Bioinformatics in the Cloud with the CGC

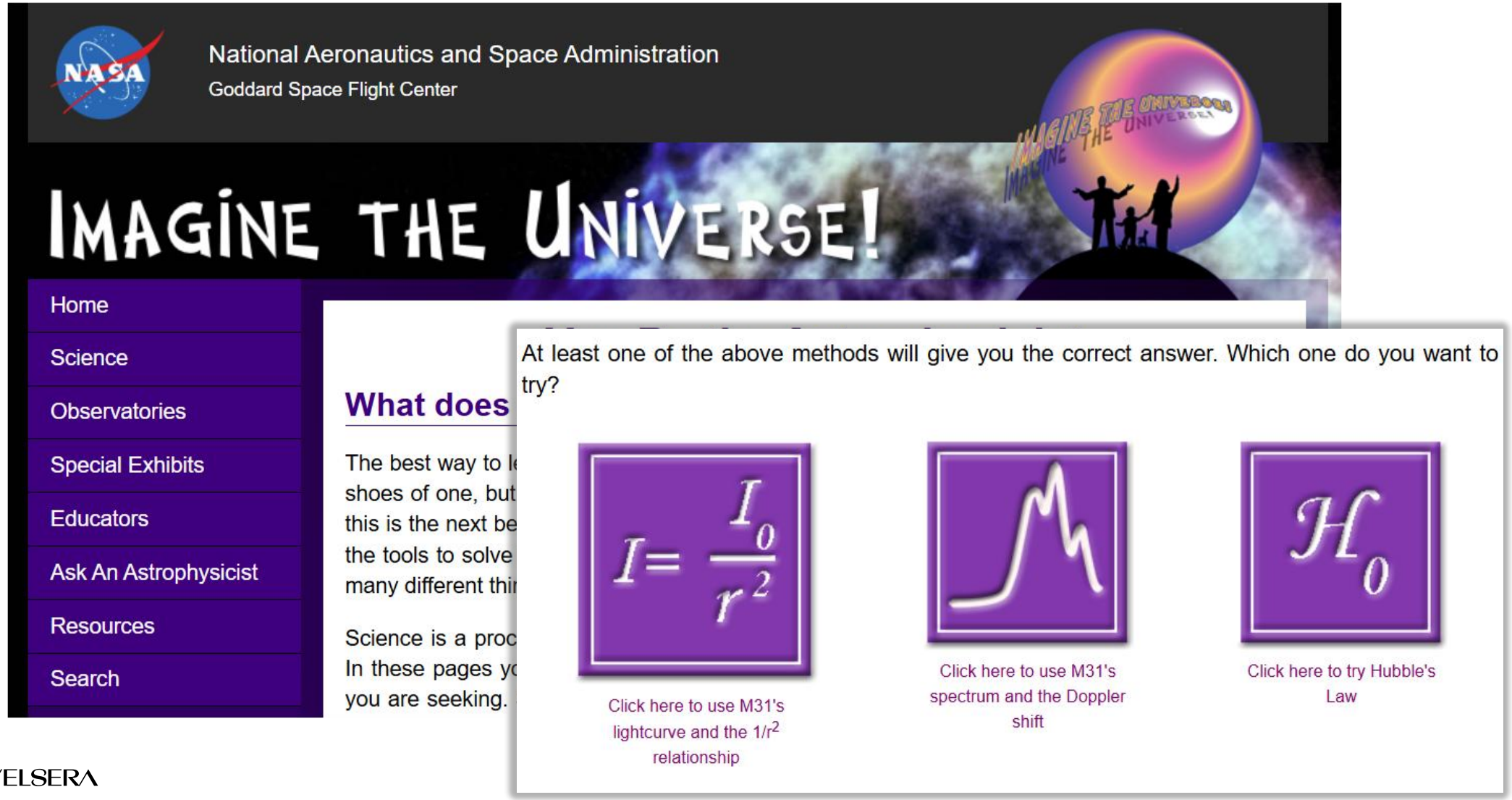
Leveraging the cloud to turbocharge your research

BTEP webinar

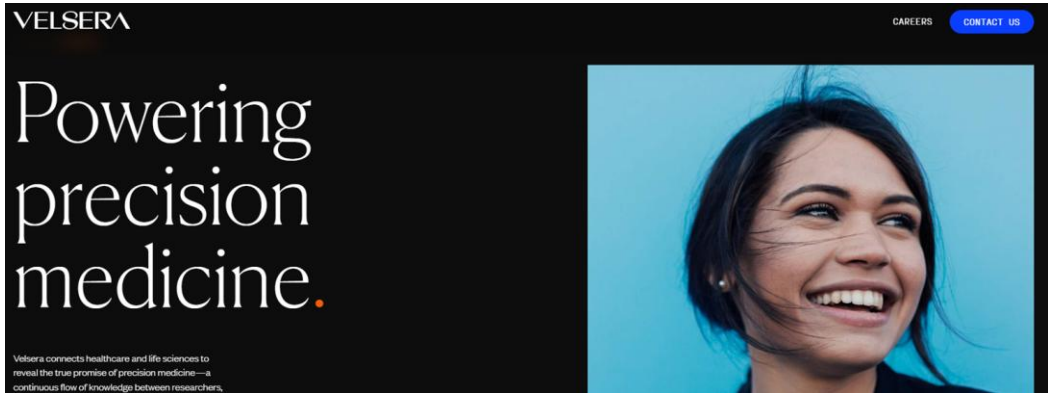
07/21/2026

Jeni Cliffe

Mini-bio – Jenepher A. Cliffe (M.S. Astrophysics)



Community Engagement Manager, Velsera



- Make NIH research better by:
  - Helping scientists and doctors analyze their research data on the Cloud
  - Teaching people how to work with and manage big data
  - Giving people better tools so research happens faster

From exploding stars to – humans?!

Agenda.

Bioinformatics in the Cloud with CGC

01	Introduction to the CGC and Cloud Computing
02	Accessing data and running tools (overview)
03	Variant analysis run-through
04	New feature highlights: OHIF viewer and 3D Slicer

Introduction to Cloud Computing with the Cancer Genomics Cloud

Let’s take a poll!

How comfortable are you with the cloud and cloud data?

1

Not comfortable

I’ve used it very little, or never

2

Somewhat comfortable

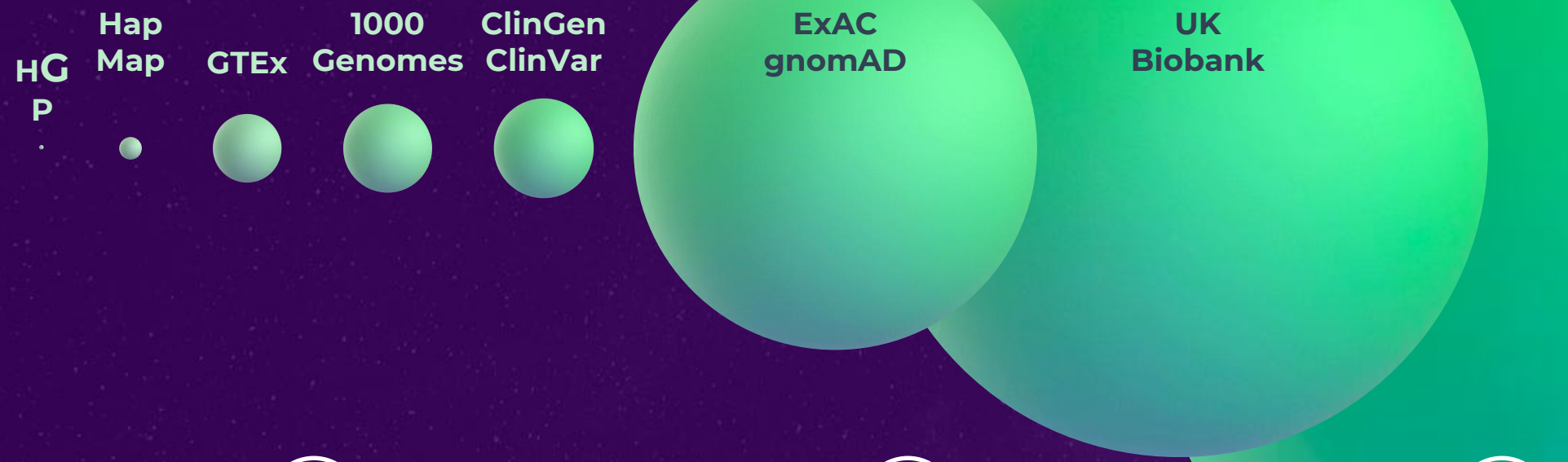
I’ve used it before

3

Very comfortable

I use it all the time

Data generation is on a roll...



2001
1
Human Genome

2010
1000
Human Genomes

2020
1M
Human Genomes

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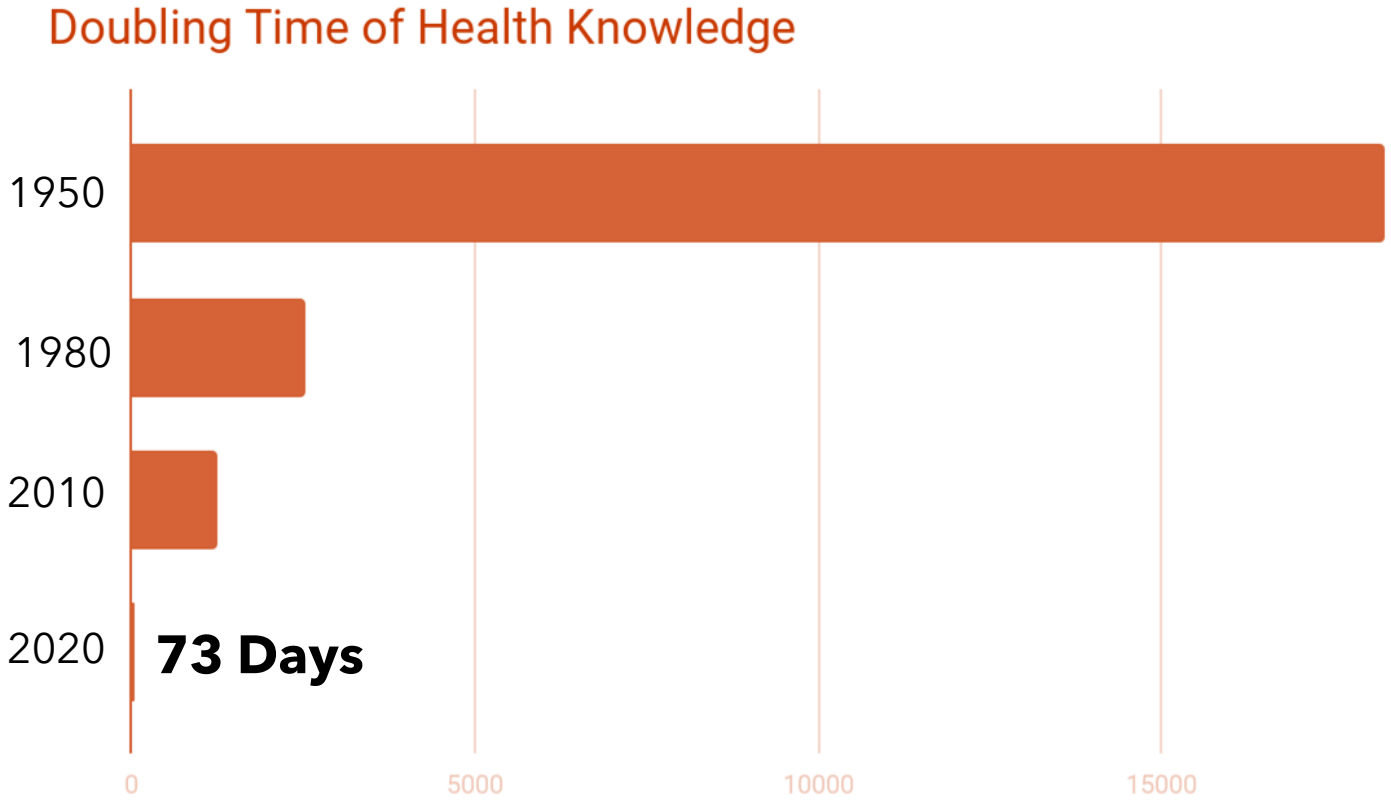
The Era of Big Data in Health

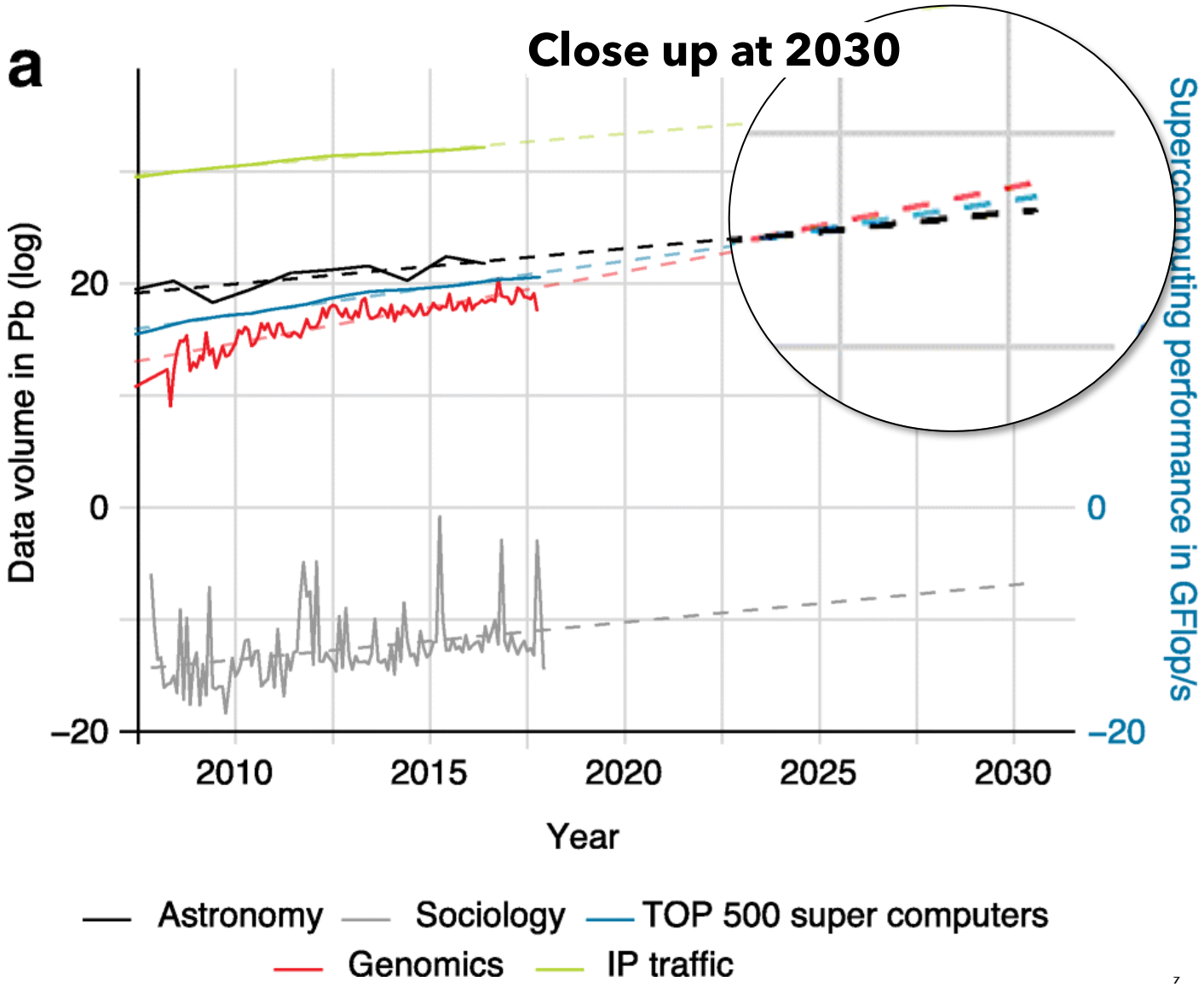


More biomedical data were generated in 2021 than all previous years **combined**

More different ***kinds*** of data – gene and genome sequencing, imaging, sensors (i.e. Fitbit), cellular measurement data, and more

How much data is it?

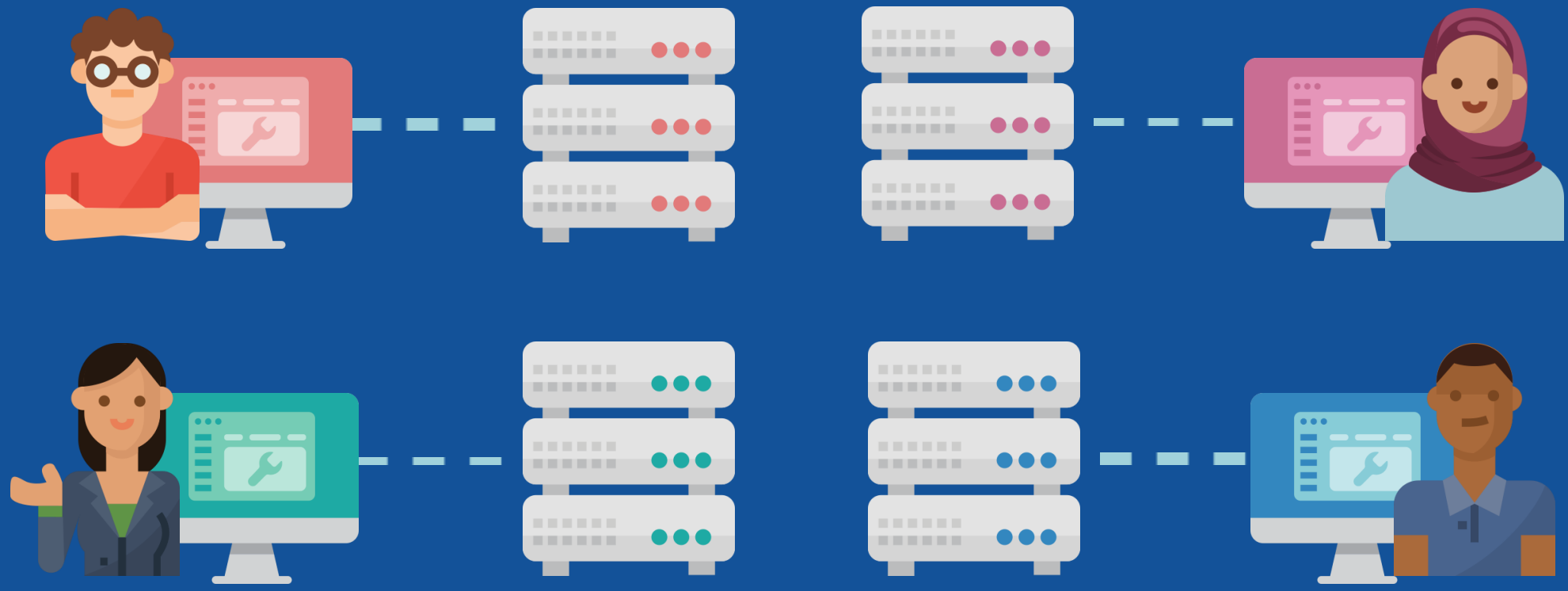
- *Estimated* between 2 and 40 exabytes of new data per year (Stephens *et al.* 2015)
- Genomics data is growing **faster than *the internet***
- Analysis-to-Data Paradigm – analyze data "where it lives"



How do we share and analyze datasets?

Traditional Approach

Bring data to researchers



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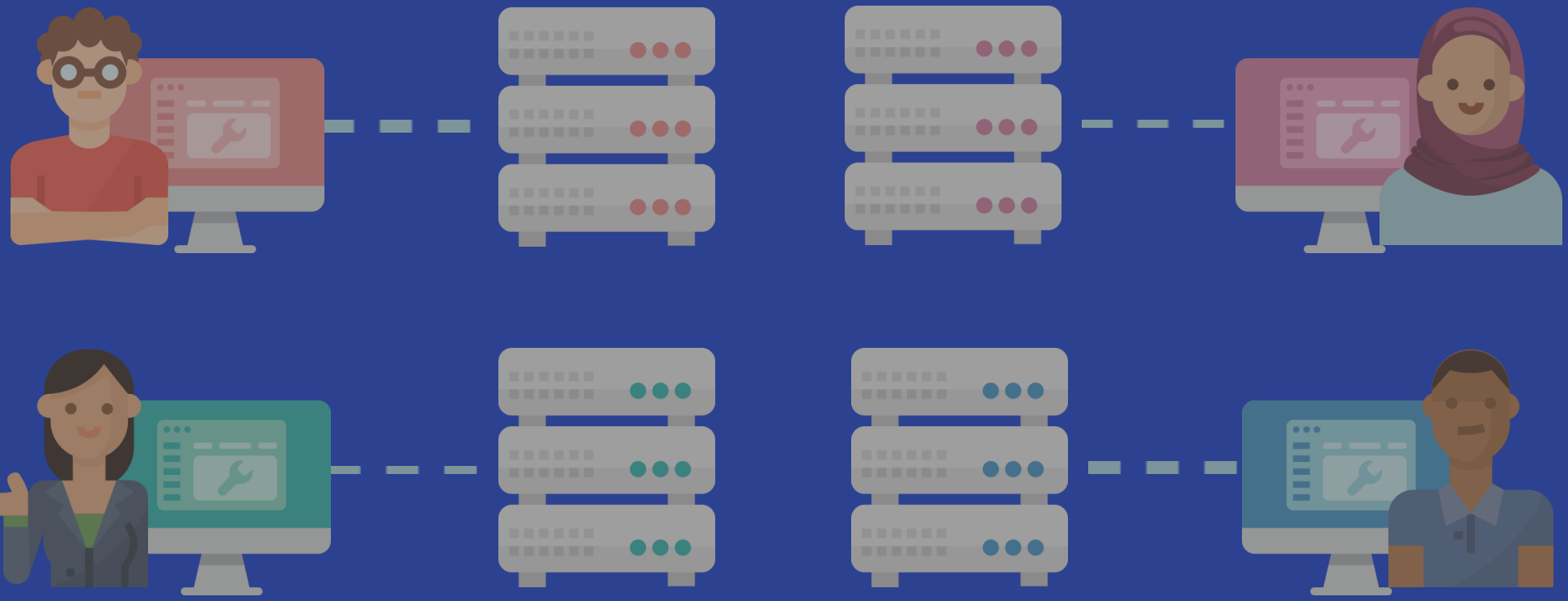
What’s wrong with this traditional approach? ?

Data is copied, not shared

High storage & infrastructure costs

Hard to share/ reproduce

Security on individuals



A new cloud-native vision for biomedical research

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A new cloud-native vision for biomedical research

~~Data is copied, not shared~~

True immediate data sharing

~~High storage & infrastructure costs~~

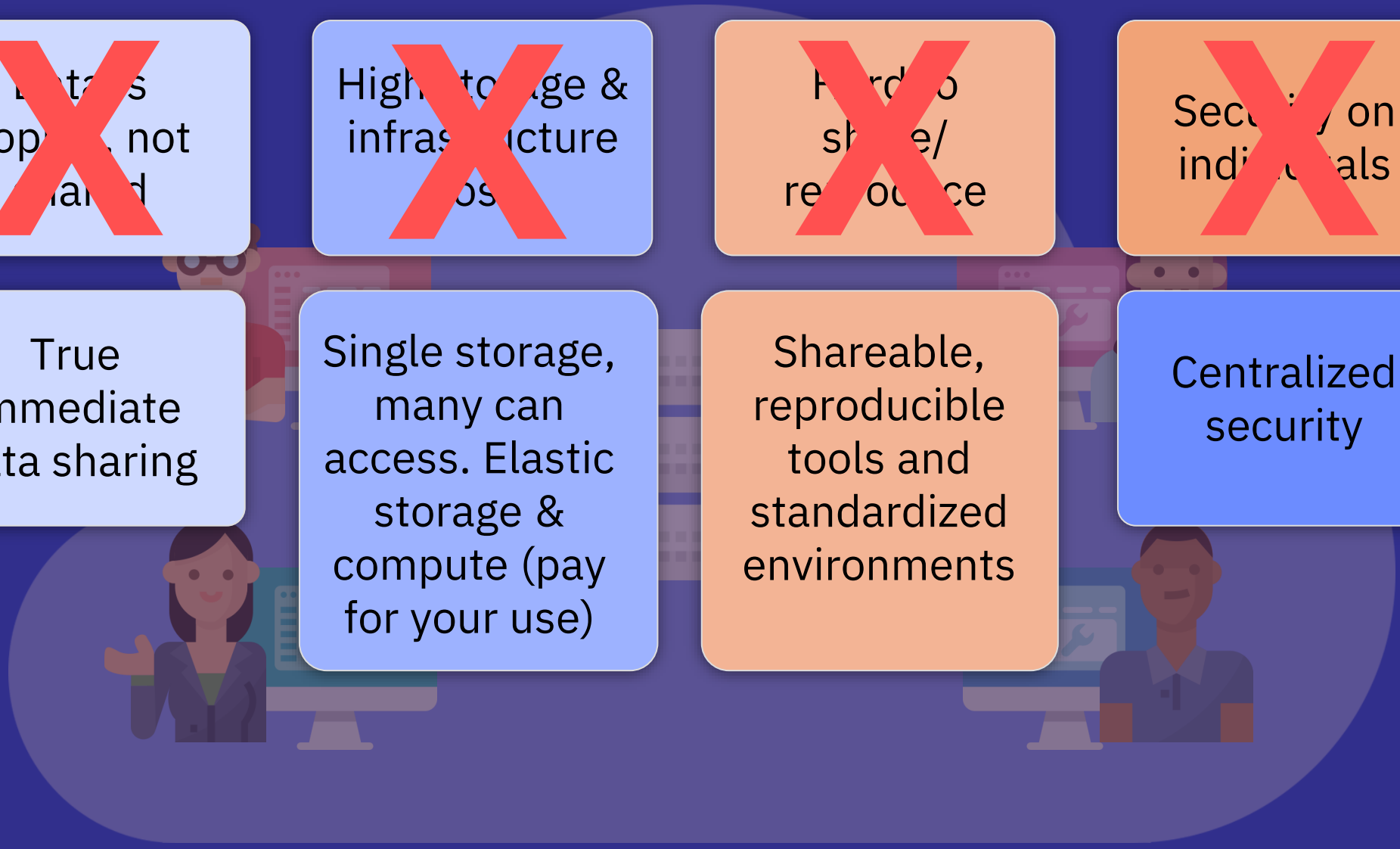
Single storage, many can access. Elastic storage & compute (pay for your use)

~~Hard to share/ reproduce~~

Shareable, reproducible tools and standardized environments

~~Security on individuals~~

Centralized security



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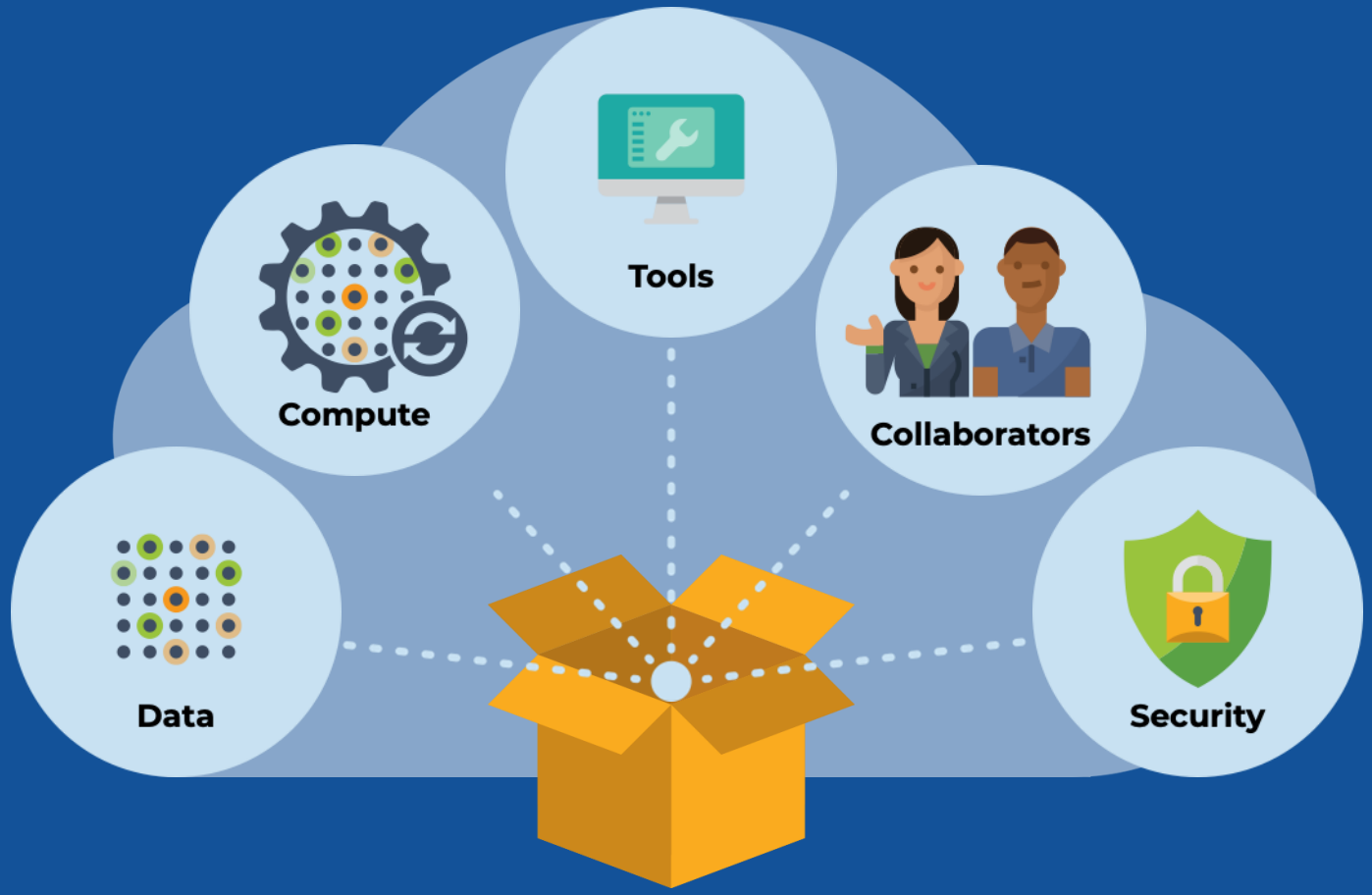
A new cloud-native vision for bioinformatics

Migrating to the cloud can be challenging!!



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cancergenomicscloud.org

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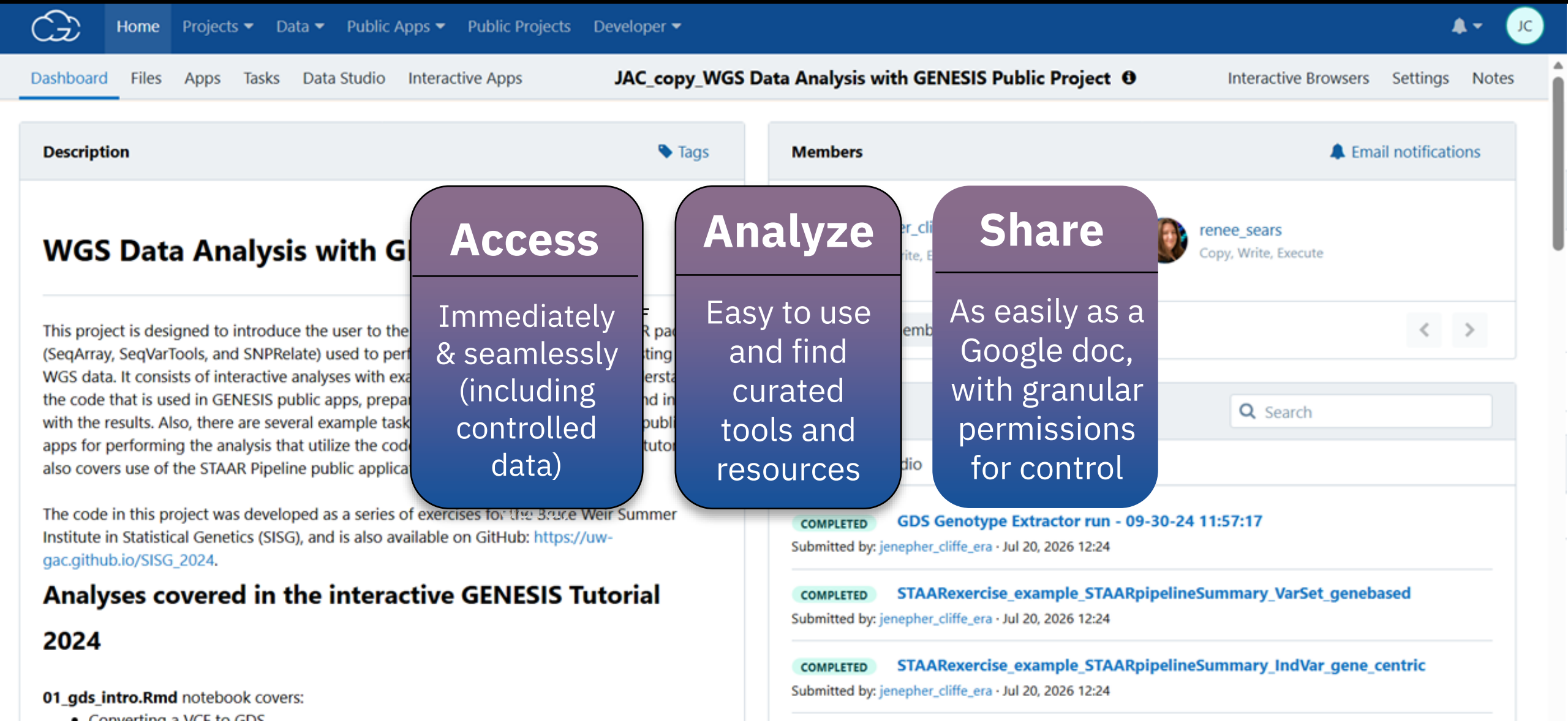
A new cloud-native vision for biomedical research



Access

Immediately & seamlessly (including controlled data)

Analyze

Easy to use and find curated tools and resources

Share

As easily as a Google doc, with granular permissions for control

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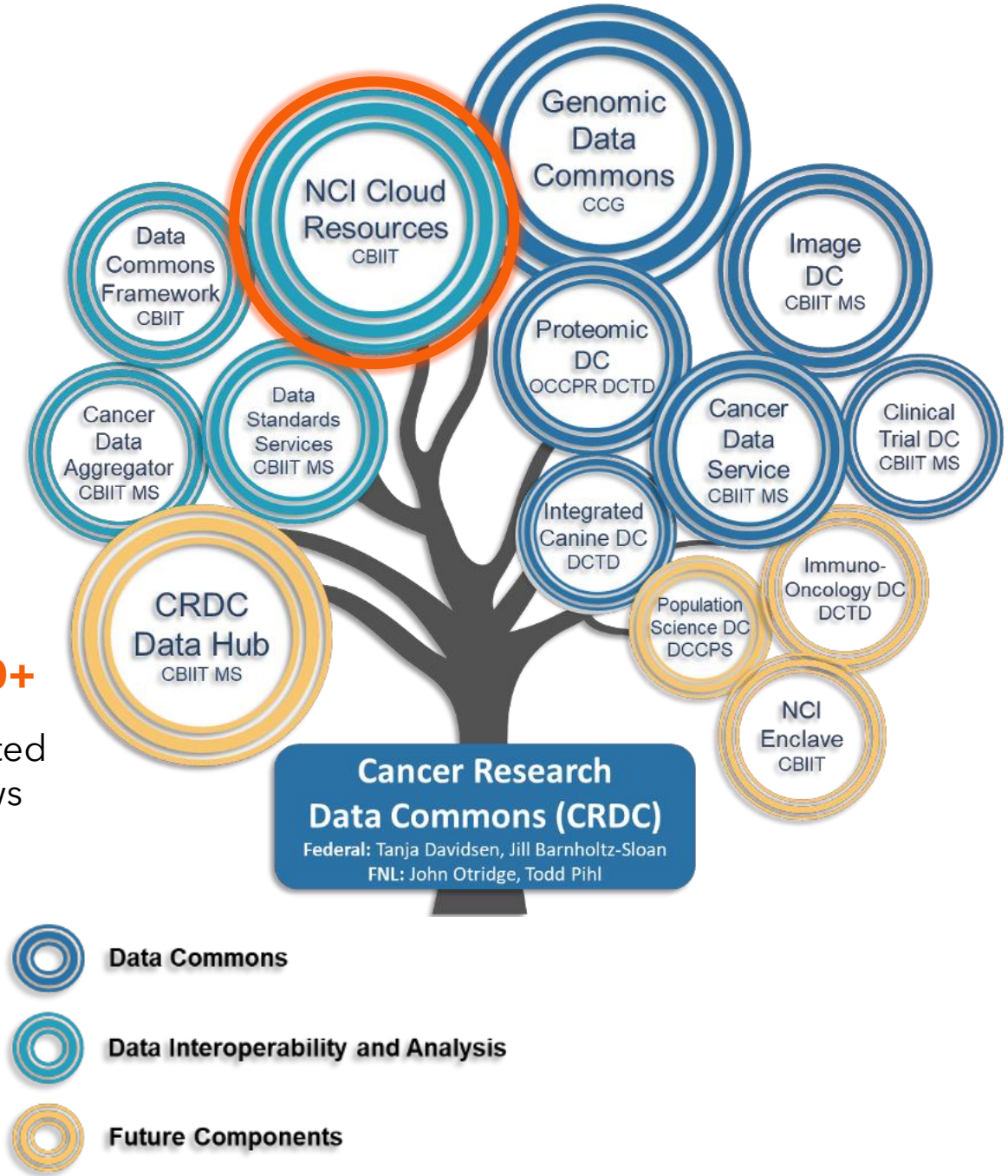
Powerful, yet easy to use interfaces to empower cancer researchers to draw new insights from petabyte scale data.

Stable, secure, and highly customizable cloud storage and computing platform

3+	2.4M+	1300+	12,500+	109,000+
Petabytes Public Data	Years of Compute	Public Tools & Workflows	Users	User-Created Workflows



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Who are CGC Users?

The CGC is designed to serve a wide range of scientists and users with varying skill sets

ADMINISTRATORS

- Manage and control users
- Monitor and control institutional assets
- Manage and monitor projects
- Monitor and control costs
- Create reports

BIOINFORMATICIANS

- Store, manage, and share data
- Access public and proprietary datasets
- Query, build, and investigate cohorts of interest
- Access optimized tools and workflows
- Create, optimize, maintain, and distribute new tools and workflows
- Create bush-button automation solutions
- Analyze data at scale with tools and workflows
- Conduct interactive exploratory analyses
- Explore/visualize results/gather insights
- Easily collaborate with stakeholders
- Integrate with external systems

BENCH SCIENTISTS

- Store, manage, and share data
- Run optimized tools/ workflows at scale
- Conduct defined analyses via push-button solutions
- Investigate/visualize results
- Easily collaborate with other stakeholders

CLINICIANS

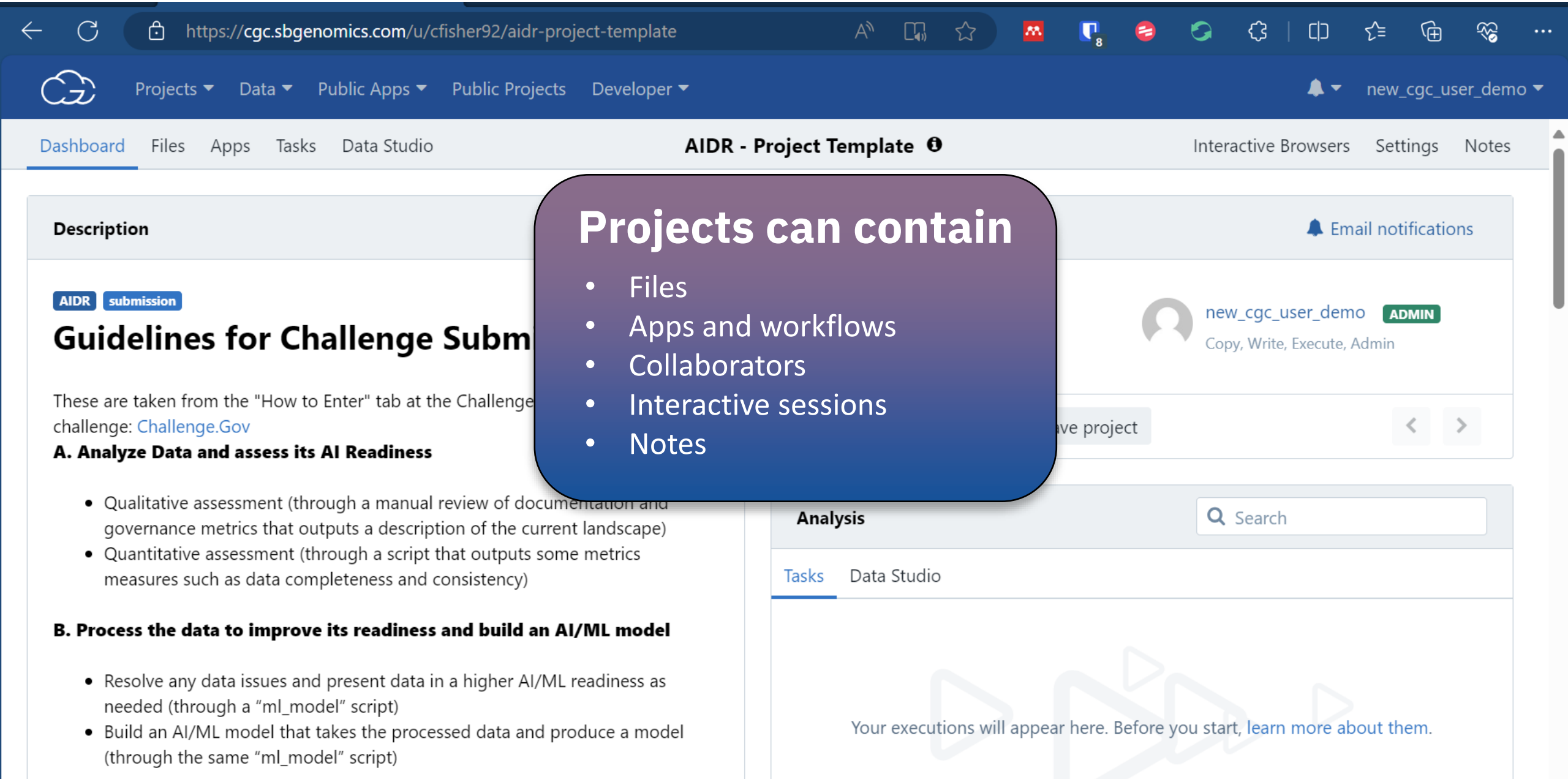
- Conduct validated analyses via push-button solutions
- Query, build, and investigate cohorts of interest
- Create reports
- Investigate/visualize results
- Easily collaborate with other stakeholders

DEVELOPERS

- Create, optimize, and maintain new tools and workflows
- Create push-button automation solutions
- Create custom interfaces for specific use cases
- Distribute proprietary tools/workflows
- Integrate upstream/downstream

Navigating the Cancer Genomics Cloud

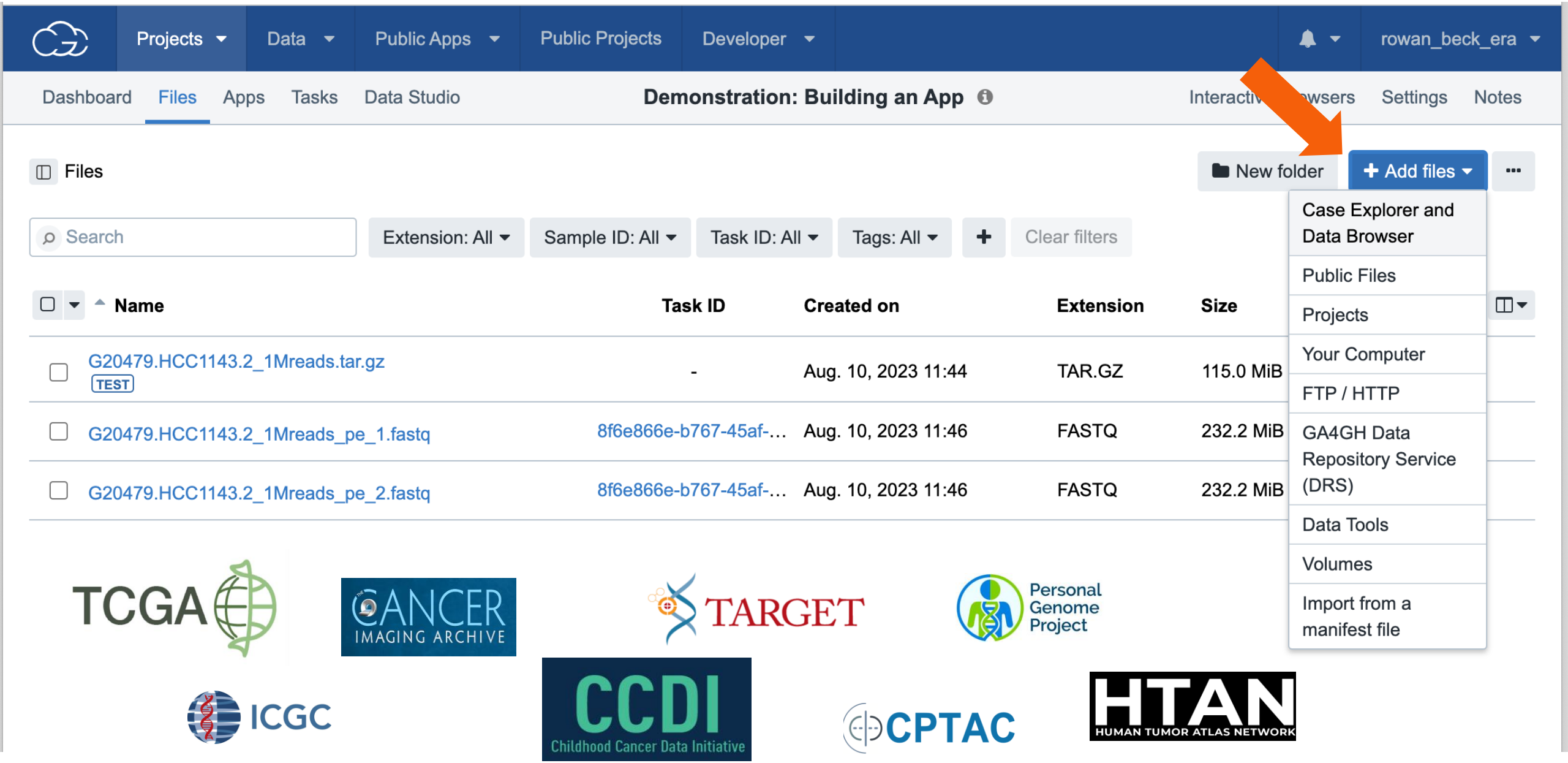
“Projects” are the main unit of Organization



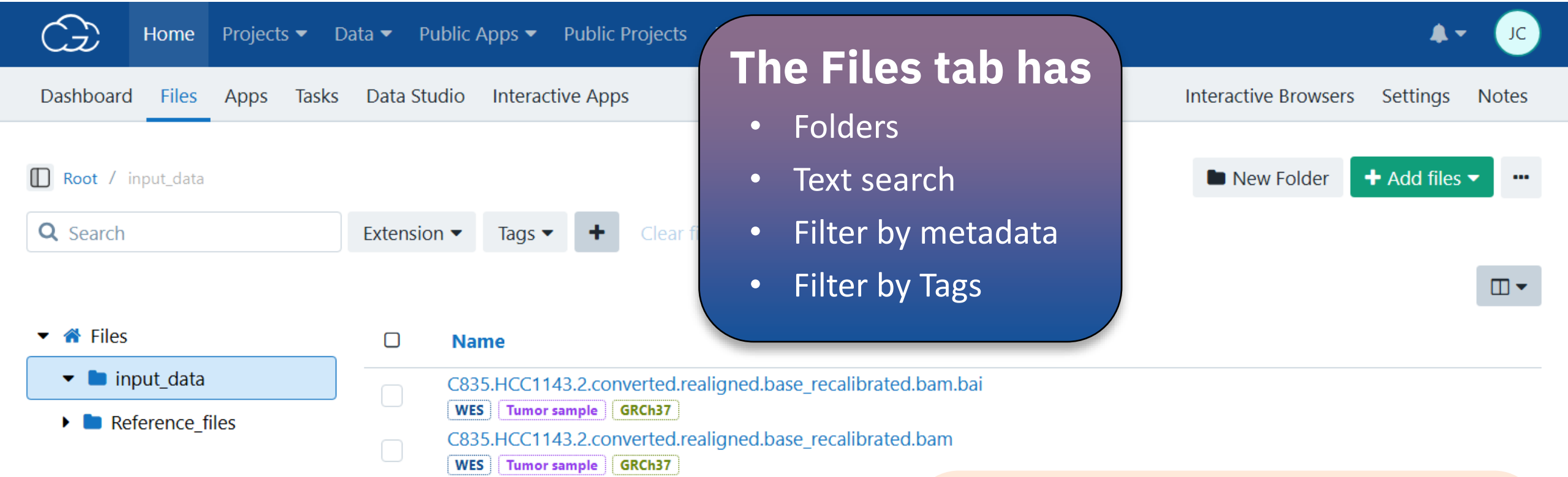
Projects can contain

- Files
- Apps and workflows
- Collaborators
- Interactive sessions
- Notes

Access Public Data, or Use Your Own



Files and file management



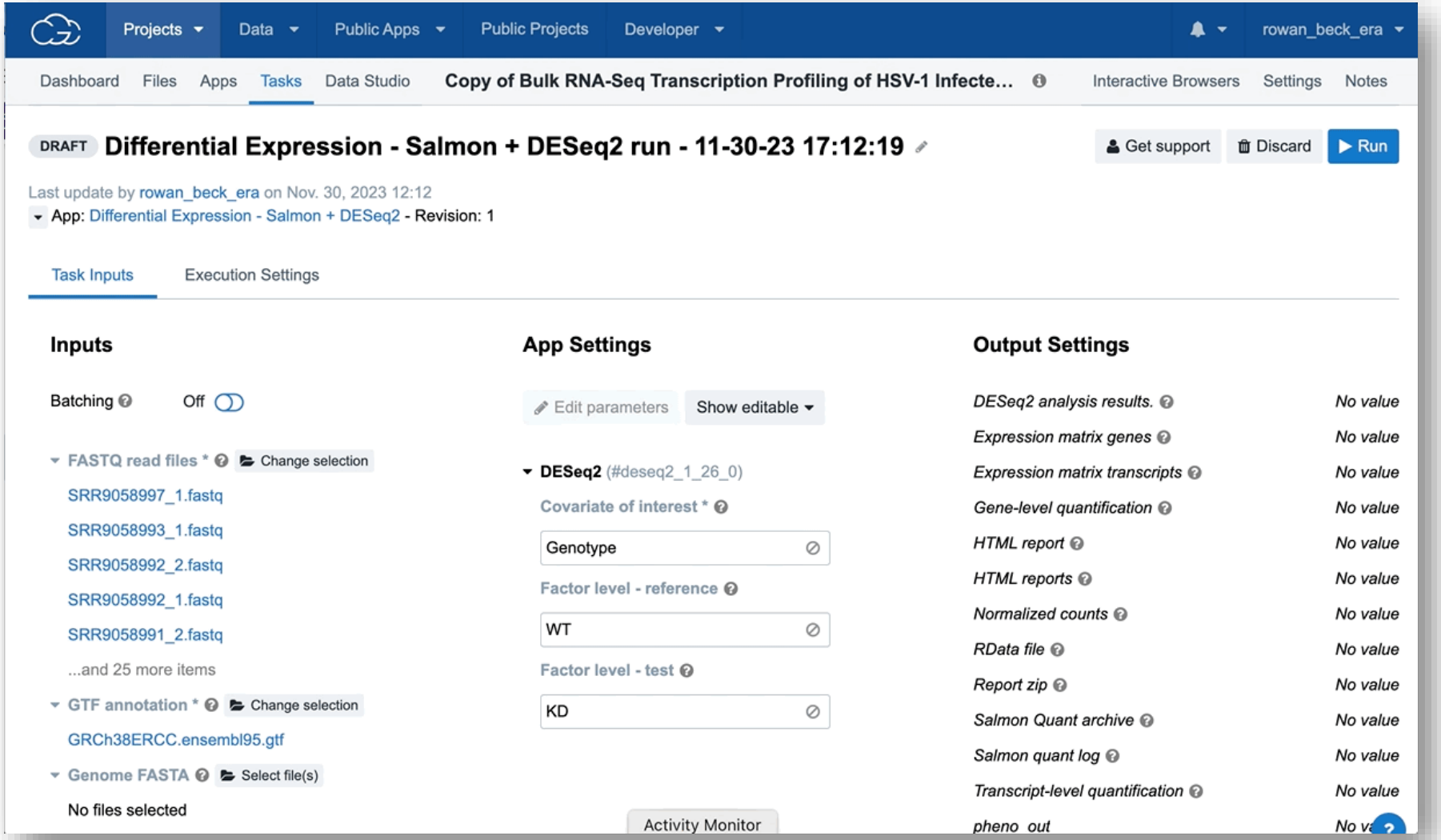
The Files tab has

- Folders
- Text search
- Filter by metadata
- Filter by Tags

LEARN

File Management:
https://youtu.be/Z4ygBEBunuY
Knowledge Center:
Files and metadata (cancergenomicscloud.org)

No coding required to run an analysis



Over 1300 curated tools and workflows

High quality apps & documentation

Customized user tools/workflows

Updated regularly

Optimized to run on cloud

Secure

Apps and Workflows: https://youtu.be/ayCKOafCGB0

Knowledge Center: Workflows and tools (cancergenomicscloud.org)

Data Studio – Interactive Data Analysis

Data Studio

Derive new insights using interactive analysis environments with Data Studio environments. Code in Python, SAS, and R to record and share your analyses.

Interact with files directly using our OHIF image viewer and Galaxy.

Videos:
R Studio on the CGC: https://youtu.be/_f8DWRTS0rE
JupyterLab on the CGC: https://youtu.be/iycWVHhqgXg

Documentation:
About Data Studio (cancergenomicscloud.org) | https://docs.cancergenomicscloud.org/docs/about-data-cruncher

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Open Health Imaging Foundation

Apps – Bulk Processing Analysis

Command Tools and Workflows

- Convert any R or Python or bash script into an app that can be optimized and automated.
- Automated and optimize to scale up.

Videos:
CGC Onboarding:
https://youtube.com/playlist?
Public Apps Gallery:
https://youtu.be/ayCKOafCGB0?si=ps0O3ihGvgNvanB_

Documentation:
Apps on the CGC (cancergenomicscloud.org) | https://docs.cancergenomicscloud.org/docs/apps-on-the-cgc

CGC Democratizes Complex Analyses

A FAIR data ecosystem

- **F**indable, **A**ccessible, **I**nteroperable and **R**eusable (FAIR)
- Immediate scaling (“Rent” vs “Buy”)
- Levels the playing field across institutions
- Many researchers can access data - no duplicate copies.
- Reproducibility - data and methods together.

HANDS-ON DEMO

cgc.SBGenomics.com

Variant Calling

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Coming soon to the Cancer Genomics Cloud

Quantitative QC for Lung CT: 3D slicer

Dashboard | Files | Apps | Tasks | Data Studio | Interactive Apps | **Copy of COVID-19 Image Segmentation with Deep...** | Interactive Browsers | Notes

What it does

- Computes spatial overlap and boundary metrics
- Quantifies volume bias and over-segmentation
- Categorizes masks into pass, review, or fail
- Generates auditable segmentation quality records

Description

Email notifications

This project provides deep learning image seg
notebook, along with a pretrained model for s
images. The model was trained on a publicly a
Analysis files include:

- A Jupyter notebook walking through th
model. This notebook can be repurpos
applications by replacing the image pre
code and datasets.
- A Keras model based off of a UNet arch
encoder pretrained with ImageNet weig
- Images and masks in NIfTI (.nii) format,
masks for ground glass opacities and p
- Images and lung masks in NumPy array
images are shuffled from the order in th
- A plot of loss history over the course of t
will be overwritten if a new model is trained.
- Utility and dependency files.

To use the tools, select **Interactive Analysis > Data Cruncher > JupyterLab**. The notebook can be run using CPU, single-GPU, or multi-GPU instances in the **SB Machine Learning environment**. To use the model as is for predictions,

yachna
Copy, Write, Execute

yachnajain
Copy, Write, Execute

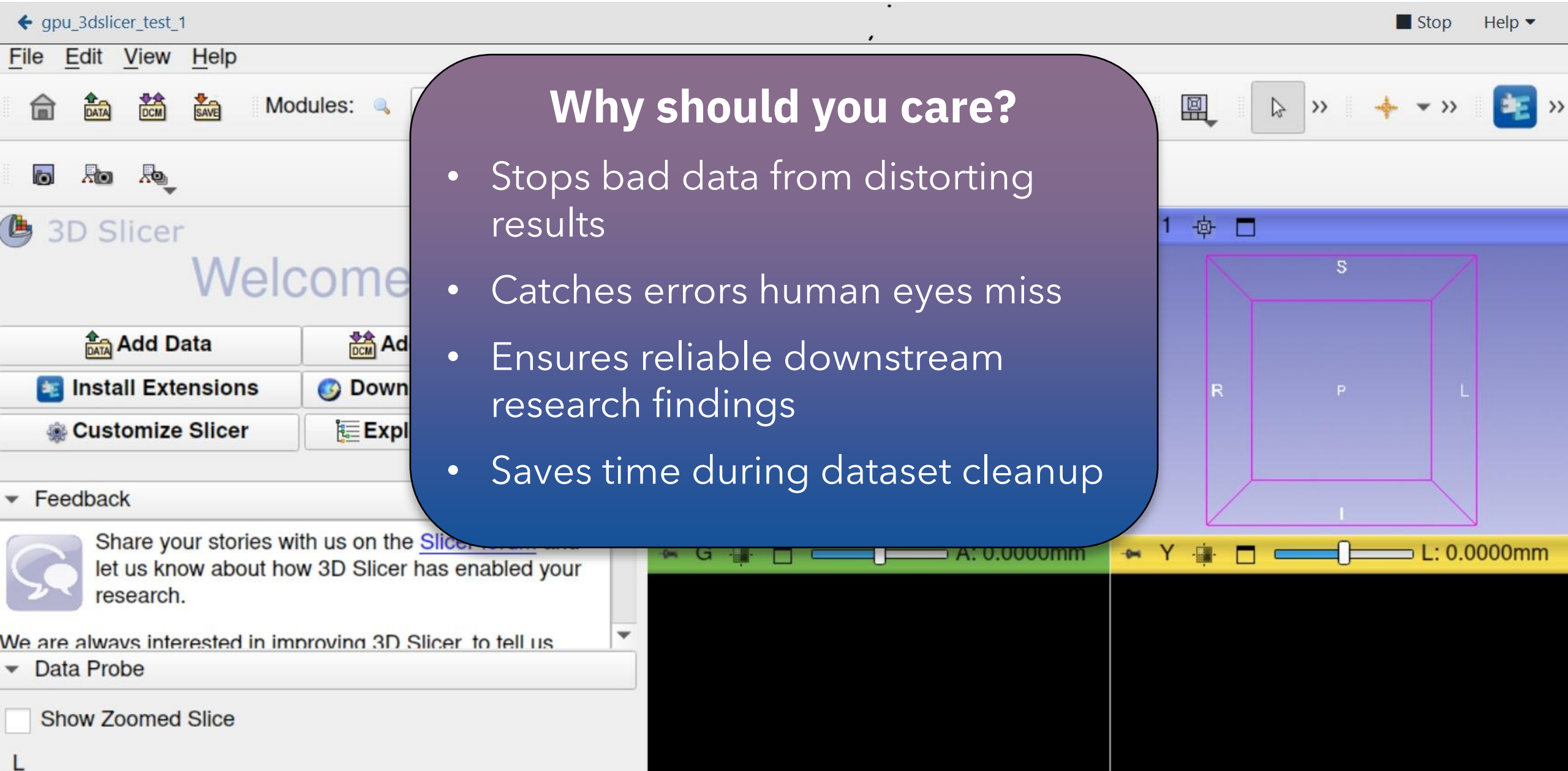
jenepher_cliffe_era_login
Copy, Write, Execute

Search

Tasks | Data Studio

COMPLETED **SBG Compressor CWL1.0 run - 06-29-26 07:48:48**
Submitted by: yatishp · Jun 29, 2026 3:48

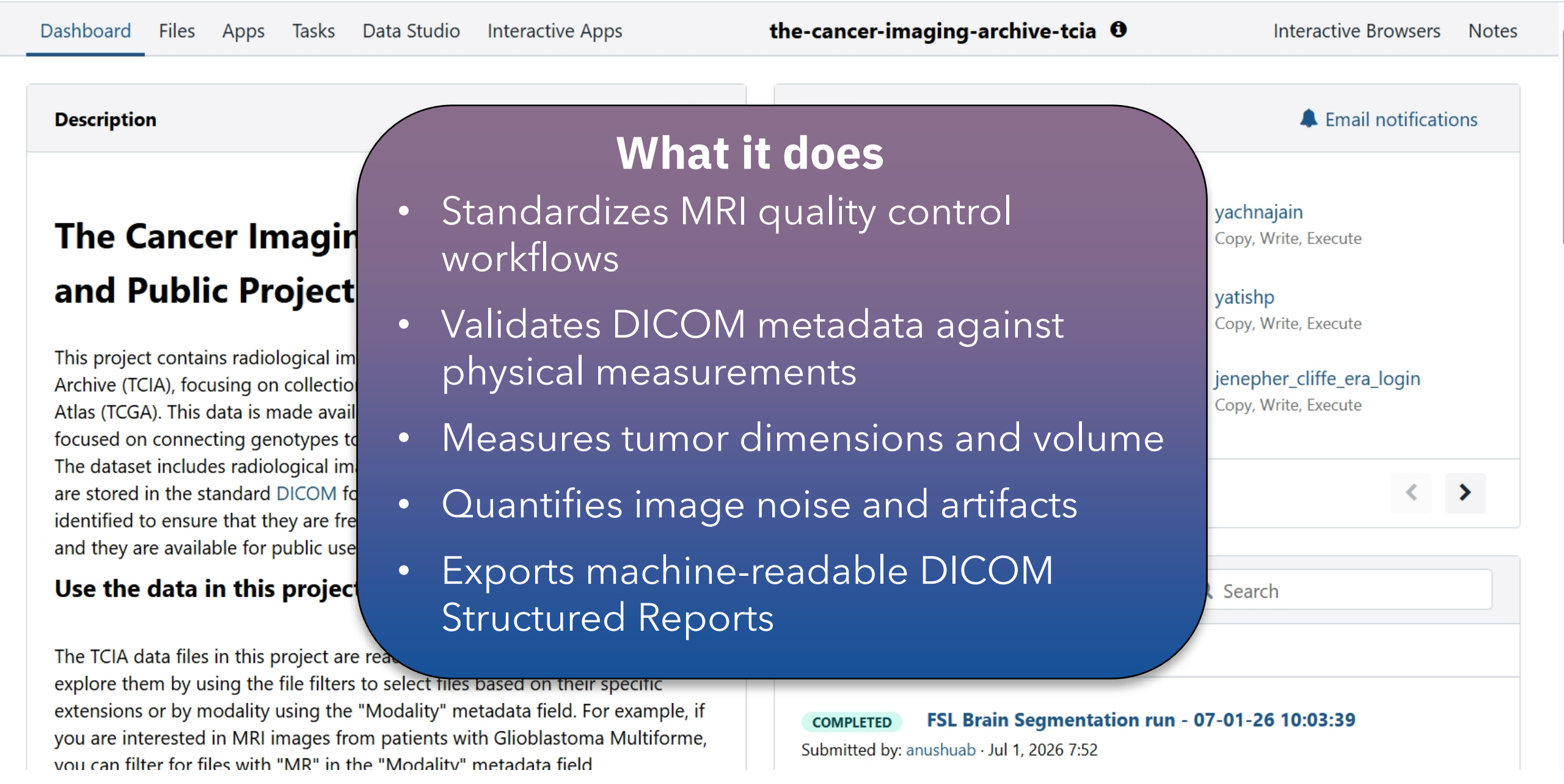
Quantitative QC for Lung CT: 3D slicer



Why should you care?

- Stops bad data from distorting results
- Catches errors human eyes miss
- Ensures reliable downstream research findings
- Saves time during dataset cleanup

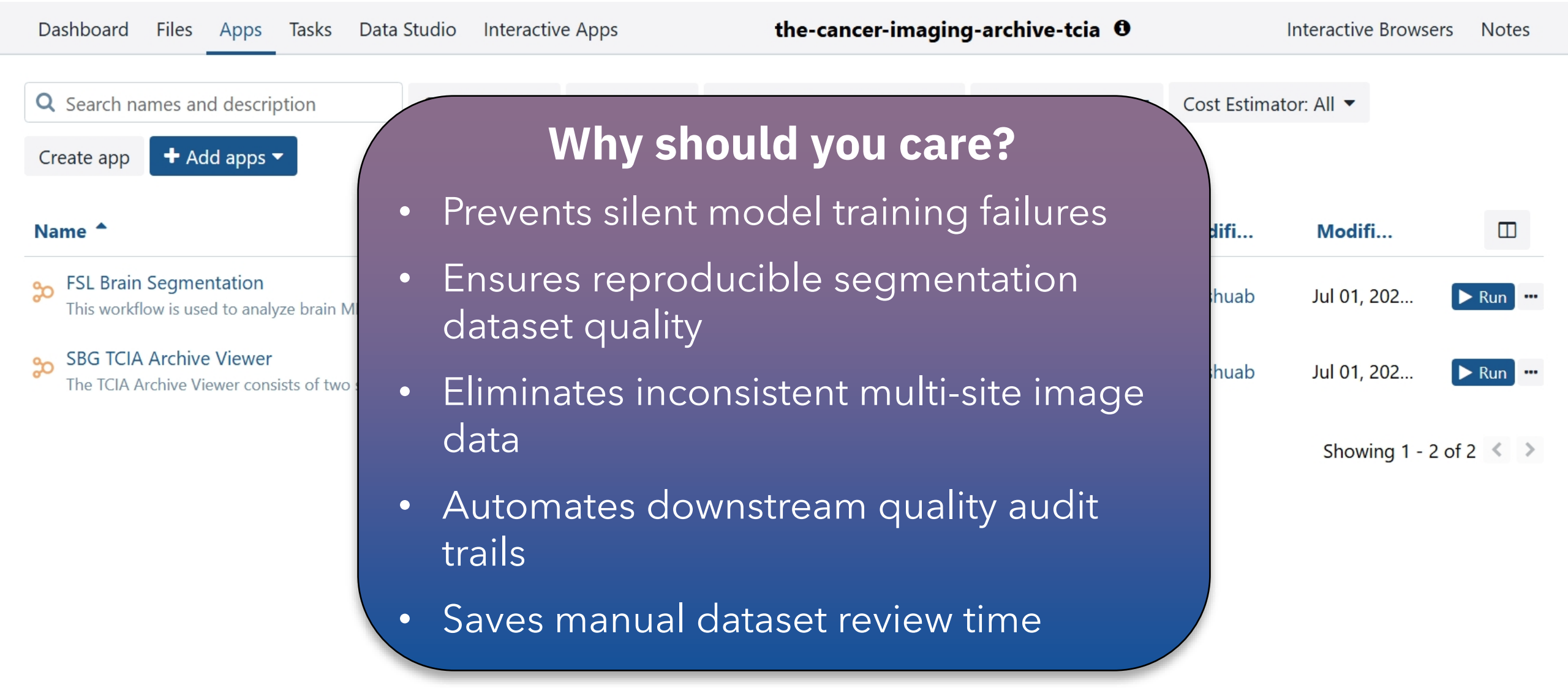
OHIF viewer: Data-Driven QC for Brain MRI



What it does

- Standardizes MRI quality control workflows
- Validates DICOM metadata against physical measurements
- Measures tumor dimensions and volume
- Quantifies image noise and artifacts
- Exports machine-readable DICOM Structured Reports

OHIF viewer: Data-Driven QC for Brain MRI



Why should you care?

- Prevents silent model training failures
- Ensures reproducible segmentation dataset quality
- Eliminates inconsistent multi-site image data
- Automates downstream quality audit trails
- Saves manual dataset review time

INTEGRATED TOOLS ENABLING

- Streamlined data access
- Reproducible
- High-throughput gating for AI pipelines
  (garbage in, garbage out protection)
- Democratized computational oncology

Resources for Working on the Cancer Genomics Cloud

You are not alone!

Onboarding resources

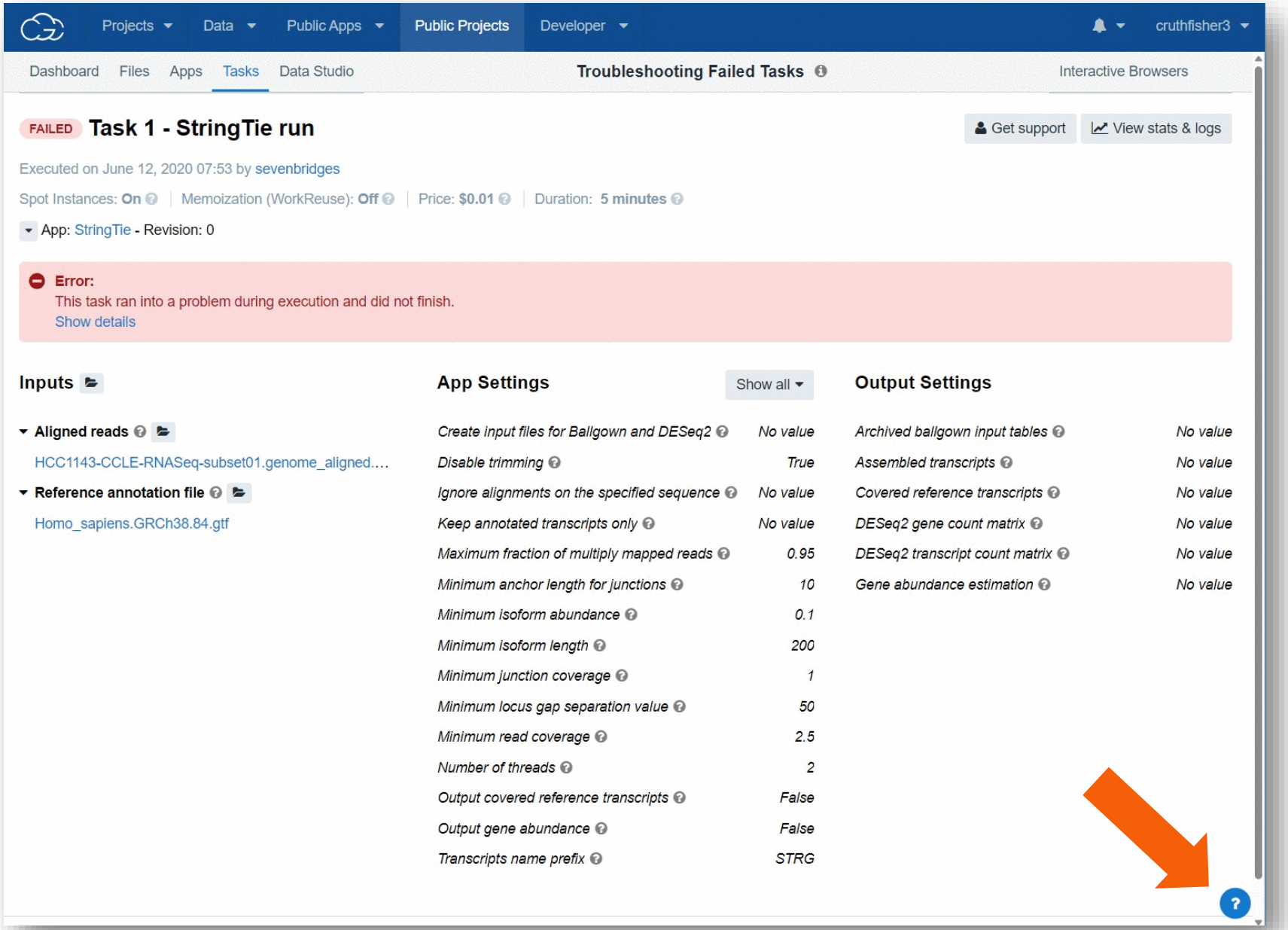
- **$300 pilot cloud credits (how to apply)**
- **Getting Started playlist on YouTube**
- **Extensive Knowledge Center**

Public apps and projects

- Curated tutorials and templates to adapt to your data.
- Vetted and tested apps and tools

New Public Projects (Template projects)	37
Public Apps (Published via projects)	33
Public Shiny-based Apps (PUBLIC_WEB_APP)	15

Get The Support You Need



Get The Support You Need

Every Week:

- 10:00 am ET Tuesday
- 2:00 pm ET Thursday

NCI Funding Is Available on the CGC

Pilot Credit Funds

- **$300 of cloud credits**
- Free for new CGC users
- Easy to request when signing up (see Getting Started – Cancer Genomics Cloud)
- Fast approval

NIH NATIONAL CANCER INSTITUTE

Collaborative Projects

- Cost estimation, optimization, and planning support
- Great for researchers new to bioinformatics and cloud approaches
- **Up to $10k compute/storage costs**
- Fast, rolling applications
- To date > 60 projects
- Apply at Collaborative Projects – Cancer Genomics Cloud

Stay in touch.

Support@Velsera.Com

https://meet.google.com/kbs-ojnj-dcg

Every Week:

- 10:00 am ET Tuesday
- 2:00 pm ET Thursday

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Thank you.

Learn more at
CancerGenomicsCloud.org

VELSERA

COMING SOON!
cgc.SBGenomics.com

OHIF viewer and 3D slicer

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