

cBioPortal

for Cancer Genomics

Webinar 1: Introduction to cBioPortal

April 30, 2020

Webinar Schedule

- April 30: Introduction to cBioPortal
- May 7: Mutation Details & Patient View
- May 14: OQL & Expression
- May 21: Group Comparison
- May 28: API & R Client

All webinars are on Thursdays 11am-12pm EDT

Acknowledgements



Memorial Sloan Kettering
Cancer Center™

Nikolaus Schultz
Jianjiong Gao
Benjamin Gross
S. Onur Sumer
Yichao Sun
Hongxin Zhang
Adam Abeshouse
Ritika Kundra
Ino de Bruijn
Robert Sheridan
Angelica Ochoa
Aaron Lisman
Manda Wilson
Avery Wang
Jing Su
Ramyasree Madupuri
Gaofei Zhao
Xiang Li



Dana-Farber
Cancer Institute

Ethan Cerami
Chris Sander
Tali Mazor
Luke Sikina
Pieter Lukasse
Priti Kumari
Augustin Luna
James Lindsay



The Children's Hospital *of* Philadelphia

Adam Resnick
Allison Heath
Karthik Kalletla
John Maris



Weill Cornell
Medicine

Olivier Elemento
Alexandros Sigaras



Fedde Schaeffer
Oleguer Plantalech
Pim van Nierop
Riza Nugraha
Sander Rodenburg
Sjoerd van Hagen
Kees van Bochove



Trevor Pugh
Kelsey Zhu

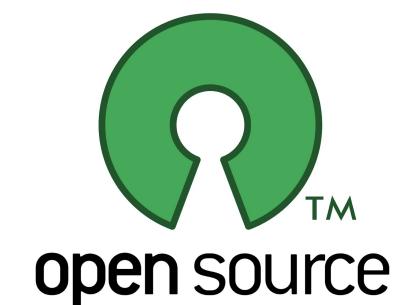


Bilkent University

Ugur Dogrusoz
Ziya Erkoc

Alumni

B. Arman Aksoy
Istemci Bahceci
Caitlin Byrne
Hsiao-Wei Chen
Ersin Ciftci
Fred Criscuolo
Leonard Dervishi
Gideon Dresdner
Andy Dufilie
Catherine Del Vecchio Fitz
Arthur Goldberg
Zachary Heins
Michael Heuer
Anders Jacobsen
Erik Larsson
Dong Li
Tamba Monroe
Peter Kok
Irina Pulyakhina
Pichai Raman
M. Furkan Sahin
Kaan Sancak
Sander Tan
Jiaojiao Wang
Stuart Watt
James Xu
Dionne Zaal



Email: cboportal@googlegroups.com

@cBioPortal

github.com/cBioPortal

Funding: Present & past



NATIONAL
CANCER
INSTITUTE



NCI CANCER MOONSHOT
Human Tumor Atlas Network
A program of the National Cancer Institute
of the National Institutes of Health



American Association
for Cancer Research



Prostate Cancer
Foundation
Curing Together.



Kravis Center for
Molecular Oncology



Dana-Farber
Cancer Institute



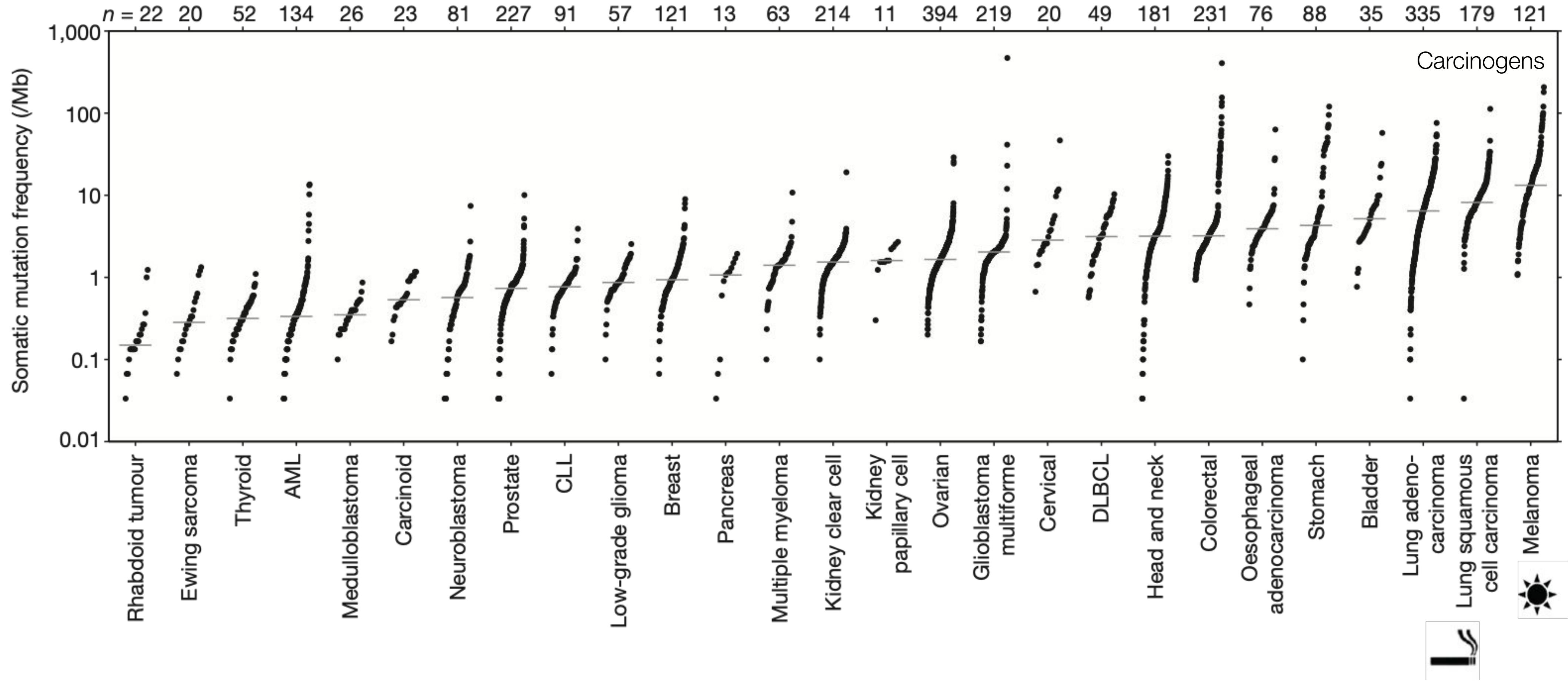
cBioPortal overview

- Platform for **exploratory and interactive visualization, analysis and download** of large-scale cancer genomics data sets
- **Open source** software jointly developed by Dana-Farber Cancer Institute, Memorial Sloan Kettering Cancer Center, Princess Margaret Cancer Centre, Children's Hospital of Philadelphia, and The Hyve
- **Public website** (cBioPortal.org) with public data (TCGA, ICGC, published sequencing studies)
 - Private instances are installed at academic and commercial institutions world-wide
 - You can make OncoPrints and Lollipop plots with your own data (“Visualize Your Data” page)

cBioPortal addresses challenges in cancer -omics

- Large cancer -omics datasets are becoming increasingly common. But they can be hard to access, analyze & visualize, especially without a computational skillset
 - cBioPortal hosts data from many studies, including TCGA, for analysis and easy download
- It can be hard to interpret the data or identify the “important” events (e.g. which mutations are drivers vs passengers) in such large datasets

cBioPortal addresses challenges in cancer -omics

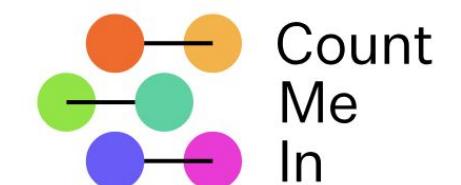


cBioPortal addresses challenges in cancer -omics

- Large cancer -omics datasets are becoming increasingly common. But they can be hard to access, analyze & visualize, especially without a computational skillset
 - cBioPortal hosts data from many studies, including TCGA, for analysis and easy download
- It can be hard to interpret the data or identify the “important” events (e.g. which mutations are drivers vs passengers) in such large datasets
 - cBioPortal integrates many data resources/knowledgebases

What data is in cBioPortal?

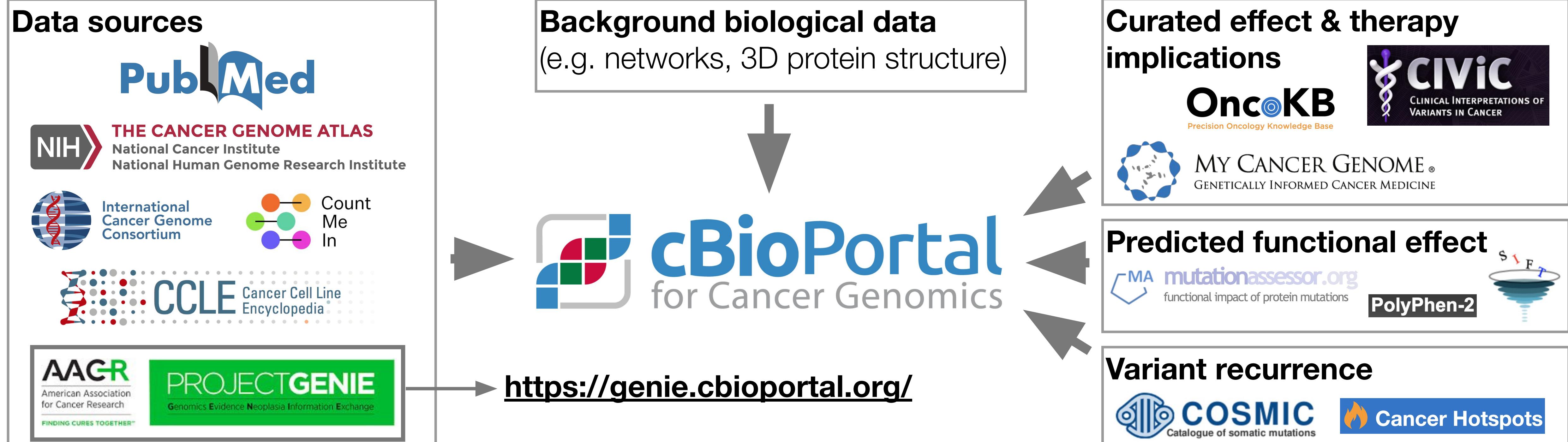
Data sources



Project:	NIH-sponsored research project	Clinical sequencing data from 19 cancer centers worldwide
Samples:	Primary, untreated tumors	Primary and metastatic tumors Pre- and post- treatment
Assays:	Whole exome sequencing + aCGH + mRNA array/seq + ...	Targeted gene panels (genes vary across cancer centers)
Data:	Mutations + copy number alterations + mRNA expression + ...	Mutations + some samples have copy number alterations

**** Read the original publication and understand your data source(s)**

What data is in cBioPortal?



- Clinical data:**
- Treatments
 - Survival
 - etc
- omic data:**
- Mutations
 - Fusions
 - Copy number
 - mRNA expression
 - Protein levels
 - DNA Methylation*

cBioPortal features & analysis tools (a subset)

- Visualize distribution of genomic alterations in multiple genes across many samples
- Calculate mutual exclusivity of genomic events
- Visualize distribution of mutations within a gene
- Visualize copy number vs expression for a gene
- Perform survival analysis
- Identify which genes are mutated in the same samples as your gene of interest
- Define and compare groups of samples/patients

Getting help

cBioPortal
FOR CANCER GENOMICS

Data Sets Web API R/MATLAB **Tutorials** FAQ News

Tutorials

Tutorial #1: Single Study Exploration

Tutorial Objectives

- Introduc
- Show tw
- Front
- Front
- Walk thr
- Stud
- Clin
- Mut
- Cop
- Show ho

< > |

Tutorial #2: Single Study Query

Tutorial Objectives

- Show ho
- Walk thr
- Onc
- Cane
- Mutu
- Plots
- Mutu
- Co-E
- Show ho

< > |

Tutorial #3: Patient View

Tutorial Objectives

- Show di
- Walk thr
- Sum
- Clin
- Path
- Tiss
- Show ho

< > |

Tutorial #4: Virtual Studies

Tutorial Objectives

- Explain
- Delinea
- Show ho

< > |

Tutorial #5: Onco Query Language (OQL)

Tutorial Objectives

- Introduc
- Explain
- Show t

< > |

Tutorial #6: Group Comparison

Tutorial Objectives

- Explain what the new group comparison functionality enables
- Delineate the different ways to define groups and enter the group comparison view
- Highlight potential use cases for group comparison functionality

< > |

< > | Slide 2 | ⚡ [] ⚙ Google Slides

 **cBioPortal**
FOR CANCER GENOMICS

Data Sets Web API R/MATLAB Tutorials **FAQ** News

FAQs

- General Questions
 - What is the cBioPortal for Cancer Genomics?
 - How do I get started?
 - What data types are in the portal?
 - What is the process of data curation?
 - How do I get updates on new portal developments and new data sets?
 - Does the portal work on all browsers and operating systems?
 - How do I cite the cBioPortal?
 - Can I use figures from the cBioPortal in my publications or presentations?
 - Can I save or bookmark my results in cBioPortal?

cBioPortal for Cancer Genomics Discussion Group

60 of 2034 topics (99+ unread) ★ 

PROTOCOL | CANCER

Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal

Jianjiang Gao¹, Bülent Arman Aksoy¹, Ugur Dogrusoz², Gideon Dresdner¹, Benjamin Gross¹, S. Onur Sumer¹, Yichao Sun¹, Anders Jacobsen¹, Rileen Sinha¹, Erik Larsson³, Ethan Cerami^{1,4}, Chris Sander¹, and Nikolaus Schultz¹

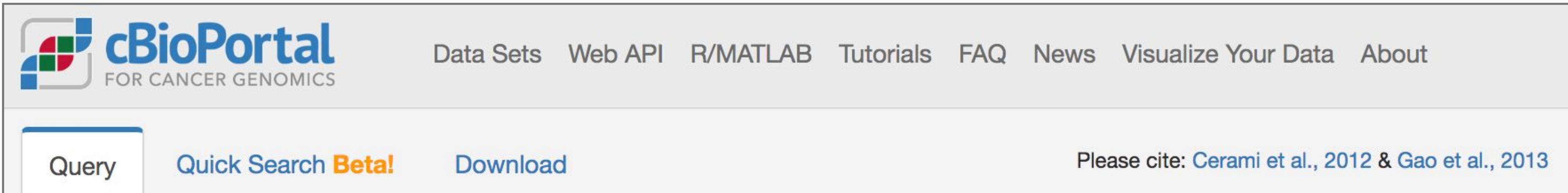
Sci. Signal. 02 Apr 2013:

Vol. 6, Issue 269, pp. pl1

DOI: 10.1126/scisignal.2004088

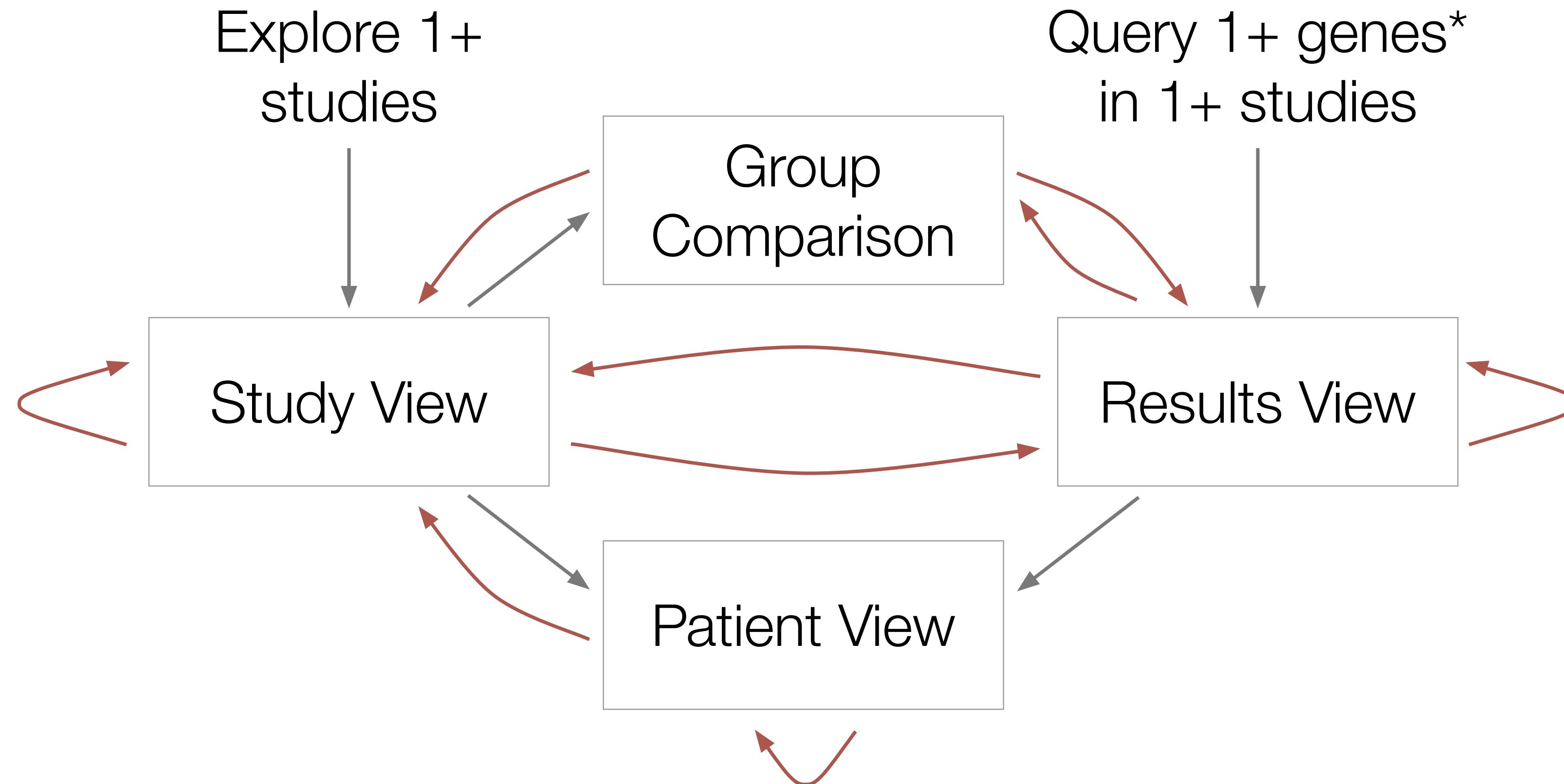
Using cBioPortal for publication

- Please use cBioPortal in your publications!
 - Figures are downloadable as PDF/SVG so you can customize them
- Cite the studies that generated the data you are using (if applicable)
- Cite cBioPortal



The screenshot shows the cBioPortal homepage. At the top, there is a navigation bar with links: Data Sets, Web API, R/MATLAB, Tutorials, FAQ, News, Visualize Your Data, and About. Below the navigation bar, there is a search bar with three buttons: Query, Quick Search Beta!, and Download. A citation reminder at the bottom right corner reads: Please cite: Cerami et al., 2012 & Gao et al., 2013.

cBioPortal workflow



* Can customize alteration types & thresholds per gene



<https://www.cbiportal.org/>

Webinar Schedule

- April 30: Introduction to cBioPortal
- May 7: Mutation Details & Patient View
- May 14: OQL & Expression
- May 21: Group Comparison
- May 28: API & R Client

All webinars are on Thursdays 11am-12pm EDT