

Integrating UCSC Cancer Genomics with Galaxy

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The UCSC Cancer Genomics Browser is a powerful tool for visual analysis of published cancer genomics datasets. Its combined visualization of genomic and clinical data allows users to dynamically sort and cluster cohorts of genomic data by clinical features, cancer subtypes and genomic signatures. It displays data from a large library of over 580 cancer genomics datasets, including TCGA, LINCS and CCLE. The Cancer Browser is currently available in the Galaxy test toolshed, providing direct export into Galaxy datasets, and will soon be available in the main toolshed.

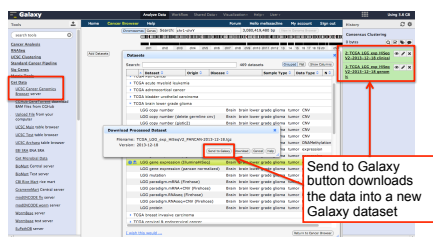
UCSC Cancer Genomics Browser



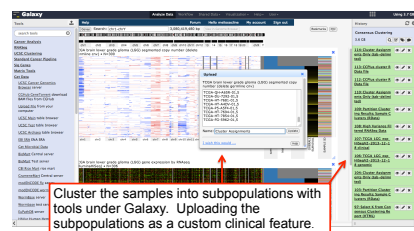
Copy Number Variation in Diffuse Intrinsic Pontine Glioma (Puget et al 2012)

UCSC Cancer Genomics Browser Integrated With Galaxy

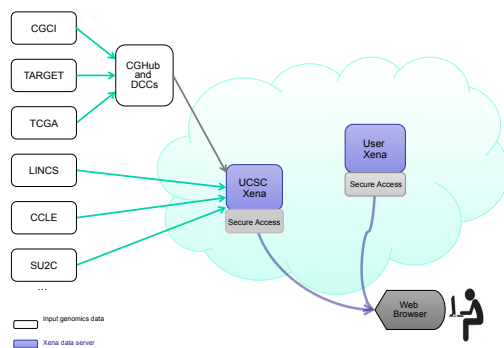
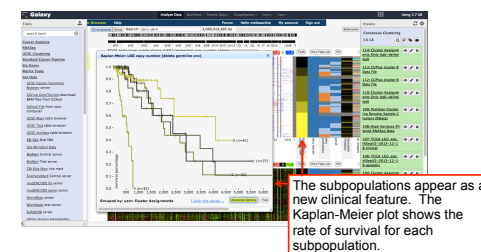
Import Data Into Galaxy



Upload Results From Galaxy



Visualize Results From Galaxy



Building on the success of the Cancer Browser, we are now developing the Xena platform to enable users to host, visualize, analyze and share their own data from within a secure virtual machine (XenaVM). Users will be able to visualize their datasets separately the Xena Browser, or integrate their data with published datasets to form larger "virtual cohorts". Data will be hosted by a network of Xena servers, with the UCSC server hosting the UCSC cancer genomics library. To provide greater analysis capabilities, Xena will be tightly integrated with Galaxy. Users will be able to export data from Xena into Galaxy datasets, analyze those datasets under Galaxy, and import the analysis results directly into Xena, facilitating cycles of analysis and visualization.

UCSC Xena Browser in Galaxy

