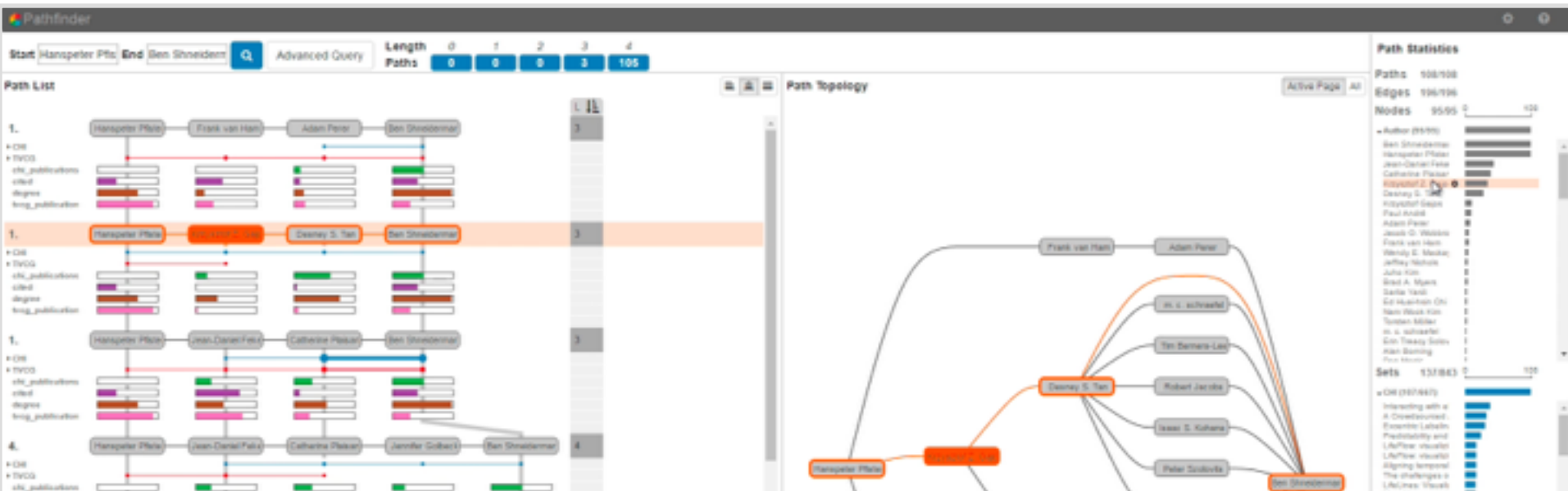


Pathfinder: Visual Analysis of Paths in Graphs

Christian Partl, Samuel Gratzl, Marc Streit, Anne Mai Wassermann,
Hanspeter Pfister, Dieter Schmalstieg, **Alexander Lex**



visualization
design lab

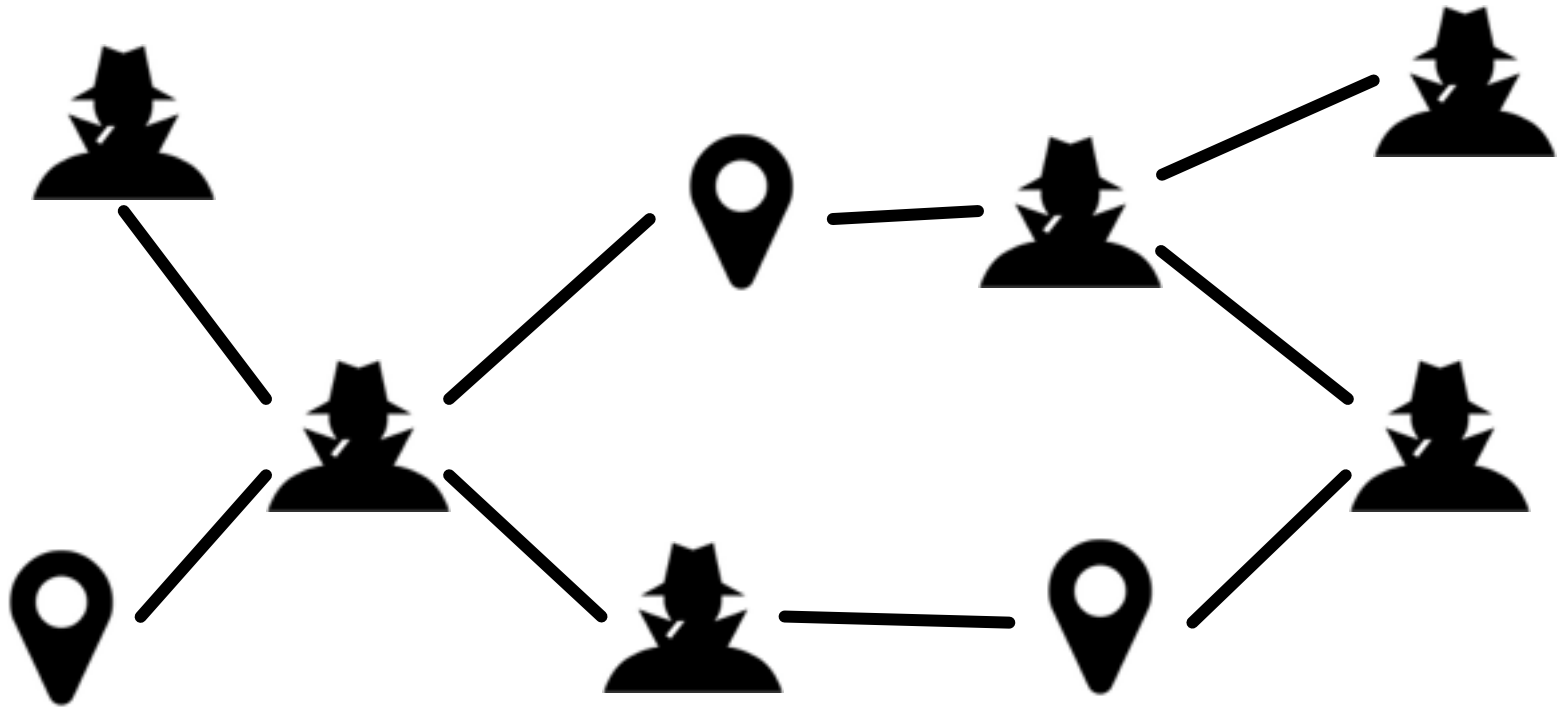


Tool / Paper

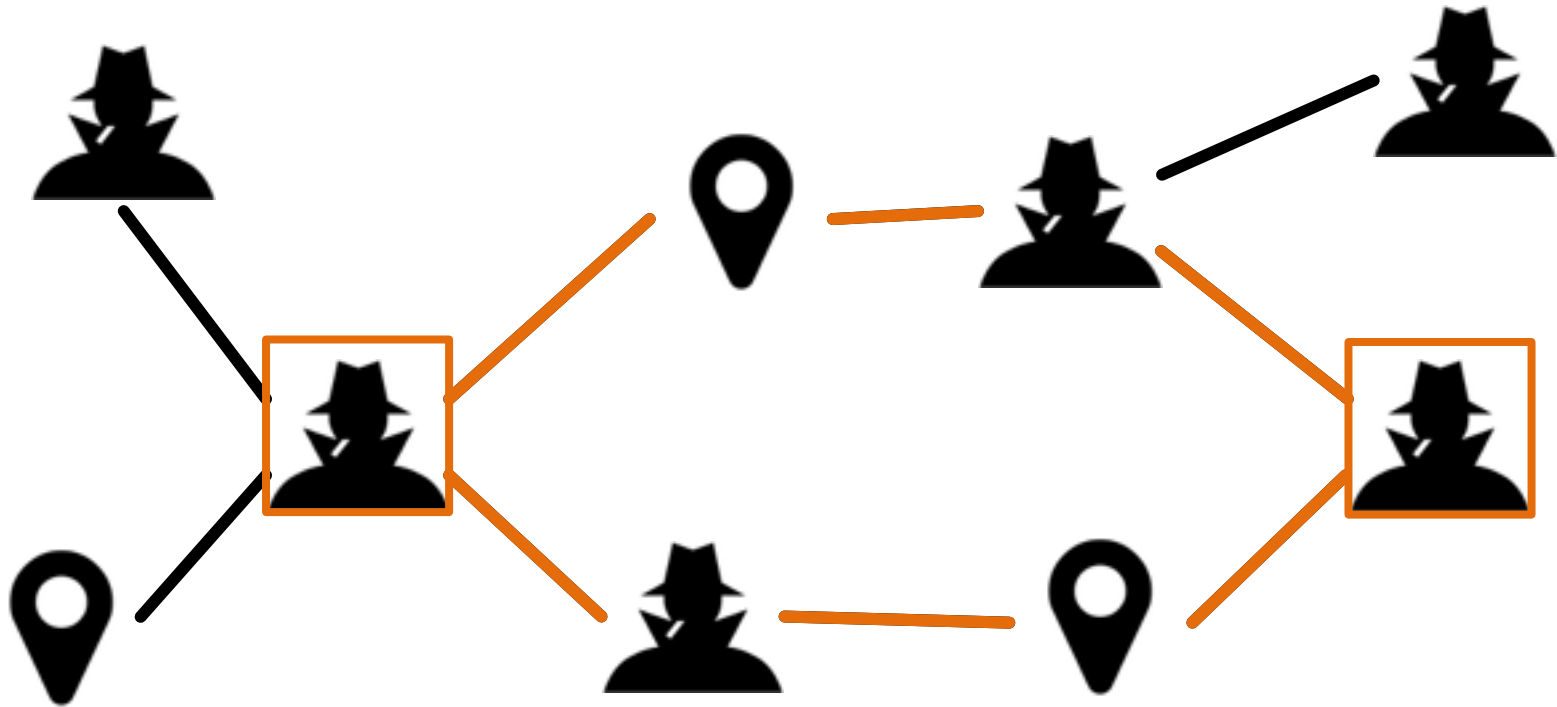
Christian Partl, Samuel Gratzl, Marc Streit, Anne Mai Wassermann, Hanspeter Pfister, Dieter Schmalstieg, Alexander Lex, **Pathfinder: Visual Analysis of Paths in Graphs**, Computer Graphics Forum (EuroVis '16) (to appear), 2016.

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

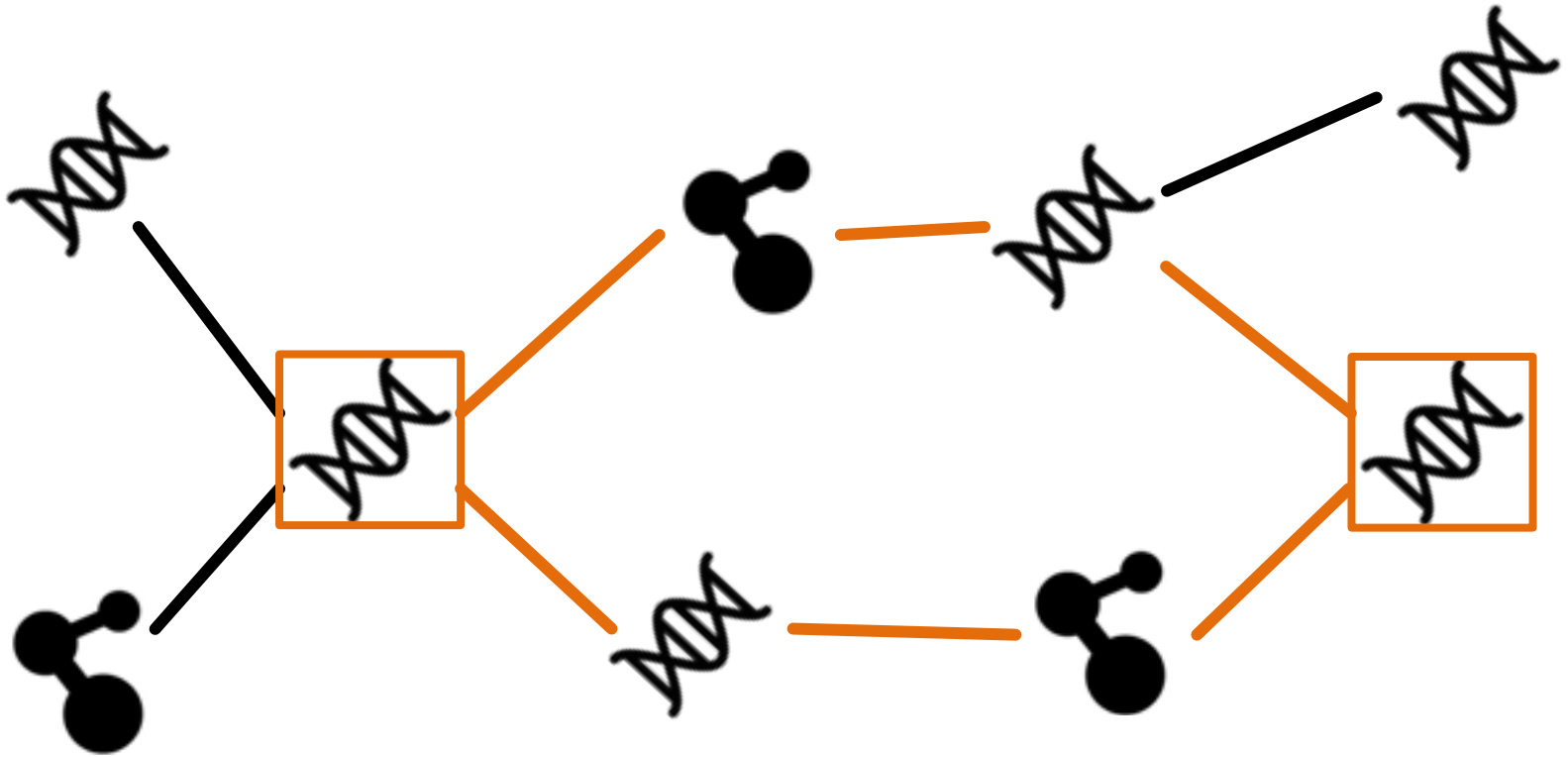
Info: http://www.caleydo.org/publications/2016_eurovis_pathfinder/



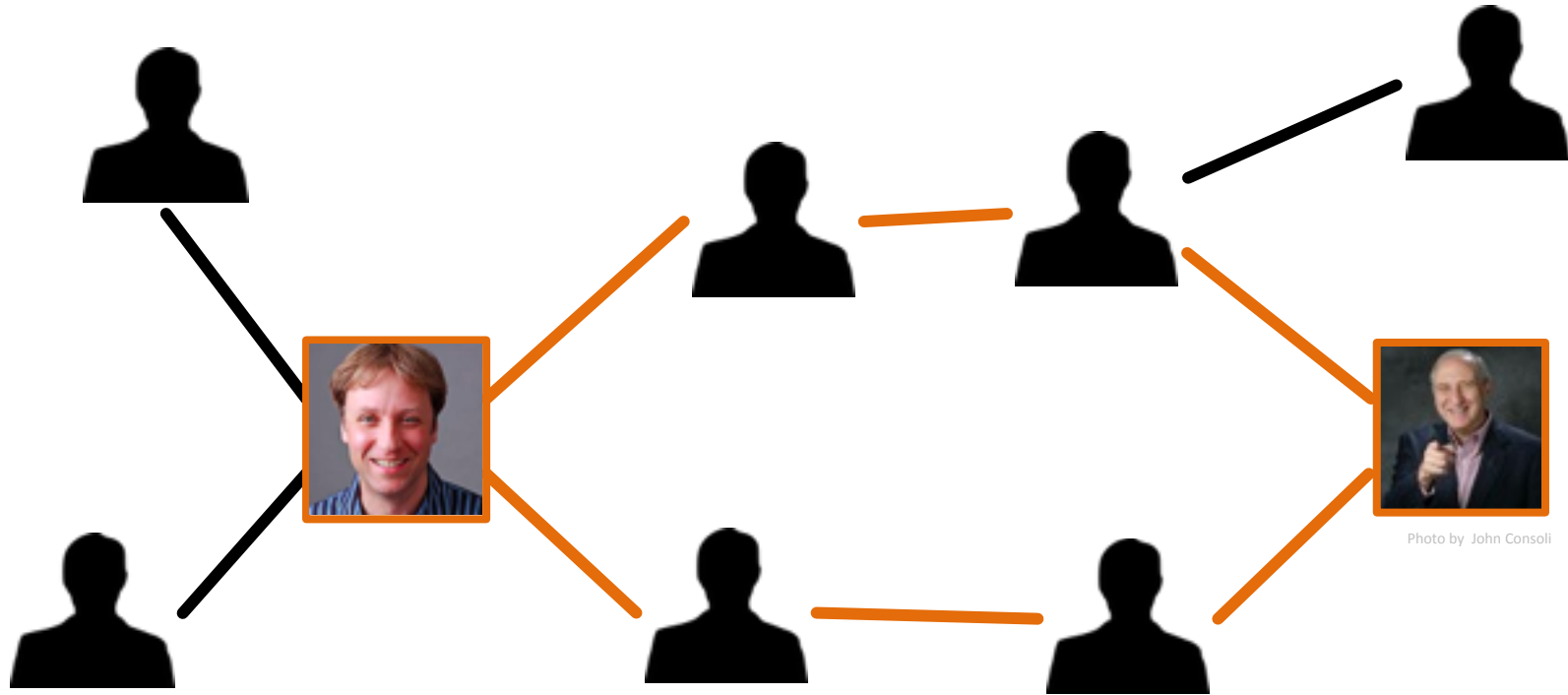
Intelligence Data: How are two suspects connected?



Intelligence Data: How are two suspects connected?



Biological Network: How do two genes interact?



Coauthor Network: How is HP Pfister connected to Ben Shneiderman?

The screenshot displays the PathVisor software interface, which is used for analyzing metabolic pathways. The interface is divided into several panels:

- Top Panel:** Contains a search bar and a list of metabolites. The list includes metabolites such as *Glucose*, *Fructose*, *Sucrose*, *Maltose*, *Mannose*, *Galactose*, *Glucose-6-phosphate*, *Fructose-6-phosphate*, *Sucrose-6-phosphate*, *Maltose-6-phosphate*, *Mannose-6-phosphate*, *Galactose-6-phosphate*, *Glucose-1-phosphate*, *Fructose-1-phosphate*, *Sucrose-1-phosphate*, *Maltose-1-phosphate*, *Mannose-1-phosphate*, *Galactose-1-phosphate*, *Glucose-5-phosphate*, *Fructose-5-phosphate*, *Sucrose-5-phosphate*, *Maltose-5-phosphate*, *Mannose-5-phosphate*, *Galactose-5-phosphate*, *Glucose-4-phosphate*, *Fructose-4-phosphate*, *Sucrose-4-phosphate*, *Maltose-4-phosphate*, *Mannose-4-phosphate*, *Galactose-4-phosphate*, *Glucose-3-phosphate*, *Fructose-3-phosphate*, *Sucrose-3-phosphate*, *Maltose-3-phosphate*, *Mannose-3-phosphate*, *Galactose-3-phosphate*, *Glucose-2-phosphate*, *Fructose-2-phosphate*, *Sucrose-2-phosphate*, *Maltose-2-phosphate*, *Mannose-2-phosphate*, *Galactose-2-phosphate*, *Glucose-1,6-bisphosphate*, *Fructose-1,6-bisphosphate*, *Sucrose-1,6-bisphosphate*, *Maltose-1,6-bisphosphate*, *Mannose-1,6-bisphosphate*, *Galactose-1,6-bisphosphate*, *Glucose-1,5-bisphosphate*, *Fructose-1,5-bisphosphate*, *Sucrose-1,5-bisphosphate*, *Maltose-1,5-bisphosphate*, *Mannose-1,5-bisphosphate*, *Galactose-1,5-bisphosphate*, *Glucose-1,4-bisphosphate*, *Fructose-1,4-bisphosphate*, *Sucrose-1,4-bisphosphate*, *Maltose-1,4-bisphosphate*, *Mannose-1,4-bisphosphate*, *Galactose-1,4-bisphosphate*, *Glucose-1,3-bisphosphate*, *Fructose-1,3-bisphosphate*, *Sucrose-1,3-bisphosphate*, *Maltose-1,3-bisphosphate*, *Mannose-1,3-bisphosphate*, *Galactose-1,3-bisphosphate*, *Glucose-1,2-bisphosphate*, *Fructose-1,2-bisphosphate*, *Sucrose-1,2-bisphosphate*, *Maltose-1,2-bisphosphate*, *Mannose-1,2-bisphosphate*, *Galactose-1,2-bisphosphate*, *Glucose-1,1-bisphosphate*, *Fructose-1,1-bisphosphate*, *Sucrose-1,1-bisphosphate*, *Maltose-1,1-bisphosphate*, *Mannose-1,1-bisphosphate*, *Galactose-1,1-bisphosphate*, *Glucose-1,0-bisphosphate*, *Fructose-1,0-bisphosphate*, *Sucrose-1,0-bisphosphate*, *Maltose-1,0-bisphosphate*, *Mannose-1,0-bisphosphate*, *Galactose-1,0-bisphosphate*, *Glucose-0-bisphosphate*, *Fructose-0-bisphosphate*, *Sucrose-0-bisphosphate*, *Maltose-0-bisphosphate*, *Mannose-0-bisphosphate*, *Galactose-0-bisphosphate*, *Glucose-0,0-bisphosphate*, *Fructose-0,0-bisphosphate*, *Sucrose-0,0-bisphosphate*, *Maltose-0,0-bisphosphate*, *Mannose-0,0-bisphosphate*, *Galactose-0,0-bisphosphate*, *Glucose-0,0,0-bisphosphate*, *Fructose-0,0,0-bisphosphate*, *Sucrose-0,0,0-bisphosphate*, *Maltose-0,0,0-bisphosphate*, *Mannose-0,0,0-bisphosphate*, *Galactose-0,0,0-bisphosphate*, *Glucose-0,0,0,0-bisphosphate*, *Fructose-0,0,0,0-bisphosphate*, *Sucrose-0,0,0,0-bisphosphate*, *Maltose-0,0,0,0-bisphosphate*, *Mannose-0,0,0,0-bisphosphate*, *Galactose-0,0,0,0-bisphosphate*, *Glucose-0,0,0,0,0-bisphosphate*, *Fructose-0,0,0,0,0-bisphosphate*, *Sucrose-0,0,0,0,0-bisphosphate*, *Maltose-0,0,0,0,0-bisphosphate*, *Mannose-0,0,0,0,0-bisphosphate*, *Galactose-0,0,0,0,0-bisphosphate*, *Glucose-0,0,0,0,0,0-bisphosphate*, *Fructose-0,0,0,0,0,0-bisphosphate*, *Sucrose-0,0,0,0,0,0-bisphosphate*, *Maltose-0,0,0,0,0,0-bisphosphate*, *Mannose-0,0,0,0,0,0-bisphosphate*, *Galactose-0,0,0,0,0,0-bisphosphate*, *Glucose-0,0,0,0,0,0,0-bisphosphate*, *Fructose-0,0,0,0,0,0,0-bisphosphate*, *Sucrose-0,0,0,0,0,0,0-bisphosphate*, *Maltose-0,0,0,0,0,0,0-bisphosphate*, *Mannose-0,0,0,0,0,0,0-bisphosphate*, *Galactose-0,0,0,0,0,0,0-bisphosphate*, *Glucose-0,0,0,0,0,0,0,0-bisphosphate*, *Fructose-0,0,0,0,0,0,0,0-bisphosphate*, *Sucrose-0,0,0,0,0,0,0,0-bisphosphate*, *Maltose-0,0,0,0,0,0,0,0-bisphosphate*, *Mannose-0,0,0,0,0,0,0,0-bisphosphate*, *Galactose-0,0,0,0,0,0,0,0-bisphosphate*, *Glucose-0,0,0,0,0,0,0,0,0-bisphosphate*, *Fructose-0,0,0,0,0,0,0,0,0-bisphosphate*, *Sucrose-0,0,0,0,0,0,0,0,0-bisphosphate*, *Maltose-0,0,0,0,0,0,0,0,0-bisphosphate*, 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*Fructose-0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0-bisphosphate*, *Sucrose-0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0-bisphosphate*, *Maltose-0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0-bisphosphate*, *Mannose-0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0-bisphosphate*, *Galactose-0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0-bisphosphate*, *Glucose-0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0-b*

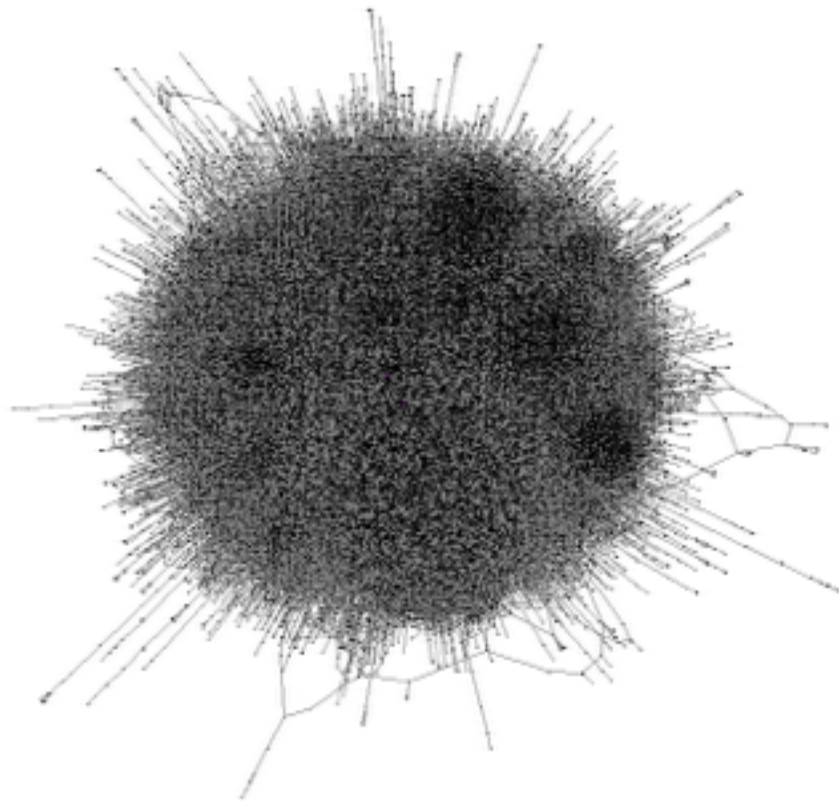
Visual Analysis of Paths

in Large Multivariate Graphs

Challenge 1: Graph Size

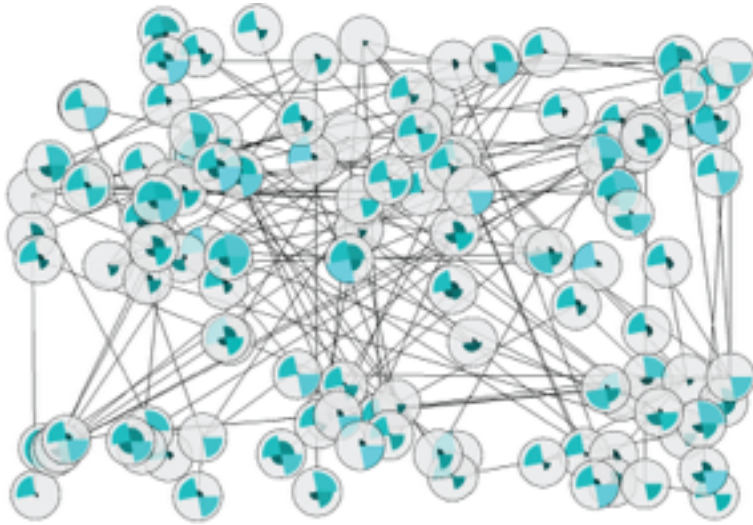
How can we deal with graphs too large to sensibly render at once?

Approach: **(Path) Queries**

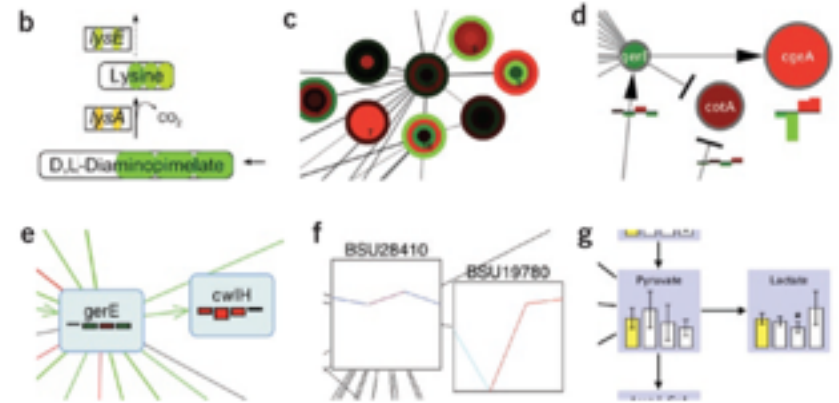


Challenge 2: Multivariate Attributes

How can we deal with graphs that contain **rich attribute data**?



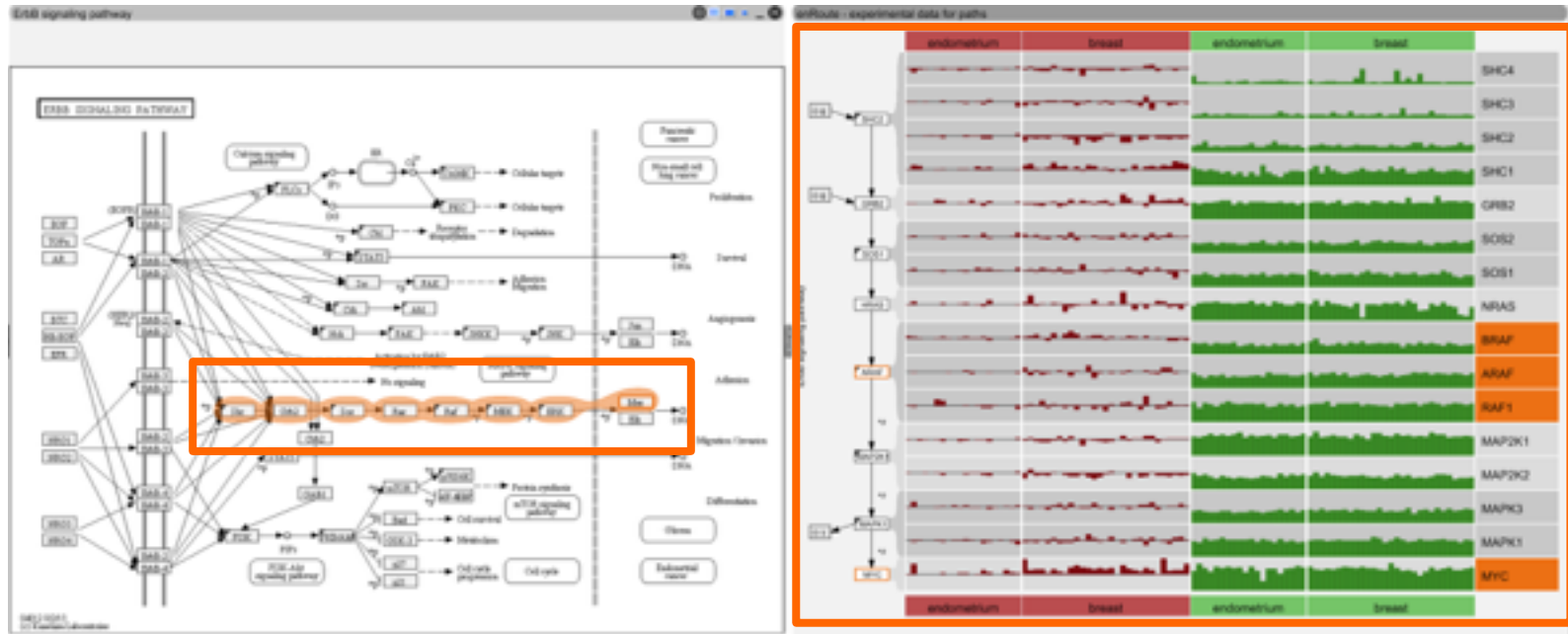
[McDonnel2009]



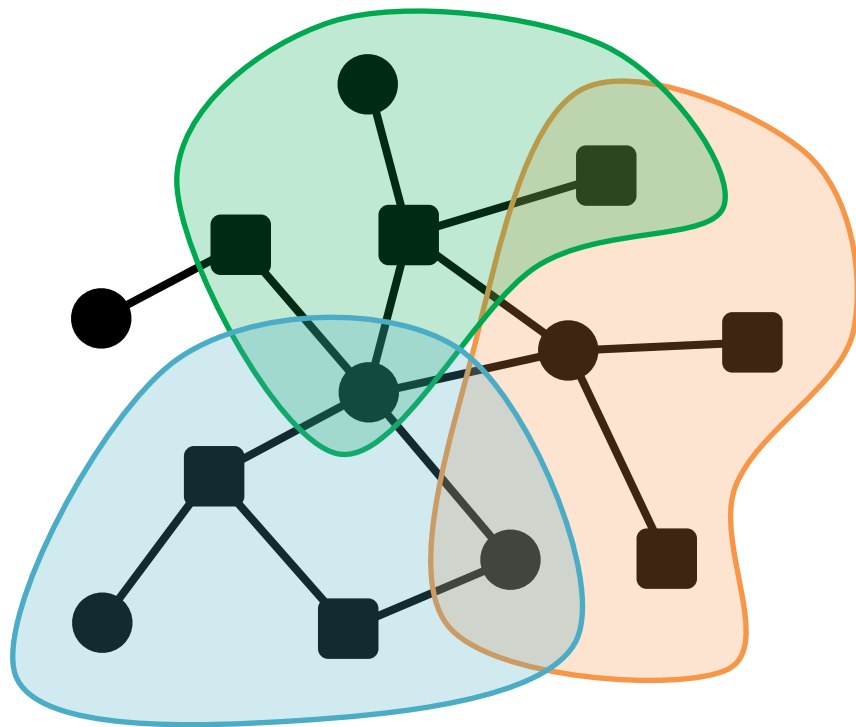
[Gehlenborg2010]

Approach: Attribute Visualization for Paths

EnRoute <http://enroute.caleydo.org>



Network Data



Nodes



Edges



Attributes

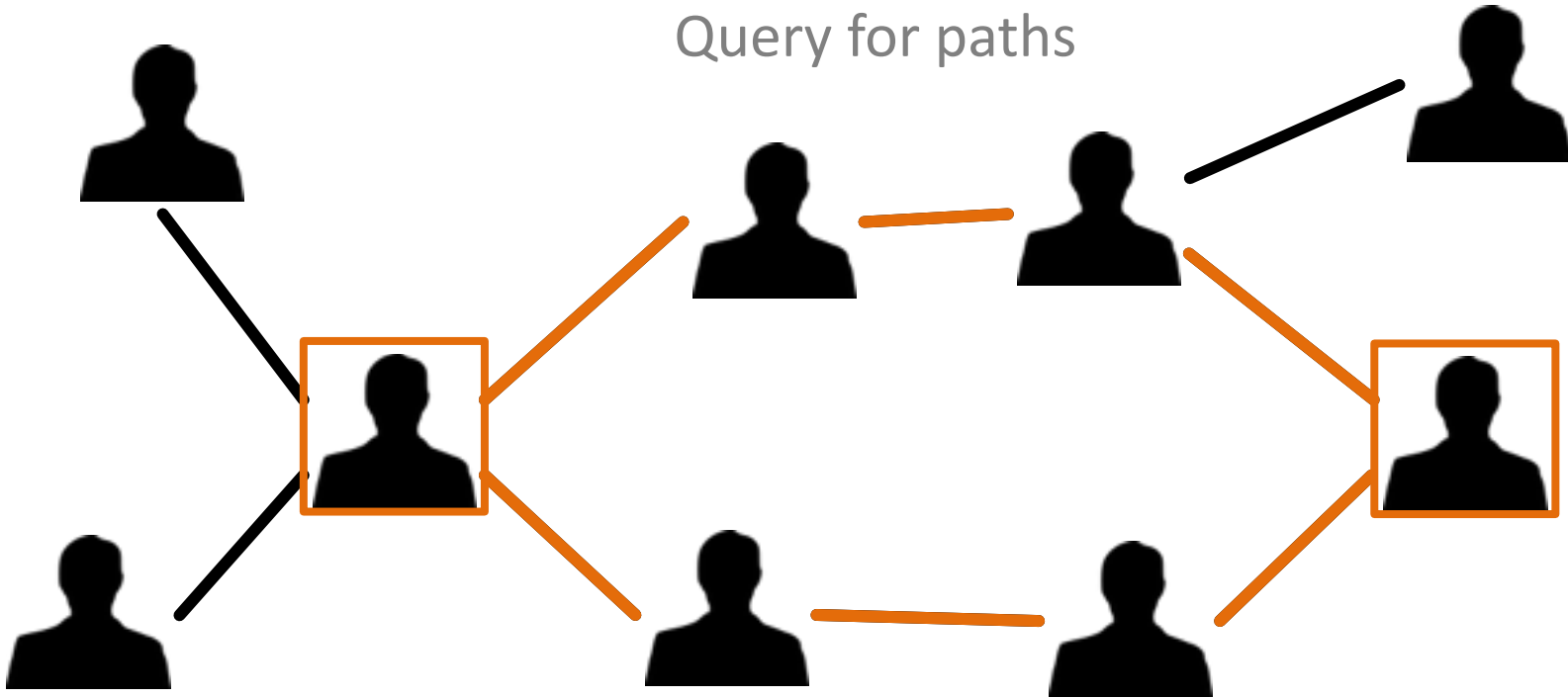


Sets



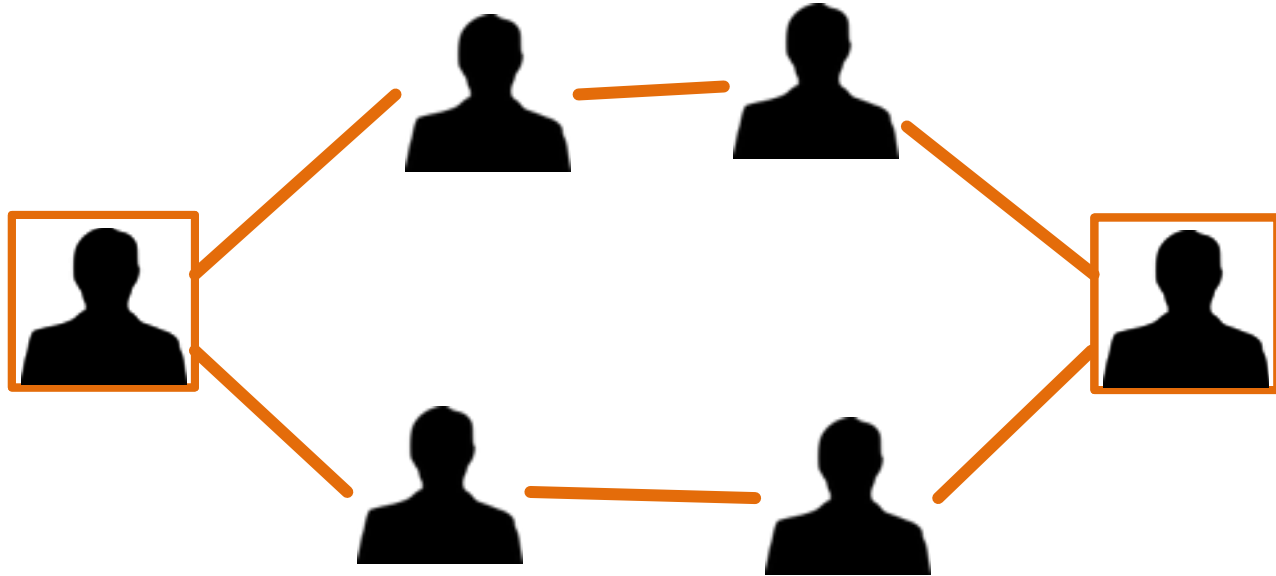
Pathfinder Approach

Query for paths



Pathfinder Approach

Show query links diagram..

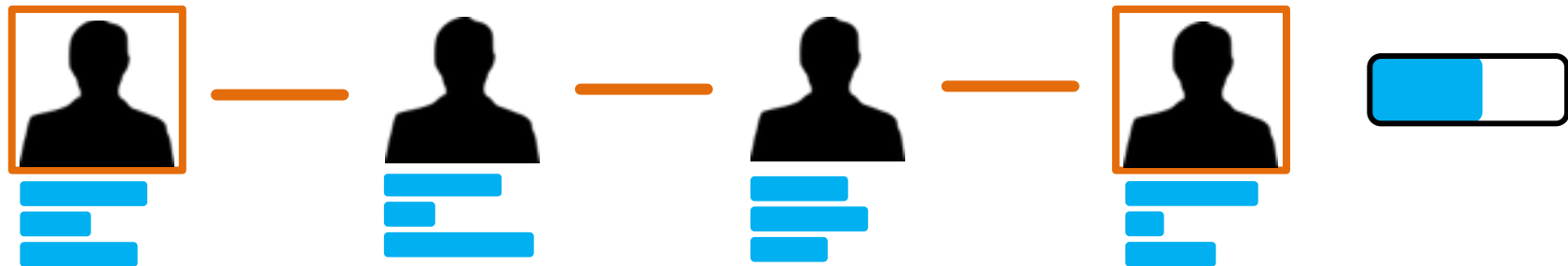


Pathfinder Approach

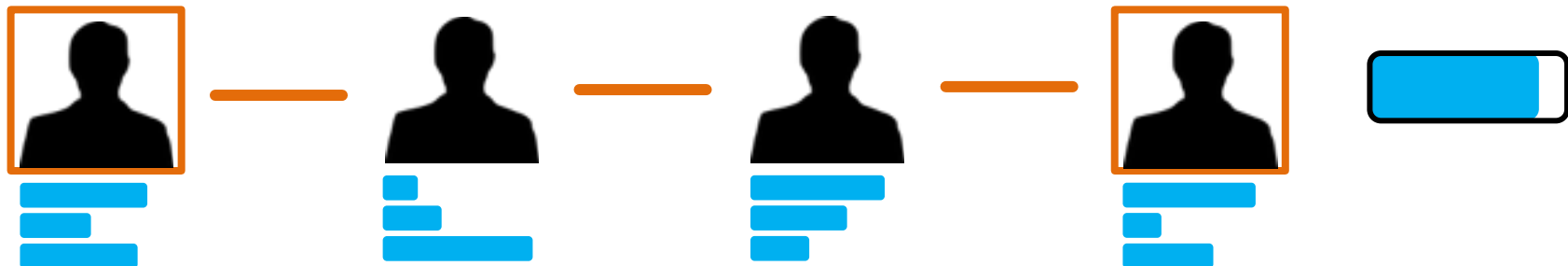
Update ranking to identify important paths

Path Score

1.



2.



Pathfinder Approach

Update ranking to identify important paths

Path Score

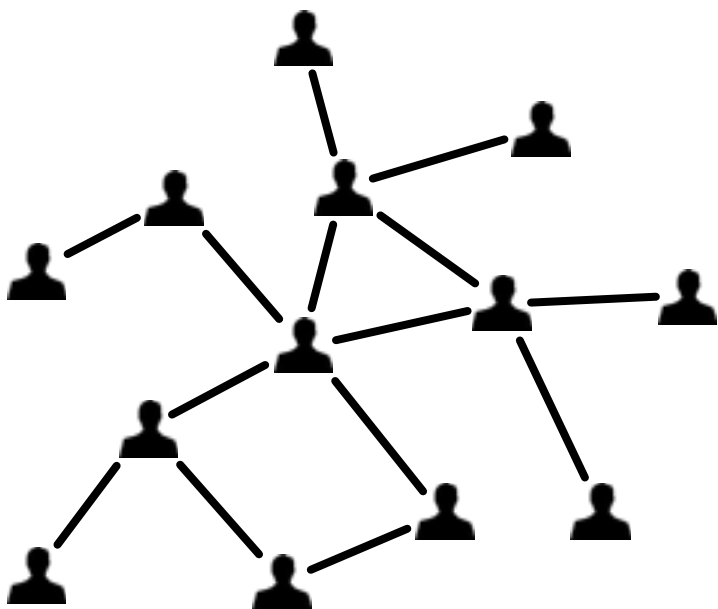
1.



2.



Coauthor Network



Nodes: Author **Edges: Co-authorship**
Generated from TVCG and CHI
publication data in DBLP



34k Nodes, 45k Edges

Attributes

Publications

Citations

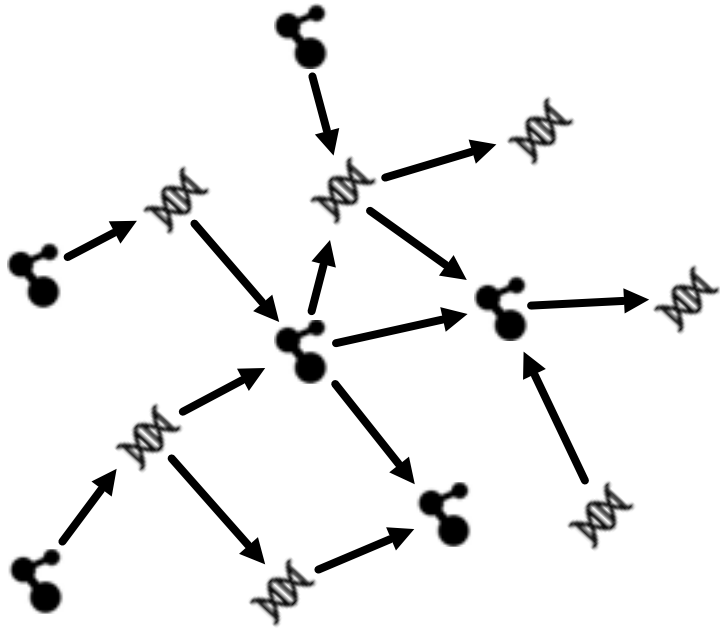
...

Sets



CHI/TVCG Publications

Biological Network



Gene
Generated from
KEGG Pathway Data

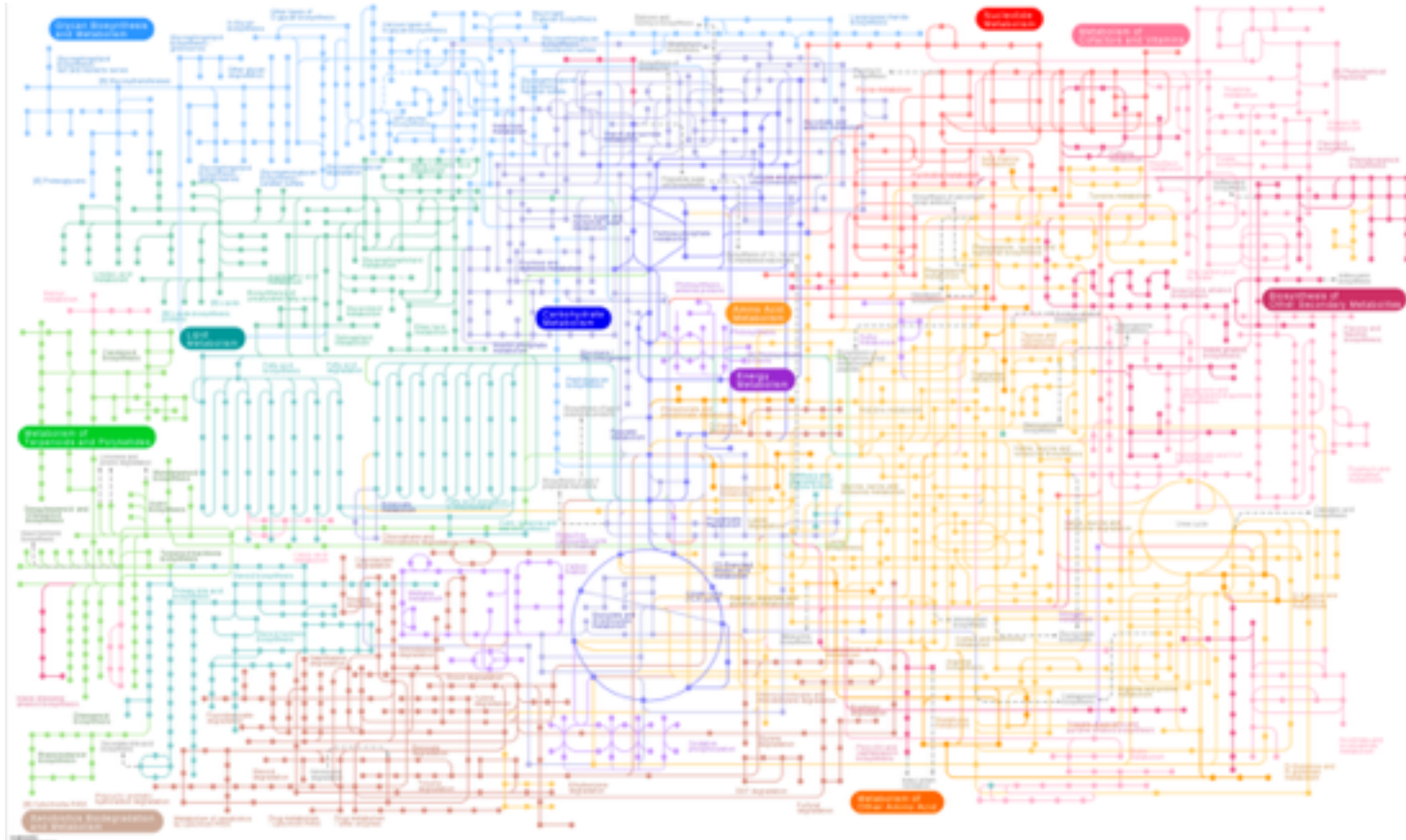
Attributes 
11k Nodes, 71k Edges
Gene Expression Data
Copy Number Data

Sets 
Biological Pathways

Compound

Attributes 
-
Sets 
Biological Pathways

Example: KEGG Metabolism Overview



Analysis Questions

Two genes are co-expressed. What is their **underlying connection**?

What are **alternative routes** connecting A to B?

How is **gene A connected to Pathway B**?

Is the connection from **A to B the same in many pathways**?

Is the **route connecting A and B active**?

Pathfinder Views

Path List View

Path Statistics View

Path Query and Search

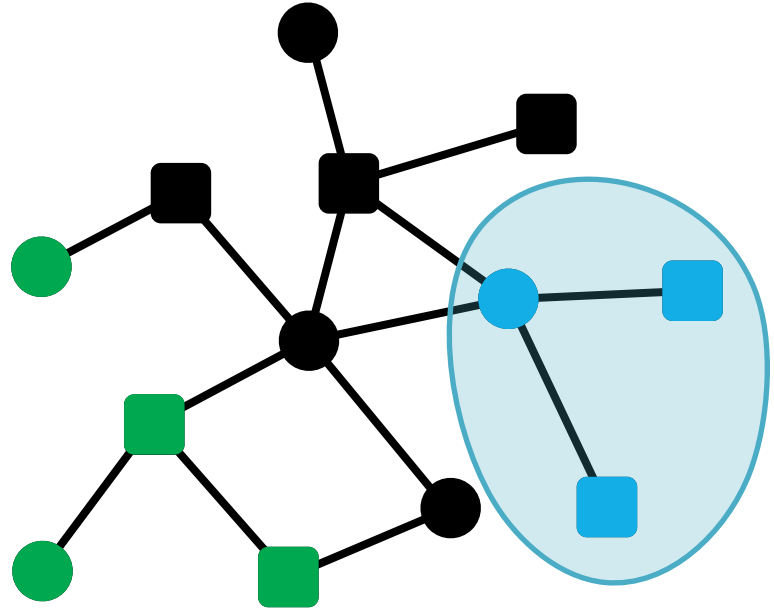
Finding Path Relationships

Query and Search

Specify **start** and **end**

Start/end can be node lists

Start/end can be defined
through set membership

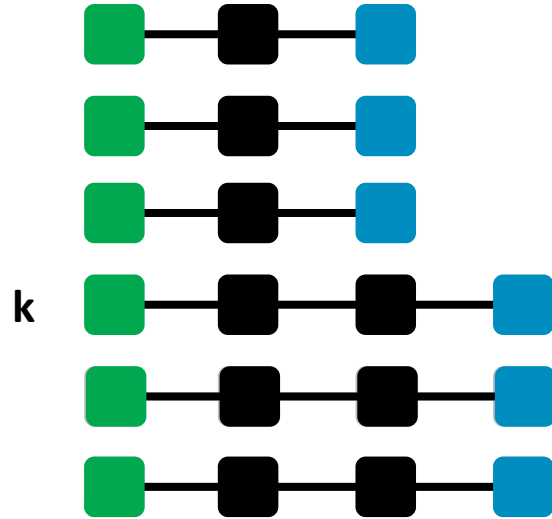


Query and Search

Specify **start** and **end**

K-shortest path search

Continue until all path of
length(k) are found



Start End

Path List



Path Topology

 All

Path Statistics

Query Interface

Query Interface

Simple

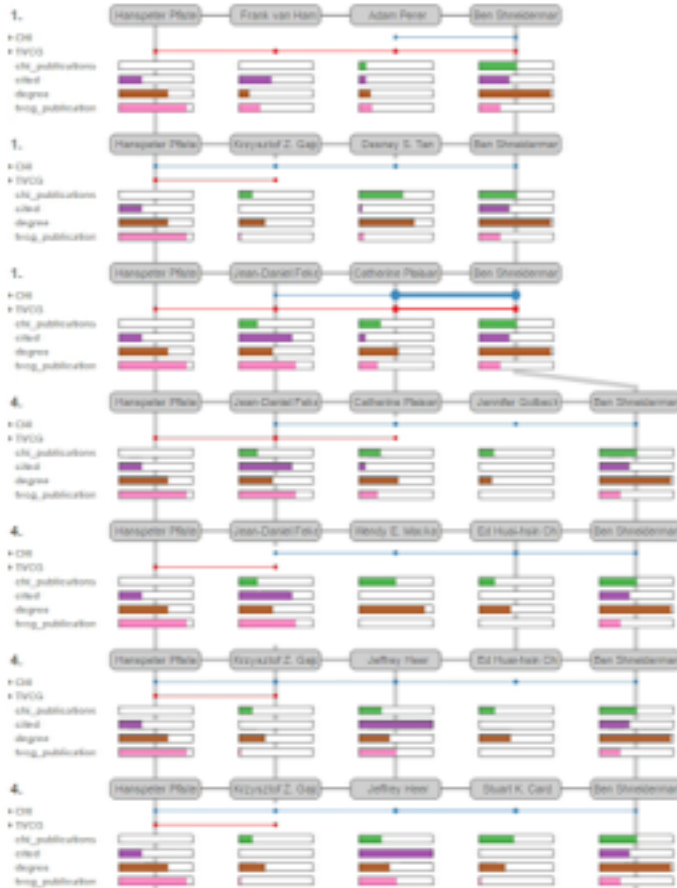
Start End

Length	0	1	2	3	4
Paths	0	0	0	3	105

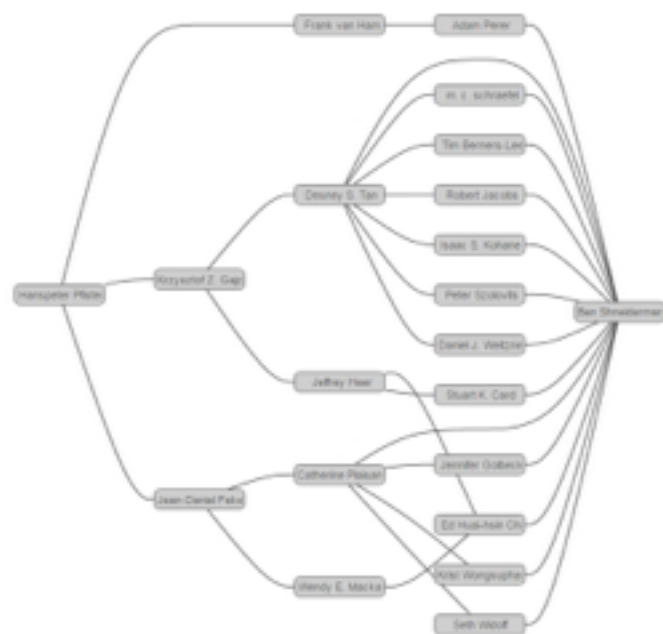
Advanced



Path List



Path Topology



Path Statistics

Paths 108/108

Edges 108/108

Nodes 95/95

Author (25/70)

Ben Shneiderman

Hanspeter Pfc

Jean-Daniel Falc

Catherine Pfc

Krzysztof Z. Gap

Deany S. Tan

Paul Kish

Adam Pfc

David G. Weller

Frank van Ham

Wendy E. Mack

Jeffrey Hark

Julia Kim

Brad A. Myers

Sarah Yadi

Ed Huah-hu Ch

Nam Hark Kim

Torben Miler

in a software

Ed Deany Gales

Adam Benning

Paul Kish

Ben Shneiderman

Ben Shneiderman

Ben Shneiderman

Ben Shneiderman

Ben Shneiderman

Ben Shneiderman

Ben Shneiderman

Ben Shneiderman

Ben Shneiderman

Ben Shneiderman

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Ben Shneiderman

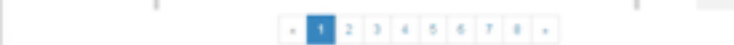
Ben Shneiderman

Ben Shneiderman

Ben Shneiderman

Path Topology View

Getting an Overview



Active Page All

```

graph LR
    Root[Academic Year 2010-2011] --> MT[Master's Thesis]
    Root --> AS[Academy of Sciences]
    Root --> PT[PhD Thesis]
    
    MT --> FvH[Frank van Ham]
    MT --> AP[Adam Pinar]
    
    AS --> KGZ[Krzysztof Z. Gaj]
    AS --> JH[Jeffrey Heer]
    
    PT --> JDF[Jean-Daniel Falcou]
    PT --> CF[Catherine Flacco]
    
    KGZ --> DST[Deenay S. Tan]
    KGZ --> JH
    
    JDF --> CF
    JDF --> NEM[Nancy E. Mack]
    
    DST --> MCS[m. c. schraafl]
    DST --> TBL[Tim Berners-Lee]
    DST --> RJ[Robert Jacobs]
    DST --> ISK[Isaac S. Kohane]
    DST --> PS[Peter Scroby]
    DST --> DJW[Daniel J. Williams]
    
    CF --> JG[Jennifer Golbeck]
    CF --> EHC[Ed Hsieh-Chi]
    CF --> KH[Kirsti Hwangphoe]
    
    JH --> SKC[Stuart K. Card]
    
    AP --> BS[Ben Shneiderman]
    AP --> JG
    AP --> EHC
    AP --> KH
    AP --> SV[Seth Vassell]
    
    BS --> MCS
    BS --> TBL
    BS --> RJ
    BS --> ISK
    BS --> PS
    BS --> DJW
    BS --> JG
    BS --> EHC
    BS --> KH
    BS --> SV
  
```

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Path List View

Investigating Paths in Detail

Path Representation

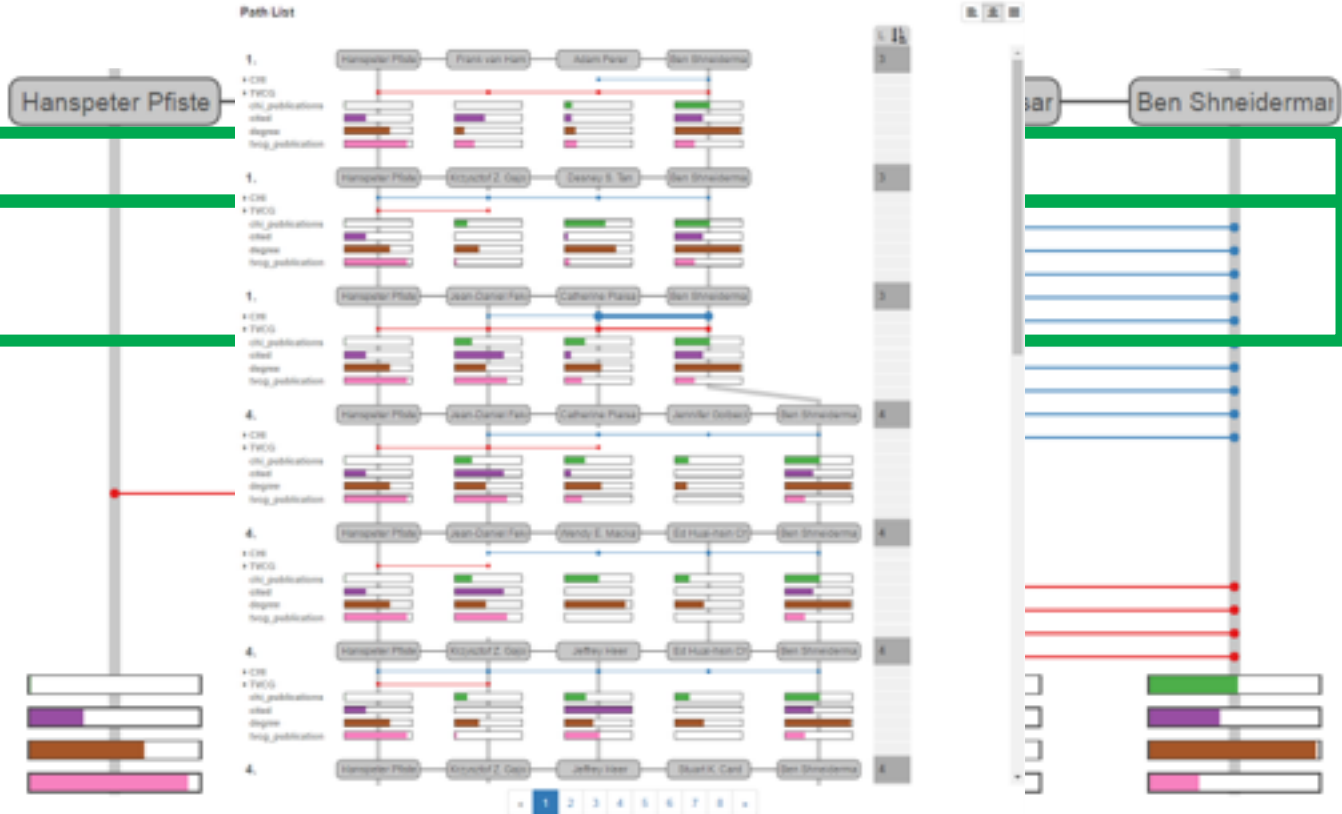
2.

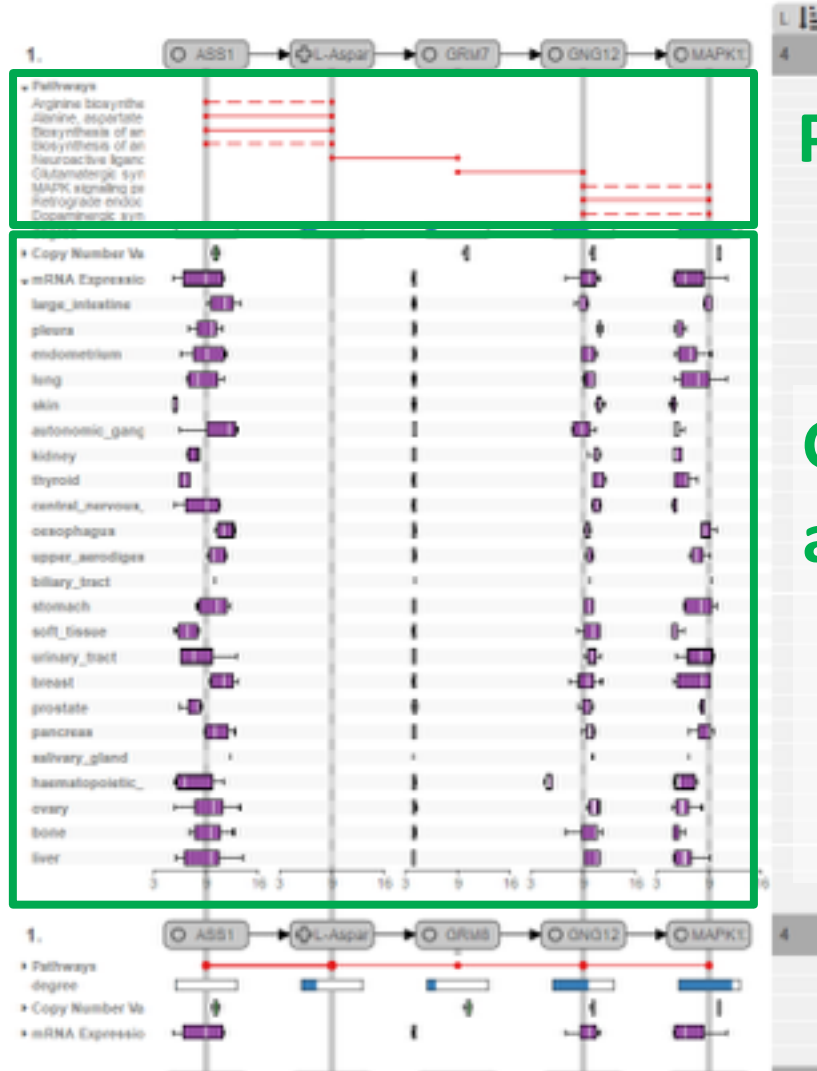
CHI

A table: improving
 Extensive Labeling
 LifeFlow: visualiz
 Query Previews in
 LifeLines: Visualiz
 The challenges of
 Organization over

TVCG

UpSet: Visualizati
 Visual Sedimentat
 SoccerStories: A I
 Promoting Insight
 Temporal Summar
 Temporal Event S
 A Task Taxonomy
 Visualizing Chang
 chi_publications
 cited
 degree
 tvcg_publication





Pathways

Grouped Copy Number
and Gene Expression Data

Path Ranking

Identifying Relevant Paths

Path Alignment

Facilitating Path Comparison

Align the Pivot Node

Figure 1 displays a grid of 24 network diagrams, organized into 6 rows and 4 columns. Each row represents a different combination of network types (DE, TVGO) and publication metrics (chi_publications, cited, degree, freq_publication). The columns represent different individuals: Hanspeter Pfister, Frank van Ham, John Doe, Catharina Olsan, and Ben Shroederma. Each diagram shows a network of connections between these individuals, with colors indicating different network types and metrics. The diagrams are arranged in a 4x6 grid, with rows 1-4 showing combinations of network types and metrics, and rows 5-6 showing combinations of network types and metrics.

Active Page All

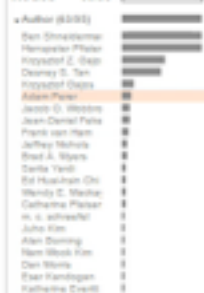
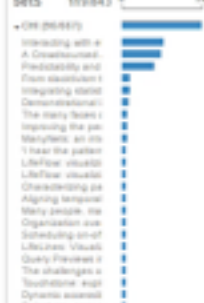


Path Statistics

Patha 50/100

Edges 158195

Nodes 6195

[illegible]

• TVCIS-031170



Align All

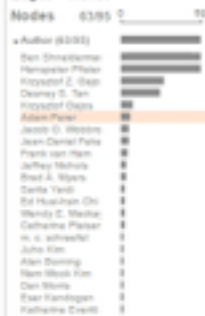


Active Page All

Path Statistics

Pathways 50-100

Edges: 10376



Set(s): 159843



• TVC02 (23.97%)



Comparison to Reference Path

Path List



Path Topology

Difference to Reference Path



Path Statistics

Paths 59/108

Edges 108/196

Nodes 63/95

Author (63/95)

Ben Shneiderman

Hanspeter Pfister

Jean-Daniel Fekete

Enrico Bertini

John Foweraker

Catherine Pisker

Ben Shneiderman

Jean-Daniel Fekete

Enrico Bertini

John Foweraker

Catherine Pisker

Ben Shneiderman

Jean-Daniel Fekete

Enrico Bertini

John Foweraker

Catherine Pisker

Ben Shneiderman

Jean-Daniel Fekete

Enrico Bertini

John Foweraker

Catherine Pisker

Ben Shneiderman

Jean-Daniel Fekete

Enrico Bertini

John Foweraker

Catherine Pisker

Ben Shneiderman

Jean-Daniel Fekete

Enrico Bertini

John Foweraker

Catherine Pisker

Ben Shneiderman

Jean-Daniel Fekete

Enrico Bertini

John Foweraker

Catherine Pisker

Ben Shneiderman

Jean-Daniel Fekete

Enrico Bertini

John Foweraker

Catherine Pisker

Ben Shneiderman

Jean-Daniel Fekete

Enrico Bertini

John Foweraker

Catherine Pisker

Ben Shneiderman

Jean-Daniel Fekete

Enrico Bertini

John Foweraker

Catherine Pisker

Ben Shneiderman

Jean-Daniel Fekete

Enrico Bertini

John Foweraker

Catherine Pisker

Ben Shneiderman

Jean-Daniel Fekete

Enrico Bertini

John Foweraker

Catherine Pisker

Ben Shneiderman

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Enrico Bertini

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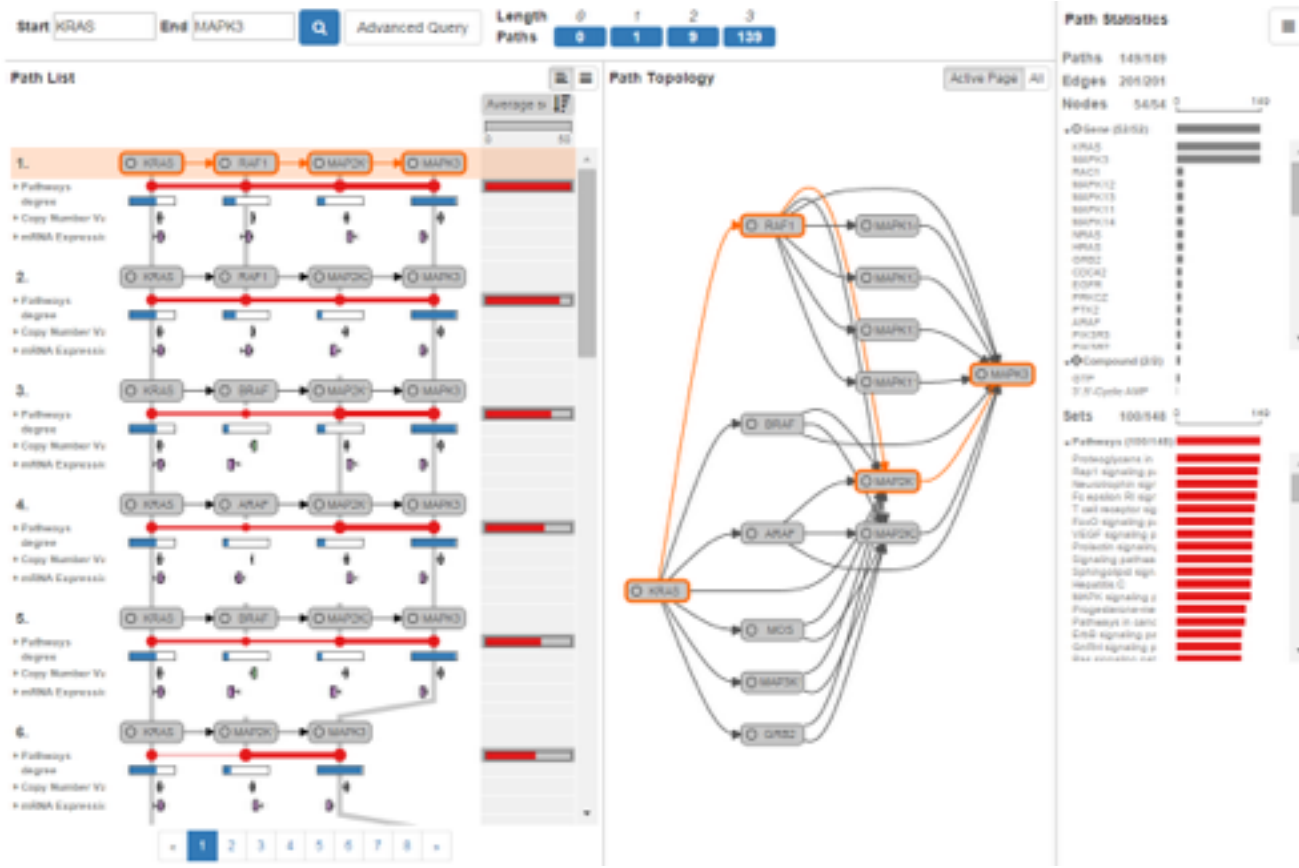
Enrico Bertini

John Foweraker

Case Study:

Biological Network

ERK-MAPK signaling cascade



Search Paths from KRAS to MAPK3

Ranking by set connection reveals ERK-MAPK signaling cascade

ERK-MAPK signaling cascade



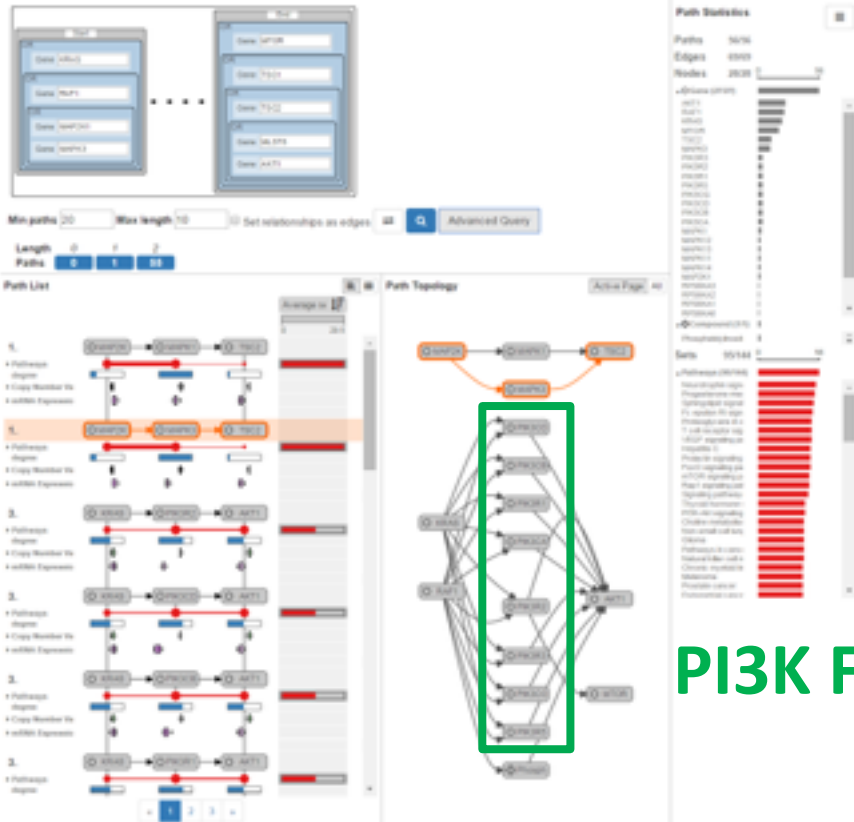
This cascade is important in many pathways.

ERK-MAPK signaling cascade



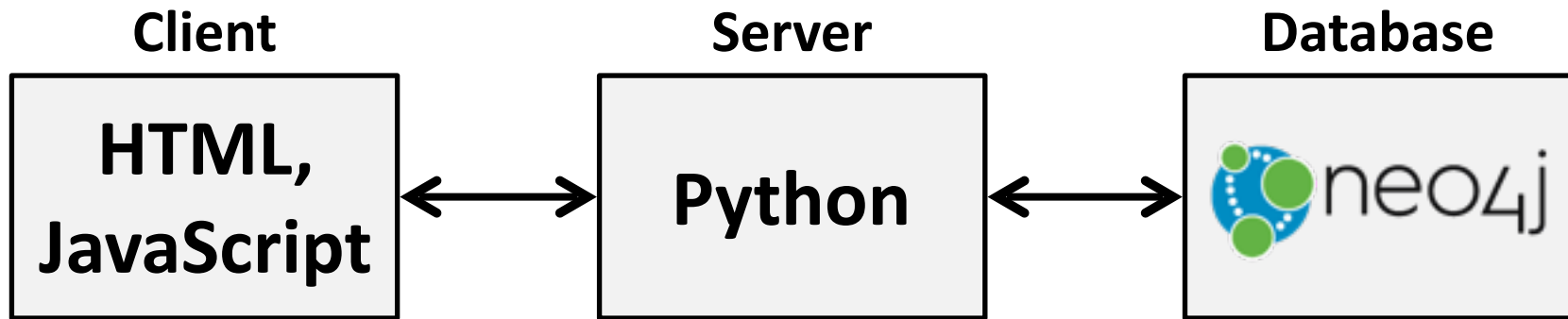
This cascade is expressed ubiquitously in all cancer tissue types

Crosstalk between ERK-MAPK and mTOR



Implementation

Implementation

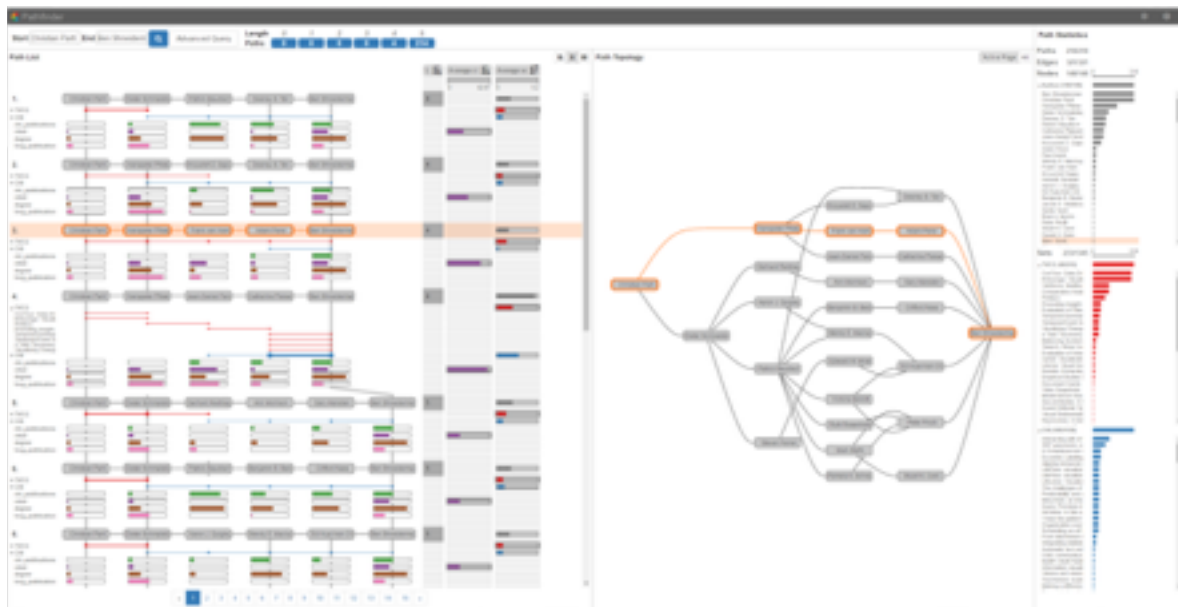


Immediate feedback to queries through intermediate results

Rendering: D3, Dagre



Pathfinder in a Nutshell



Query-based Technique
for Path Analysis

Results in Topology-
and List View

Path Exploration by
Query Refinement
Ranking

Questions?



pathfinder.caleydo.org

Interactive Demo:

demo.caleydo.org/pathfinder/

Source Code:

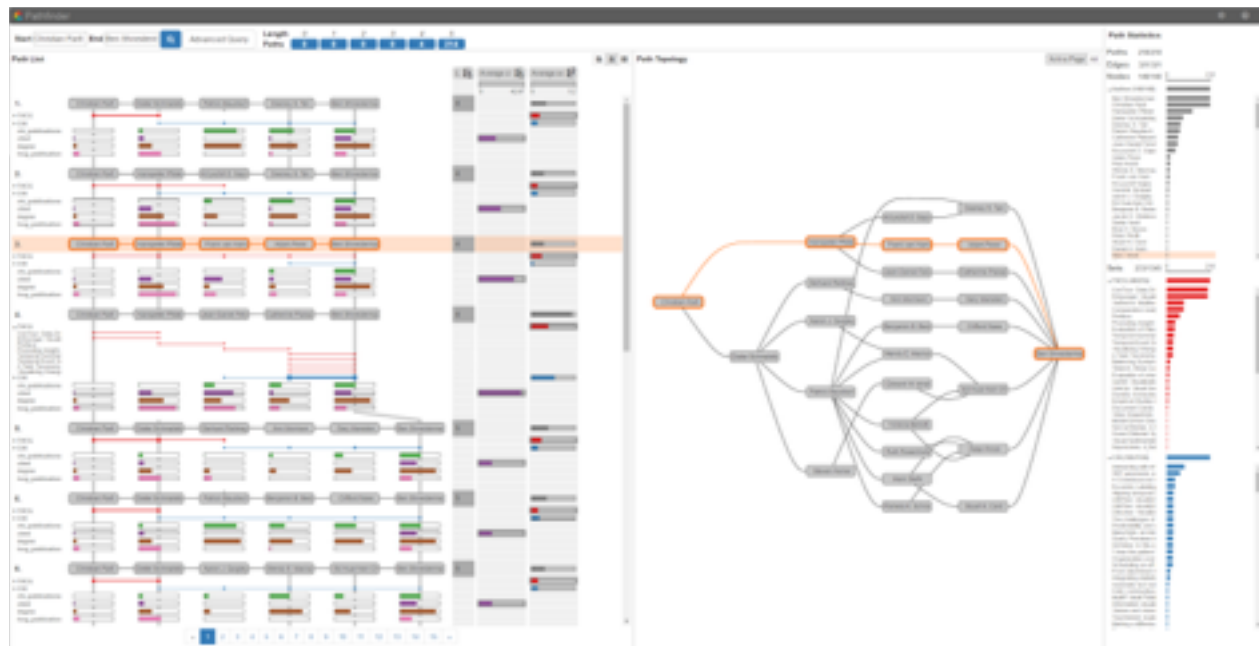
github.com/Caleydo/pathfinder/

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visualization
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Miriah Meyer



Alexander Lex

<http://goo.gl/Zmm4L8>



Future Work

Integrate with general graph exploration tools

Provide overview of similar paths

- Grouping based on similarity

- Dimensionality reduction and show in scatterplot

Cost-based path search

Scalability

Network Size

Coauthor Network: 34k nodes, 45k edges

Biological Network: 11k nodes, 71k edges

600+ Paths

Path length

Depends on screen size/resolution and node size

7-10 hops, more with scrolling