

# StratomeX: Enabling Visualization-Driven Cancer Subtype Analysis



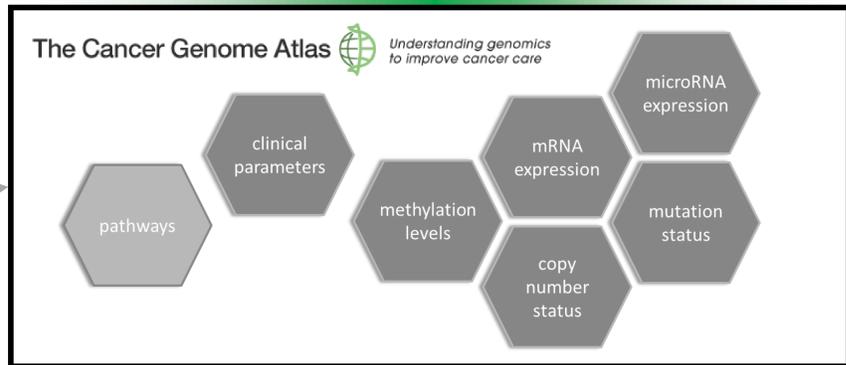
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Header Bricks show a summary of the whole dataset.

Each Brick represents a candidate subtypes, a group of patients.

## Motivation

The traditional classification of cancer based on the tissue in which they arise is nowadays supplemented by biomolecular subtypes. Knowledge about cancer subtypes promises improved patient outcomes through refined therapeutic targeting. Gaining such knowledge is an important goal of integrative cancer genomics projects such as *The Cancer Genome Atlas*

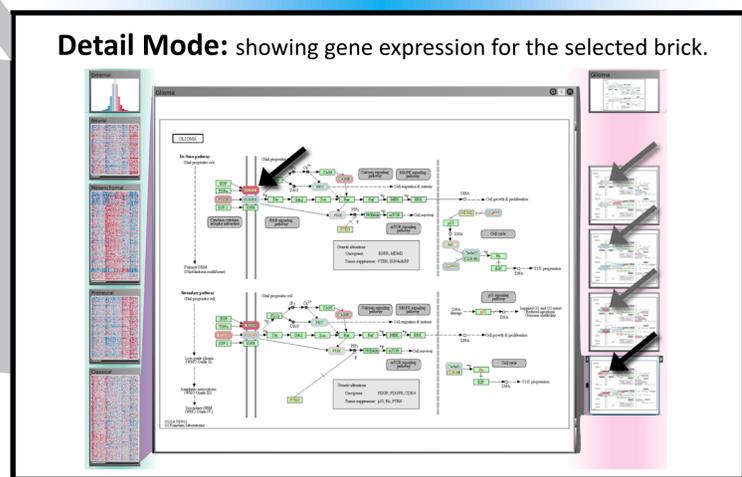
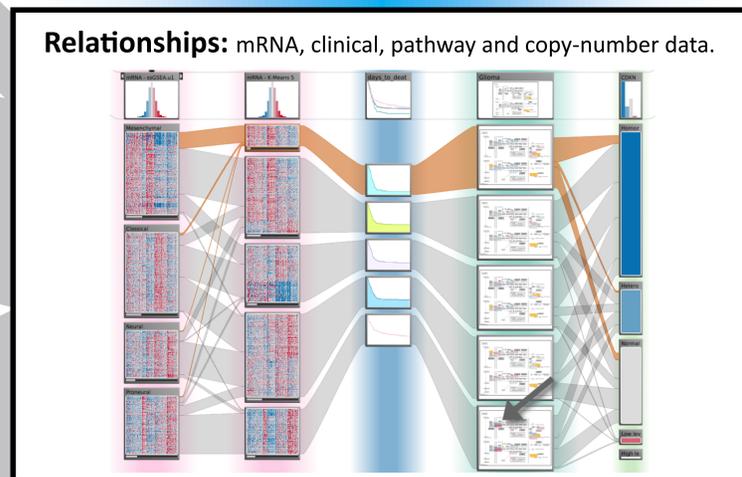
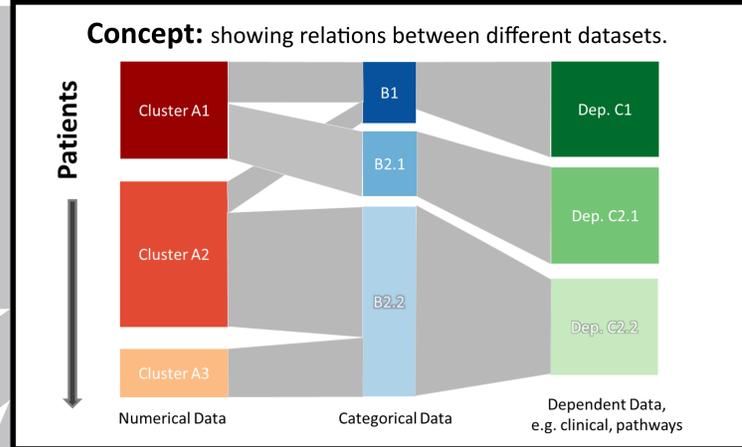


The analysis of cancer subtypes is based on the integrated analysis of multiple biomolecular datasets. Methods such as clustering of a dataset are used to stratify a dataset into candidate subtypes. The challenge is to find candidate subtypes which are backed up by other data, such as

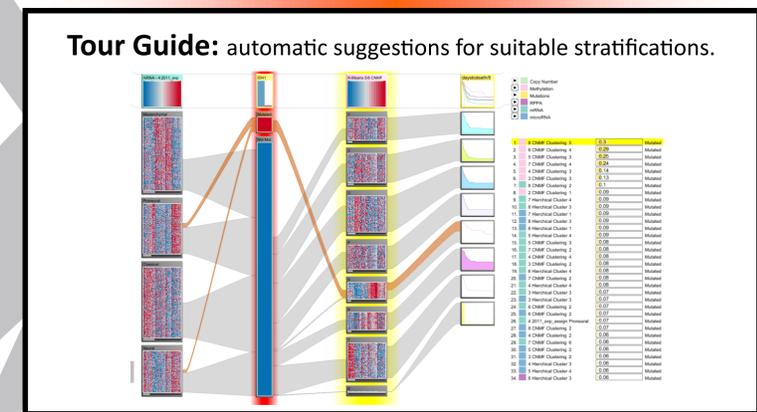
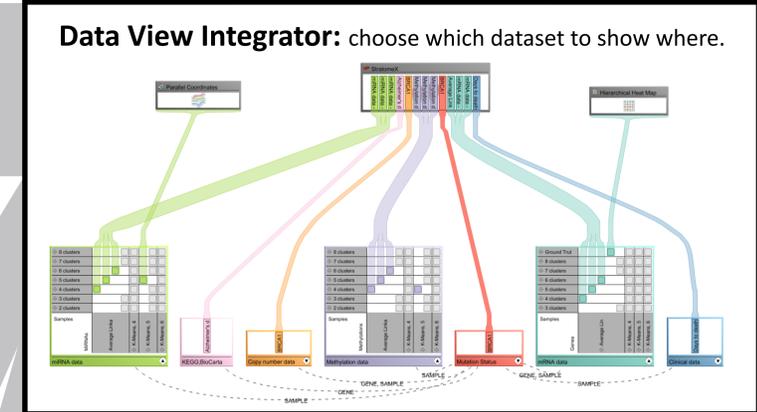
- differences in clinical outcome
- indication of causality based on mutations or copy number alterations
- differences in biological processes

Columns represent a dataset.

## Technique



## Smart Support



Ribbons between Columns show how strong two bricks are related.

Download and learn about StratomeX:  
<http://stratomeX.caleydo.org>  
 Explore TCGA Data:  
<http://tcga.caleydo.org>  
 Contact:  
[lex@seas.harvard.edu](mailto:lex@seas.harvard.edu)

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