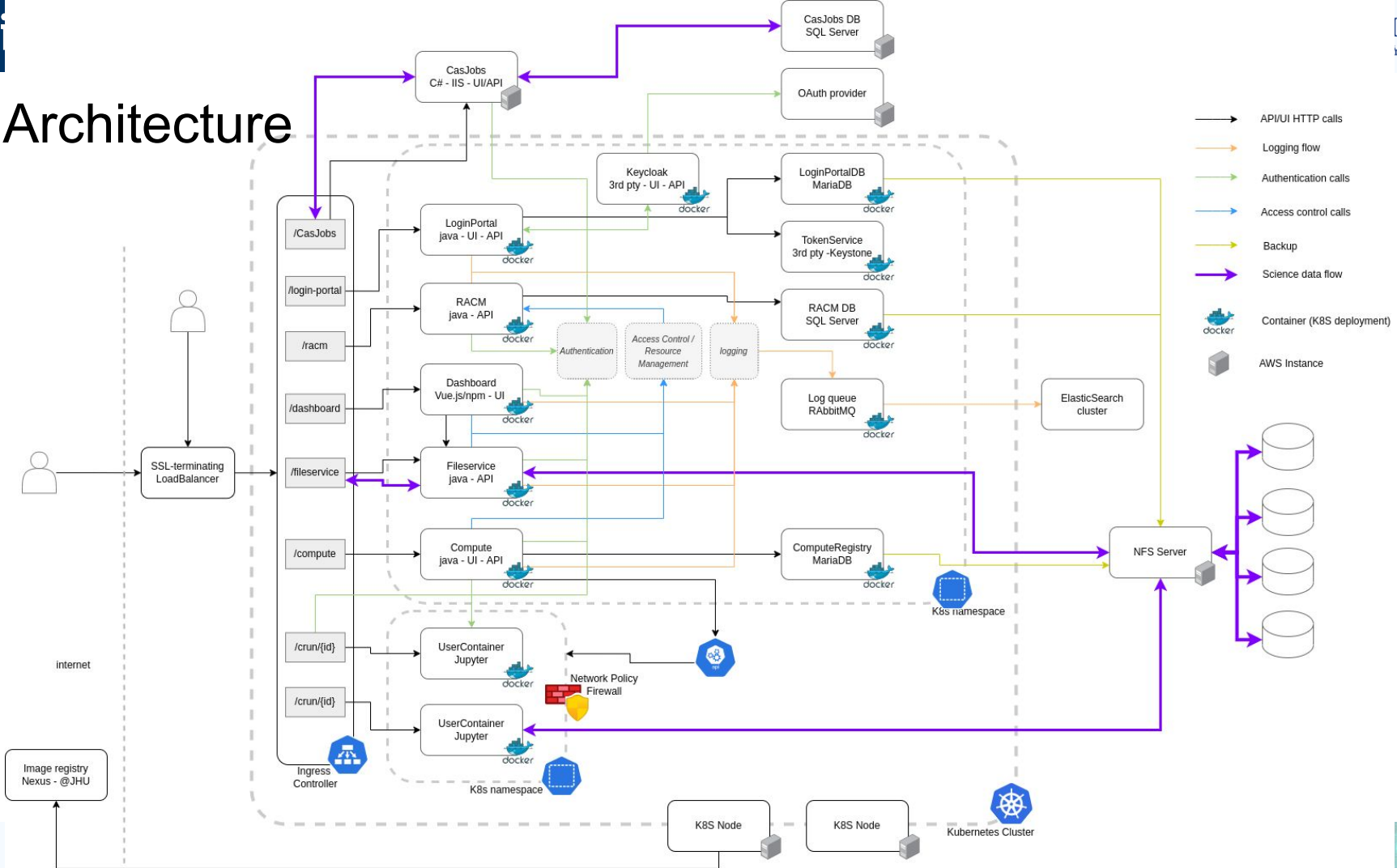
Submit Answer

What is the function of the Reverse Transcriptase enzyme?

- Makes DNA using DNA as a template
- Makes RNA using DNA as a template


SciServer as a service


Architecture





Deployments


- All the same features:
 - In another datacenter on own hardware
 - Behind a VPN
 - For specific insiders
 - In a HIPAA-safe environment
- A number of partners
- Active development

 **JOHNS HOPKINS**
UNIVERSITY
 @JHU (sciserver.org)
On premise

@NIST 
AWS VPC, k8s

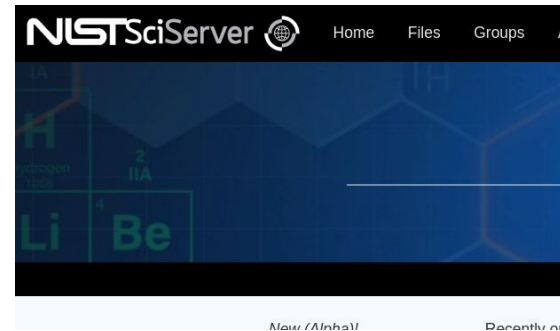
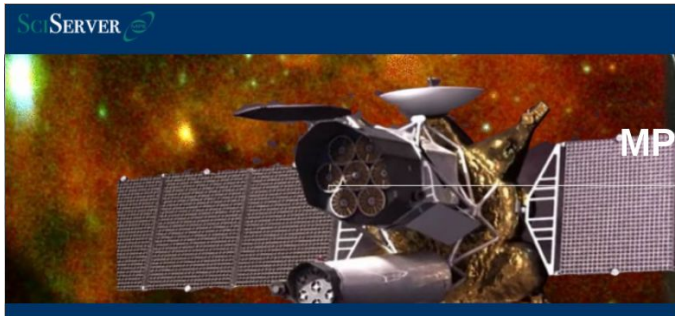
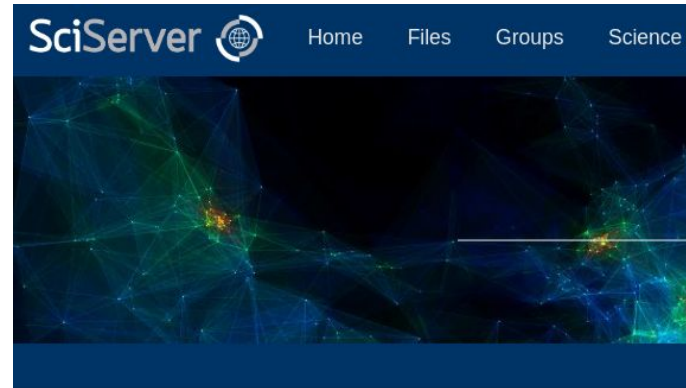
@NAOJ 
On premise, k8s

@MPE 
On premise, k8s

@Precision-Medic 
Azure, secure-desktop

Deployments

- Branding
 - Theme customizations
 - links
 - etc



Deployments

- Leverage Kubernetes and helm
- Bundle SciServer + 3rd party dependencies
- Configurable with a single file

```
$ helm install sciserver -f config.yaml sciserver-k8s/charts/sciserver
```



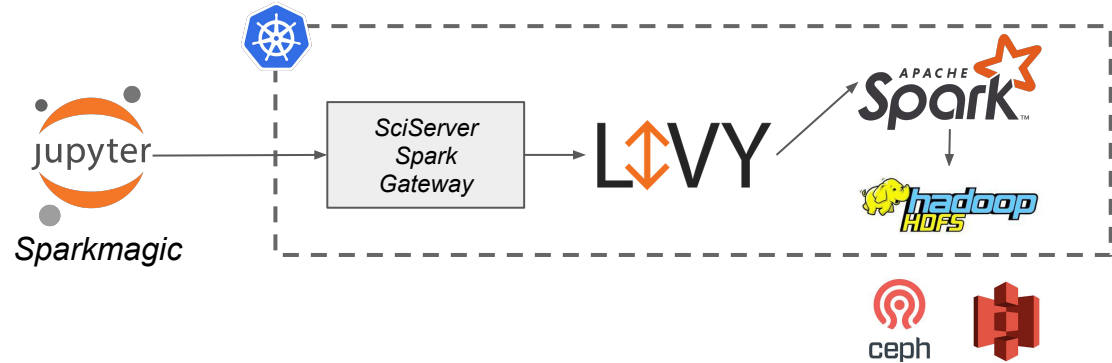
Extra Features

Extra features

- Accelerated computing
 - GPU
 - Spark
 - Dask
- Interactive and/or Jobs

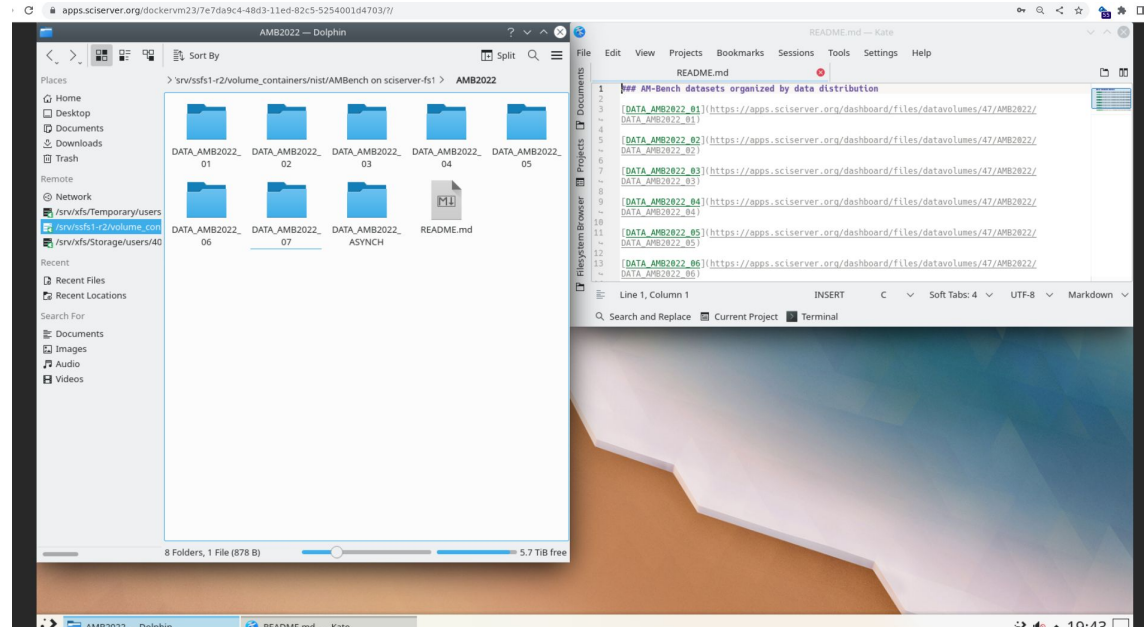


 PyTorch  TensorFlow



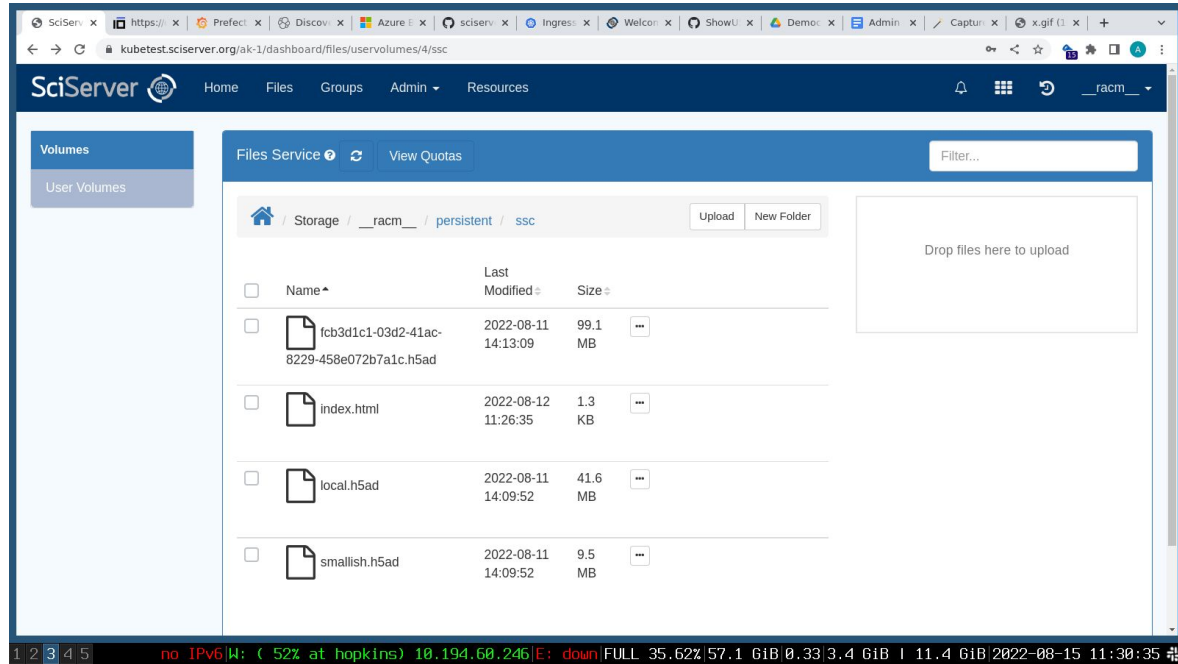
Extra Features

- Not Just Jupyter
- Compute exposes service that listens to single port
- VNC, for example



Extra Features

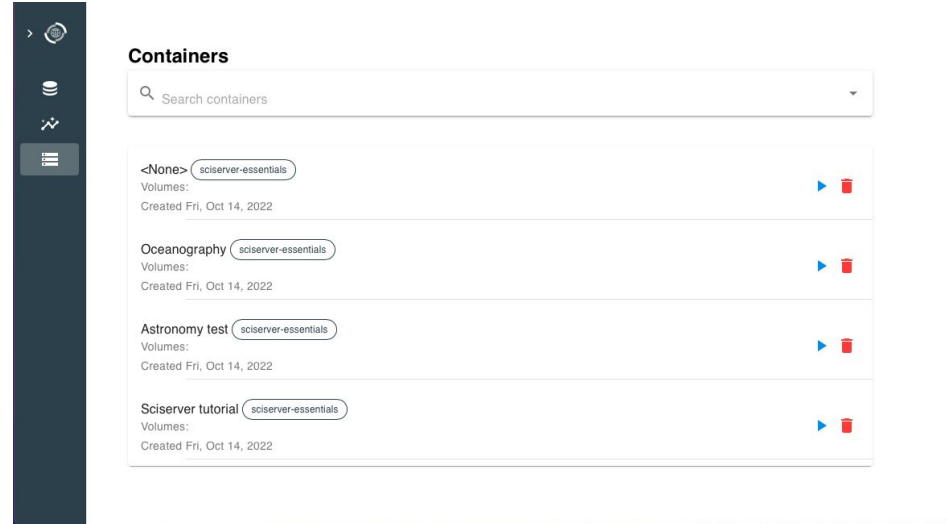
- “One-click apps”
- Shareable links
- Argument passing
 - Can do in one-click what would take steps using generic compute containers
- Operate on files
- Embedded feel



Future Directions

Future Directions

- UI consolidation / improvements
 - Simplify development
 - Simplify branding and customizations
 - Improved layout and features

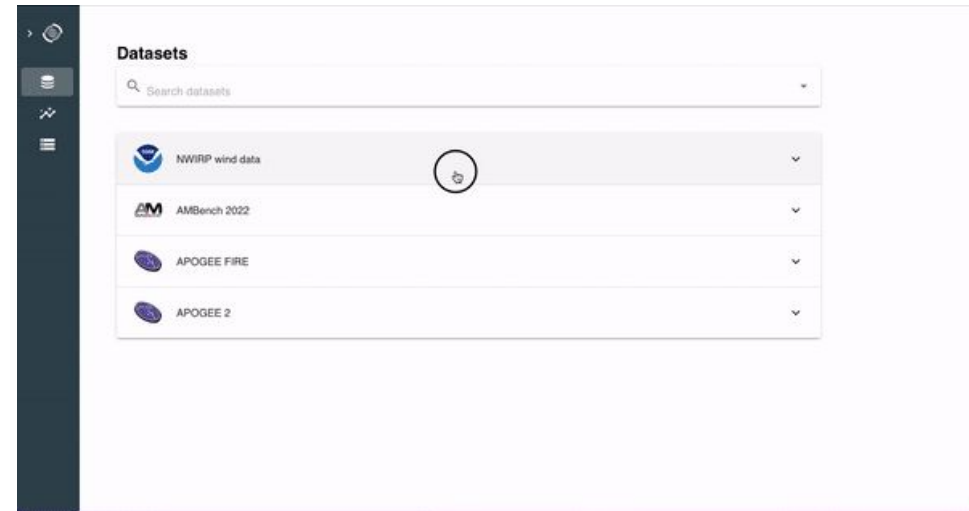


The screenshot displays the 'Containers' management interface. On the left is a dark sidebar with navigation icons. The main content area features a search bar at the top, followed by a list of containers. Each container entry includes a name, a volume label, and creation details, with play and delete icons for management.

Container Name	Volume Label	Created	Actions
<None>	sciserver-essentials	Fri, Oct 14, 2022	▶ 🗑️
Oceanography	sciserver-essentials	Fri, Oct 14, 2022	▶ 🗑️
Astronomy test	sciserver-essentials	Fri, Oct 14, 2022	▶ 🗑️
Sciserver tutorial	sciserver-essentials	Fri, Oct 14, 2022	▶ 🗑️

Future Directions

- UI consolidation / improvements
- Data discoverability
 - “Documents close to the data”
 - Leverage built-in access control
 - Human and machine writable
 - Just documentation, not full ontology




Future Directions

- UI consolidation / improvements
- Data discoverability
- One-click simplicity / link-share
 - Combine with data discoverability
 - Notebooks, quicker start
 - Jupyter widgets based apps
 - Sends links, not wordy instructions



New (Alpha)

[Quick Notebook](#) 

Recently opened notebooks: (see all)

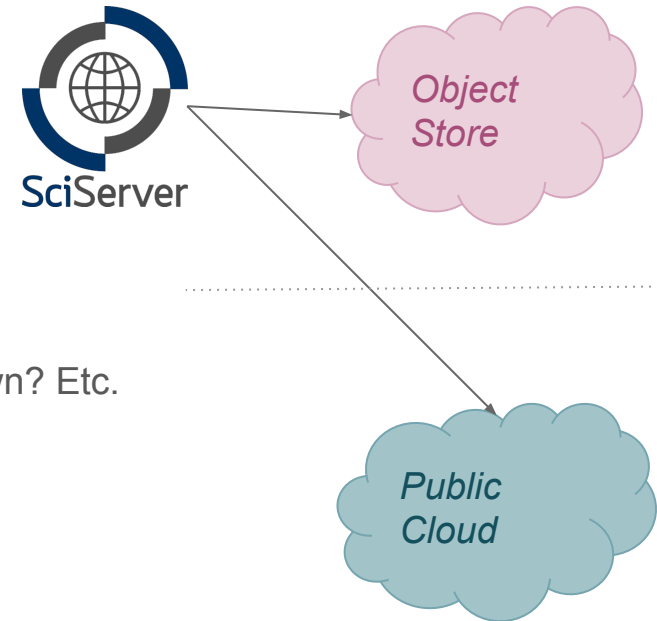
- [explore-single-cell-data](#) (in `persistent/SSC`) SciServer Essentials 3.0
- [new-notebook-1663858207935](#) (in `scratch/sciserver`) SciServer Essentials 2.0
- [abuse_detection_cpu](#) (in `gerard/SciServerUsageStatistics/elasticsearch`) SciServer Essentials

Your Activities

The screenshot shows the SciServer file browser interface. The top navigation bar includes 'Home', 'Files', 'Groups', 'Admin', and 'Resources'. The main content area shows a file named 'HISAKWE.md' with a last modified date of '2020-10-11 15:23:46' and a size of '305 Bytes'. Below the file list, there are 'Example applications' listed: 'Intro-scrapy-persisngreen-out', 'scrap-learning-knowledge', 'distributed-cluster-trading-in-Spark', and 'wslgpt-service'. A 'Drop files here to upload' area is visible on the right side of the interface.

Future Directions

- UI consolidation / improvements
- Data discoverability
- One-click simplicity / link-share
- Cloud integrations
 - Object storage integration
 - Compute: site-wide? Research group? Bring-your-own? Etc.
 - Cloud-only datasets



Future Directions

- UI consolidation / improvements
- Data discoverability
- One-click simplicity / link-share
- Cloud integrations
- Others on the radar
 - Extended login sessions / api keys
 - Scheduled / cron-like jobs
 - Anonymous file sharing

Thanks!



2012-2016

