

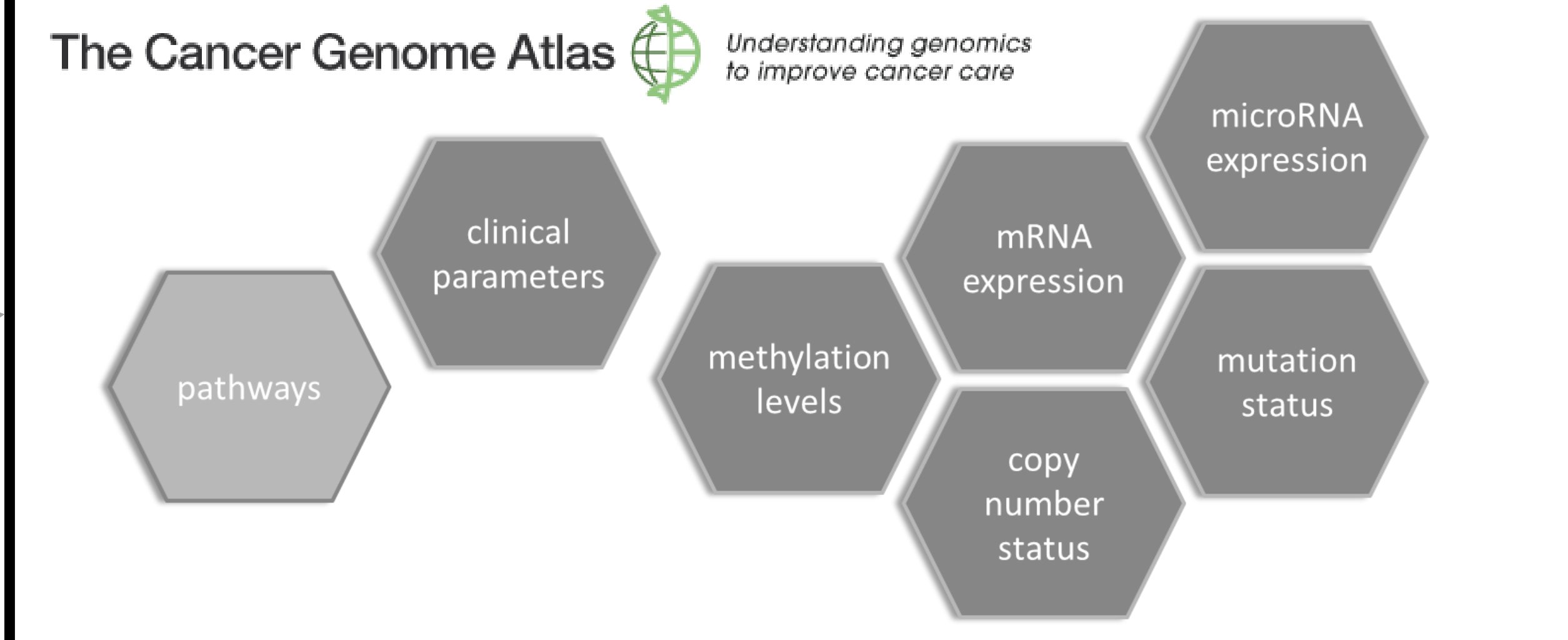
# StratomeX: Enabling Visualization-Driven Cancer Subtype Analysis



Alexander Lex, Marc Streit, Hans-Jörg Schulz, Christian Partl, Dieter Schmalstieg, Peter J. Park, Nils Gehlenborg

## 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 are used to stratify datasets. The resulting stratifications represent potential cancer subtypes. The challenge we address 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, or
- differences in biological processes.

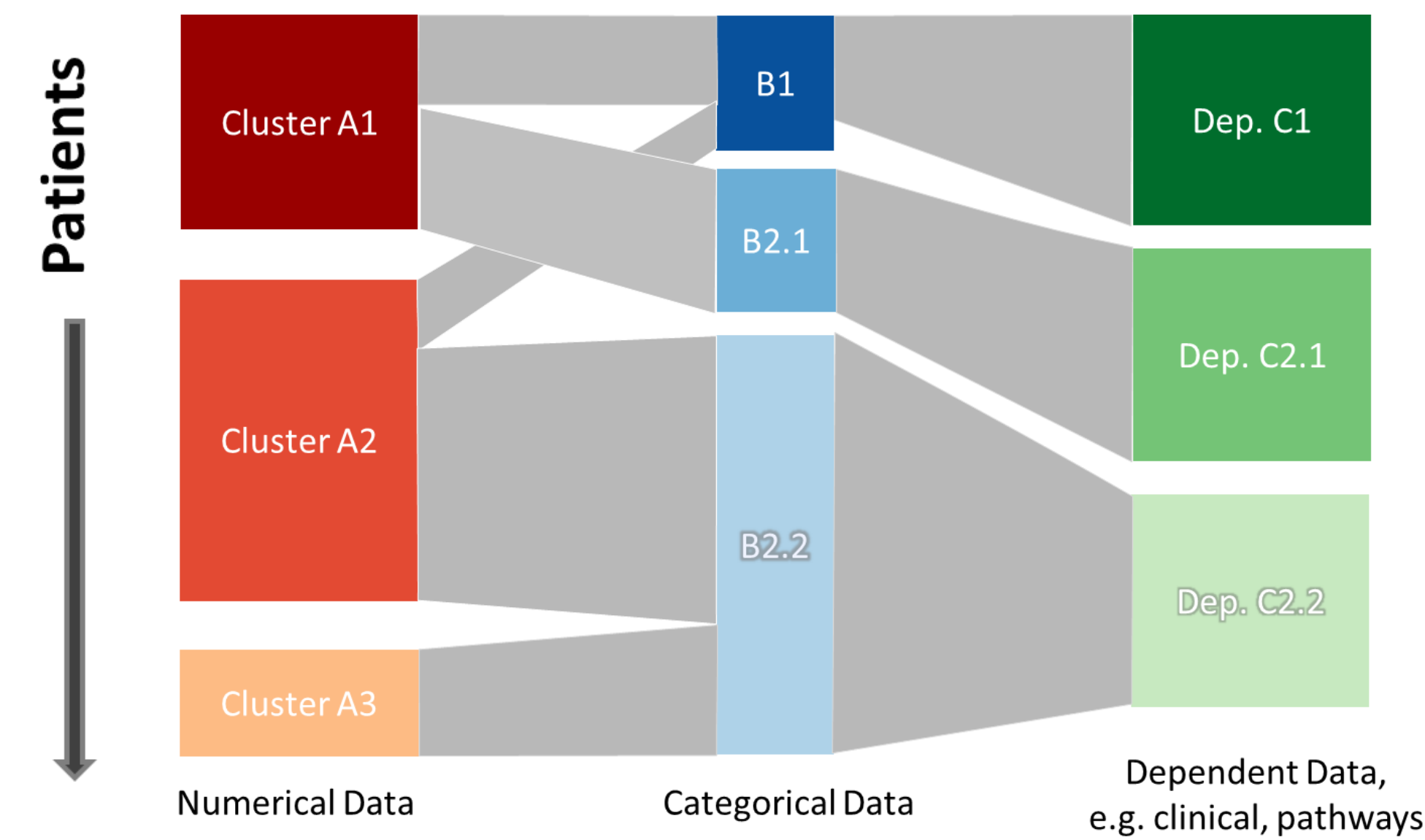
Columns represent a stratification of a dataset.

Header Bricks show a summary of the whole dataset.

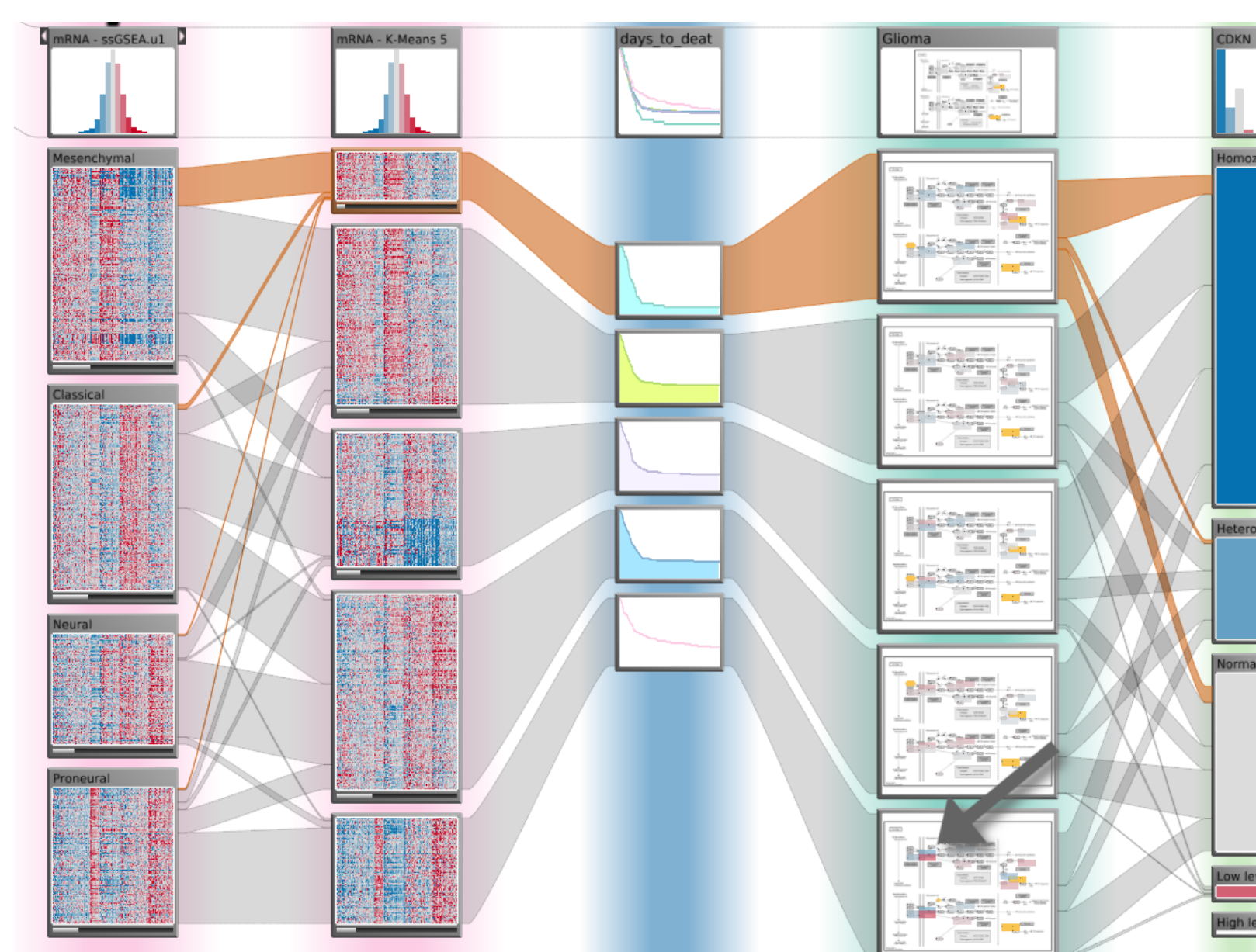
Each Brick represents a candidate subtype, a group of patients.

## Technique

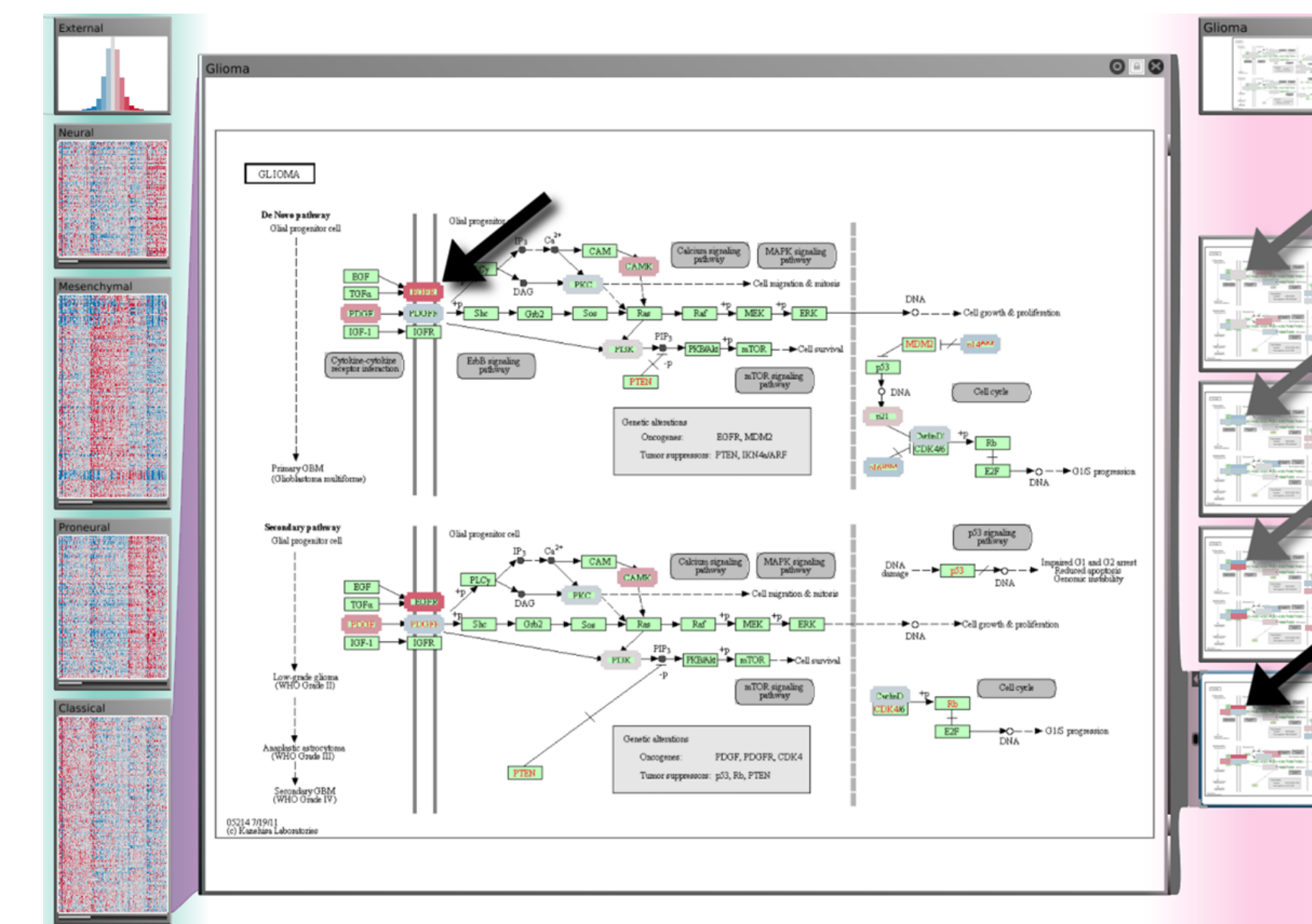
**Concept:** showing relations between different datasets.



**Relationships:** mRNA, clinical, pathway and copy-number data.

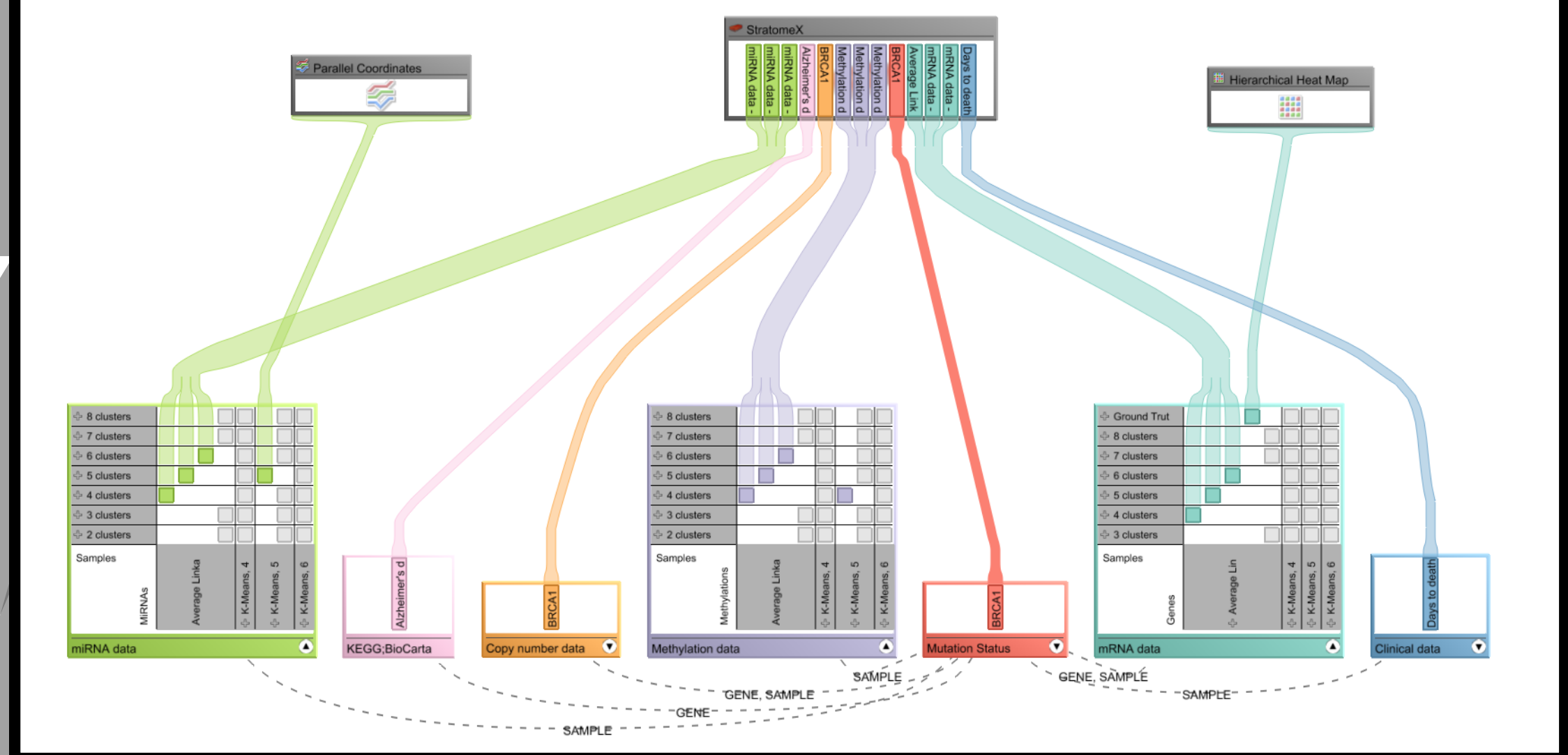


**Detail Mode:** showing gene expression for the selected brick.

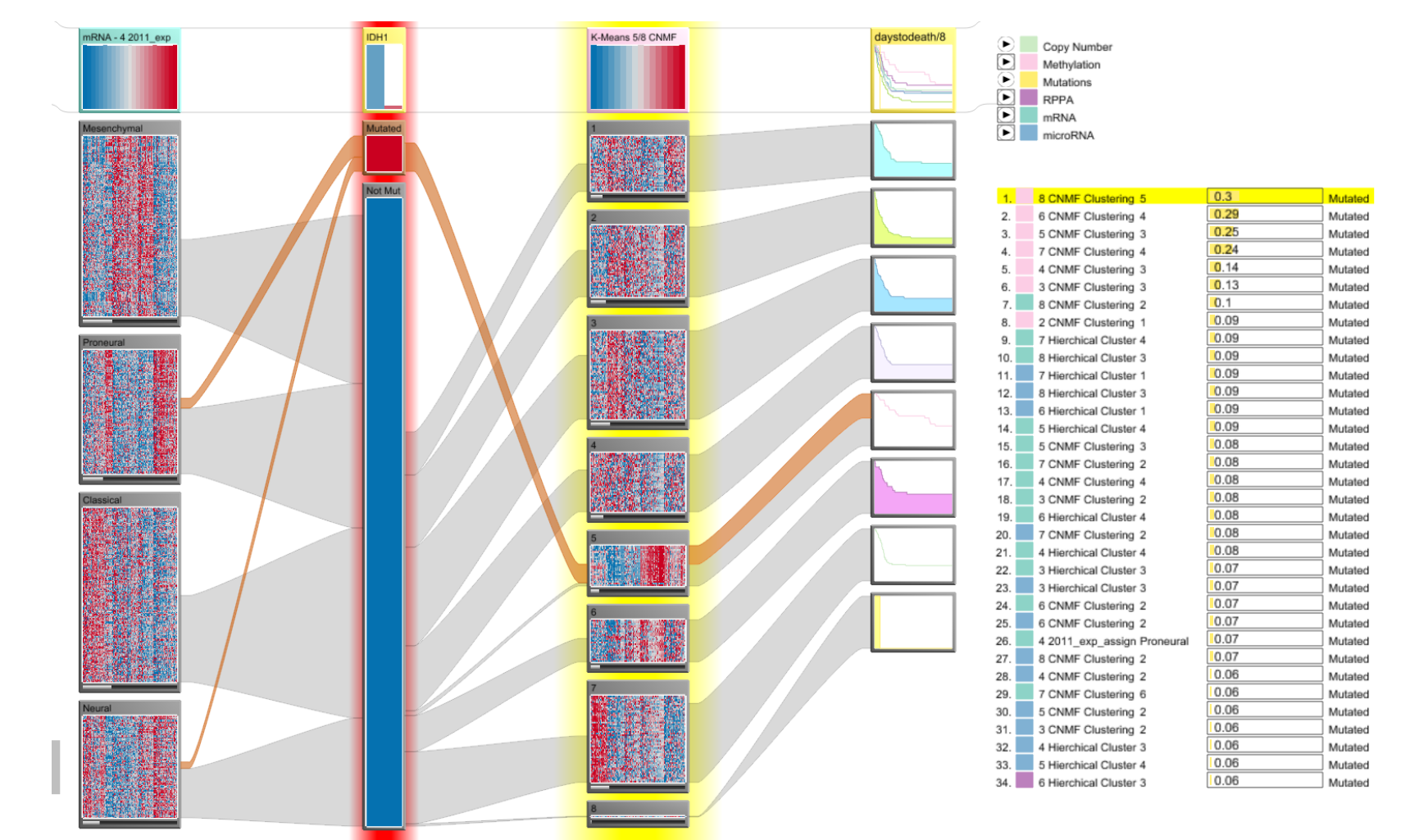


## Smart Support

**Data View Integrator:** choose which dataset to show where.



**Tour Guide:** automatic suggestions for suitable stratifications.



Ribbons between Columns show how strongly two groups 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)