https://www.cbioportal.org/

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Memorial Sloan-Kettering Cancer Center

Memorial Sloan-Kettering Cancer Center
Dana-Farber Cancer Institute
The Children's Hospital of Philadelphia
UHN Toronto General Toronto Western Princess Margaret Toronto Rehab
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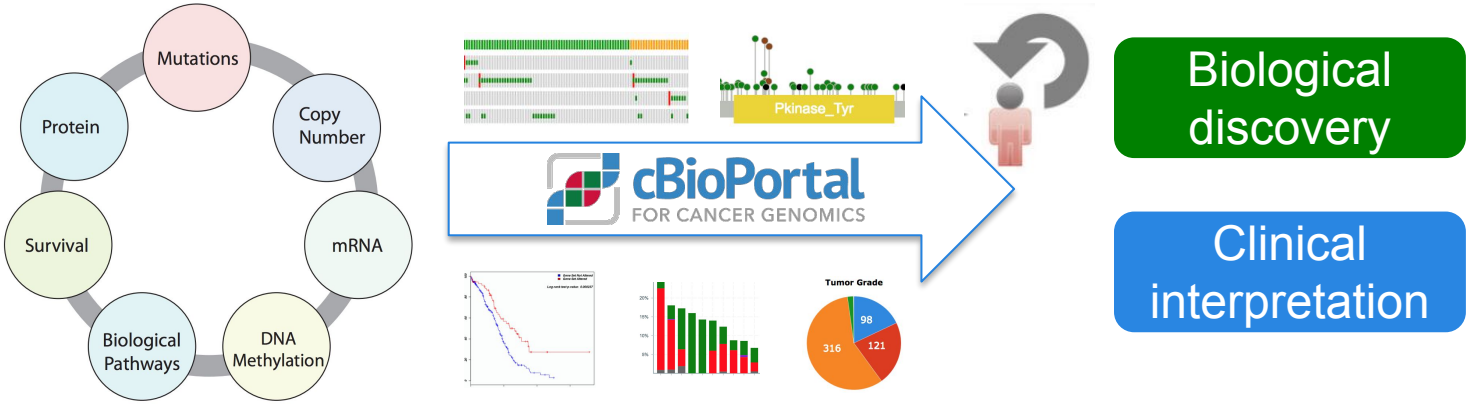
Goal of cBioPortal

Make complex cancer genomic data **accessible** and **interpretable** for cancer biologists and clinicians



Cohort exploration

Cancer Type

	#	Freq
Non-Small Cell Lung Cancer	1,668	15.2%
Breast Cancer	1,324	12.1%
Colorectal Cancer	1,007	9.2%
Prostate Cancer	717	6.6%
Glioma	553	5.1%
Pancreatic Cancer	502	4.6%
Soft Tissue Sarcoma	443	4.0%
Bladder Cancer	423	3.9%
Melanoma	365	3.3%
Renal Cell Carcinoma	361	3.3%
Hepatobiliary Cancer	355	3.2%

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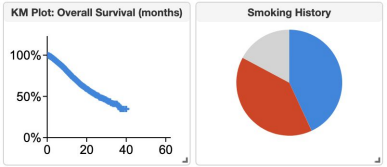
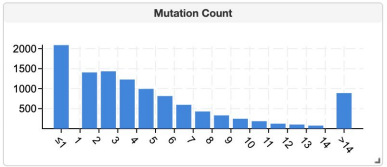
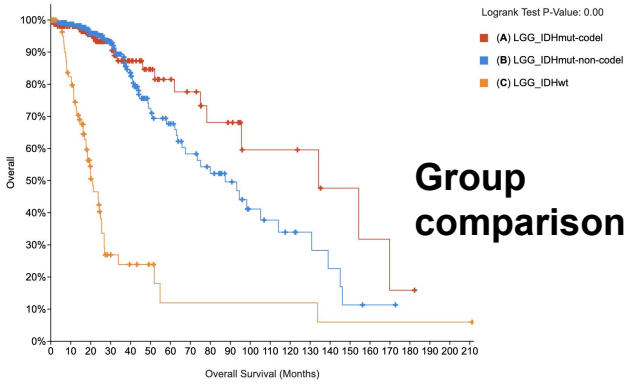




Mutated Genes (10945 profiled samples)

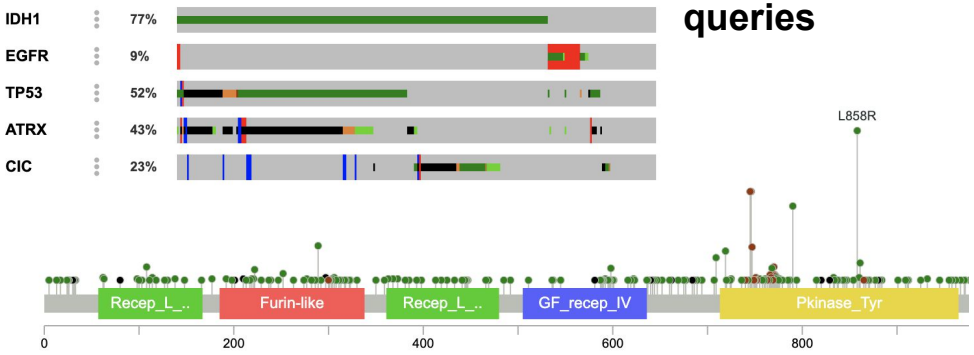
Gene	# Mut	#	Freq
TP53	4,954	4,538	41.5%
KRAS	1,670	1,643	15.0%
TERT	1,549	1,460	13.3%
PIK3CA	1,517	1,355	12.4%
APC	1,674	1,121	10.2%
ARID1A	1,072	875	8.0%
KMT2D	1,210	851	7.8%
PTEN	764	665	6.1%
KMT2C	818	642	5.9%
EGFR	799	636	5.8%
FAT1	773	595	5.4%

Search...

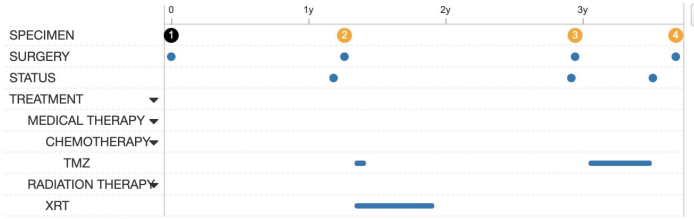


Group comparison

Gene-centric queries



Patient visualization



Samples	Gene	Protein Change	Annotation
1 2 3 4	IDH1	*R132C*	
1 2 3 4	TP53	*R248Q*	
4	ERC1	*L283Ffs*20*	
4	HSP90AB1	*K72E*	
4	SPRTN	*F404Lfs*3*	
1	OR10V1	*R273W*	
1 2 3 4	TEAD3	*P51L*	

cBioPortal has an awesome team 🤗

cBioPortal
FOR CANCER GENOMICS

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The Children's Hospital of Philadelphia

thehyve

Say hi to us (Poster #39) 👋

Aaron Lisman

Onur Sumer

Ino de Bruijn

cBioPortal
FOR CANCER GENOMICS

Memorial Sloan Kettering
Cancer Center

Open source and open data

Code is open https://github.com/cBioPortal/
Data is open https://github.com/cBioPortal/datahub/

Free to download and install
Modifications and contributions are welcome

Maintained by multiple institutions

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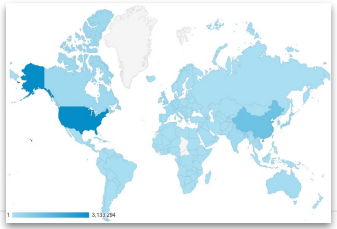
cBioPortal is used a lot

Monthly Users	~34k
Total Citations	~18k
Curated Studies	325

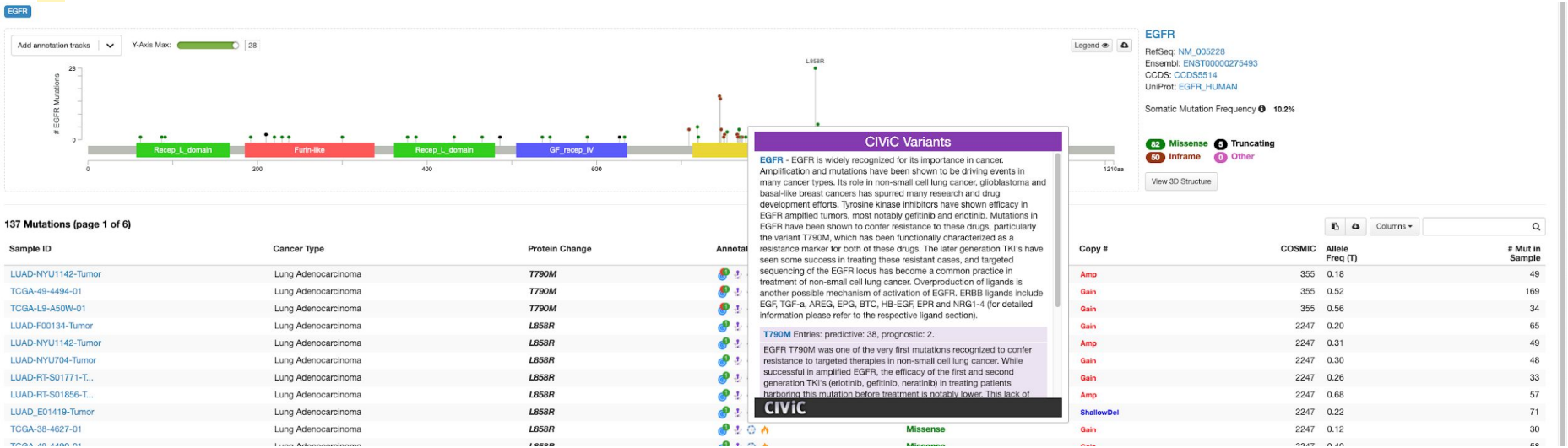


> 7,000,000 visits to cBioPortal.org since 2011

>70 institutional instances globally

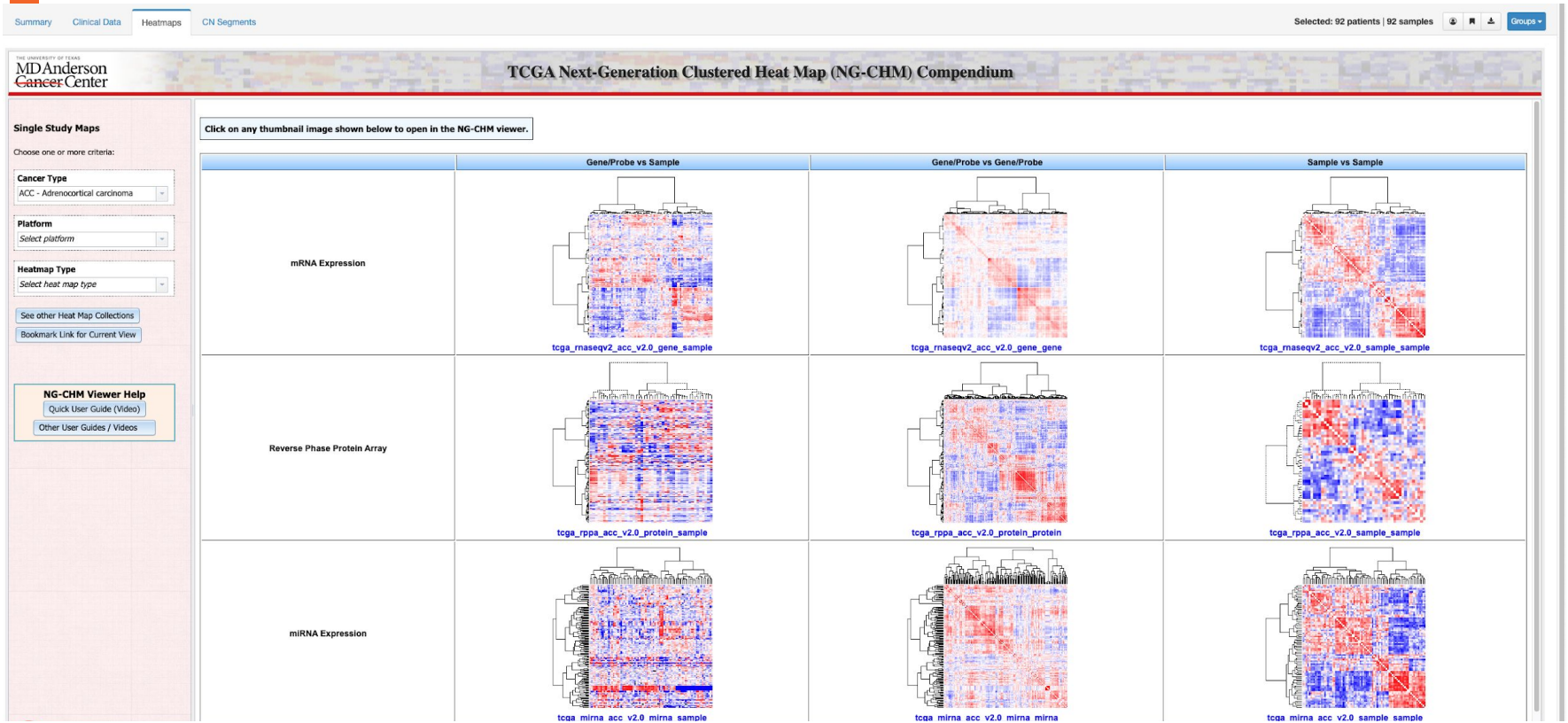
Integrations with 6 Projects

1. Clinical Interpretation of Variants In Cancer (CIViC)

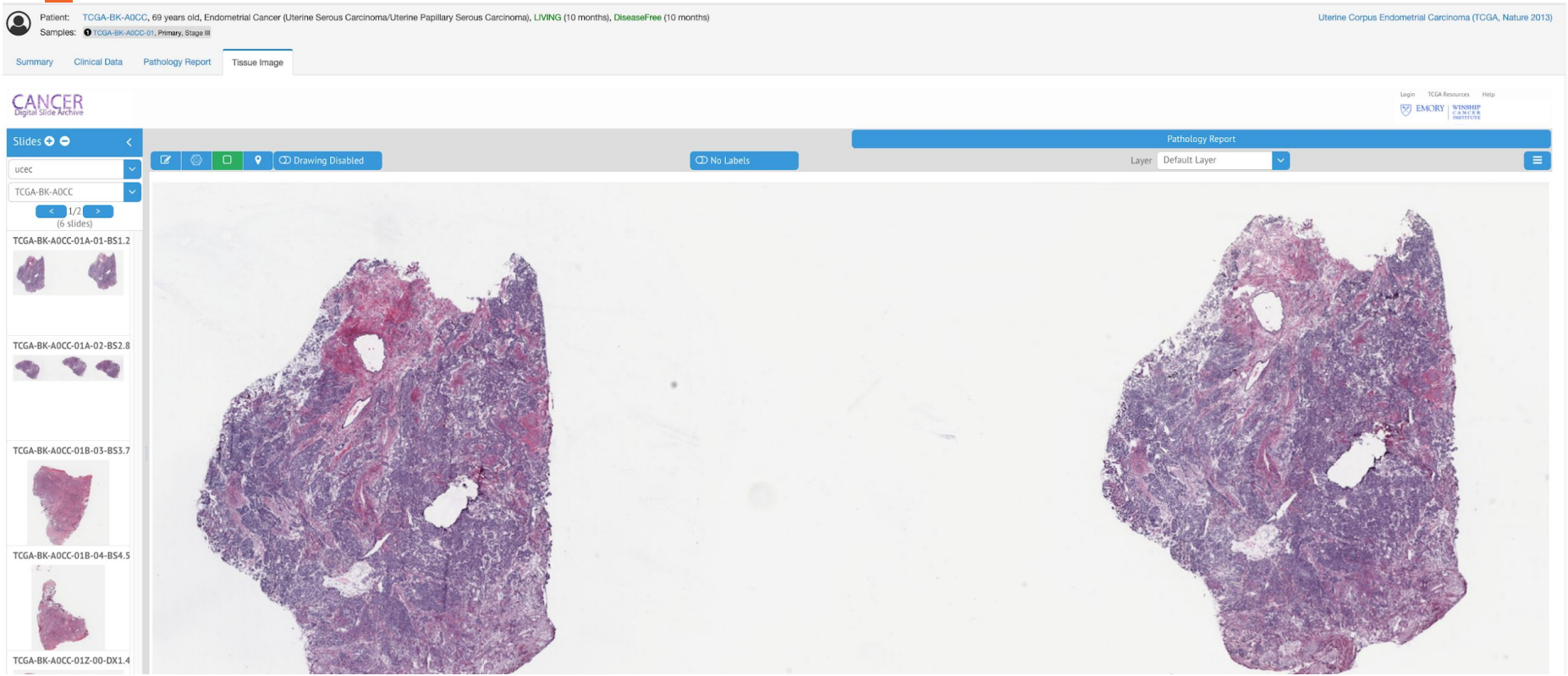


2. Integrative Genomics Viewer (IGV)

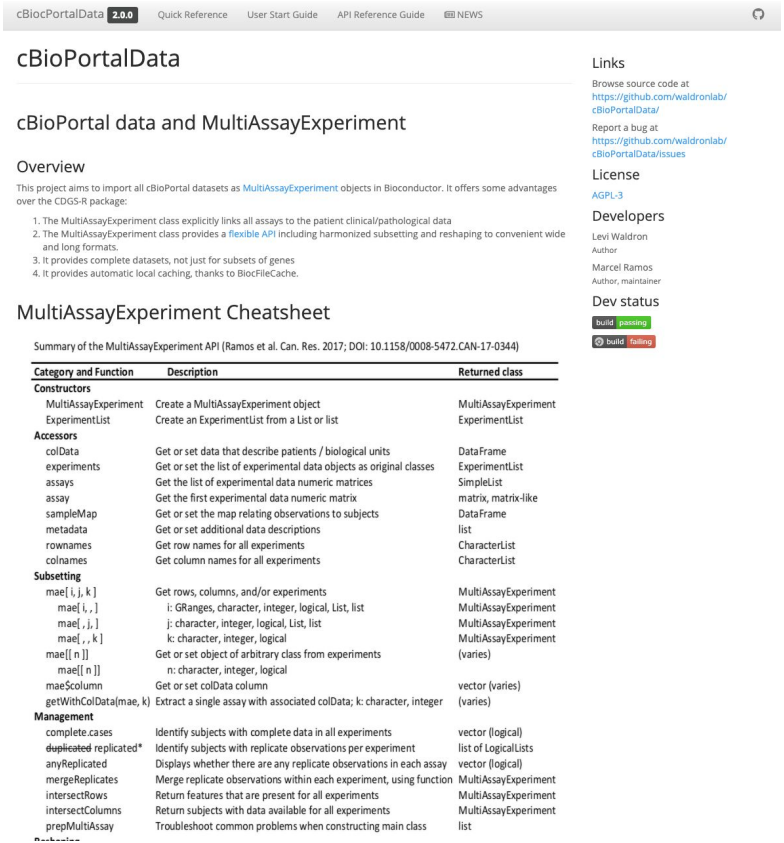
3. Next Generation Clustered Heat Map (NG-CHM)



4. Cancer Digital Slide Archive (CDSA)



5. R Package cBioPortalData - Bioconductor



cBiocPortalData 2.0.0 Quick Reference User Start Guide API Reference Guide NEWS

cBioPortalData

cBioPortal data and MultiAssayExperiment

Overview

This project aims to import all cBioPortal datasets as MultiAssayExperiment objects in Bioconductor. It offers some advantages over the CDGS-R package:

1. The MultiAssayExperiment class explicitly links all assays to the patient clinical/pathological data
2. The MultiAssayExperiment class provides a flexible API including harmonized subsetting and reshaping to convenient wide and long formats.
3. It provides complete datasets, not just for subsets of genes
4. It provides automatic local caching, thanks to BiocFileCache.

MultiAssayExperiment Cheatsheet

Summary of the MultiAssayExperiment API (Ramos et al. Can. Res. 2017; DOI: 10.1158/0008-5472.CAN-17-0344)

Category and Function	Description	Returned class
Constructors		
MultiAssayExperiment	Create a MultiAssayExperiment object	MultiAssayExperiment
ExperimentList	Create an ExperimentList from a List or list	ExperimentList
Accessors		
colData	Get or set data that describe patients / biological units	DataFrame
experiments	Get or set the list of experimental data objects as original classes	ExperimentList
assays	Get the list of experimental data numeric matrices	SimpleList
assay	Get the first experimental data numeric matrix	matrix, matrix-like
sampleMap	Get or set the map relating observations to subjects	DataFrame
metadata	Get or set additional data descriptions	list
rownames	Get row names for all experiments	CharacterList
colnames	Get column names for all experiments	CharacterList
Subsetting		
mae[i, j, k]	Get rows, columns, and/or experiments	MultiAssayExperiment
mae[i, ,]	i: GRanges, character, integer, logical, List, list	MultiAssayExperiment
mae[, j,]	j: character, integer, logical, List, list	MultiAssayExperiment
mae[, , k]	k: character, integer, logical	MultiAssayExperiment
mae[[n]]	Get or set object of arbitrary class from experiments	(varies)
mae[[n]]	n: character, integer, logical	
mae$column	Get or set colData column	vector (varies)
getWithColData(mae, k)	Extract a single assay with associated colData; k: character, integer	(varies)
Management		
complete.cases	Identify subjects with complete data in all experiments	vector (logical)
~~duplicated~~ replicated*	Identify subjects with replicate observations per experiment	list of LogicalLists
anyReplicated	Displays whether there are any replicate observations in each assay	vector (logical)
mergeReplicates	Merge replicate observations within each experiment, using function	MultiAssayExperiment
intersectRows	Return features that are present for all experiments	MultiAssayExperiment
intersectColumns	Return subjects with data available for all experiments	MultiAssayExperiment
prepMultiAssay	Troubleshoot common problems when constructing main class	list

Links

Browse source code at https://github.com/waldronlab/cBioPortalData/

Report a bug at https://github.com/waldronlab/cBioPortalData/issues

License

AGPL-3

Developers

Levi Waldron
Author

Marcel Ramos
Author, maintainer

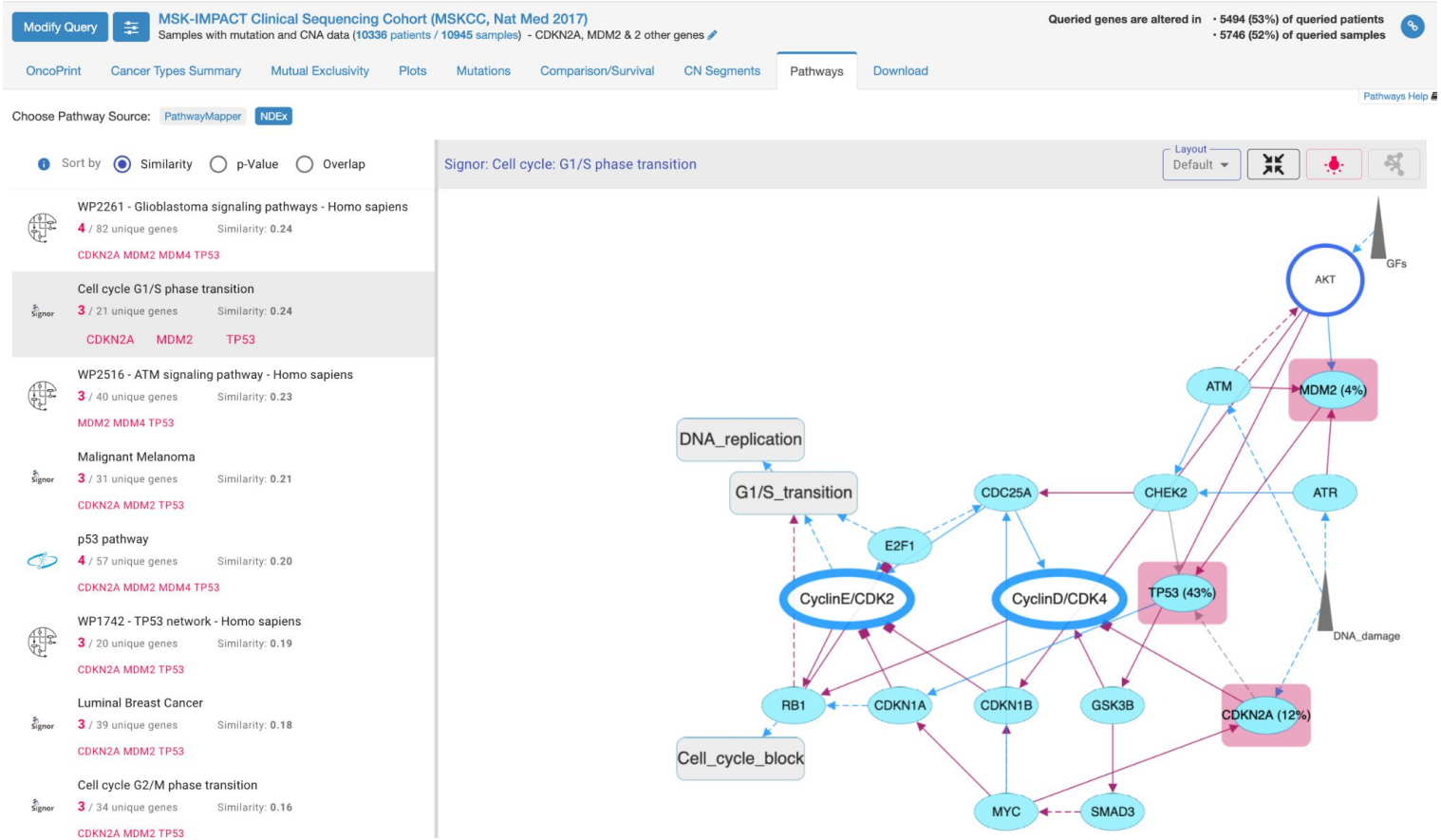
Dev status

build passing

build failing

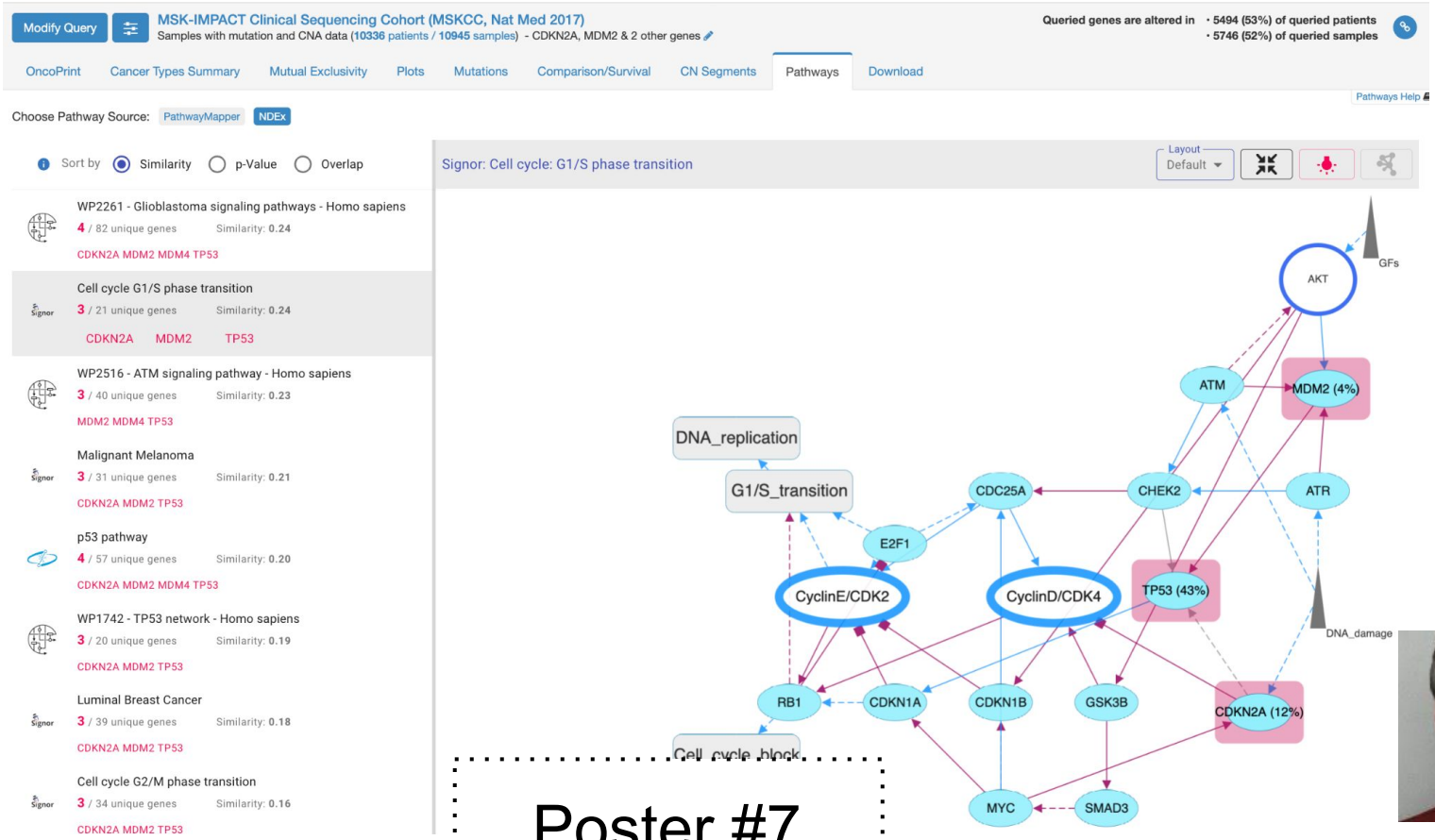
6. NDEx Pathway Analysis

NEW



6. NDEx Pathway Analysis

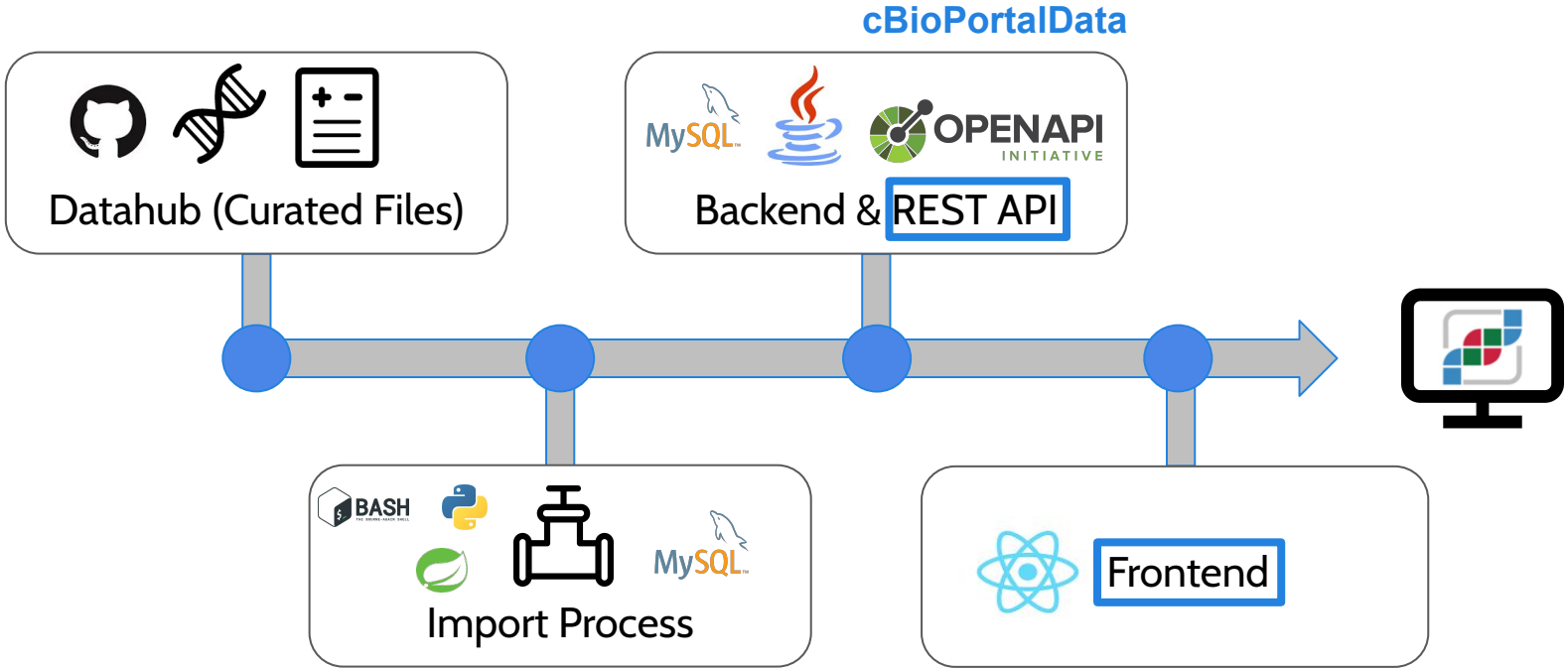
NEW



Poster #7

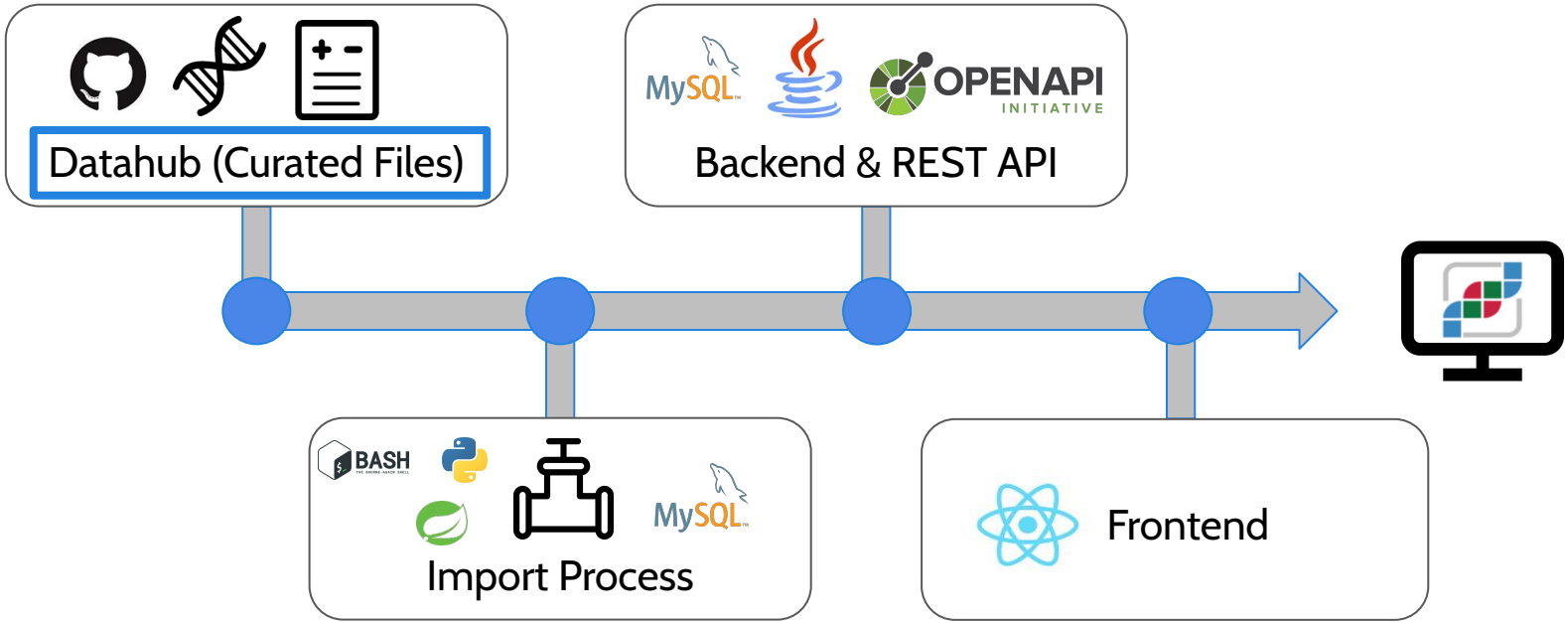
Dexter Pratt

Existing ITCR Collaborations

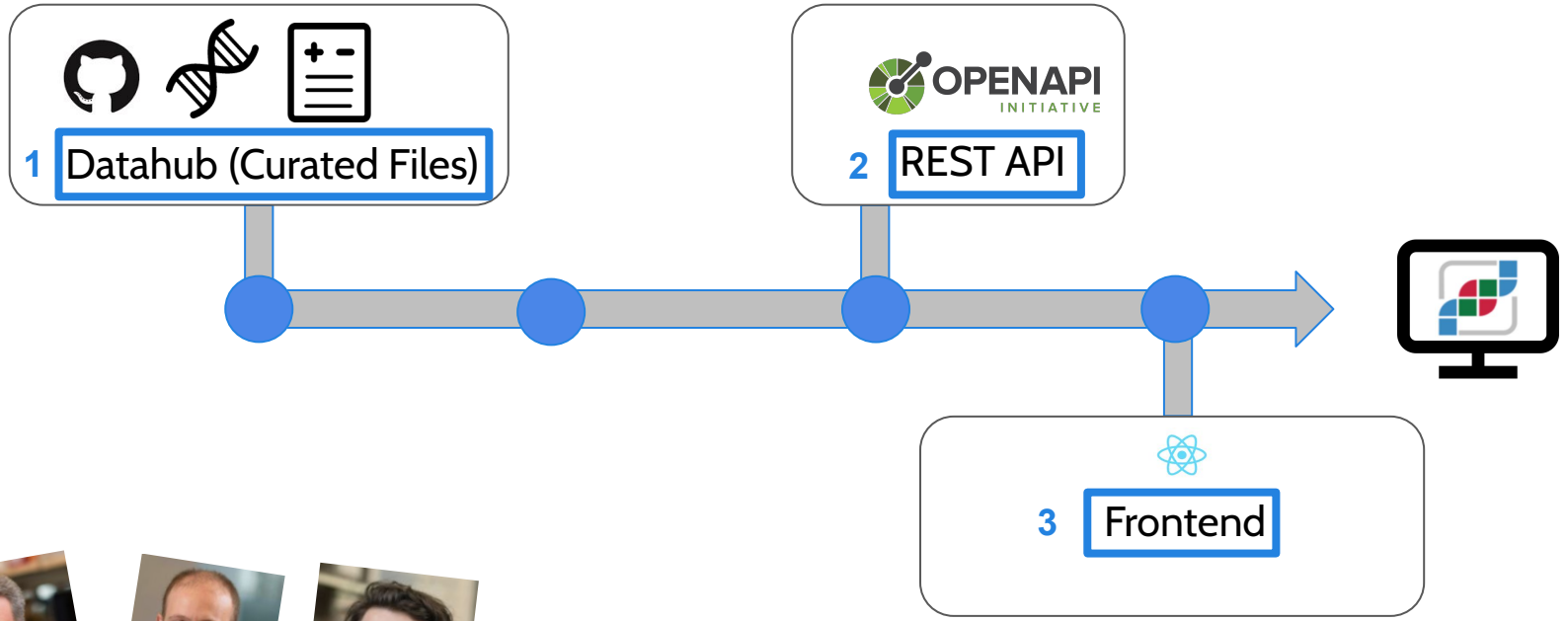


New tab (IFrame): CDSA, NG-CHM, NDEx
Frontend component: IGV
Annotations: CIViC's REST API

Potential ITCR Collaborations



Potential ITCR Collaborations



Poster #39 👋