



# CALEYDO

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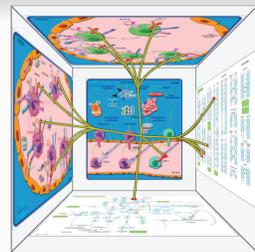
## Bucket

The main contribution of Caleydo is the integration of different visualizations.

The spatial arrangement helps coping with many visualizations simultaneously.

The connection lines show relationships between different visualizations. In this way Caleydo bridges the gap between gene expression analysis, pathways, and clinical data.

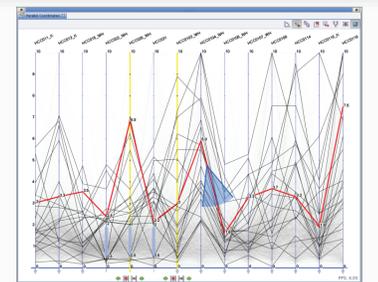
## Pathway Exploration



The Caleydo pathway explorer is a tool that integrates pathways from BioCarta and KEGG in one framework. To facilitate understanding of processes across pathway boundaries, Caleydo arranges the pathways in a 3D setup and connects identical nodes with visible links.

Navigation in the network of pathways is facilitated by a hierarchical approach which dynamically selects a working set of individual pathways for closer inspection.

## Parallel Coordinates



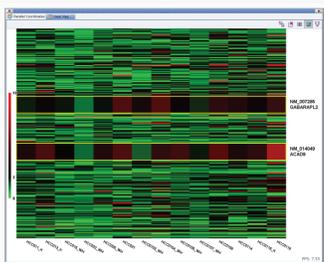
Parallel Coordinates are a well-established method to visualize multi-dimensional data. However, they have been rarely used for the visualization of gene expression.

Our implementation of parallel coordinates aims at being especially usable and explicitly targets the needs of gene expression analysis.

Among the key features are:

- Different brushes (selection tools)
- Occlusion prevention techniques
- Axis and polylines can be exchanged, thus supporting different use cases
- Moving, removing, and duplication of axis

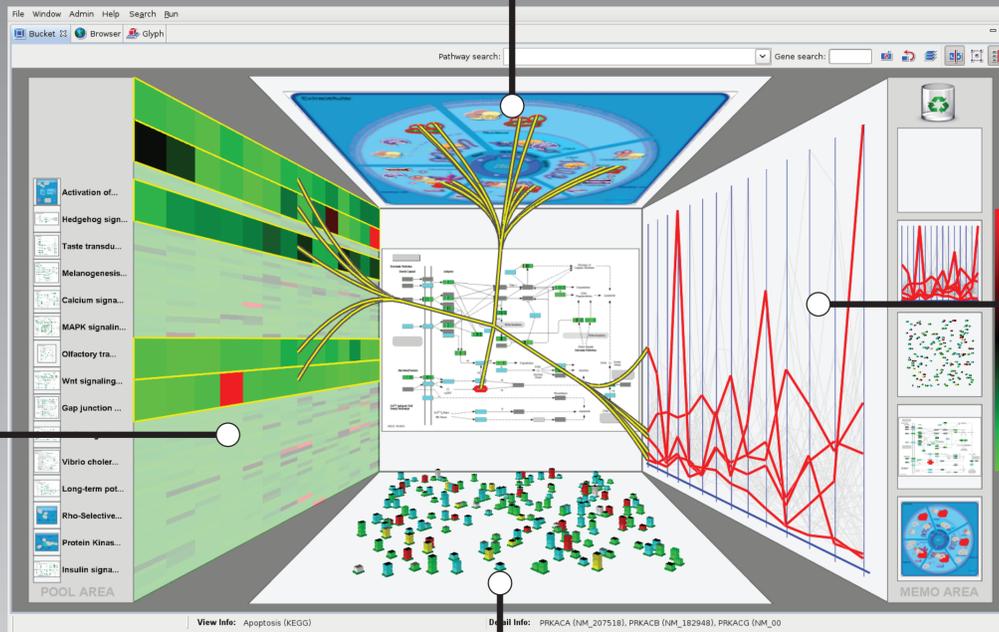
## Heatmap



A heatmap is a visualization where the magnitude of a value is correlated to a color.

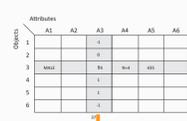
The different values are arranged in rows and columns, corresponding to their meaning. Heat maps are the standard way of visualizing gene expression regulation. Caleydo currently uses heat maps mainly to visualize contextual information. Therefore, the usually observed clustering of the elements has not yet been implemented.

- Features of the heatmap include:
- Freely selectable color mapping
  - Exchange of rows and columns to support different use cases

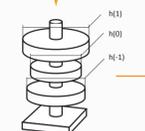


## Object Glyphs

For the visualization of medical data sets we developed two types of 3D glyphs:



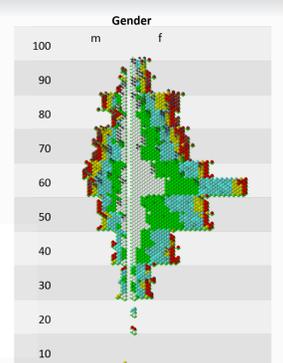
Object-glyphs representing a subset of different clinical parameters, e.g. age, staging, survival data etc.



Attribute-Glyphs for the visualization of value distributions.



Both types of glyphs have symmetry axes (like a crystal) in order to provide an efficient way of spatial arrangement for the interactive definition of hierarchical structures and subgroups.



## References:

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## Acknowledgements:

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