# The UCSC Xena system for integrating and visualizing functional genomics





Mary Goldman, Brian Craft, Jingchun Zhu, Teresa Swatloski, Melissa Cline, David Haussler

Mutations (green) clustered

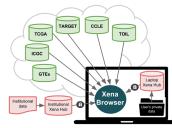
around the active site (purple).



# http://xena.ucsc.edu

## Xena: See the bigger picture

Securely analyze and visualize your private functional genomics data in the context of public data sets.



#### **Xena Browser**

Use your web browser to securely connect to public and private hubs at the same time.

#### **Xena Data Hubs**

Can be installed anywhere. Restrict access to authorized users if desired.

#### **Public Data Hubs**

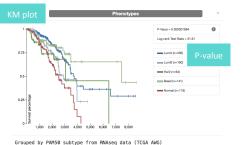
Access over 800+ datasets from TCGA. ICGC, TARGET, GTEx, **CCLE** and more. More than 35 cancer types, including Pan-Cancer.

#### **Private Data Hubs**

Easy to install on your laptop or behind a firewall. Load your data using our app or the command line. Mac, Windows and Linux.

### Xena helps you answer questions like:

- What is the pattern between my two genes?
- What is the relationship between this frequent mutation and expression?
- Where does my sample fall within the larger genomics space?
- How did drug treatment change expression of a gene in my cell line?



Overall survival by breast cancer subtype.

Compare TERT expression in GBM, LGG and single sample

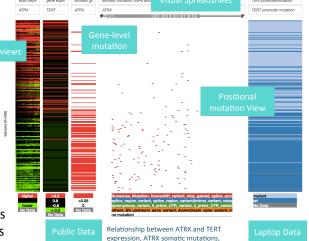
### We offer:

- Tutorials
- Forums
- Mailing lists
- Help guides

Expression of ESR1 and FOXA1

are related in breast cancer

FAQ



and TERT promoter mutations.

Data types: SNPs, Indels, SVs, expression, CNV, methylation, sample annotations (age, tumor type, clustering results, etc)

FOXM1 regulates expression of PLK1, CCNB2, BIRC5, and AURKB, FOXM1A is a transcriptional repressor, while FOXM1B/1C are transcriptional activators

https://github.com/ucscXena mary@soe.ucsc.edu



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# Watch to learn more