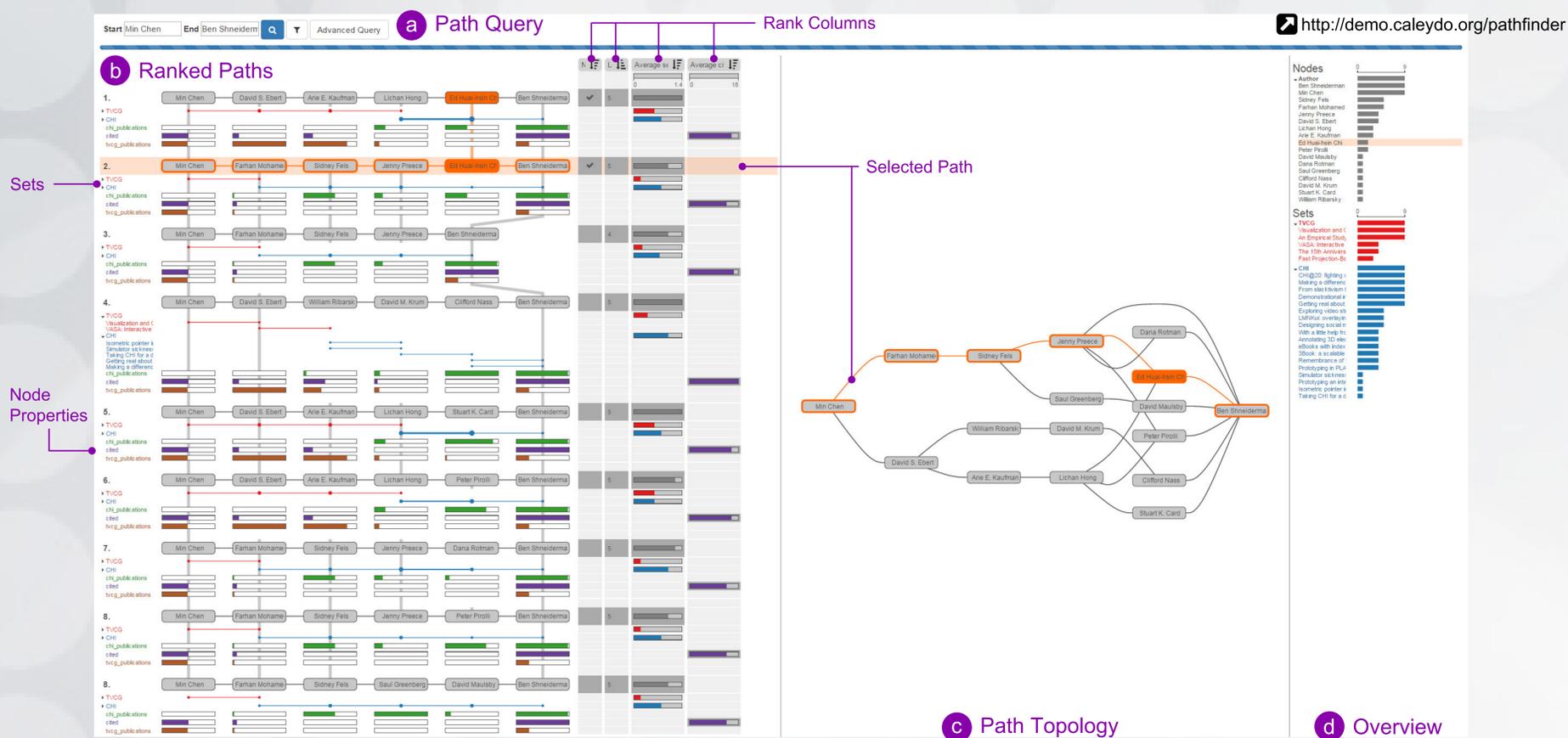


# Pathfinder: Visual Analysis of Paths in Heterogeneous Graphs

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<http://demo.caleydo.org/pathfinder>



Pathfinder displaying paths of a co-author network (DBLP data). (a) **Path Query**: A query is specified to find paths from *Min Chen* to *Ben Shneiderman*. (b) **Ranked Paths**: The paths are listed and showing sets and properties of nodes and edges. Paths can be ranked by various criteria. Columns next to the paths display scores that are used for ranking. (c) **Path Topology**: All paths are shown in a layered graph layout to provide a topological overview. (d) **Overview**: Pathfinder displays an overview of nodes (authors) and sets (publications) that are in the list of paths. The bars indicate the number of paths that contain the nodes and sets respectively.

Finding and analyzing paths in large, heterogeneous, and multivariate graphs is a common yet challenging task in many domains. Here, we introduce Pathfinder, a technique for the exploration of multiple paths and their properties through a graph. Pathfinder provides visual path query methods given user-defined constraints. The resulting set of paths is visualized in both a ranked list and in a node link diagram, showing the topology of the paths. For the paths we display rich attribute data associated with nodes and/or edges, which includes sets, categorical, and numerical data (similar to [1]) Pathfinder is based on a client-server architecture and designed to scale to networks with tens of thousands of nodes and edges. Queries to the data back-end provide continuous updates with intermediate results. Query refinements are immediately reflected on the current result set, which is updated based on back-end results as they become available. We demonstrate Pathfinder in usage scenarios with data from a co-author network and biological pathways.

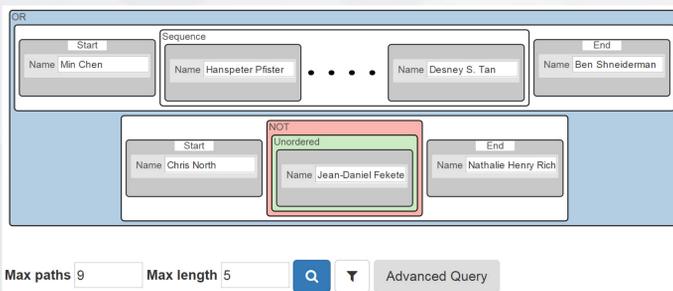
## Implementation

Pathfinder is built with Caleydo Web. It is based on a client-server architecture that uses Javascript and Typescript on the client and Python on the server. D3 is used for rendering. The network data is stored in a Neo4j graph database.

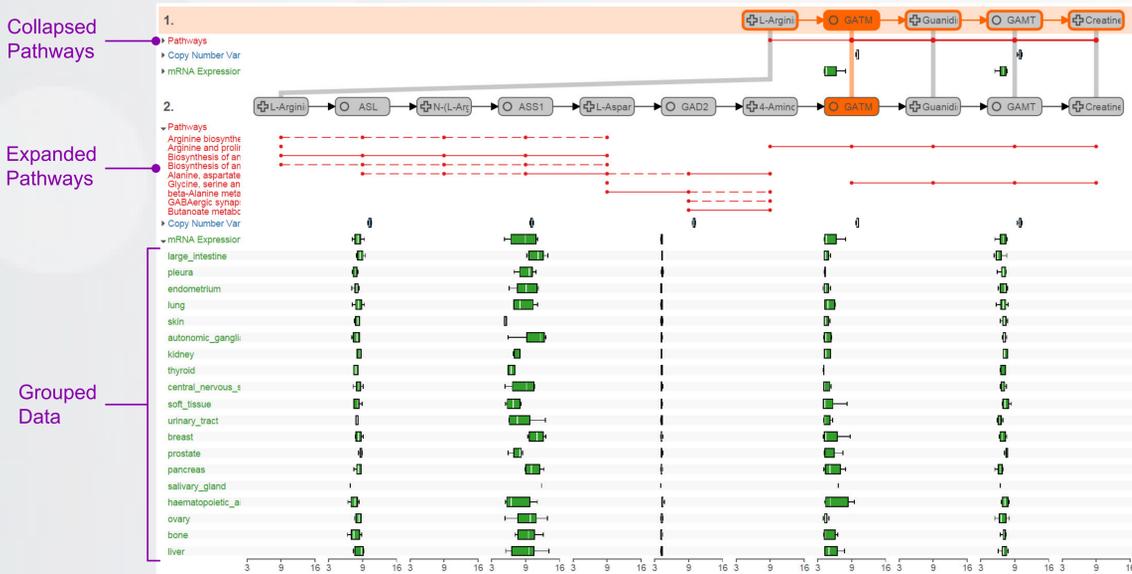
- [1] C Partl et al. enRoute: Dynamic Path Extraction from Biological Pathway Maps for Exploring Heterogeneous Experimental Datasets. BMC Bioinformatics, 14(Suppl 19):S3, 2013
- [2] M. Kanehisa et al. KEGG for integration and interpretation of large-scale molecular data sets. Nucleic Acids Research, 40(1):D109-114, 2012
- [3] J. Barretina et al. The cancer cell line encyclopedia enables predictive modelling of anticancer drug sensitivity. Nature, 483(7391): 603-607, Mar. 2012.

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**Visual Path Query**: Pathfinder provides an advanced visual interface to query for paths. Complex queries can be formulated by specifying constraints based on properties, sequences of nodes, logical expressions, etc.



**Biological Networks**: Pathfinder is domain-agnostic. Here we show a biological network based on KEGG pathways [2]. Additional gene expression and copy number variation data (taken from [3]) is shown as node attributes. The data is mapped to gene nodes of the paths, grouped and aggregated by tissue types, and displayed as box plots. Pathways are shown as sets.

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