

Overview of the NCI Cancer Research Data Commons, Genomic Data Commons (GDC), and NCI Cloud Resources

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The Cancer Data Ecosystem

The Beau Biden Cancer Moonshotsm

Overarching goals – Jan, 2016

- Accelerate progress in cancer, including prevention & screening
 - From cutting edge basic research to wider uptake of standard of care
- Encourage greater cooperation and collaboration
 - Within and between academia, government, and private sector
- Enhance data sharing

Blue Ribbon Panel – October, 2016

- Network for Direct Patient Engagement
- Cancer Immunotherapy Translational Science Network
- Therapeutic Target Identification to Overcome Drug Resistance
- A National Cancer Data Ecosystem for Sharing and Analysis
- Fusion Oncoproteins in Childhood Cancers
- Symptom Management Research
- Prevention and Early Detection – Implementation of Evidence-based Approaches
- Retrospective Analysis of Biospecimens from Patients Treated with Standard of Care
- Generation of 3D Human Tumor Atlas
- Development of New Enabling Cancer Technologies
- Full report: www.cancer.gov/brp

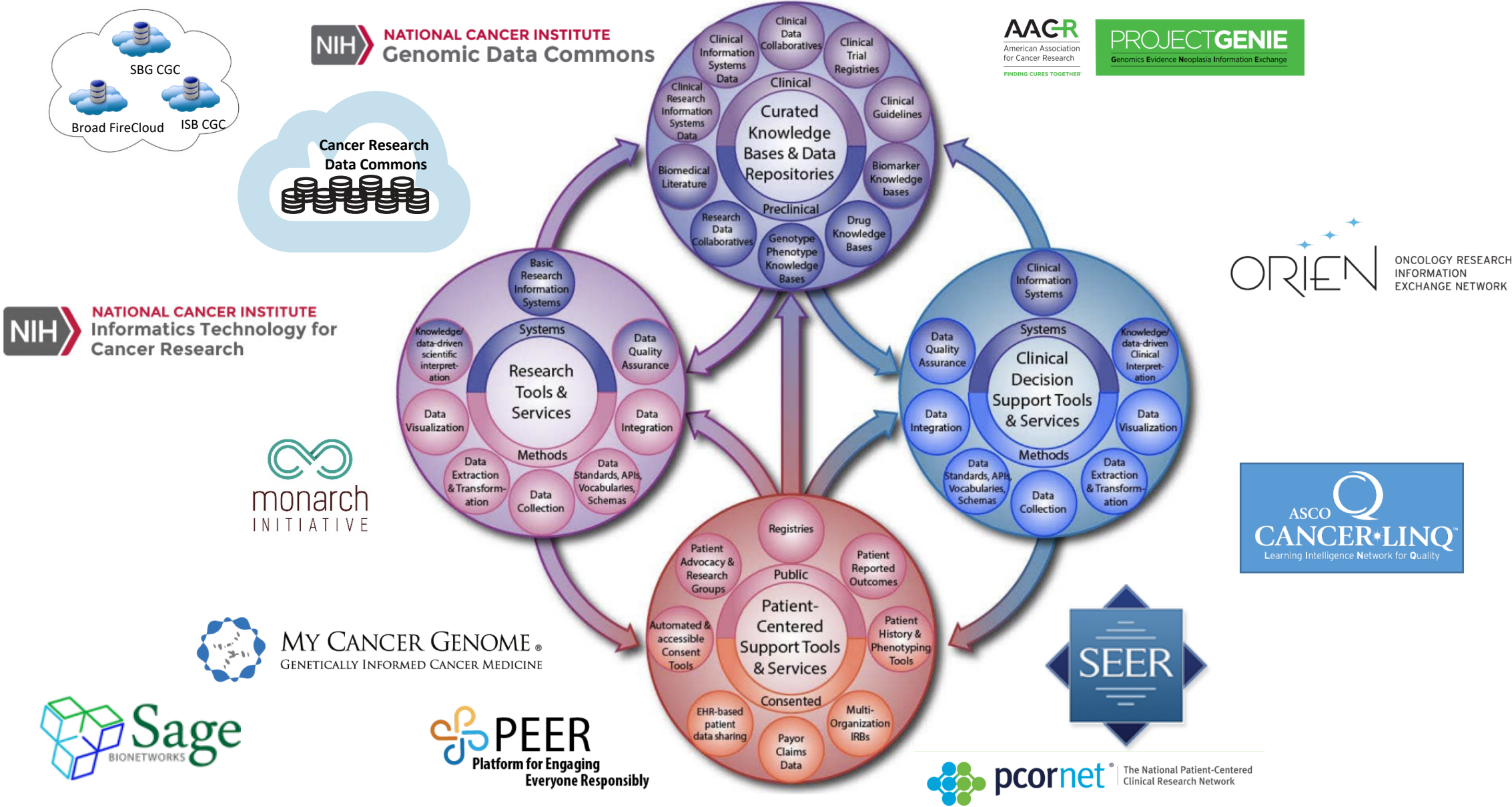
National Cancer Data Ecosystem Recommendations

Overall goal: *“Enable all participants across the cancer research and care continuum to contribute, access, combine and analyze diverse data that will enable new discoveries and lead to lowering the burden of cancer.”*

Recommendations

- **Build a National Cancer Data Ecosystem**
 - Enhanced cloud-computing platforms.
 - Services that link disparate information, including clinical, image, and molecular data.
 - Essential underlying data science infrastructure, methods, and portals for the Cancer Data Ecosystem.
 - Establish sustainable data governance to ensure long-term health of the Ecosystem.
 - Develop standards and tools so that data are interoperable.

Enhanced Data Sharing Working Group Recommendation: *The Cancer Data Ecosystem*

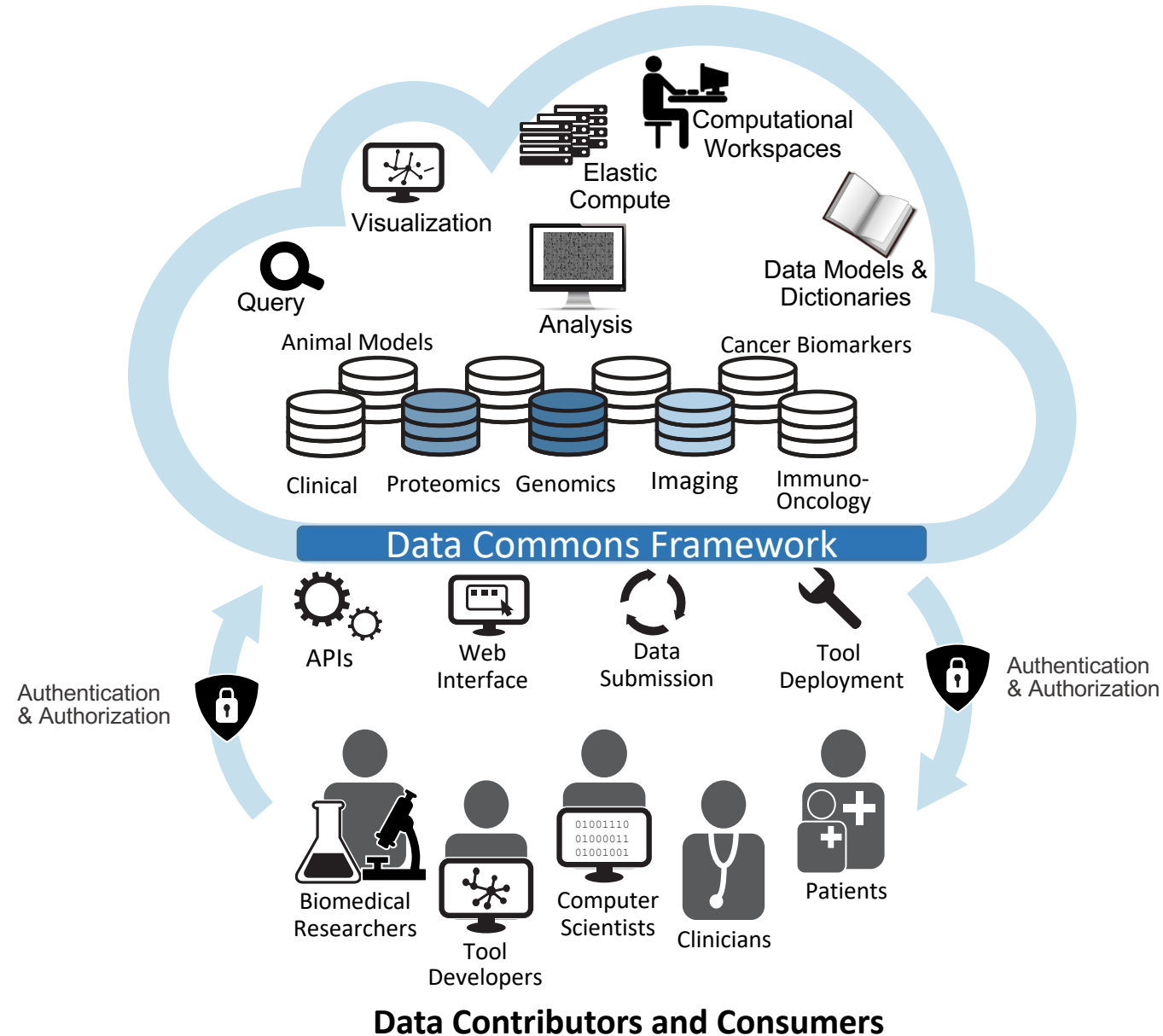


The Cancer Research Data Commons (CRDC)

NCI Cancer Research Data Commons (CRDC) - Concept

NCI Scope: *“Create a data science infrastructure necessary to connect repositories, analytical tools, and knowledge bases”*

Data commons co-locate data, storage and computing infrastructure with commonly used services, tools & apps for analyzing and sharing data to create an interoperable resource for the research community.*



*Robert L. Grossman, Allison Heath, Mark Murphy, Maria Patterson and Walt Wells, A Case for Data Commons Towards Data Science as a Service, IEEE Computing in Science and Engineer, 2016. Source of image: The CDIS, GDC, & OCC data commons infrastructure at the University of Chicago Kenwood Data Center.

Goals of the NCI CRDC

- Enable the cancer research community to share diverse data types across programs and institutions.
- Provide easy access to data, regardless of where they are stored.
- Provide mechanisms for innovative tool discovery, access, and usage, e.g., ITCR tools.
- Help Data Coordinating Centers share their data publicly.

NCI Cancer Research Data Commons

Data Sources / Contributors (Examples)



The Cancer Genome Atlas (TCGA)



Clinical Proteomic Tumor Analysis Consortium (CPTAC)



The Cancer Imaging Archive (TCIA)



NCI Individual Labs / Grants /
Contracts / Cancer Centers (GENIE)



Therapeutically Applicable Research to
Generate Effective Treatments (TARGET)



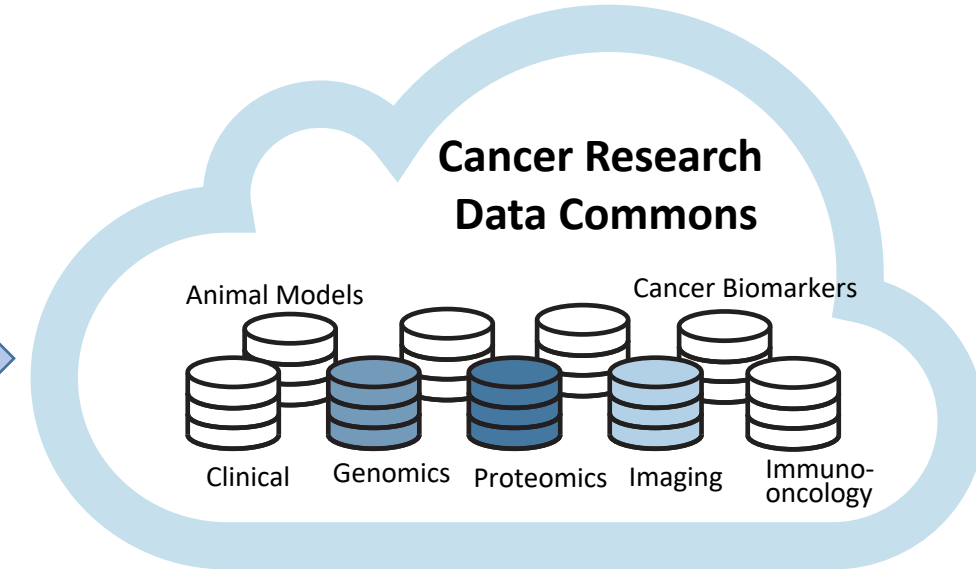
Collaborative Programs: APOLLO (Applied Proteogenomic Organizational Learning and Outcomes), ICPC (International Cancer Proteogenome Consortium)



3rd Party Programs: Foundation Medicine,
Multiple Myeloma Research Foundation



Data Submission



Data Commons Framework – What Is It?

Reusable, expandable
framework for a Data
Commons

Core principles and
structures for a Data
Commons

Set of modular
components that can be
leveraged across Data
Commons

Modular Components



Secure user authentication and authorization



Metadata validation and tools



Domain-specific, extensible data models and dictionaries



API and container environment for tools and pipelines



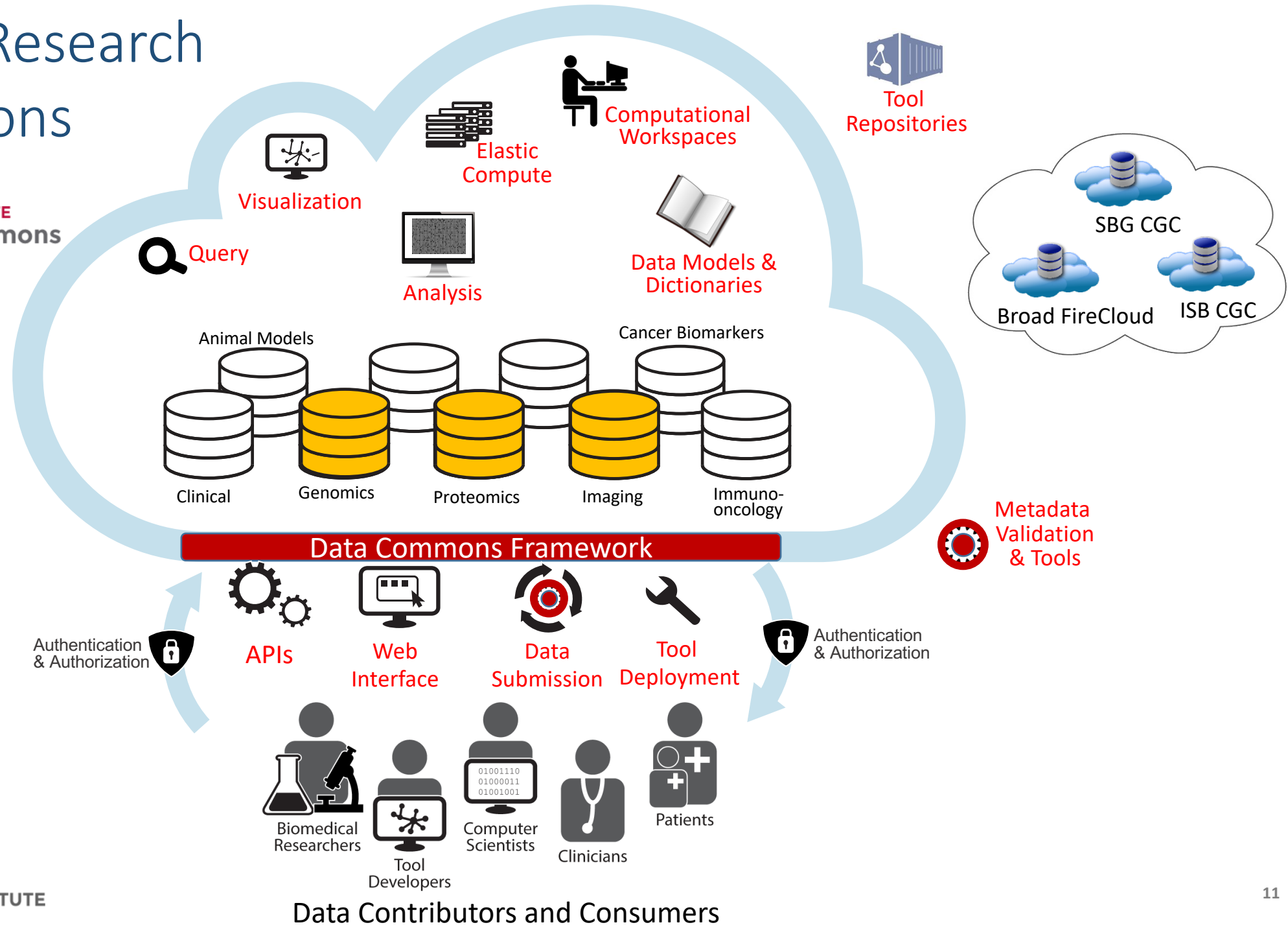
Access to computational workspaces for storing data, tools, and results

NCI Cancer Research Data Commons

NIH NATIONAL CANCER INSTITUTE
Genomic Data Commons

CPTAC
Clinical Proteomics Tumor
Analysis Consortium*

TCIA
The Cancer Imaging Archive*



The NCI Genomic Data Commons

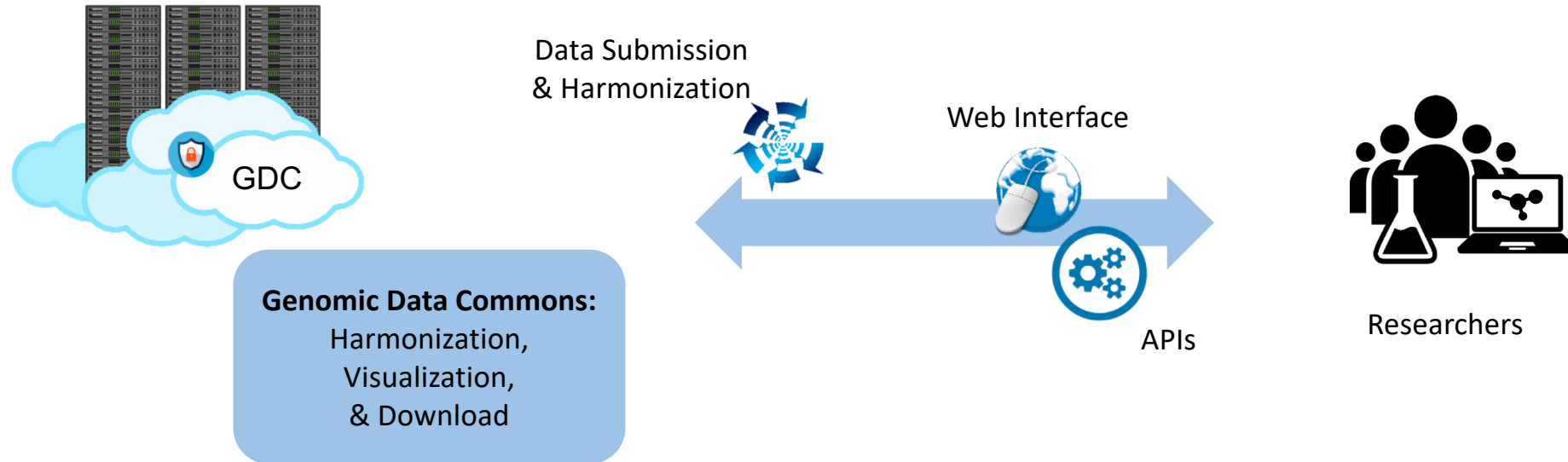
*Provide the cancer research community with
a **unified data repository** that enables **data
sharing** across **cancer genomic studies** in
support of **precision medicine***

The NCI Genomic Data Commons

- Support the *receipt, quality control, integration, storage, and redistribution* of standardized genomic data sets derived from cancer research studies
 - Available data
 - NCI Funded cancer genomics datasets
 - User submissions
 - Data searching and retrieval/downloading
 - Harmonization of raw sequence (alignment and variant calling) of all GDC data
 - Application of state-of-the-art methods of generating derived data
- Developed, supported, and hosted by U. Chicago

Genomic Data Commons (GDC):

A unified data repository for the research community developed, supported, and hosted by U. Chicago



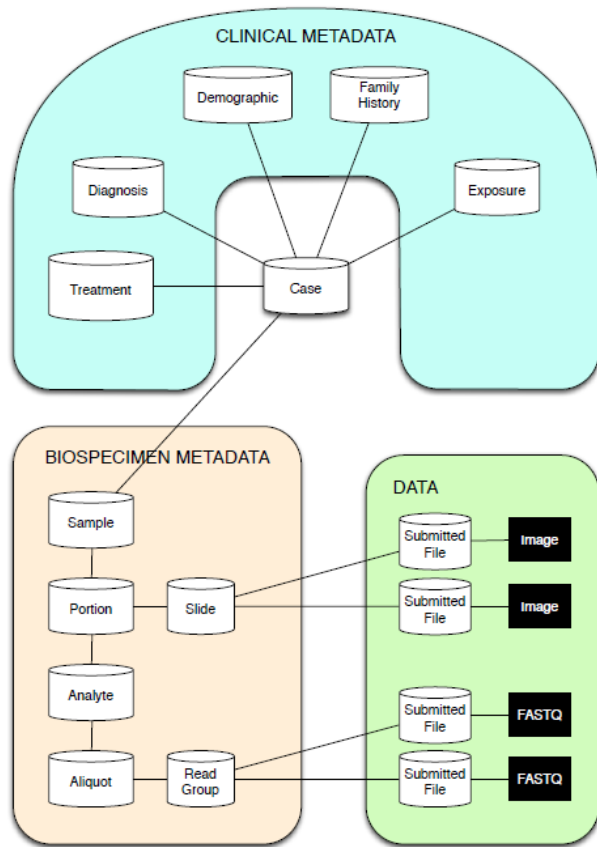
<https://gdc.cancer.gov>



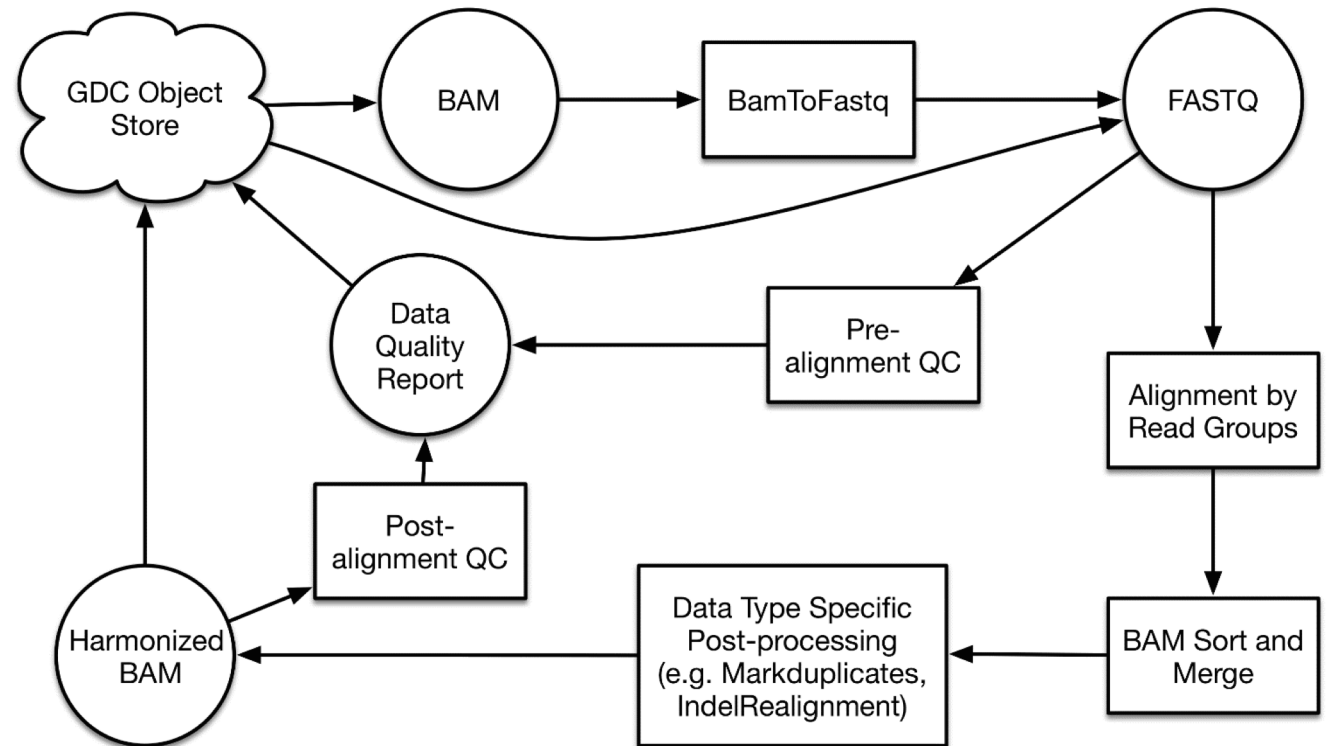
Authentication
& Authorization thru
eRA Commons & dbGaP

GDC: Data Submission & Harmonization

Data Submission



Data Harmonization



<https://gdc.cancer.gov/>

GDC: Data Retrieval

Data Portal

The screenshot shows the GDC Data Portal interface. On the left, there are filters for Project, Primary Site, Cancer Program, Disease Type, Data Type, and Experimental Strategy. The main area displays a table of projects with columns for ID, Disease Type, Primary Site, Program, Cases, Clinical, Array, Seq, SMI, CNA, SV, Exp, Ploidy, Meth, Other, Files, and File Size. A search bar at the top allows users to search for project names or IDs.

The screenshot shows the GDC Legacy Archive interface. It has a similar layout to the Data Portal but focuses on legacy data. It includes filters for Case, Case Submitter ID Prefix, Primary Site, Cancer Program, and Project. The main area displays a table of files with columns for Access, File Name, and Cases Project. A search bar at the top allows users to search for case IDs or submitter IDs.

Data Transfer Tool

The screenshot shows the GDC Data Portal interface with a terminal window open. The terminal displays a command to download data using the GDC client: `1 $ parcel udt -t token -m gdc_manifest_97a589423eb4c4e15fd29a6cb58a6c6652c21:`. The terminal output shows the progress of the download, including file names, sizes, and download speeds.

GDC Website

The screenshot shows the GDC Website homepage. It features a navigation bar with links for About GDC, Access Data, Submit Data, For Developers, Support, Reports, and News. The main content area includes a section titled "The Next Generation Cancer Knowledge Network" with a pie chart showing "Case Distribution by Disease Type". There is also a "Data Availability Summary" table showing the number of programs and projects available.

Visualization Tools

The screenshot shows the GDC API interface. It displays a mutation plot for the TP53 gene, showing the number of mutations across the gene. Below the plot is a table of mutations with columns for Sample ID, Cancer Study, AA change, Annotation, Type, COSMIC, Allele Freq (T), and #Mut in Sample. The table lists various mutations, including G302Rfs*4, P151Rfs*27, E336Sfs*9, Q144_L145dup, R175H, and R175H.

GDC API

```
{
  "data": {
    "hits": [
      { "project_id": "TCGA-SKCM", "primary_site": "Skin" },
      { "project_id": "TCGA-PCPG", "primary_site": "Nervous System" },
      { "project_id": "TCGA-LAML", "primary_site": "Blood" },
      { "project_id": "TCGA-CNTL", "primary_site": "Not Applicable" },
      { "project_id": "TCGA-UVM", "primary_site": "Eye" }
    ]
  }
}
```

Legacy Archive

API URL Endpoint URL parameters Query

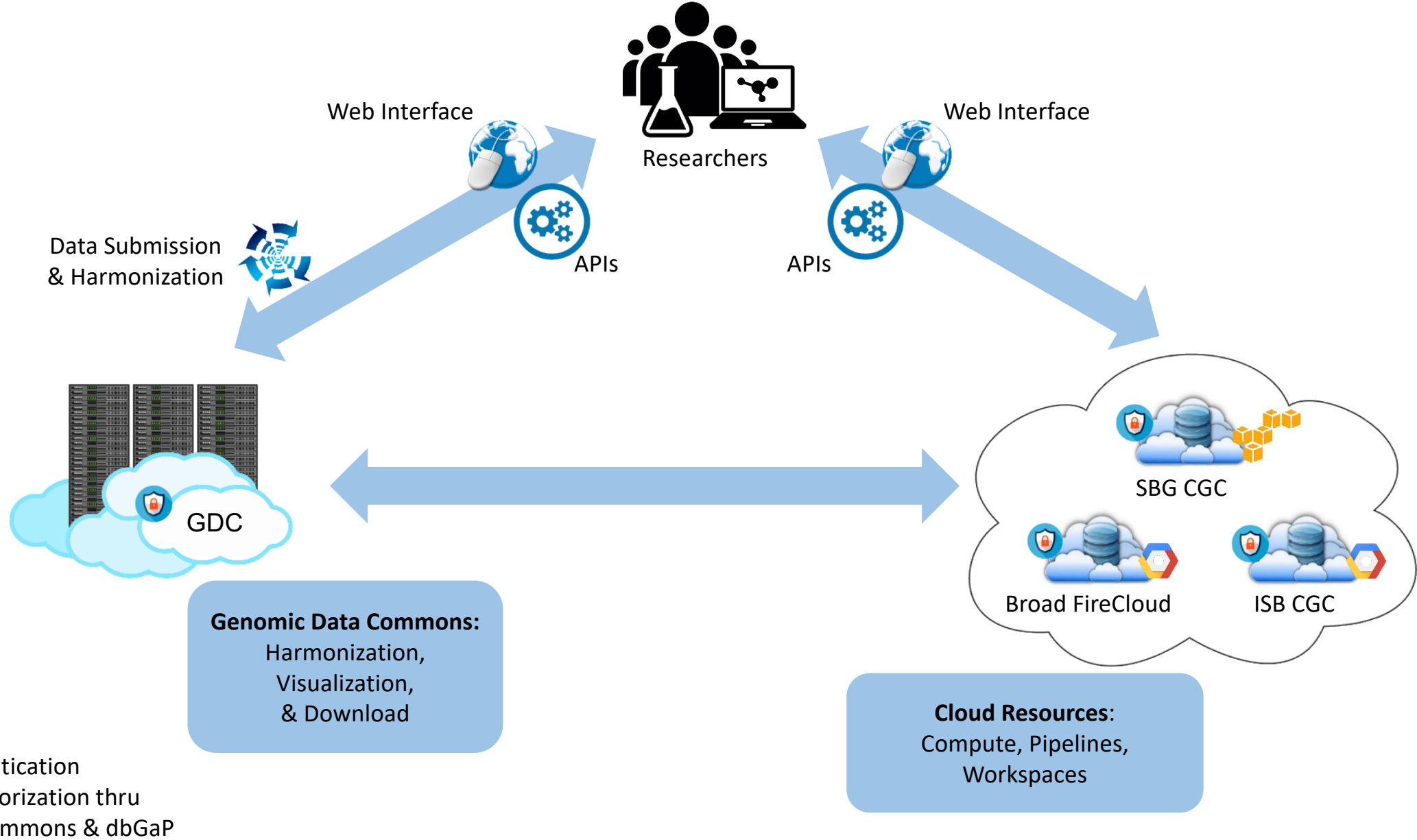
`https://gdc-api.nci.nih.gov/projects?fields=project_id,primary_site`



The NCI Cloud Resources

*Understanding how to meet the
research community's need to
analyze large-scale cancer
genomic and clinical data*

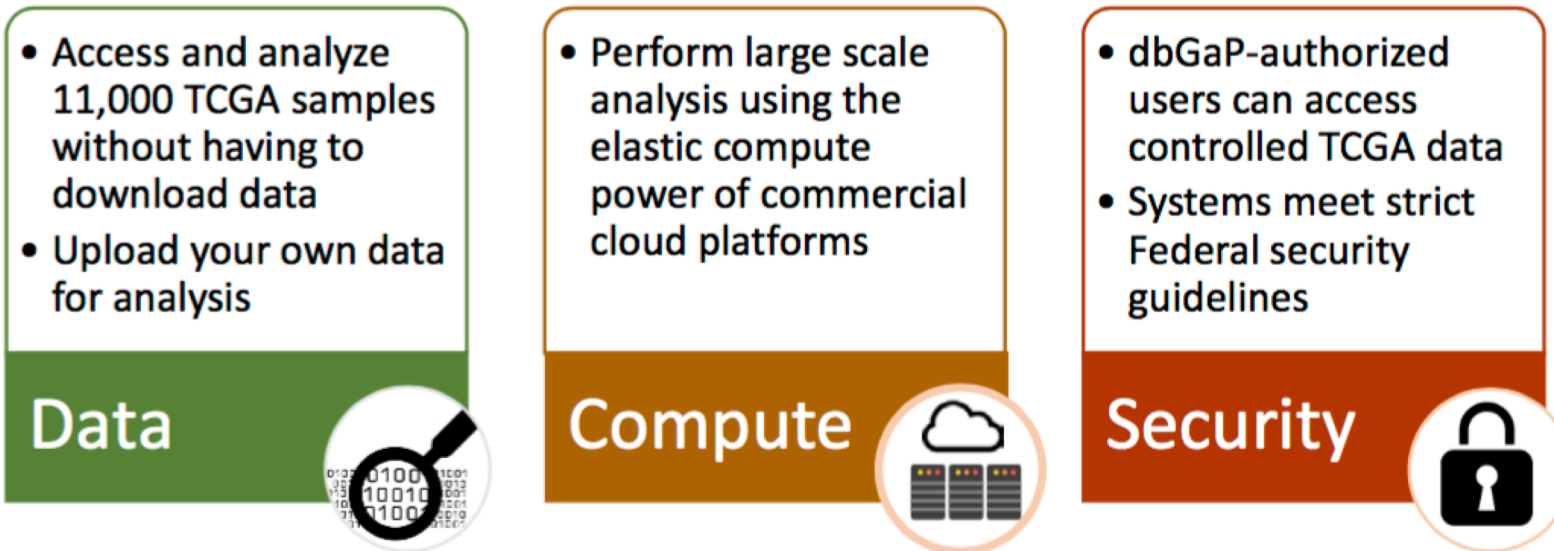
GDC and the NCI Cloud Resources



NCI Cloud Resources

The Cloud Resources provide:

- Access to large cancer data sets without need to download
- Access to popular analysis tools and pipelines
- Ability for researchers to bring their own data to the Cloud Resources
- Ability for researchers to bring their own tools and pipelines to the data
- Workspaces, for researchers to save and share their data and results of analyses



Democratize access to cancer datasets, and to provide cost-effective computational capacity to the cancer research community.

 #NCICloud

Three NCI Cloud Resources

Broad Institute

- PI: Anthony Philippakis
- Google Cloud
- Firehose in the cloud including Broad best practices workflows
- <http://firecloud.org>

Institute for Systems Biology

- PI: Ilya Shmulevich
- Google Cloud
- Leverage Google infrastructure; Novel query and visualization
- <http://cgc.systemsbiology.net/>

Seven Bridges Genomics

- PI: Brandi Davis-Dusenbery
- Amazon Web Services
- Interactive data exploration; > 30 public pipelines
- <http://www.cancergenomicscloud.org>

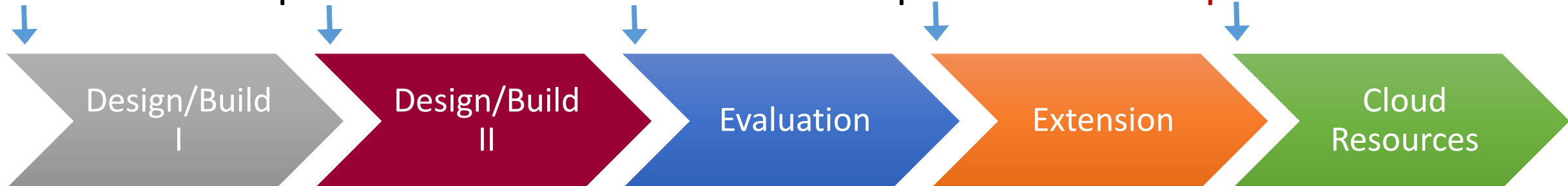
Sept 2014

April 2015

Jan 2016

Sept 2016

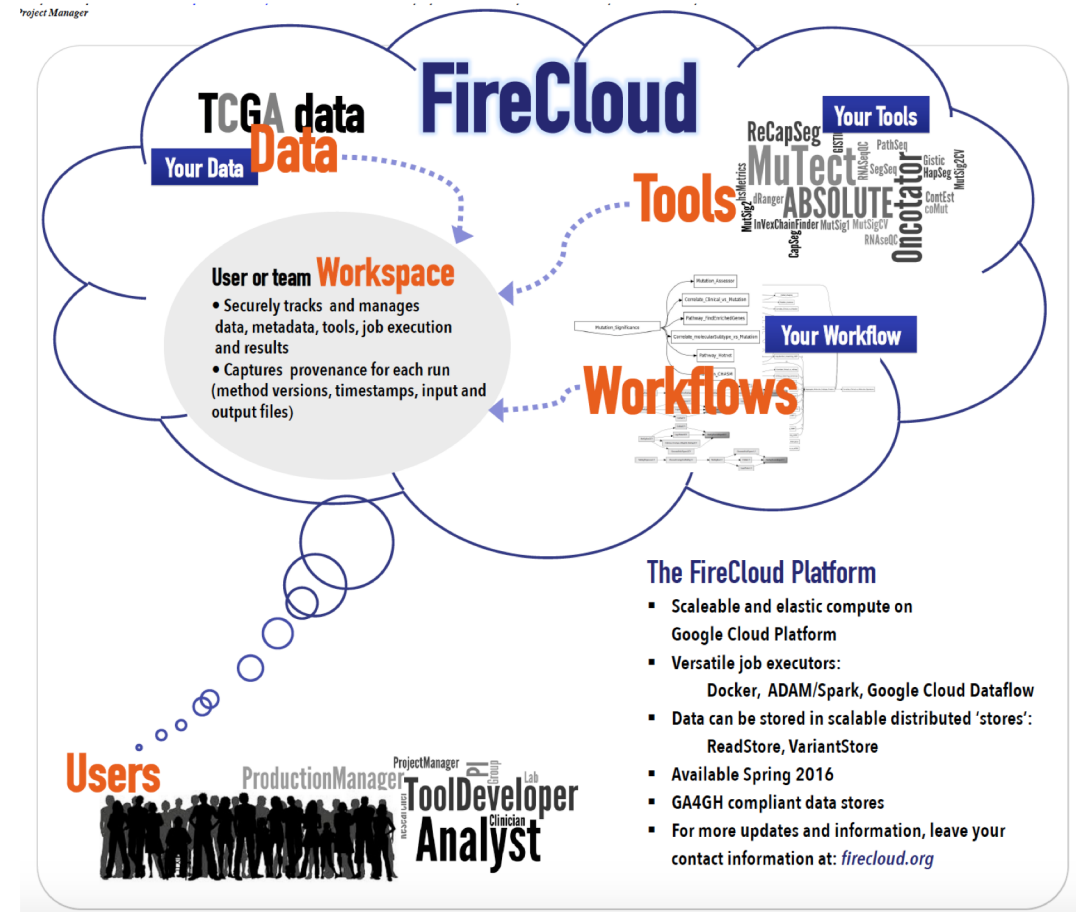
Sept 2017



Broad Institute Cloud Resource

- Targeted at users performing analyses at scale.
- Modeled after their Firehose analysis infrastructure developed for the TCGA program.
- Users can upload their own data and tools and/or run the Broad's best practice tools and pipelines on pre-loaded data.

<http://firecloud.org>



The Data Library

The primary tool for discovering datasets at Broad and beyond

Broad's Genomics Platform has been delivering all WGS projects into FireCloud for a year.

Recently begun cataloguing all data into the Data Library for discovery and access.

Users can search the datasets and filter datasets by the data use restrictions.

The screenshot displays the FireCloud Data Library interface. At the top, navigation links include 'FireCloud', 'Workspaces', 'Data Library' (which is highlighted), and 'Method Repository'. Below the navigation bar, a search bar is present. To the left of the main results area, there are several filter sections: 'Filter by Research Purpose' with a 'Clear' link, 'Tags' with a 'Clear' link, 'Cohort Phenotype/Indication' with a 'Clear' link and a list of categories (Acute Myeloid Leukemia, Adrenocortical carcinoma, Bladder Urothelial Carcino..., Brain Lower Grade Glioma, Breast Invasive Carcinoma) each with a count of 4 and a 'more...' link, 'Experimental Strategy' with a 'Clear' link and a list of categories (Genotyping Array, Methylation Array, RNA-Seq, Whole Exome, miRNA-Seq) each with a count of 132 and a 'more...' link, and 'Project Name' with a 'Clear' link and a list of categories (TCGA, Epi25, TOPMed) with counts of 133, 36, and 22 respectively. The main results area is titled 'Matching Cohorts 133 Datasets found'. It contains a table with two columns: 'Cohort Name' and 'Cohort Phenotype/Indication'. The table lists various TCGA cohorts, including 'TCGA Diagnostic Side Images' (cancer), 'TCGA_ACC_ControlledAccess' (Adrenocortical carcinoma), 'TCGA_ACC_hg38_ControlledAccess' (Adrenocortical carcinoma), 'TCGA_ACC_hg38_OpenAccess' (Adrenocortical carcinoma), 'TCGA_ACC_OpenAccess' (Adrenocortical carcinoma), 'TCGA_BLCA_ControlledAccess' (Bladder Urothelial carcinoma), 'TCGA_BLCA_hg38_ControlledAccess' (Bladder Urothelial carcinoma), 'TCGA_BLCA_hg38_OpenAccess' (Bladder Urothelial carcinoma), 'TCGA_BLCA_OpenAccess' (Bladder Urothelial carcinoma), 'TCGA_BRCA_ControlledAccess' (Breast Invasive Carcinoma), 'TCGA_BRCA_hg38_ControlledAccess' (Breast Invasive Carcinoma), 'TCGA_BRCA_hg38_OpenAccess' (Breast Invasive Carcinoma), 'TCGA_BRCA_OpenAccess' (Breast Invasive Carcinoma), 'TCGA_CESC_ControlledAccess' (Cervical Squamous Intraepithelial Neoplasia), 'TCGA_CESC_hg38_ControlledAccess' (Cervical Squamous Intraepithelial Neoplasia), 'TCGA_CESC_hg38_OpenAccess' (Cervical Squamous Intraepithelial Neoplasia), 'TCGA_CESC_OpenAccess' (Cervical Squamous Intraepithelial Neoplasia), 'TCGA_CHOL_ControlledAccess' (Cholangiocarcinoma), 'TCGA_CHOL_hg38_ControlledAccess' (Cholangiocarcinoma), and 'TCGA_CHOL_hg38_OpenAccess' (Cholangiocarcinoma).

FireCloud Workspaces Data Library Method Repository

Search

Filter by Research Purpose Clear

Tags Clear

Cohort Phenotype/Indication Clear

- Acute Myeloid Leukemia 4
- Adrenocortical carcinoma 4
- Bladder Urothelial Carcino... 4
- Brain Lower Grade Glioma 4
- Breast Invasive Carcinoma 4

more...

Experimental Strategy Clear

- Genotyping Array 132
- Methylation Array 132
- RNA-Seq 132
- Whole Exome 132
- miRNA-Seq 132

more...

Project Name Clear

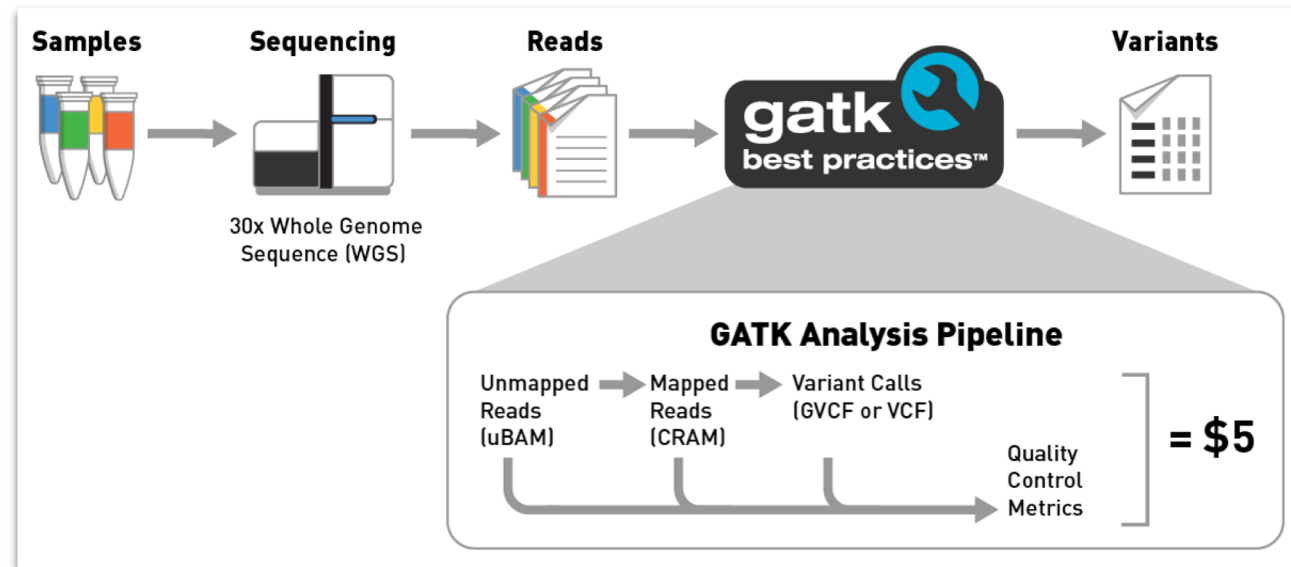
- TCGA 133
- Epi25 36
- TOPMed 22

Matching Cohorts 133 Datasets found

Cohort Name	Cohort Phenotype/Indication
TCGA Diagnostic Side Images	cancer
TCGA_ACC_ControlledAccess	Adrenocortical carcinoma
TCGA_ACC_hg38_ControlledAccess	Adrenocortical carcinoma
TCGA_ACC_hg38_OpenAccess	Adrenocortical carcinoma
TCGA_ACC_OpenAccess	Adrenocortical carcinoma
TCGA_BLCA_ControlledAccess	Bladder Urothelial carcinoma
TCGA_BLCA_hg38_ControlledAccess	Bladder Urothelial carcinoma
TCGA_BLCA_hg38_OpenAccess	Bladder Urothelial carcinoma
TCGA_BLCA_OpenAccess	Bladder Urothelial carcinoma
TCGA_BRCA_ControlledAccess	Breast Invasive Carcinoma
TCGA_BRCA_hg38_ControlledAccess	Breast Invasive Carcinoma
TCGA_BRCA_hg38_OpenAccess	Breast Invasive Carcinoma
TCGA_BRCA_OpenAccess	Breast Invasive Carcinoma
TCGA_CESC_ControlledAccess	Cervical Squamous Intraepithelial Neoplasia
TCGA_CESC_hg38_ControlledAccess	Cervical Squamous Intraepithelial Neoplasia
TCGA_CESC_hg38_OpenAccess	Cervical Squamous Intraepithelial Neoplasia
TCGA_CESC_OpenAccess	Cervical Squamous Intraepithelial Neoplasia
TCGA_CHOL_ControlledAccess	Cholangiocarcinoma
TCGA_CHOL_hg38_ControlledAccess	Cholangiocarcinoma
TCGA_CHOL_hg38_OpenAccess	Cholangiocarcinoma

The \$5 Genome: Pipeline Optimizations

- Broad is optimizing production pipelines with a commitment to openness, transparency, and continued improvements in cost and performance
- Example: Germline GATK best practices
 - \$45/sample* in 2016
 - \$13.50/sample in 2017
 - \$5/sample in 2018
- Pipelines will be available to run in FireCloud and will also be in Dockstore.



Optimized somatic best practices coming soon!

* Cloud compute costs from Google Cloud Platform

FireCloud is part of the Data Biosphere

FireCloud will evolve into a citizen of an interoperable world through principles outlined across the *Data Biosphere*.

The Biosphere is a collaboration among institutions working on data platforms that will serve several large-scale, high-profile biomedical research projects.

Principles

- Open
- Standards Based
- Modular
- Community Driven

Initial collaborators in the Data Biosphere are building data platforms for the NCI Data Commons, NIH Data Commons, All of Us Research Program, Human Cell Atlas, Gabriella Miller Kids First, and others.

First integration with Data Biosphere: Dockstore

Tools

Workflows

Search

Documentation

Available Workflows

github.com/gatk-workflows/somatic-snvs-indels/gatk4-somatic-snvs-indels-discovery:master

☆ 0

gatk4 indel mutect2 snv somatic

Last Modified: n/a

InfoLabelsVersionsFilesToolsDAG

Path : github.com/gatk-workflows/somatic-snvs-indels/gatk4-somatic-snvs-indels-discovery

GitHub : <https://github.com/gatk-workflows/somatic-snvs-indels>

Workflow Path: /mutect2.wdl

Test File Path:

Checker Workflow:

Descriptor Type: wdl

Launch With

Make a runtime JSON template and fill in desired inputs, outputs, and other parameters

```
$ dockstore workflow convert entry2json --entry github.com/gatk-workflows/somatic-snvs-indels/gatk4-somatic-snv  
$ vim Dockstore.json
```

or grab one that the workflow author has provided (if applicable)

```
$ wget --header='Accept: text/plain' https://dockstore.org:8443/api/ga4gh/v2/tools/%23workflow%2F%20%24%7B%2E
```

Recent Versions

master
0.1.0-beta
See all versions

Source Repositories

GitHub

Launch with

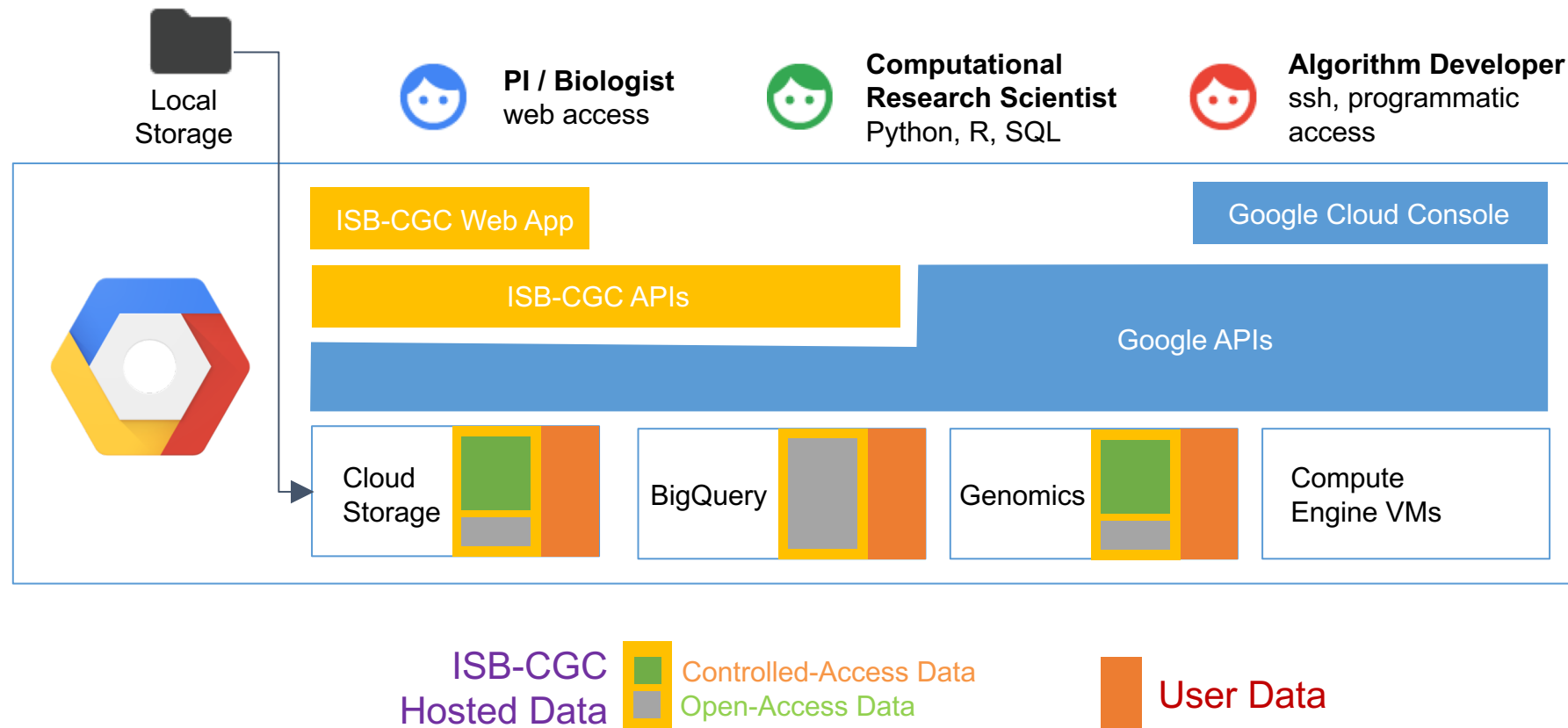
DNASTack »

FireCloud »

WDL workflows on Dockstore.org can now be launched with FireCloud!

ISB Cancer Genomics Cloud (ISB-CGC)

- Closely tied with Google Cloud Platform tools including BigQuery, App Engine, Cloud Datalab, Google Genomics, and Compute Engine



<http://cgc.systemsbiology.net/>

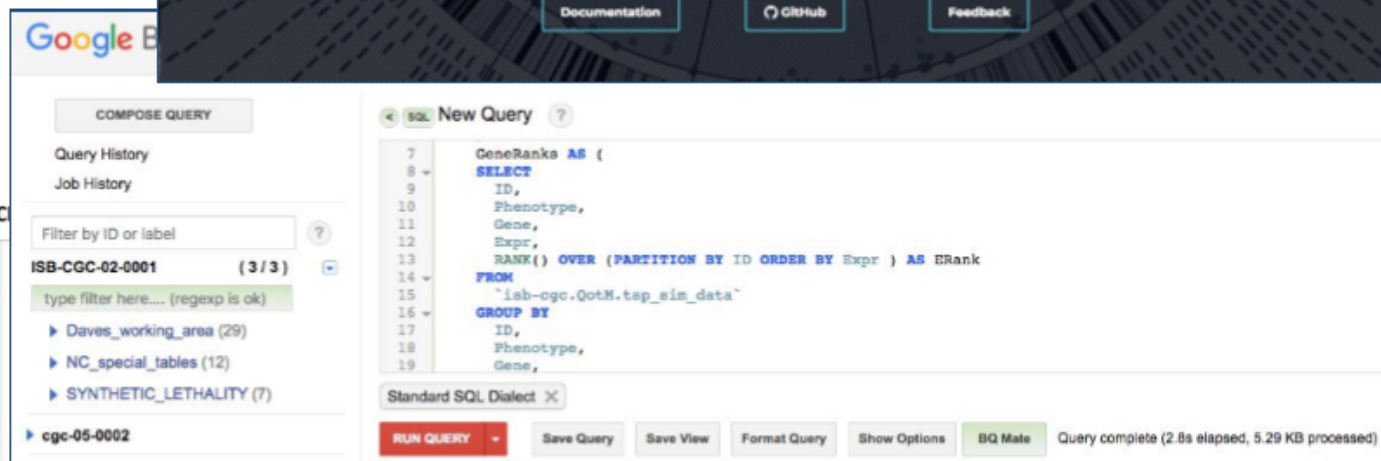
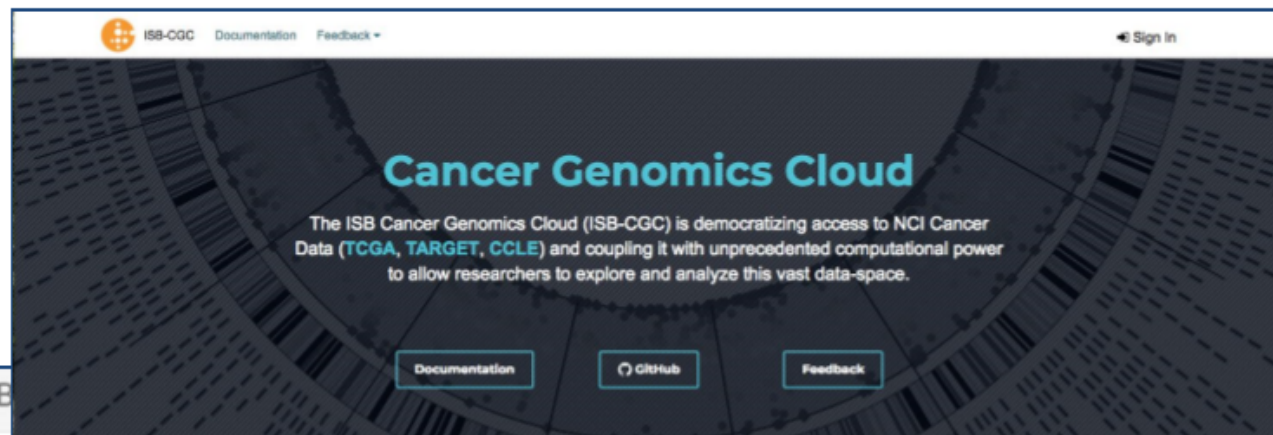
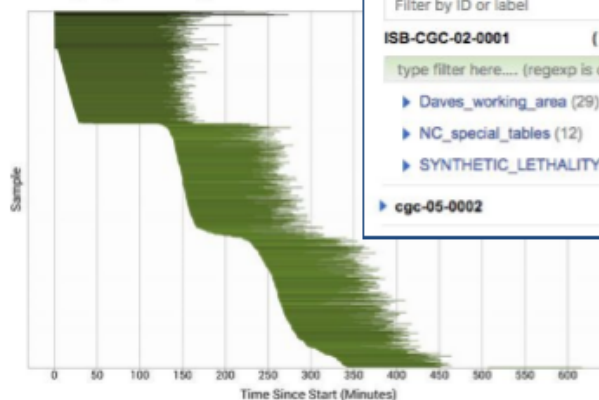
There are three primary ways of working on ISB-CGC.

ISB-CGC Web App

BigQuery

Pipelines

Sample processing over time — CC



What you choose depends on the question and what you're comfortable with

Method 2: Working with BigQuery



bigquery and
bigQueryR



googleAuthR



Pre-built VM images



Cloud notebooks
and workspaces.

Cloud Datalab



Google BigQuery

plays well with others.



Google BigQuery it's *great* for answering questions



Q: How many samples have a mutation in PARP1?

Use standard SQL to answer it:

```
SELECT
  project_short_name,
  COUNT(DISTINCT(sample_barcode_tumor)) AS n
FROM
  `isb-cgc.TCGA_hg38_data_v0.Somatic_Mutation_DR10`
WHERE
  Hugo_Symbol = 'PARP1'
GROUP BY
  project_short_name
ORDER BY
  n DESC
```

Easy to join tables on any shared variable.

Lots of built in functions for math, string processing, etc

Can process massive amounts of data in parallel.

Query Of The Month Club

Spearman correlations using RNA-seq data and pathway definitions



ISB-CGC Query of the Month, Feb 2018

This plot shows gene-gene correlations for a set of genes given by the selected pathway. The correlations can be filtered using the correlation threshold slider. BioCircos links can be Moused-Over to display the gene pair and correlation value. Also, it's possible to zoom in on portions of the circo plot by double clicking. Try searching the list of pathways by selecting the pathway drop-down, hitting delete and typing a search term.

Pathway

CELL CYCLE CHECKPOINTS (291 genes)

Cohort

TCGA-LUSC

random number of genes



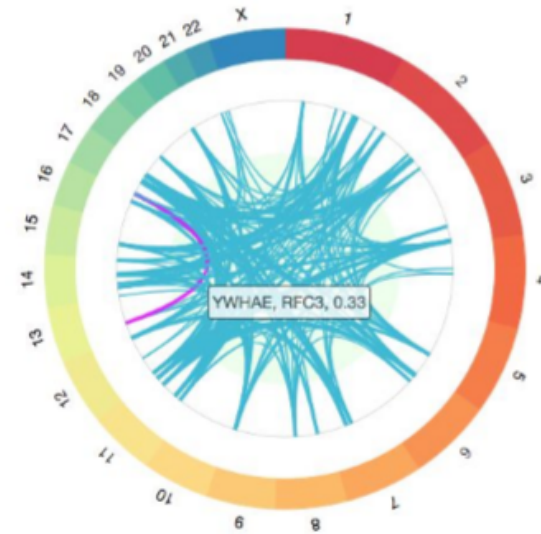
correlation threshold



Submit after selecting pathway and cohort

Packages used: BioCircos, bigquery

Data used: Reactome pathways, TCGA hg19 RNAseq UNC RSEM

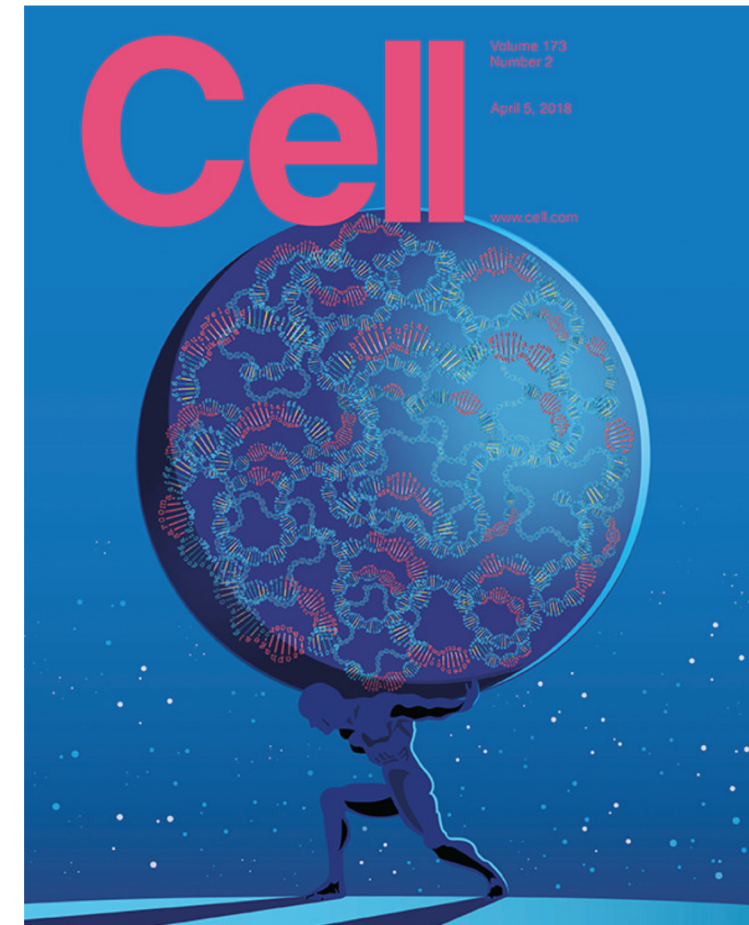
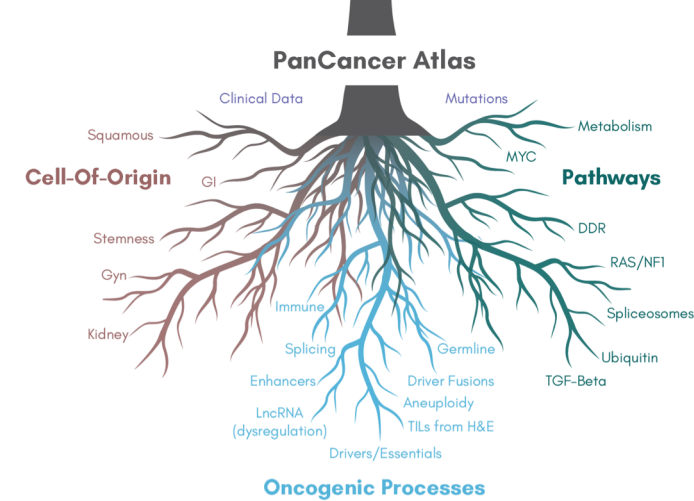


geneA	chrA	startA	geneB	chrB	startB	spearman
HIST1H4H	chr6	26277609	HIST1H2BE	chr6	26172059	0.72
PSMA6	chr14	35278633	PSMA3	chr14	58244831	0.70
SPC25	chr2	168834132	CDC25C	chr5	138285265	0.66
SPC25	chr2	168834132	SGOL2	chr2	200510008	0.63
SPC25	chr2	168834132	PSMD14	chr2	161308038	0.61
CENPO	chr2	24793136	BRIP1	chr17	61681266	0.59
HIST2H2BE	chr1	149842204	HIST1H4H	chr6	26277609	0.59
RFC4	chr3	186789880	PSMD2	chr3	184298709	0.58
SKA1	chr18	50374995	RFC5	chr12	118013588	0.58
SPC25	chr2	168834132	RFC3	chr13	33818049	0.57

Item	Count
number of edges shown:	206
number of edges total:	1059
number of genes shown:	71
number of genes total:	91

ISB-CGC a key resource for TCGA #PanCancerAtlas

- Germline, Fusion, and Immune Response papers used ISB-CGC to access and compute on TCGA sequence data on the Google Cloud Platform
- Immune, MYC, and DDR papers used BigQuery and ISB-CGC data tables
- [#PanCancerAtlas](#) open-access tables now available in BigQuery (referenced from [GDC page](#))
- The availability of PanCancer Atlas data in BigQuery enables easy integration with other public datasets through BigQuery

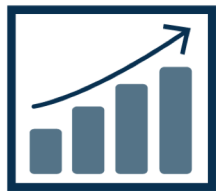


The Seven Bridges Cancer Genomics Cloud (CGC)

- A user-friendly, web-based portal for collaborative analysis of petabytes of multi-omic data alongside private data
- Built upon the SBG commercial cloud-based genomics platform
- For cancer genomics research and beyond



Easy data
management



Scalable computation



Secure collaboration



Optimized
bioinformatics
algorithms



Flexible & fully
reproducible
methods

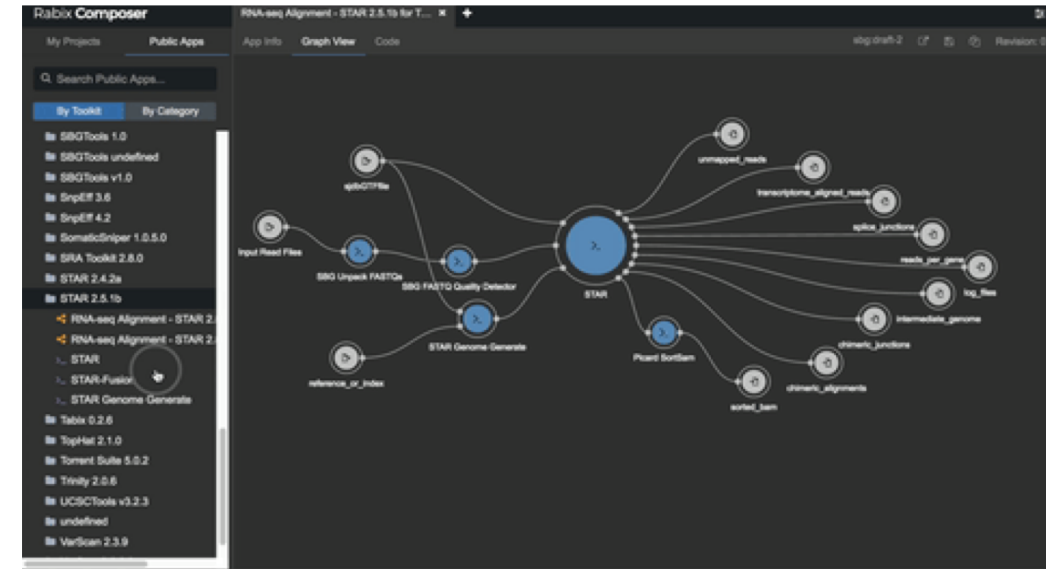
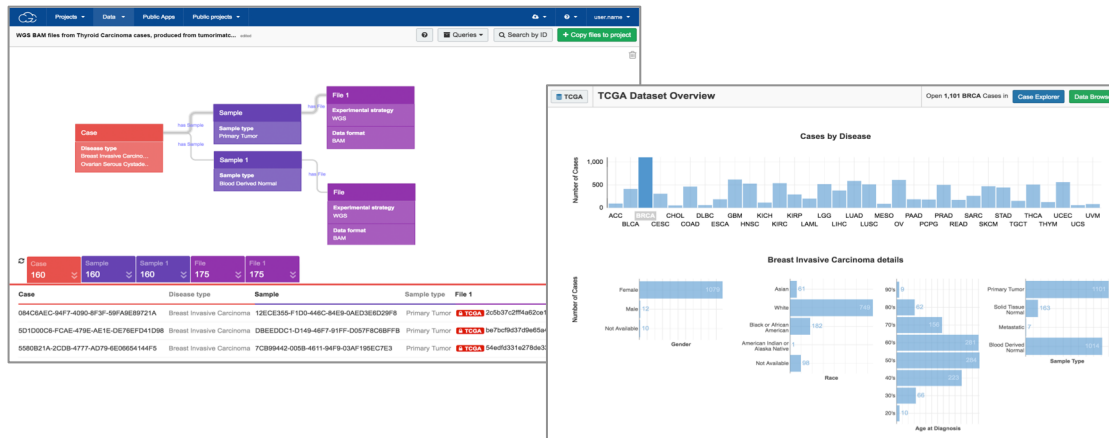


Extensible &
developer-friendly
platform

<http://www.cancergenomicscloud.org>

Available Resources

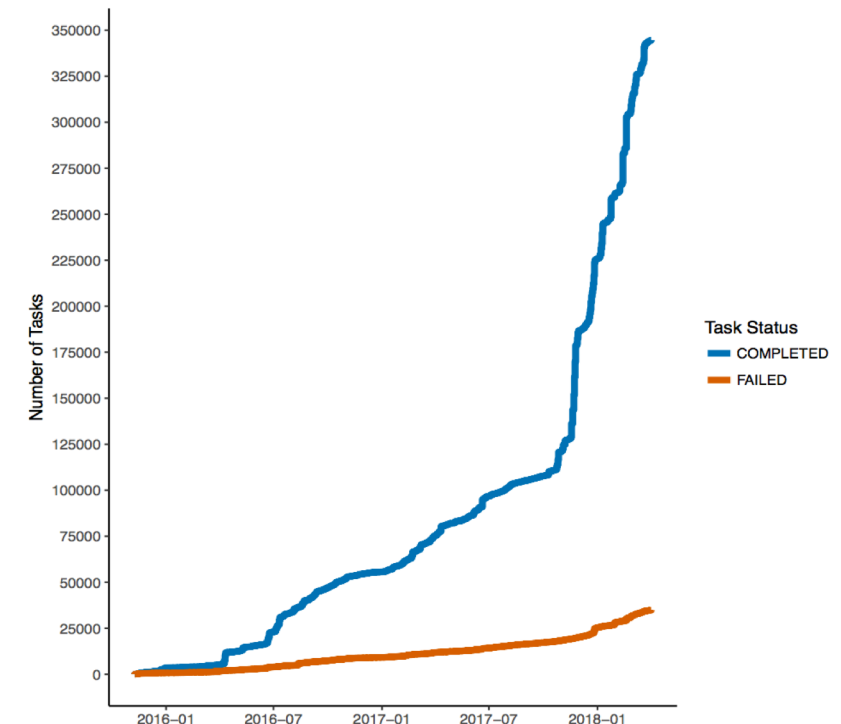
- Access **3+ PB** of multi-omic public data through interactive query tools & APIs.
- Upload private data for analysis.
- Collaborate securely with colleagues anywhere.
- Use the **360+** cloud- and cost-optimized tools in the Public Apps library.
- Deploy custom tools using SDK (**Rabix**) & Jupyter notebook (**Data Cruncher**).
- Consult with **200+** expert support staff.



Usage by the Research Community

3,100+ users from **60+** countries have used the CGC to run **347,000+** computational tasks representing **465+** years of total compute time to:

- Detect aberrant splice junctions and splicing profiles across patient populations
- Identify neoantigens arising from novel gene fusion events
- Profile miRNA expression across patient populations
- Conduct HLA typing to identify neoantigens
- Compare viral infection patterns across patient populations
- Detect novel gene fusions from RNA-Seq data
- Identify cis-regulatory region variants across patient populations
- ...and much more



Scalable, Cost-Effective Research

Case Study #1: TCGA Immune Response Working Group

- Collaborative analysis with members of the Immune Response Working Group of The Cancer Genome Atlas (TCGA) Research Network
- Outcome: cost-optimized (<\$0.30/sample), high-throughput HLA typing across ~9,000 TCGA RNA-Seq (fastq) files

Case Study #2: PanCancer Analysis of Whole Genomes (PCAWG) Study from International Cancer Genome Consortium (ICGC)

- High-throughput, harmonized analysis by Seven Bridges of all tumor and matched genomes in the dataset (~1,350)
- Outcome: rapid generation of ~65,000 output files (including ~5,000 VCFs) totaling 725 TB

Case Study #3: Independent Analysis on 45,000 Bacterial Genomes

- High-throughput analysis of 45,000 bacterial genomes accessed from SRA via API and analyzed using a custom workflow
- Outcome: analysis completed in ~1 week by a novice CGC user with no substantive assistance from the CGC team

The Seven Bridges Cloud Ecosystem: Interoperable Data Access and Analysis to Drive Precision Medicine

Infrastructure



Interoperability



Partnerships





**NATIONAL
CANCER
INSTITUTE**

www.cancer.gov

www.cancer.gov/espanol