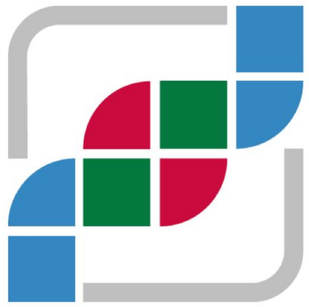


cBioPortal
for Cancer Genomics

# Webinar 1: Introduction to cBioPortal

April 30, 2020

Dana-Farber
Cancer Institute

Memorial Sloan Kettering
Cancer Center™

thehyve

The Children's Hospital *of* Philadelphia

UHN
Toronto General
Toronto Western
Princess Margaret
Toronto Rehab

# 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

thehyve

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

UHN Toronto General Toronto Western Princess Margaret Toronto Rehab

Trevor Pugh
Kelsey Zhu

Bilkent University

Ugur Dogrusoz
Ziya Erkoc

**Alumni**

B. Arman Aksoy
Istemi 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 Monrose
Peter Kok
Irina Pulyakhina
Pichai Raman
M. Furkan Sahin
Kaan Sancak
Sander Tan
Jiaojiao Wang
Stuart Watt
James Xu
Dionne Zaal

open source

**Funding: Present & past**

NIH National Cancer Institute
ITCR
NCI Cancer Moonshot Human Tumor Atlas Network
AACR American Association for Cancer Research
Prostate Cancer Foundation Curing Together.
Movember Foundation
Kravis Center for Molecular Oncology
Dana-Farber Cancer Institute
Robertson Foundation
TCGA
NRNB
S2C
Starr Cancer Consortium
BCRF Breast Cancer Research Foundation
IVY Foundation The Ben and Catherine
POETIC


Email: cbioportal@googlegroups.com @cBioPortal github.com/cBioPortal

# 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

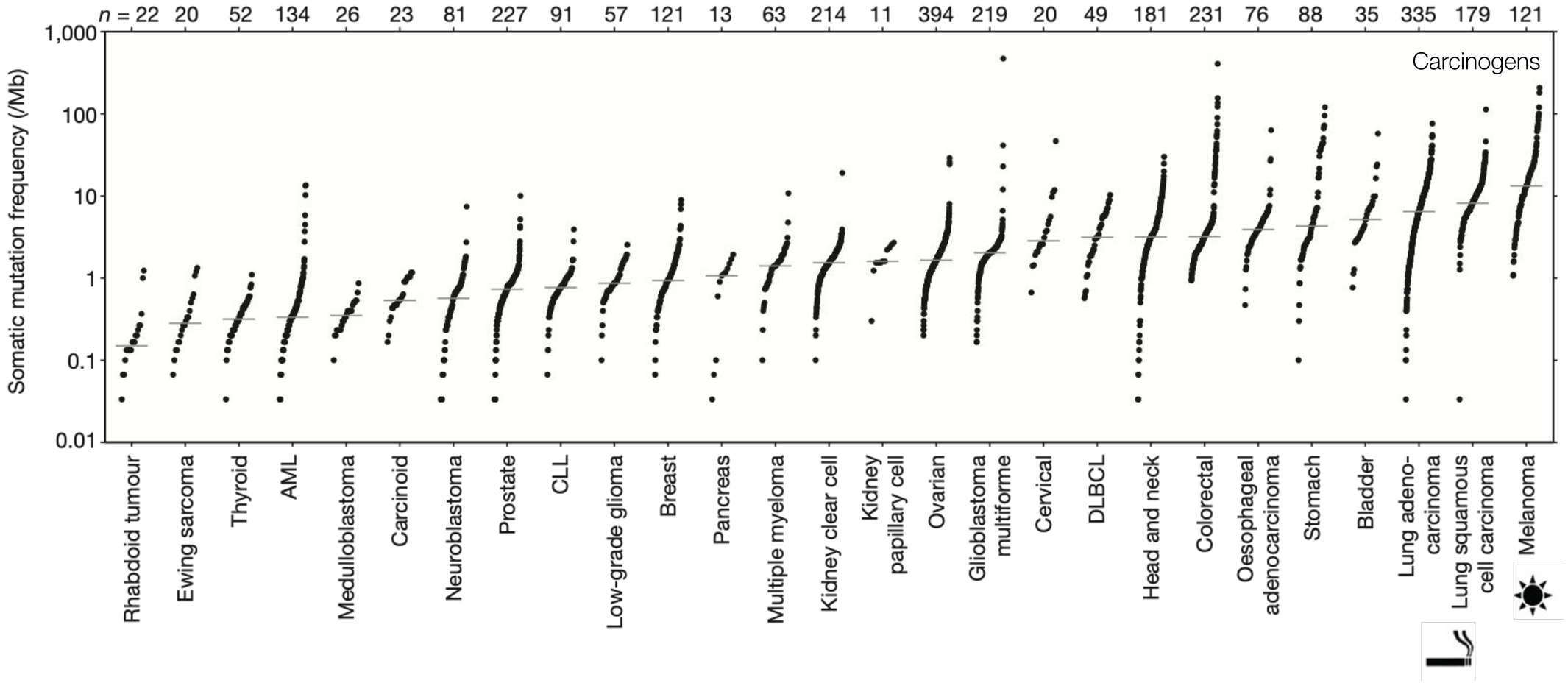
- **Public website** (cBioPortal.org) with public data (TCGA, ICGC, published sequencing studies)
    - Private instances are installed at academic and commercial institutions world-wide
    - You can make OncoPrints and Lollipop plots with your own data ("Visualize Your Data" page)

# 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




Lawrence MS et al, Nature, 2013

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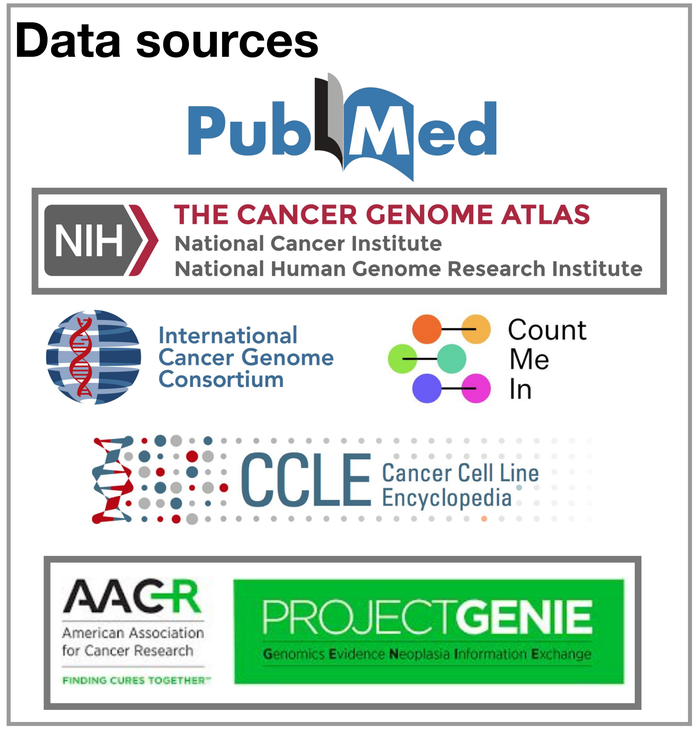
- It can be hard to interpret the data or identify the “important” events (e.g. which mutations are drivers vs passengers) in such large datasets
    - cBioPortal integrates many data resources/knowledgebases

# What data is in cBioPortal?



cBioPortal for Cancer Genomics

NIH THE CANCER GENOME ATLAS
National Cancer Institute
National Human Genome Research Institute

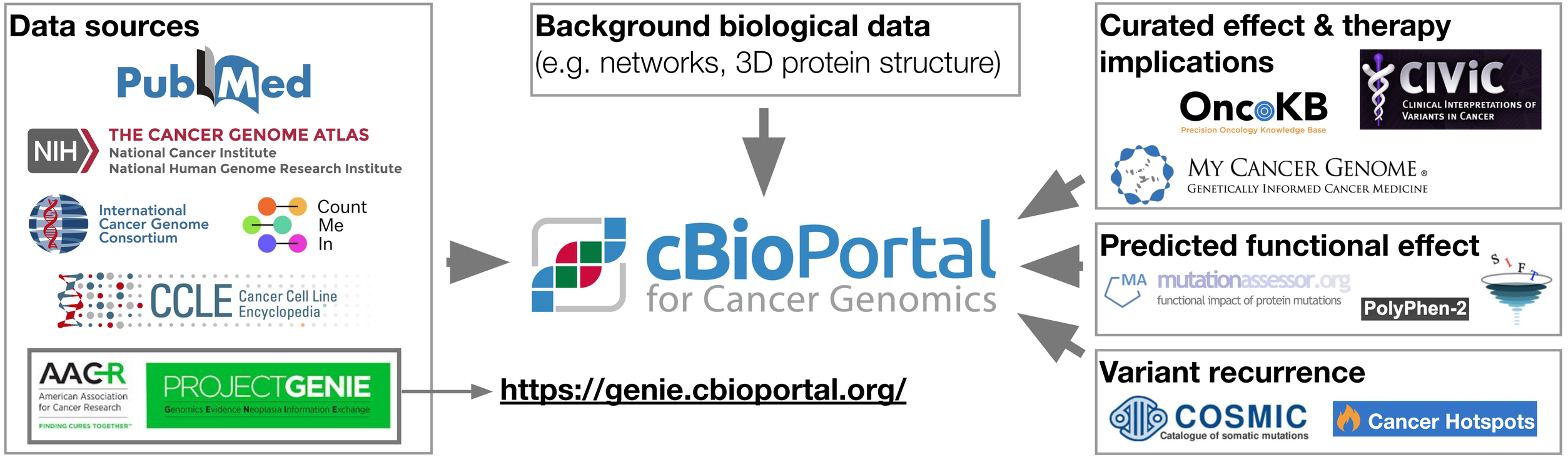
AACR American Association for Cancer Research FINDING CURES TOGETHER™

PROJECT GENIE
Genomics Evidence Neoplasia Information Exchange

| | | |
|---|---|---|
| **Project:** | NIH-sponsored research project | Clinical sequencing data from 19 cancer centers worldwide |
| **Samples:** | Primary, untreated tumors | Primary and metastatic tumors<br>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

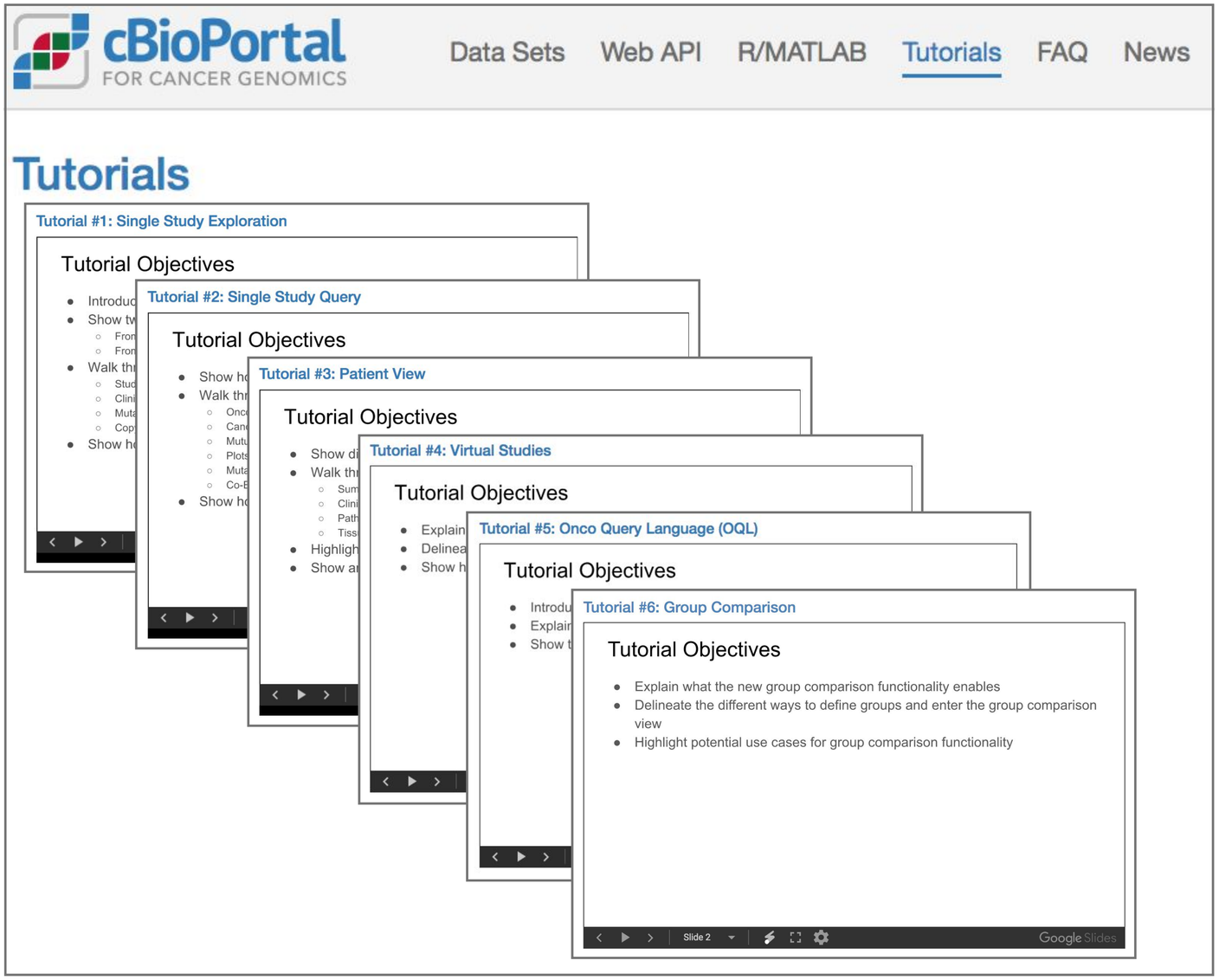
-omic data:

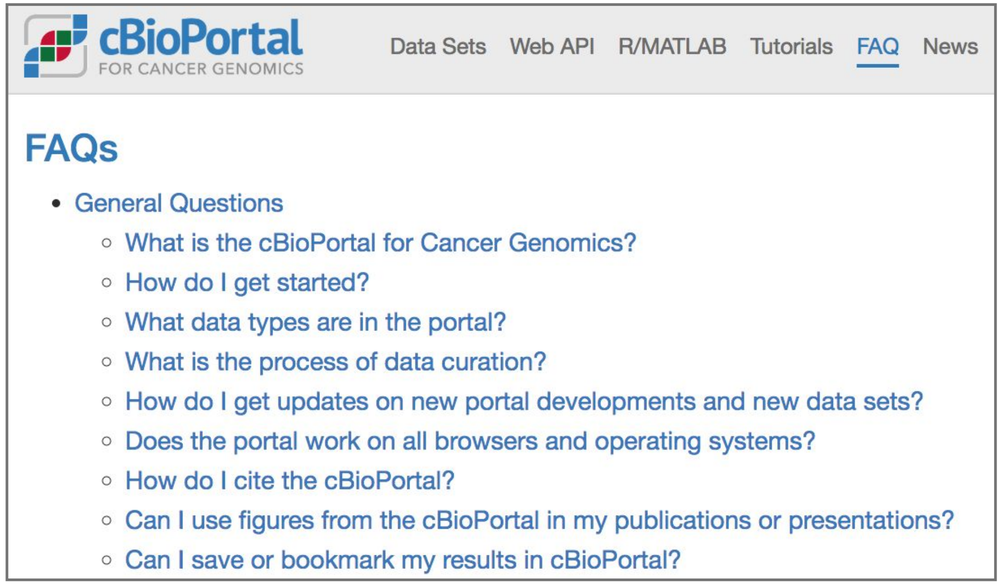
- Mutations
- Fusions
- Copy number
- mRNA expression
- Protein levels
- DNA Methylation*

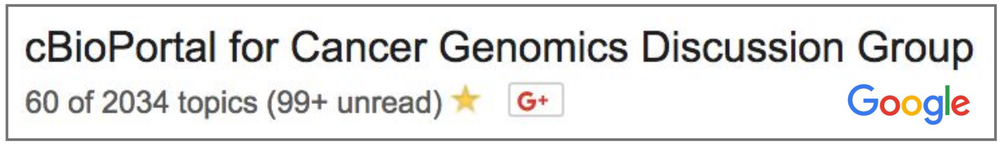
# cBioPortal features & analysis tools (a subset)

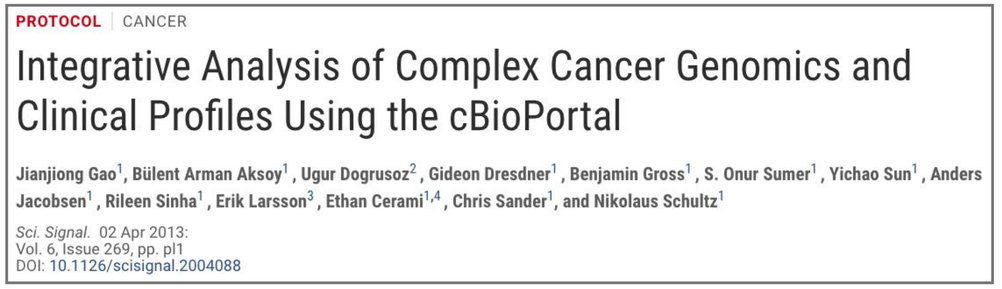
- Visualize distribution of genomic alterations in multiple genes across many samples
- Calculate mutual exclusivity of genomic events
- Visualize distribution of mutations within a gene
- Visualize copy number vs expression for a gene
- Perform survival analysis
- Identify which genes are mutated in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

# Getting help



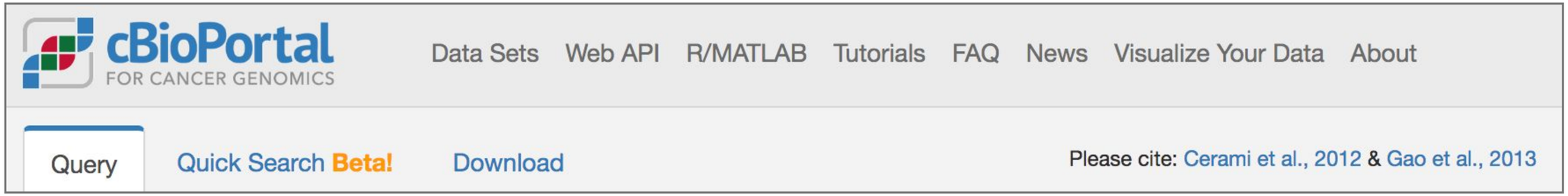



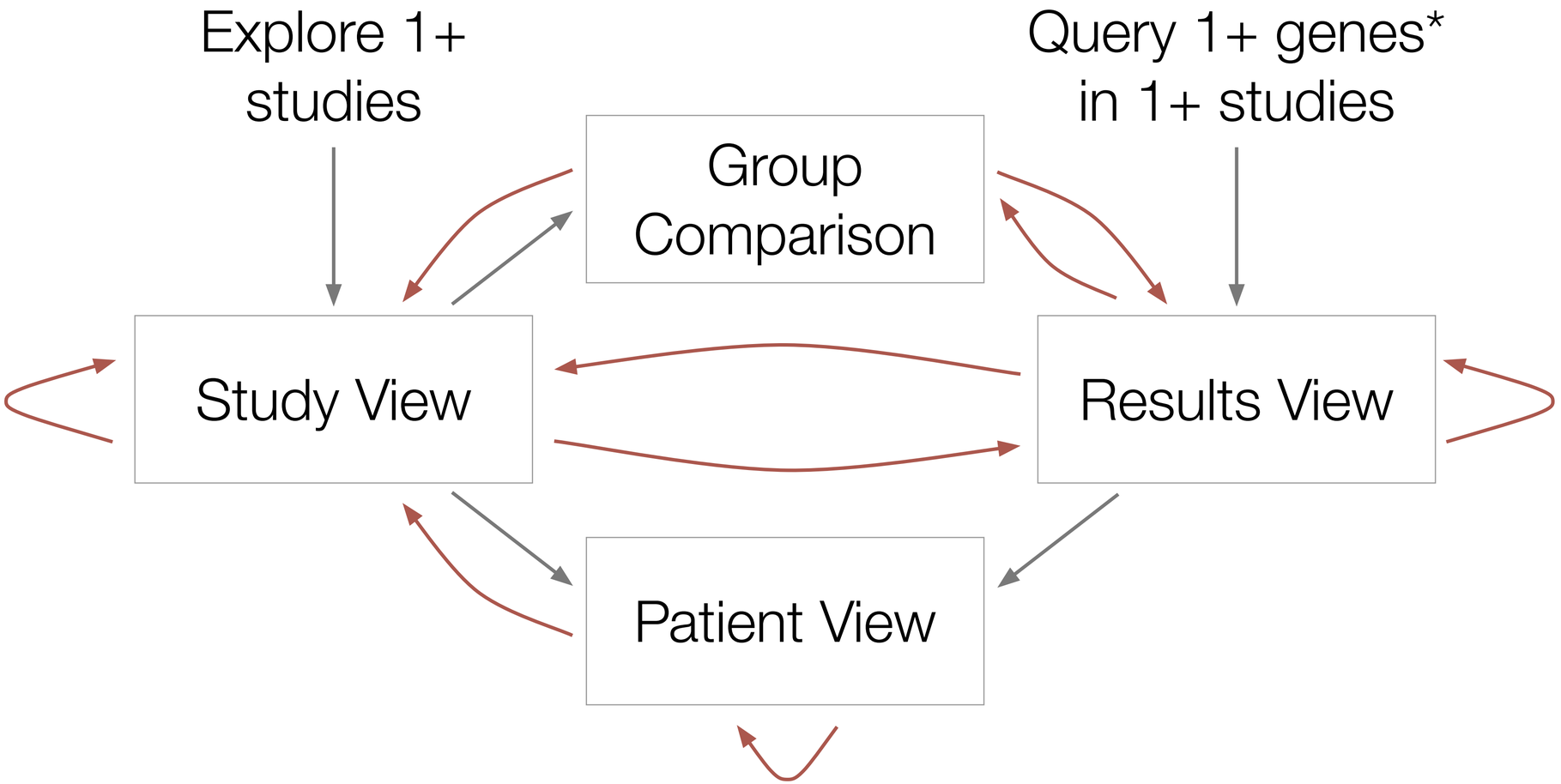



# Using cBioPortal for publication

- **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



# cBioPortal workflow




* Can customize alteration types & thresholds per gene

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https://www.cbioportal.org/

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