Alexander Lex
@alexander_lex
http://alexander-lex.net

THE UNIVERSITY OF UTAH

Visualizing Biological Data: Pathway Graphs, Genealogies, and Alternative Splicing

visualization
design lab

SCI
www.sci.utah.edu

visualization
design lab

Miriah Meyer

Alexander Lex

Ethan Kerzner

Alex Bigelow

Sean McKenna

Sam Quinan

Nina McCurdy

Jimmy Moore

Cameron Waller

Carolina Nobre

SCI
www.sci.utah.edu

http://vdl.sci.utah.edu/

visualization
design lab

Applied Visualization Research

Biology, Medicine, Humanities, …

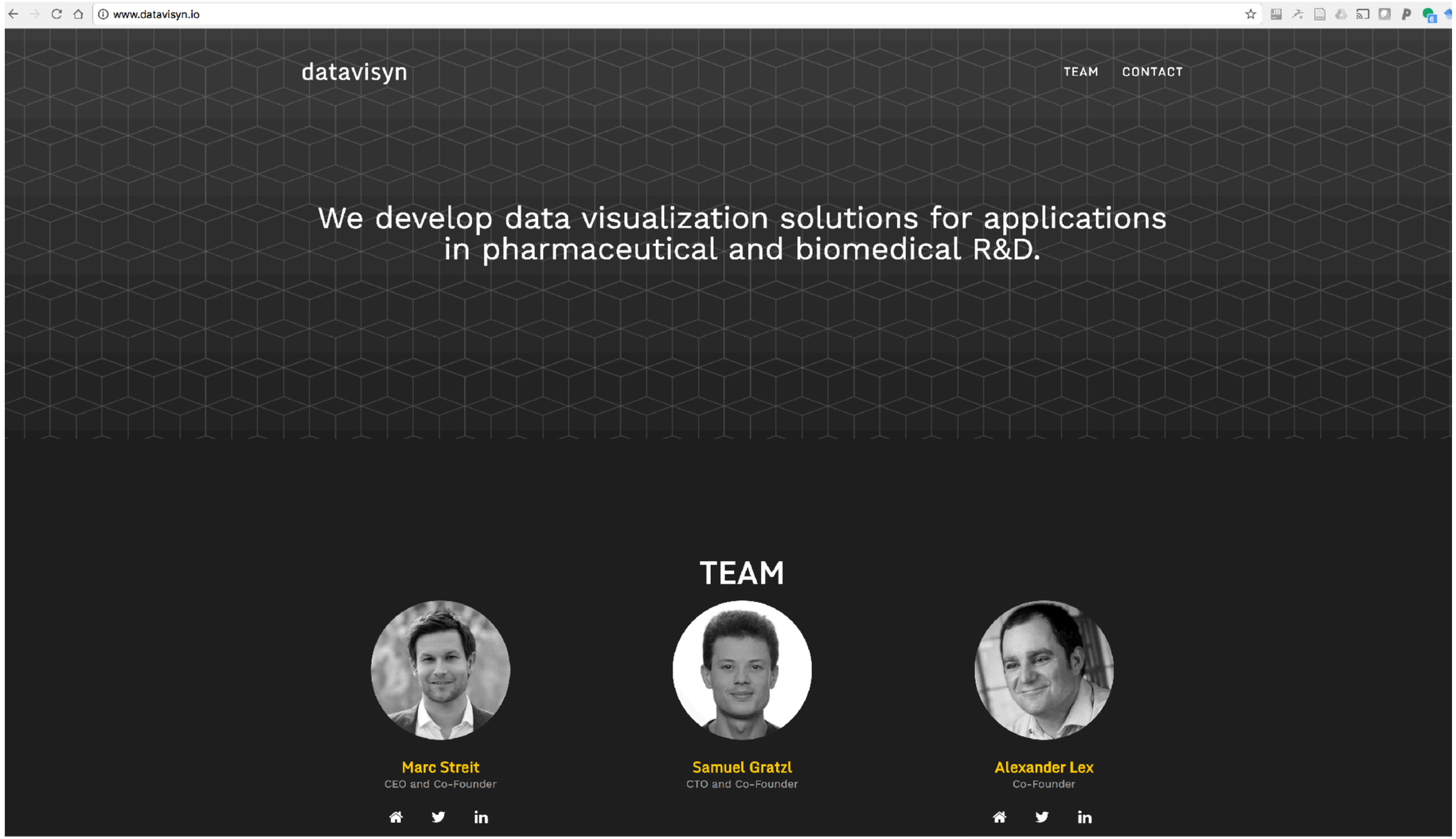
Visualization Design Models

User-centered Design

Visualization Techniques

Visualization Frameworks

datavisyn.io



visualization

The purpose of computing is insight,
not numbers.

pictures

- Card, Mackinlay, Shneiderman
- Richard Wesley Hamming

Banana	***M. acuminata***
Date	***P. dactylifera***
Cress	***Arabidopsis thaliana***
Rice	***Oryza sativa***
Sorghum	***Sorghum bicolor***
Brome	***Brachypodium distachyon***

[D'Hont et al., Nature, 2012]

Good Data Visualization

… makes data accessible

… combines strengths of humans and computers

… enables insight

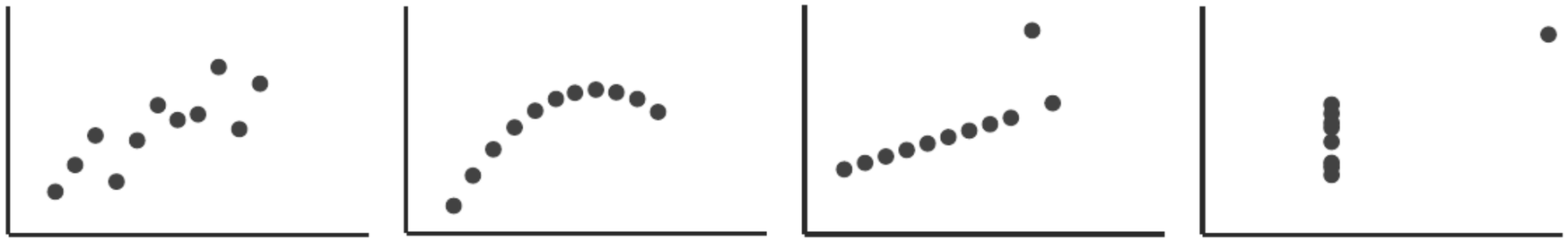
… communicates

Can We Trust Statistics?

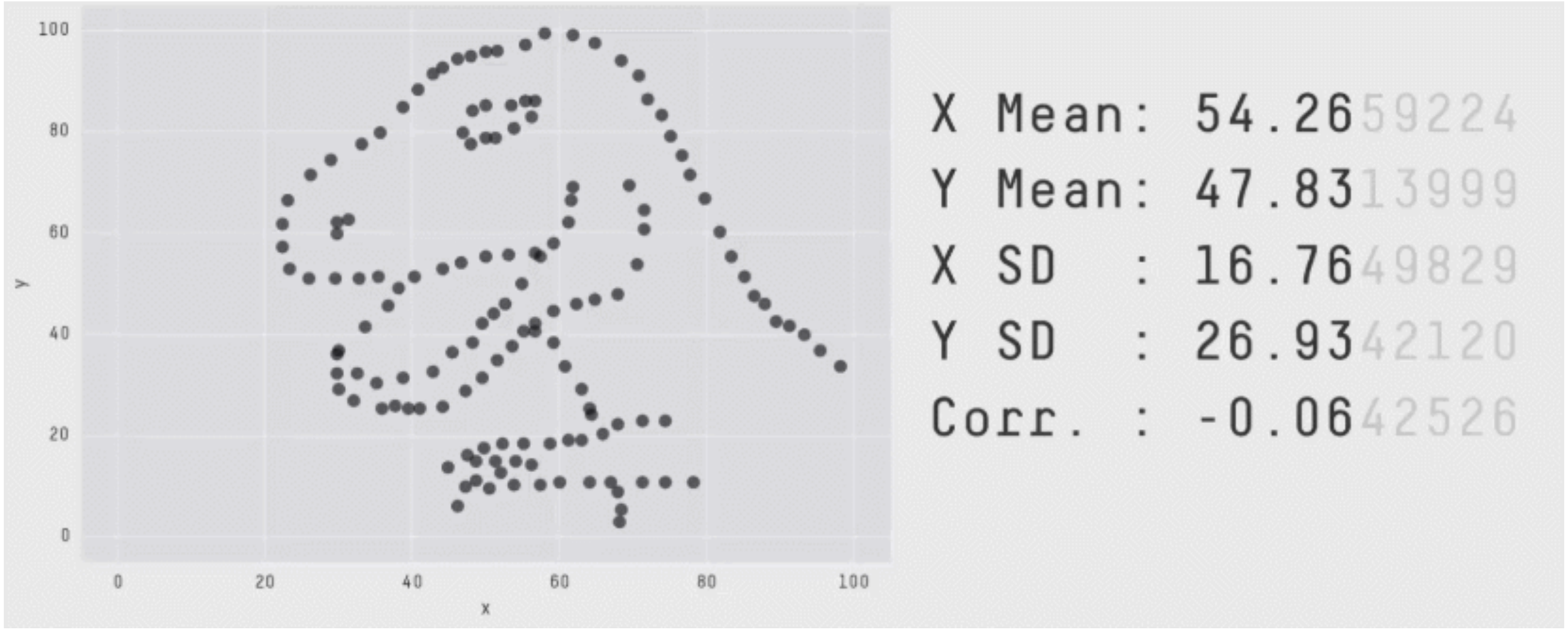
I		II		III		IV	
x	y	x	y	x	y	x	y
10	8.04	10	9.14	10	7.46	8	6.58
8	6.95	8	8.14	8	6.77	8	5.76
13	7.58	13	8.74	13	12.74	8	7.71
9	8.81	9	8.77	9	7.11	8	8.84
11	8.33	11	9.26	11	7.81	8	8.47
14	9.96	14	8.1	14	8.84	8	7.04
6	7.24	6	6.13	6	6.08	8	5.25
4	4.26	4	3.1	4	5.39	19	12.5
12	10.84	12	9.13	12	8.15	8	5.56
7	4.82	7	7.26	7	6.42	8	7.91
5	5.6					8	6.89

Mean x: 9 y: 7.50
Variance x: 11 y: 4.122
Correlation x – y: 0.816
Linear regression: y = 3.00 + 0.500x

Anscombe’s Quartett



Mean x: 9 y: 7.50
Variance x: 11 y: 4.122
Correlation x – y: 0.816
Linear regression: y = 3.00 + 0.500x



Same Stats, Different Graphs: Generating Datasets with Varied Appearance and Identical Statistics through Simulated Annealing, CHI 2017, Justin Matejka, George Fitzmaurice

Visualization in the Data Science Process

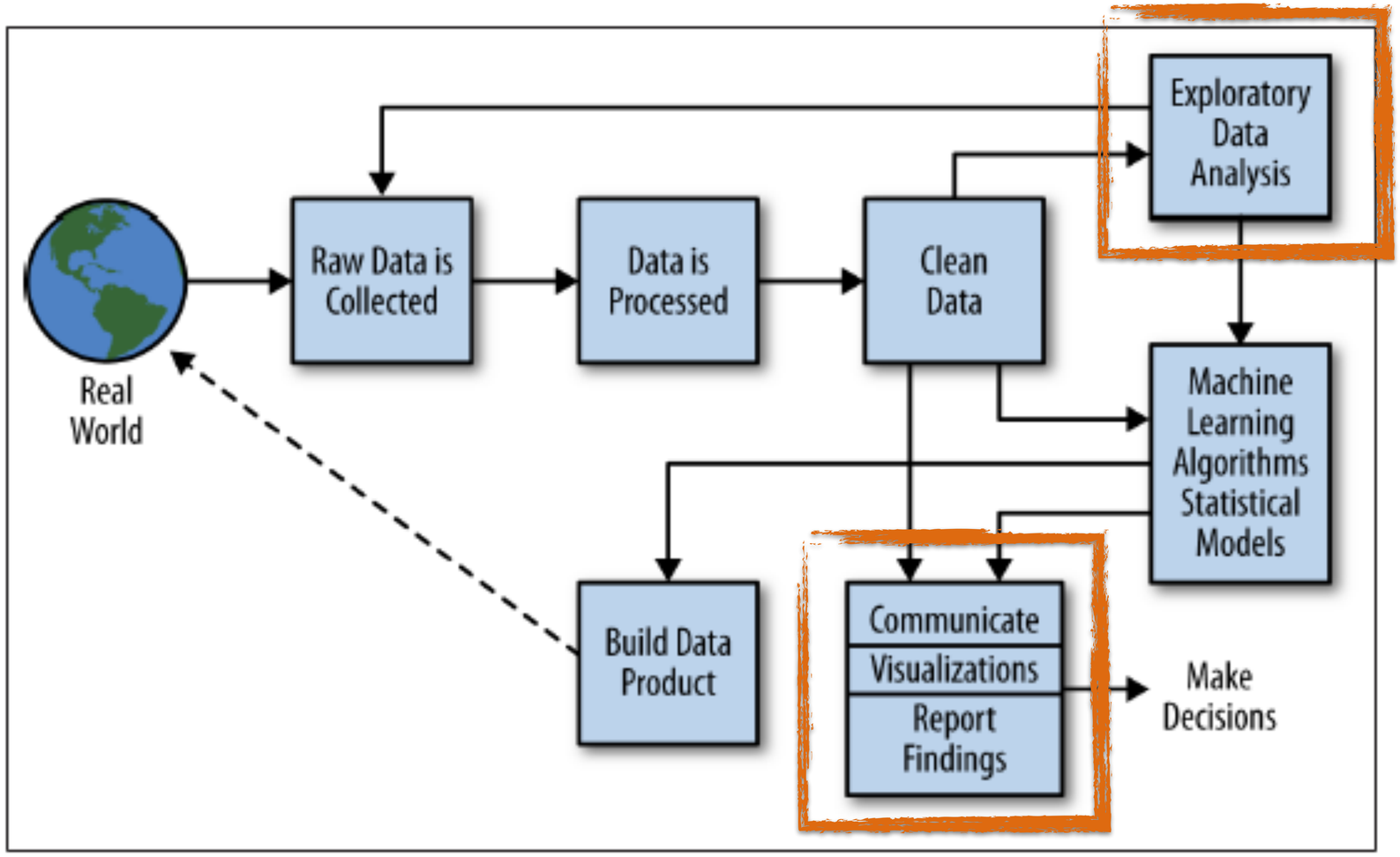
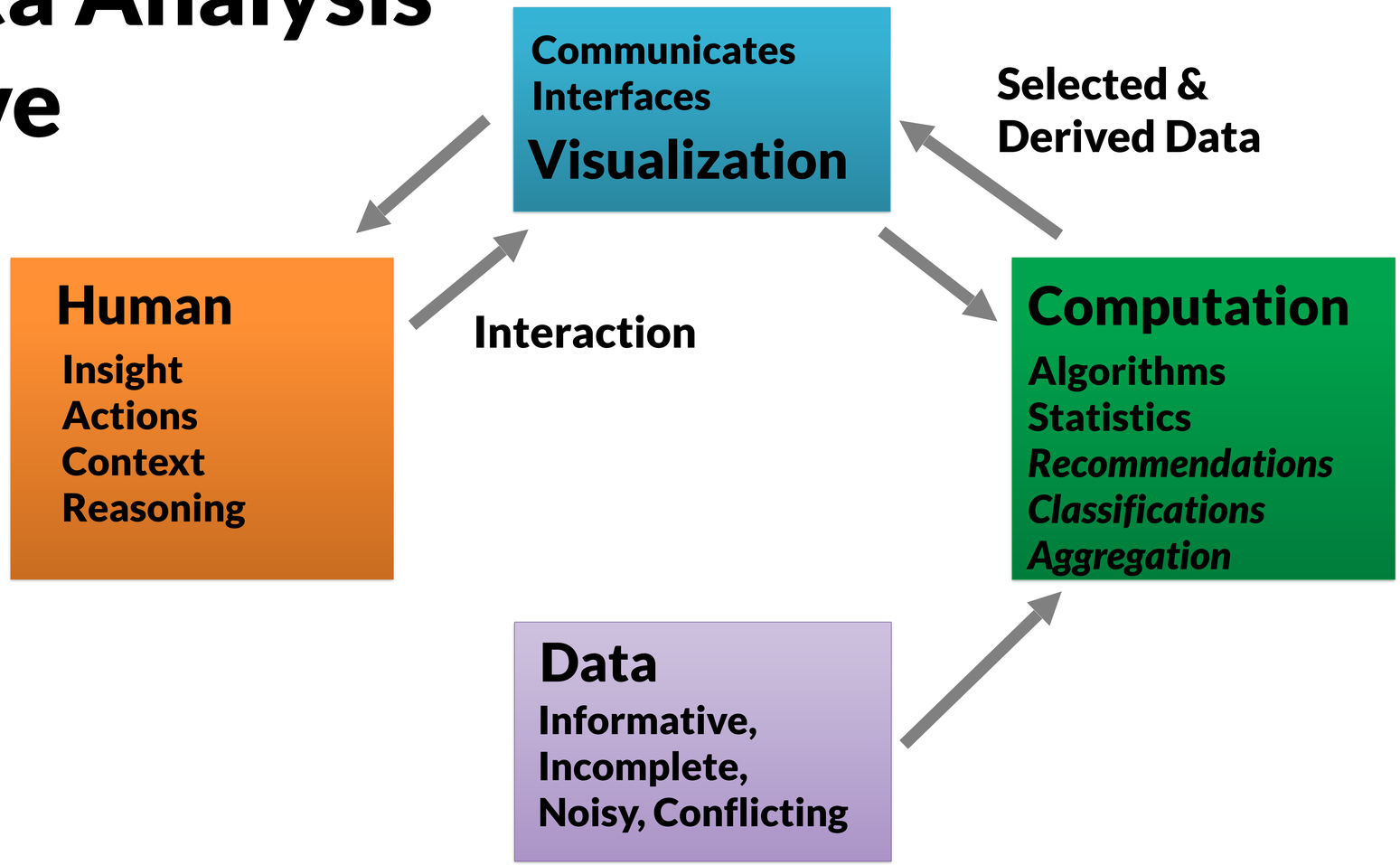


Figure 2-2. The data science process

Interacting with Data

The Future of Data Analysis is (also) Interactive

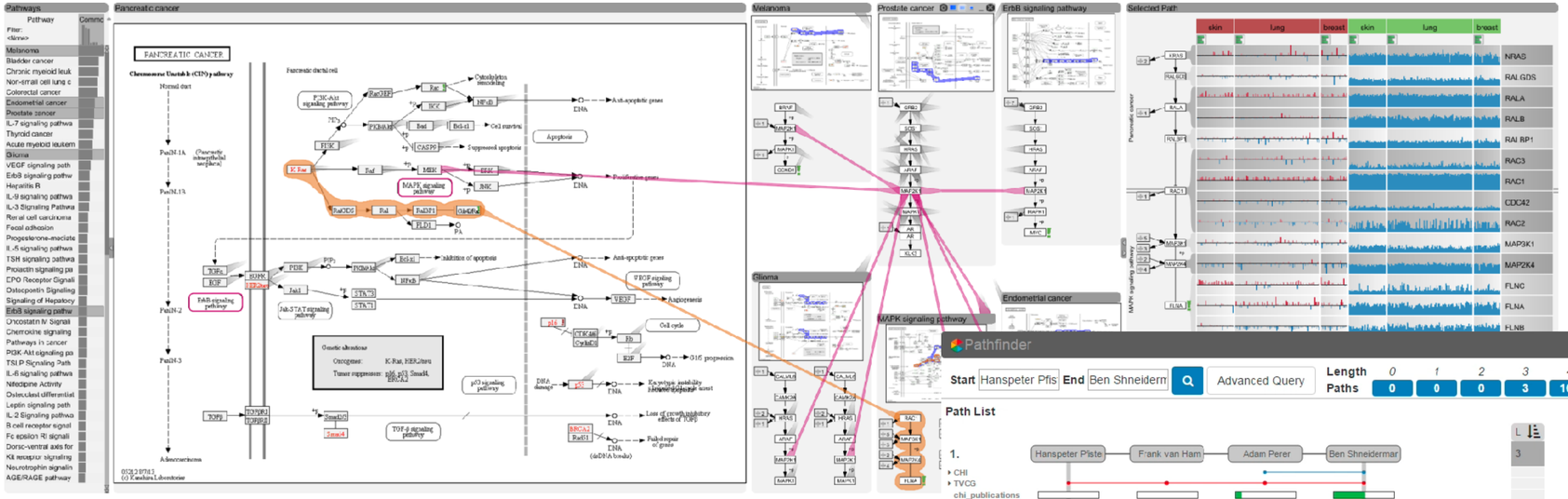


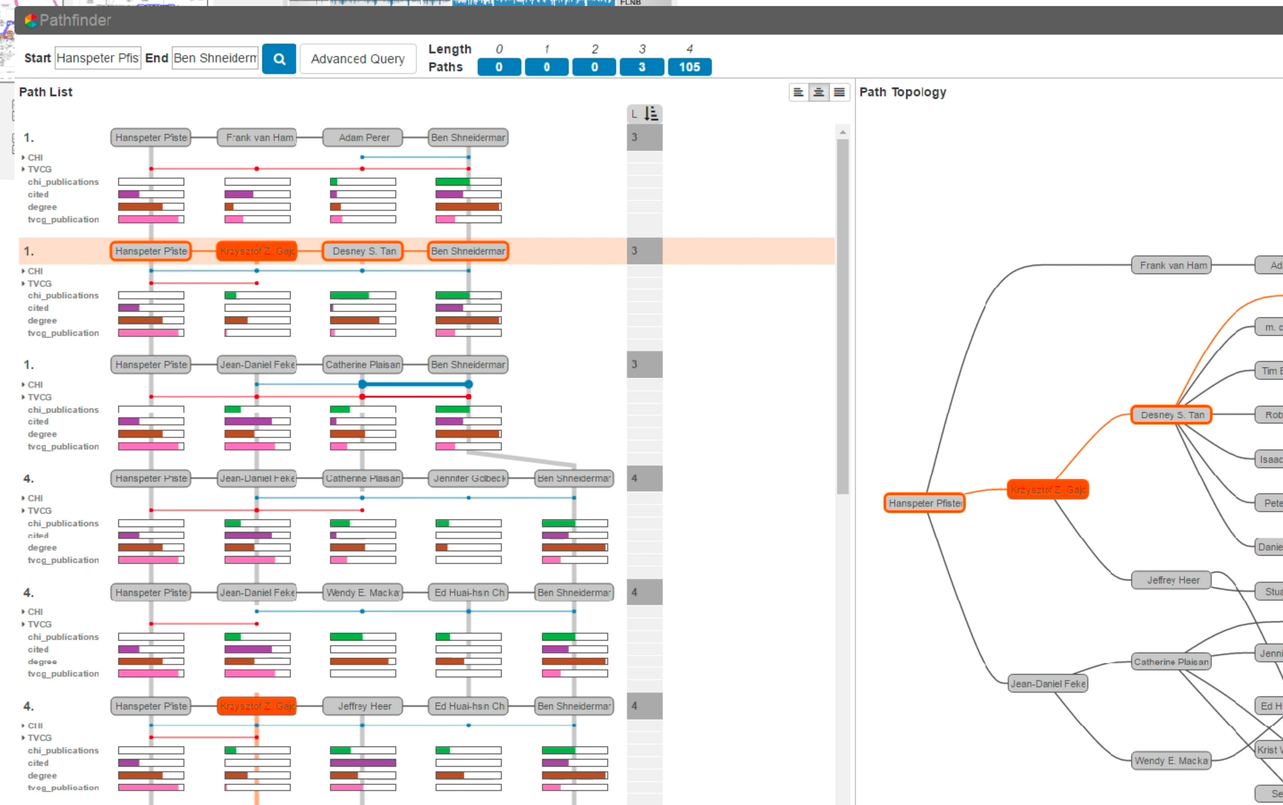
Visualization =

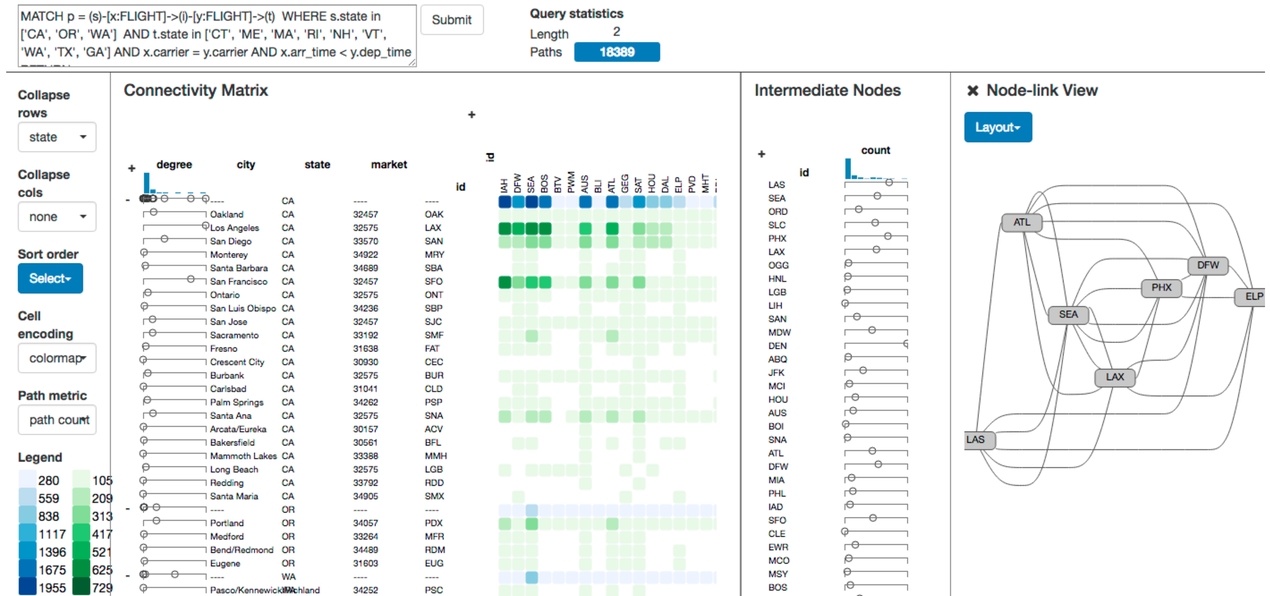
Human Data Interaction

Research Areas

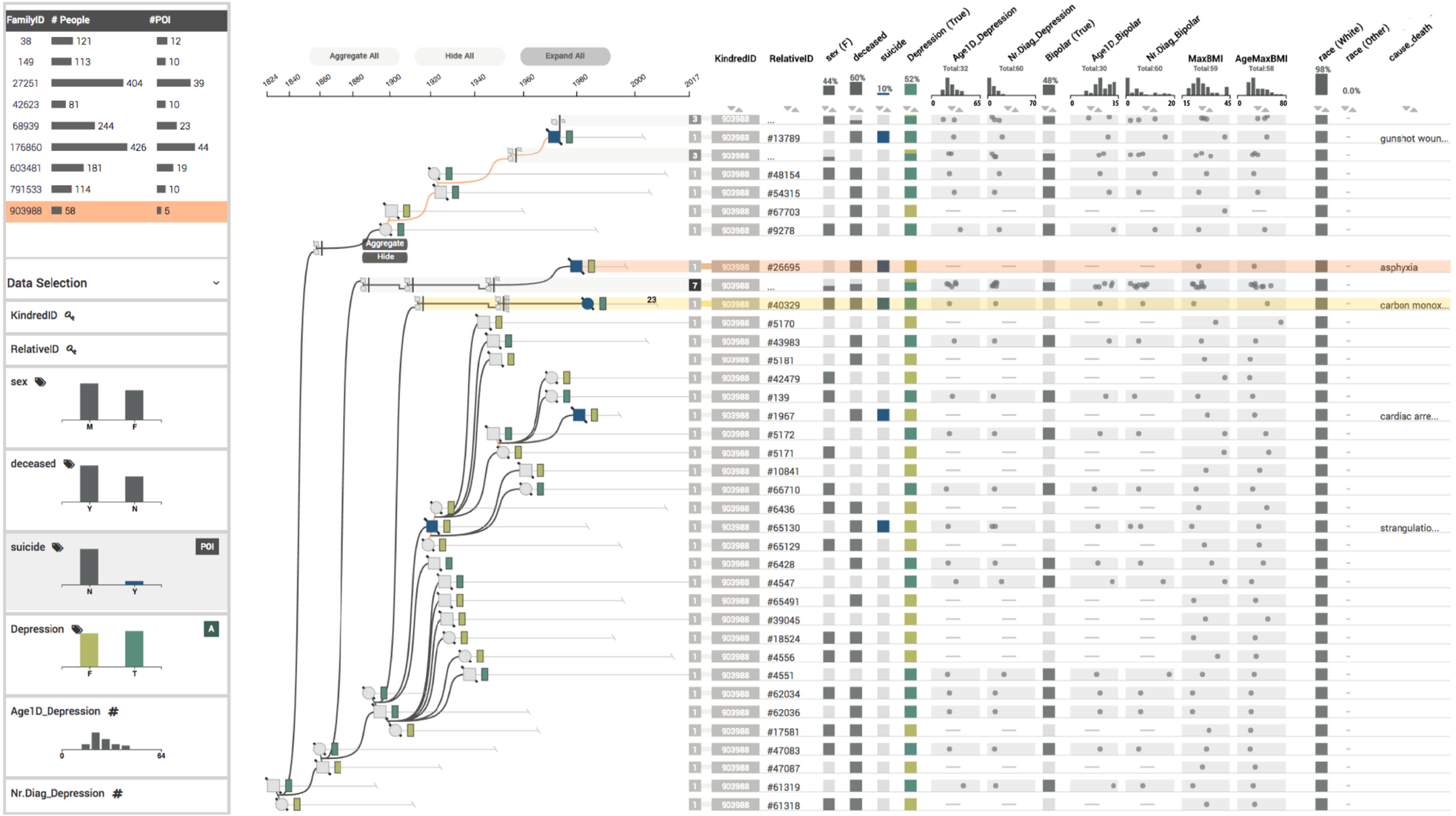
Large, Multivariate (Biological) Networks



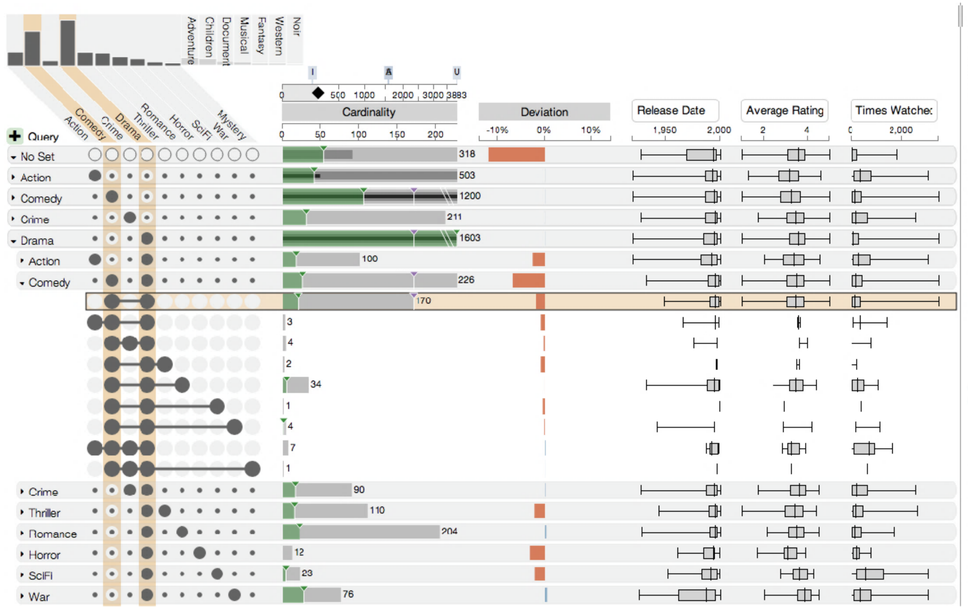




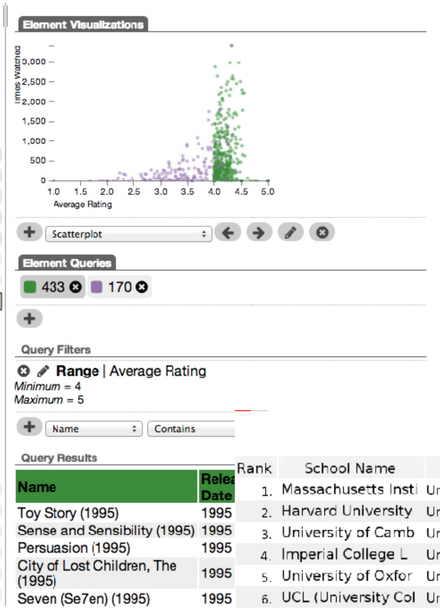
Genealogies & Clinical Data



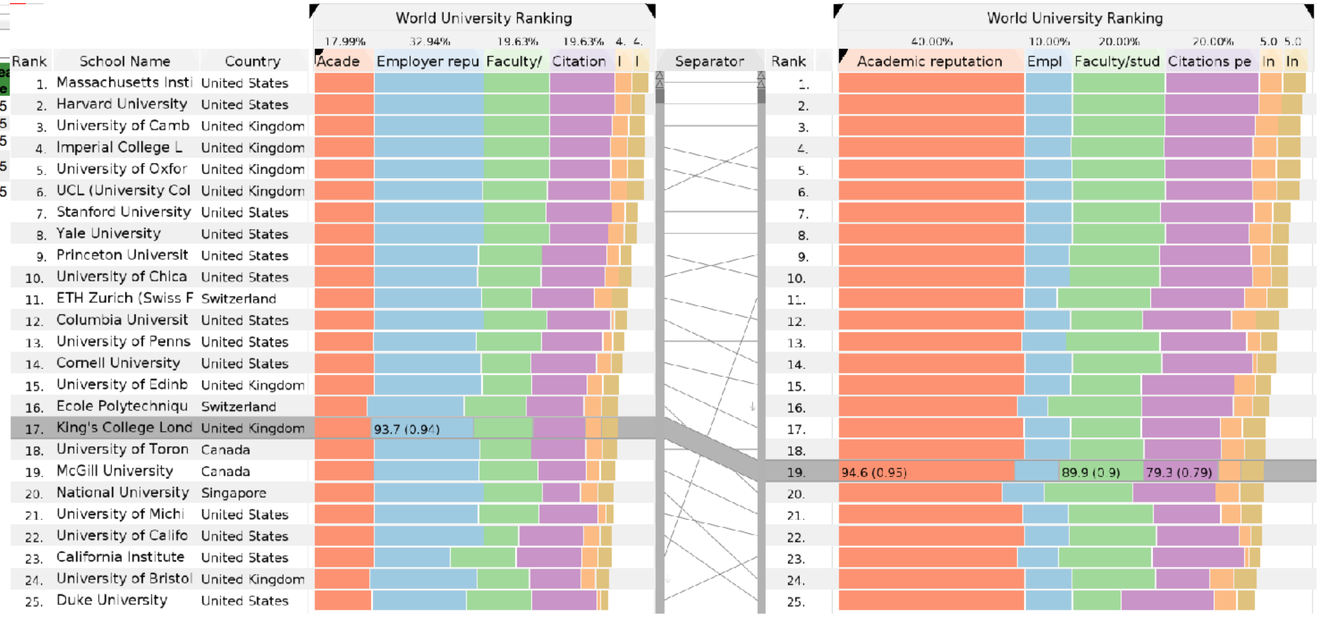
Multidimensional Data

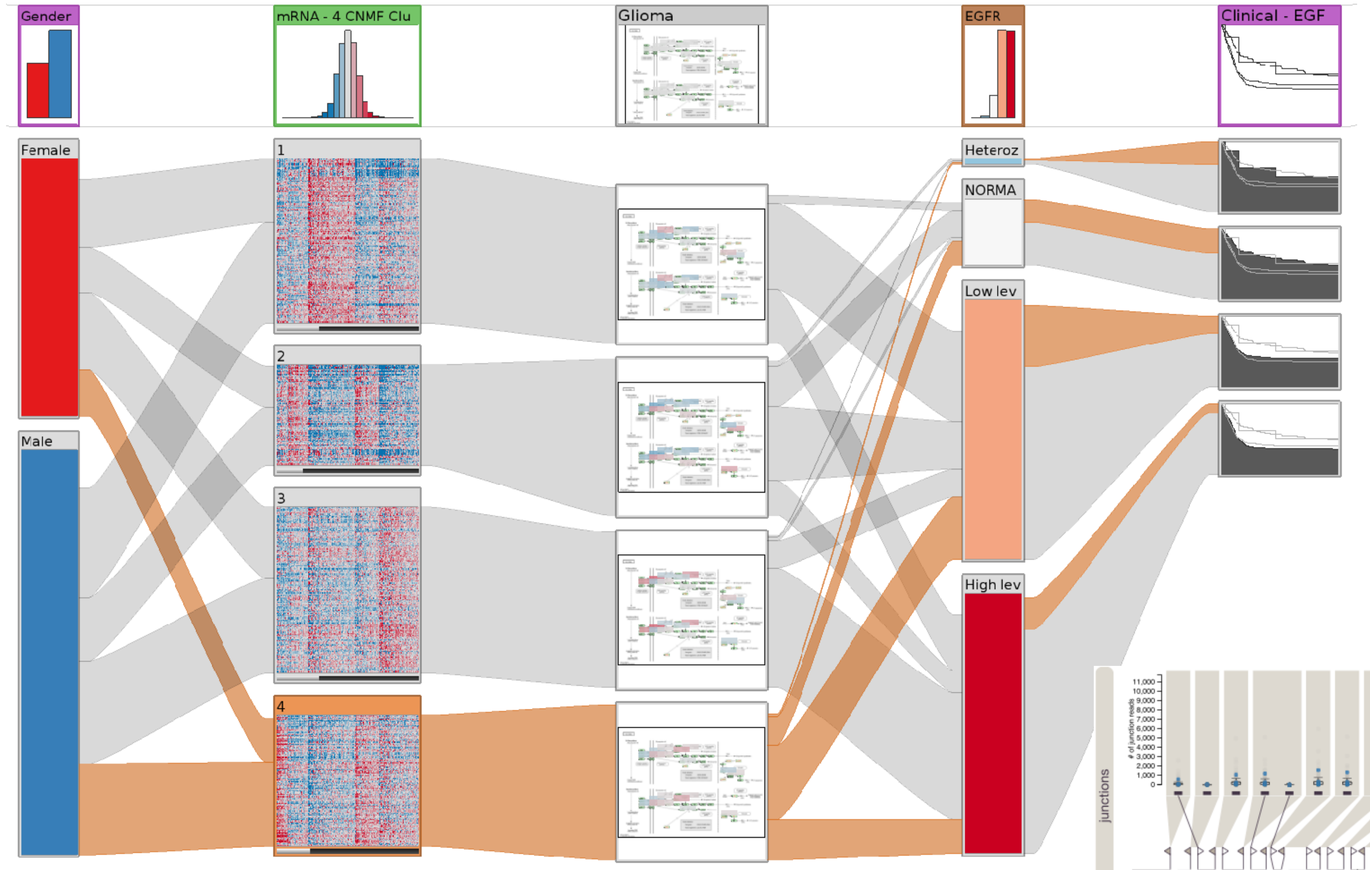


Set Visualization



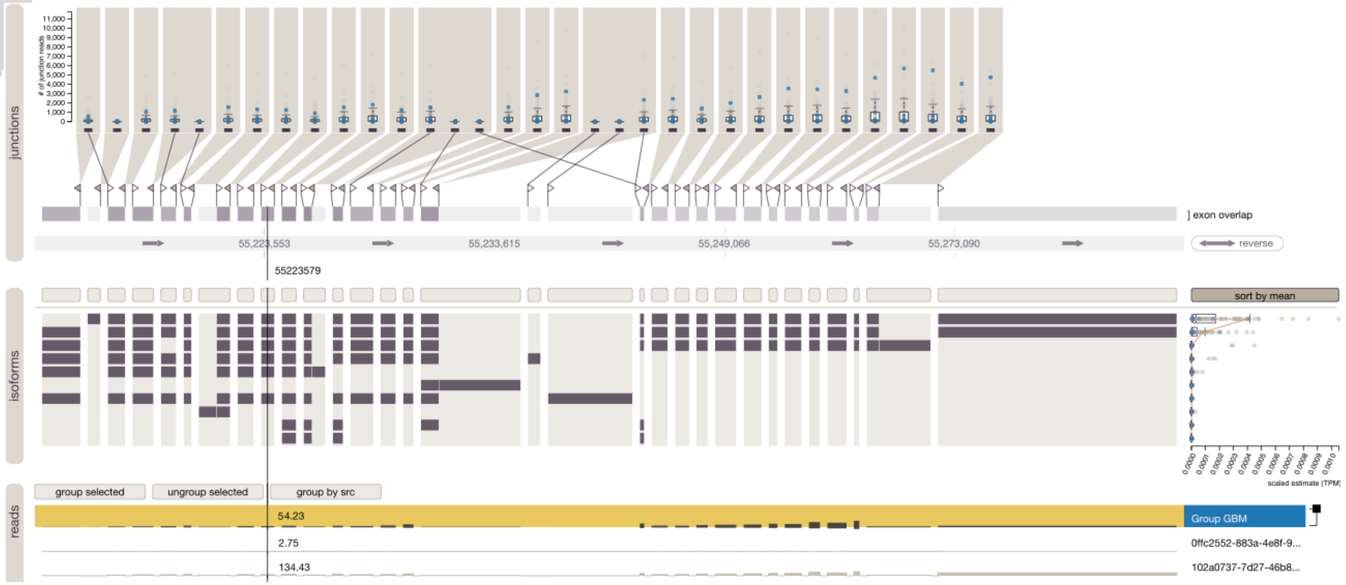
Multivariate Rankings





Cancer Subtypes / Omics Clustering and Stratification

Alternative Splicing / mRNA-seq



Vials
Visualizing Alternative Splicing

[InfoVis'15]

Hendrik Strobelt

Bilal Alshallak

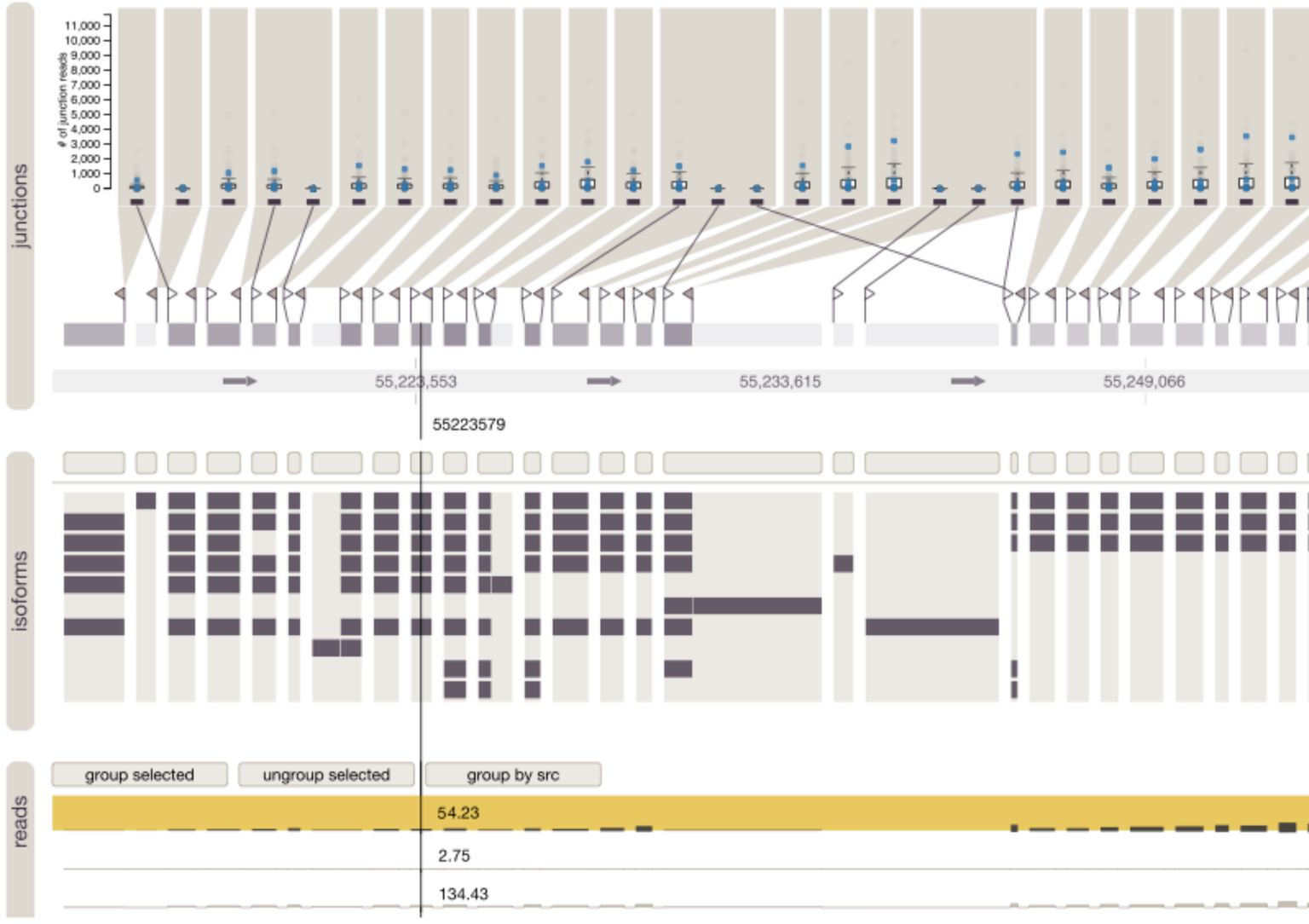
Joseph Botros

Brant Peterson

Mark Borowsky

Hanspeter Pfister

Alexander Lex

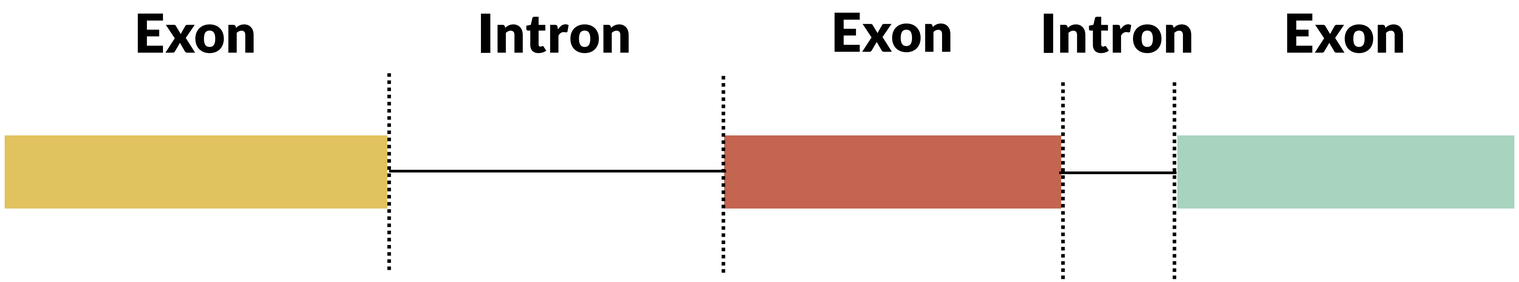


Scalable solution for isoform / alternative splicing analysis

Visualize measures for
isoform abundance,
base-pair/exon expression,
junction reads

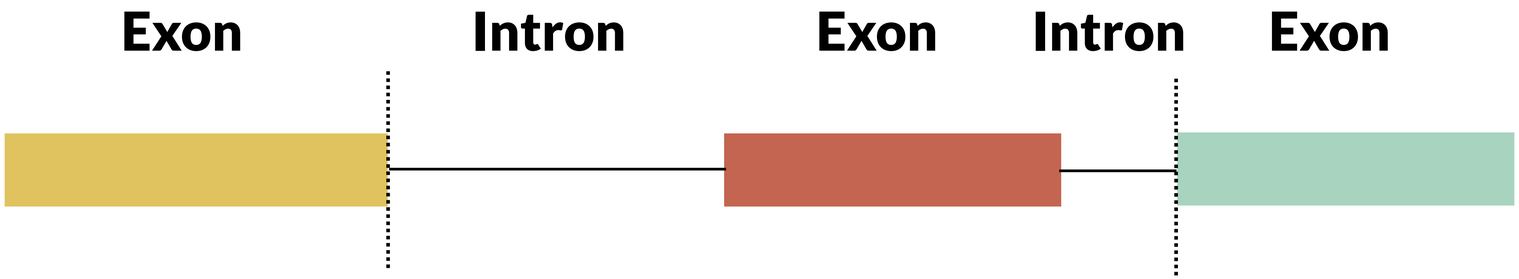
for a large set of samples

Splicing

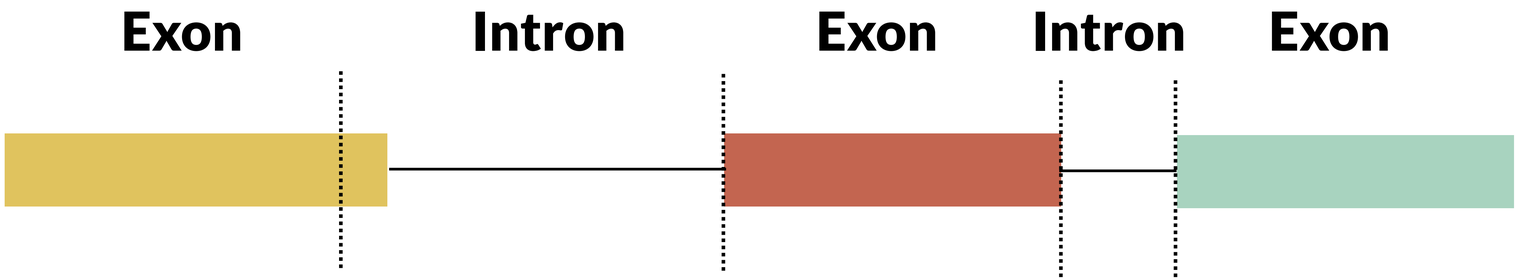


Remove introns as part of the transcription process

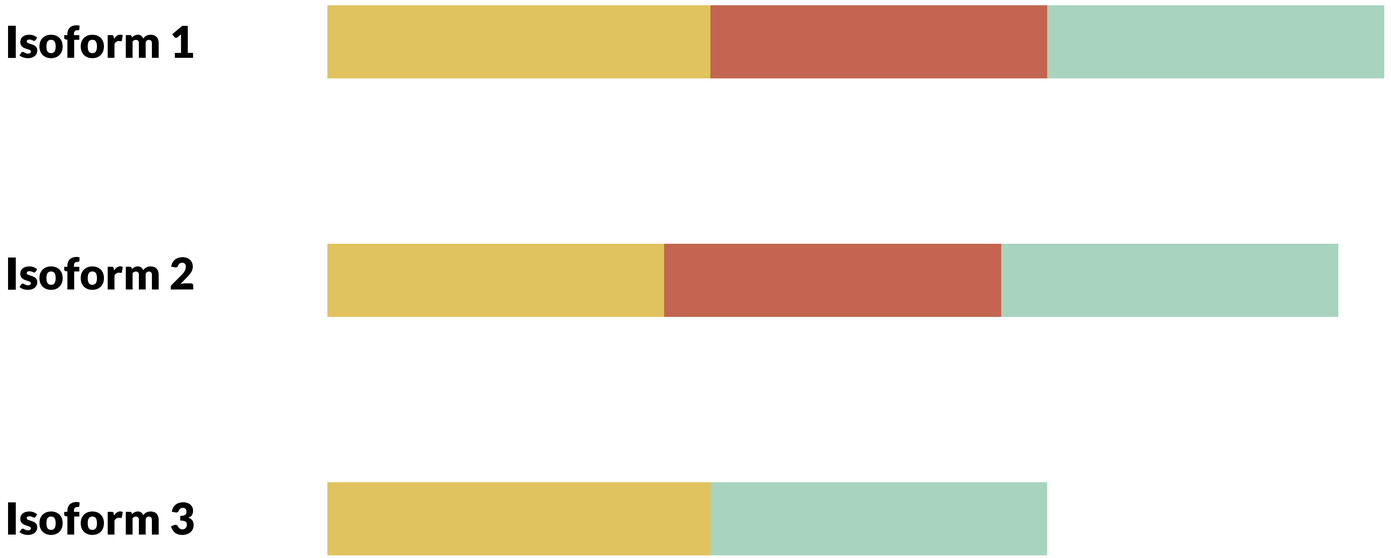
Omitted Exons



Truncated Exons



Isoforms

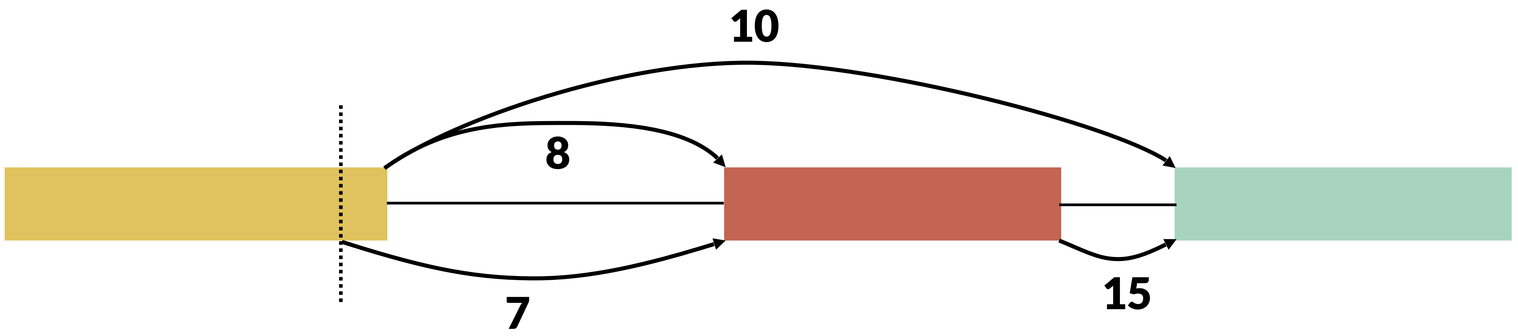


Reads

Reads from mRNA-seq data tell us about expression of exons

Junction reads tell us about which (parts of) exons are spliced out

Junction Information



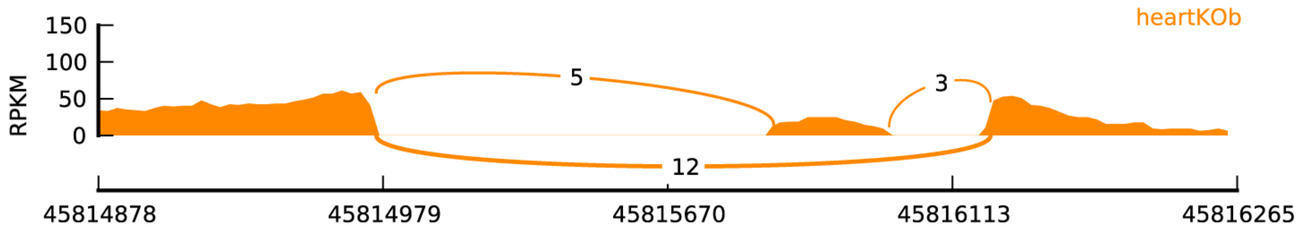
Goals

Explore differences between samples and groups of samples

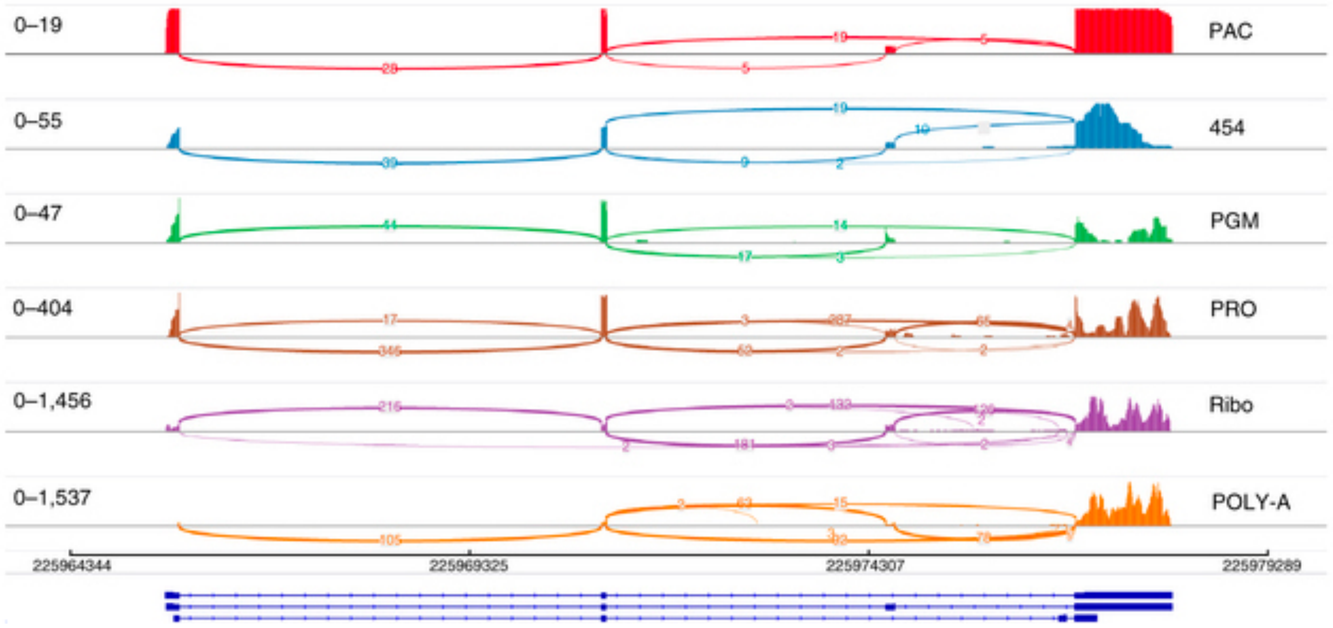
Quality control

Discover novel isoforms

The Competition: Sashimi Plots



[Katz et al, 2010]



[Sheng et al, 2014]

Data & Visualization

Isoform abundance

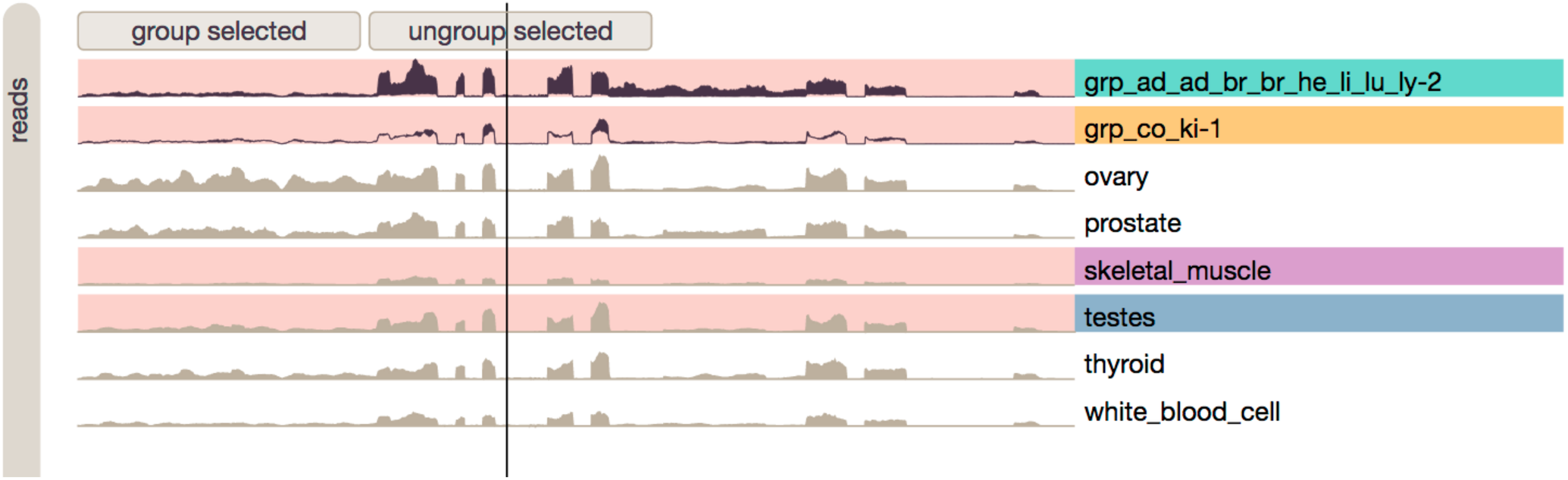
Exon expression

Junction reads

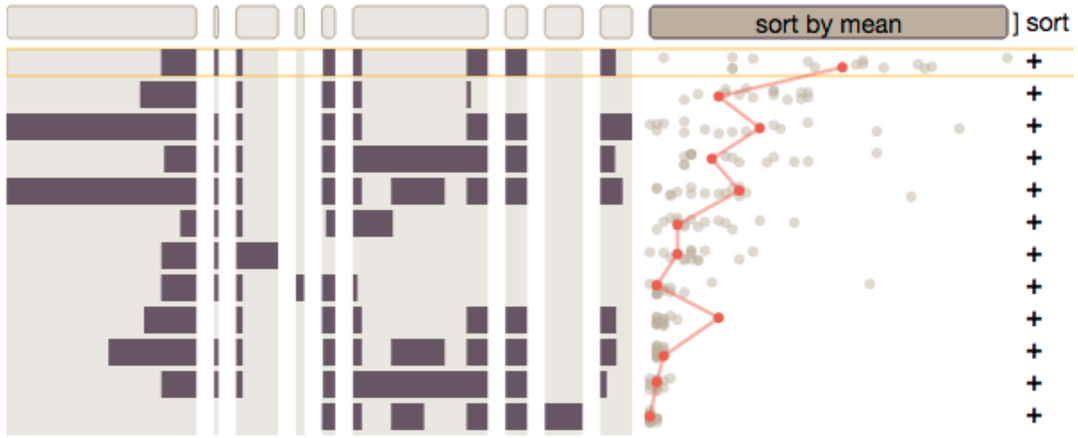
…for hundreds of samples

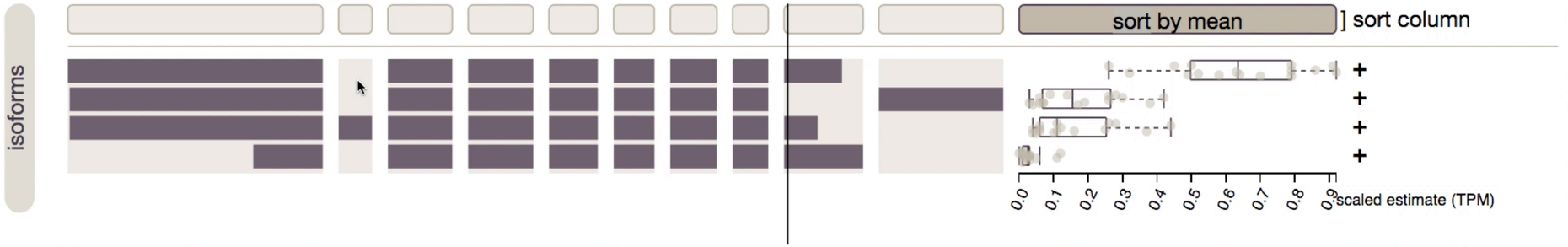
…for multiple groups

Expression View

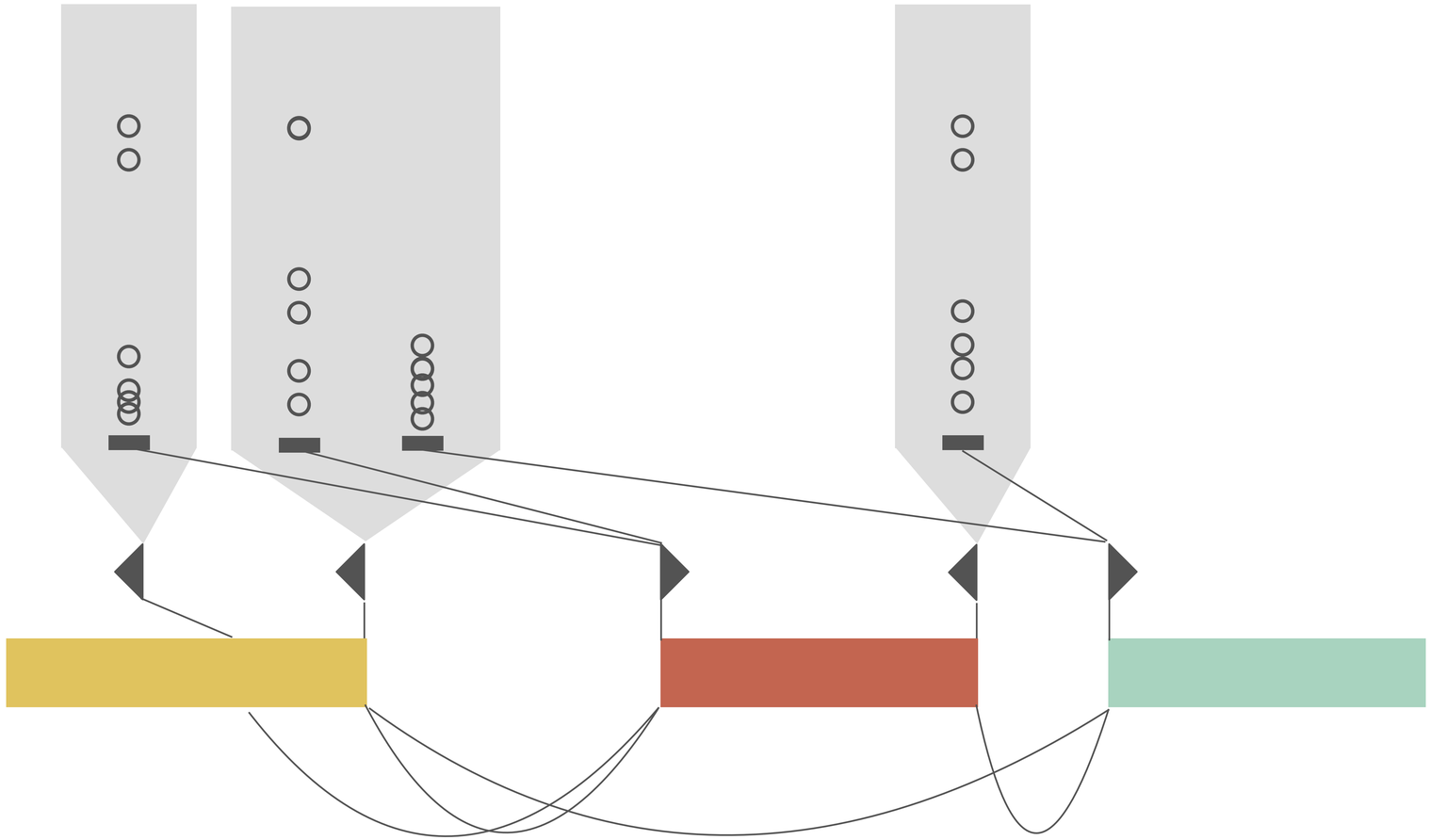


Isoform View

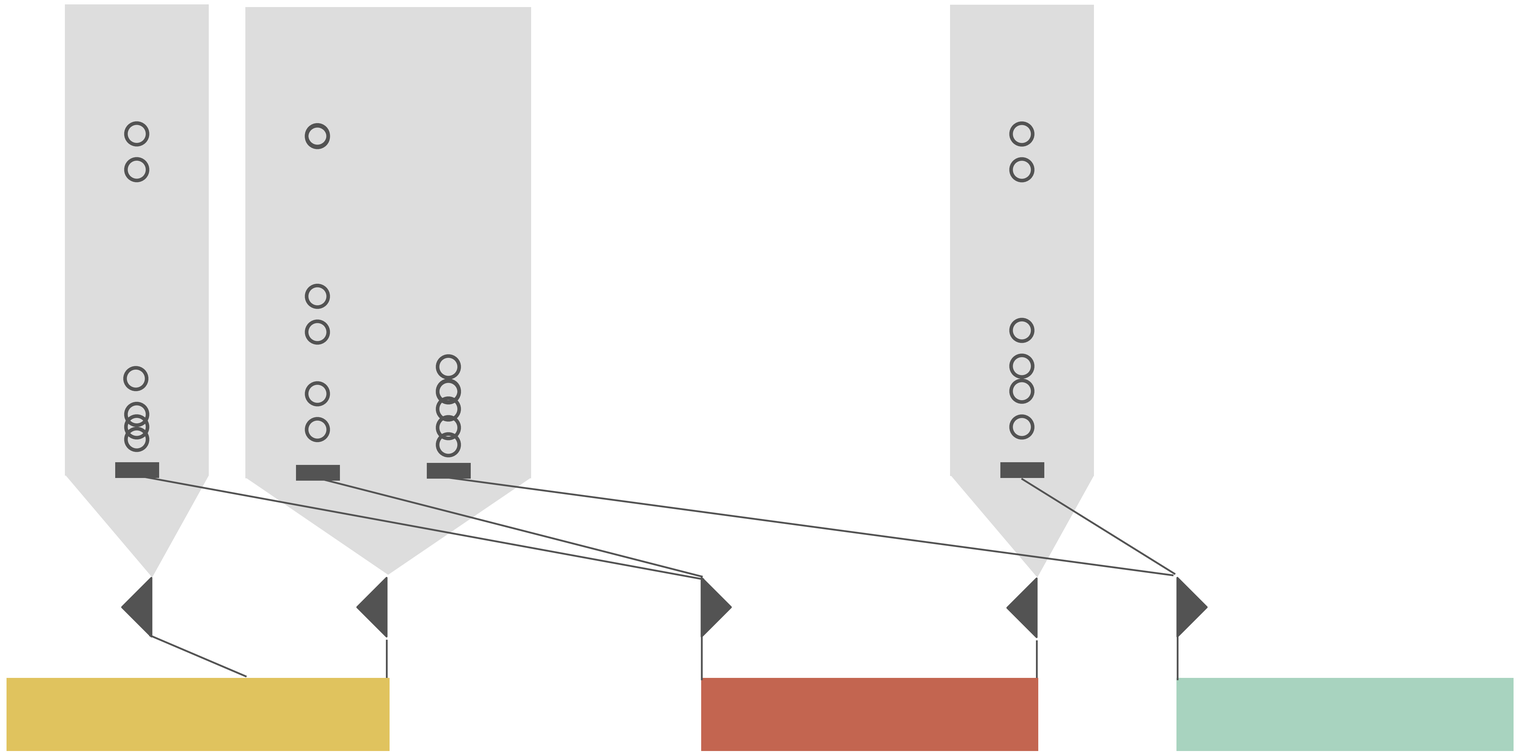




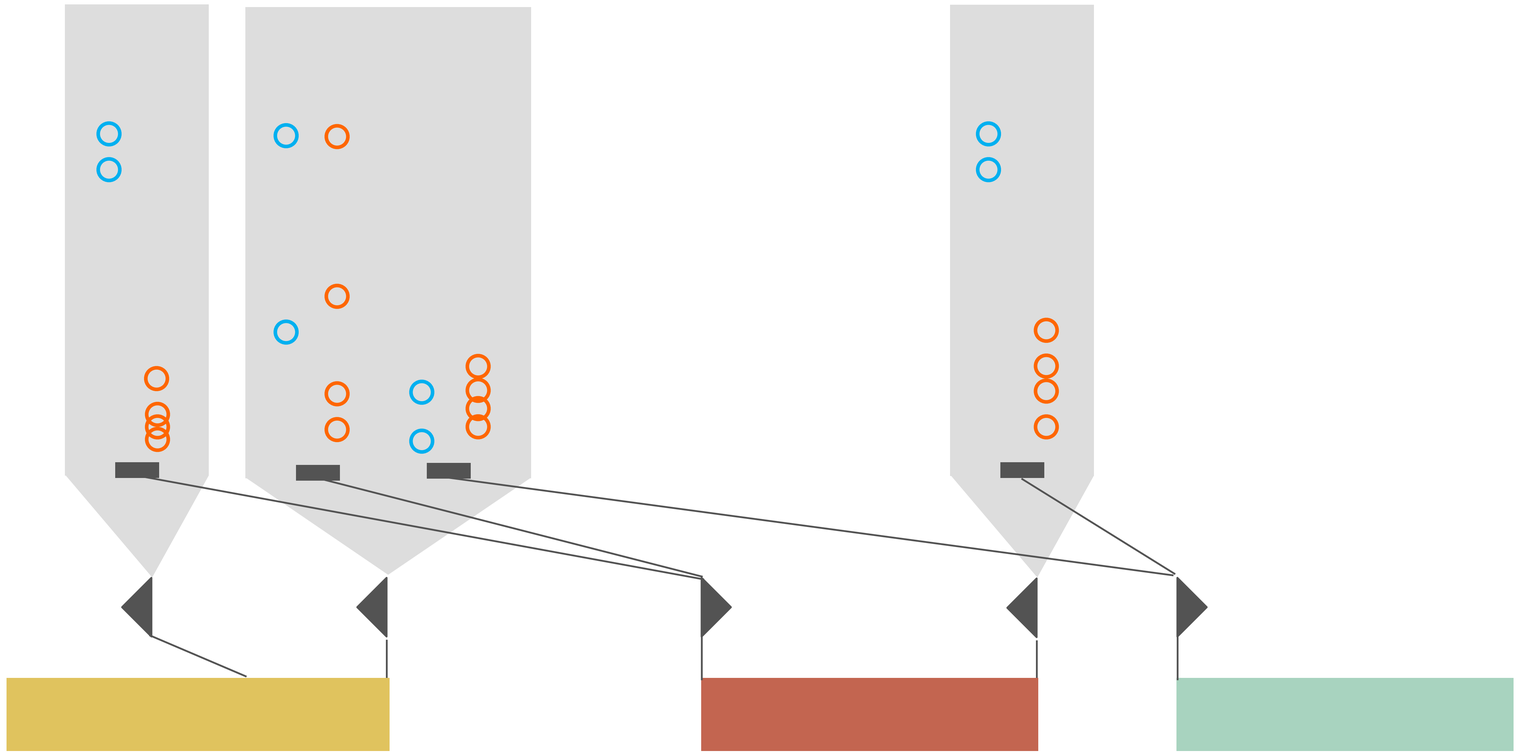
Junction View



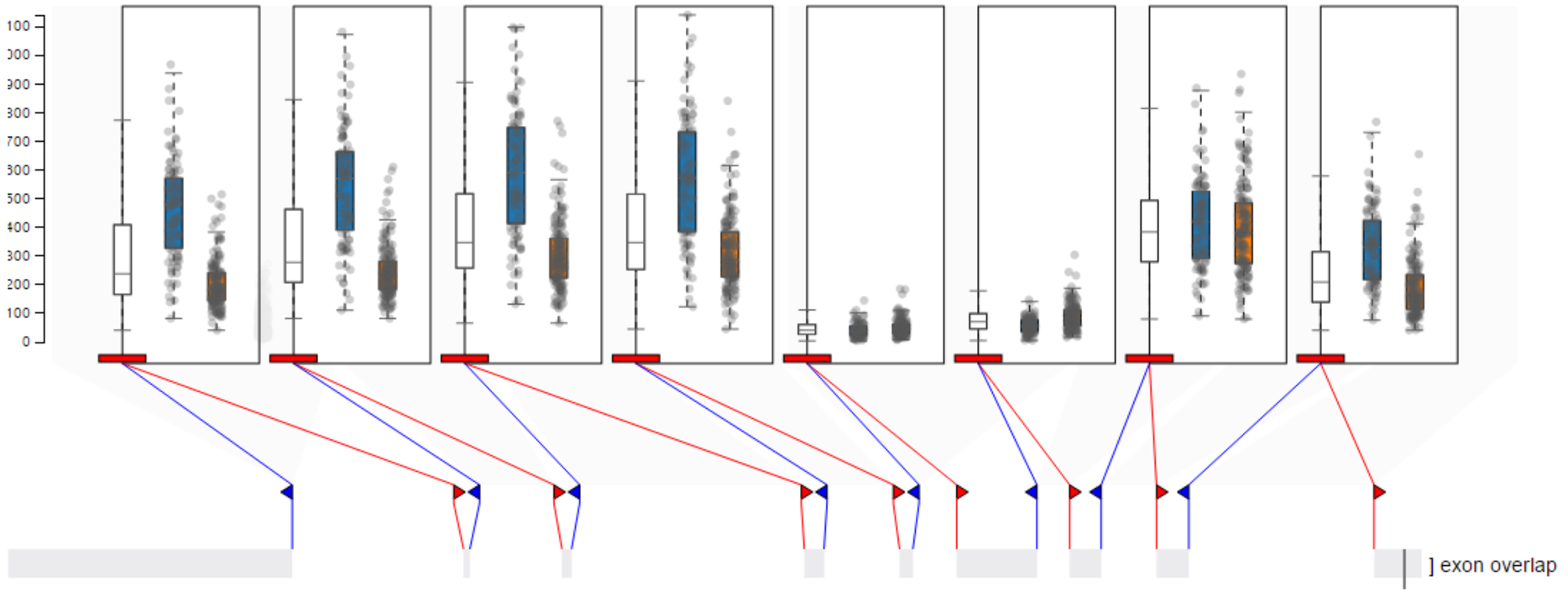
Junction View - Group Comparison



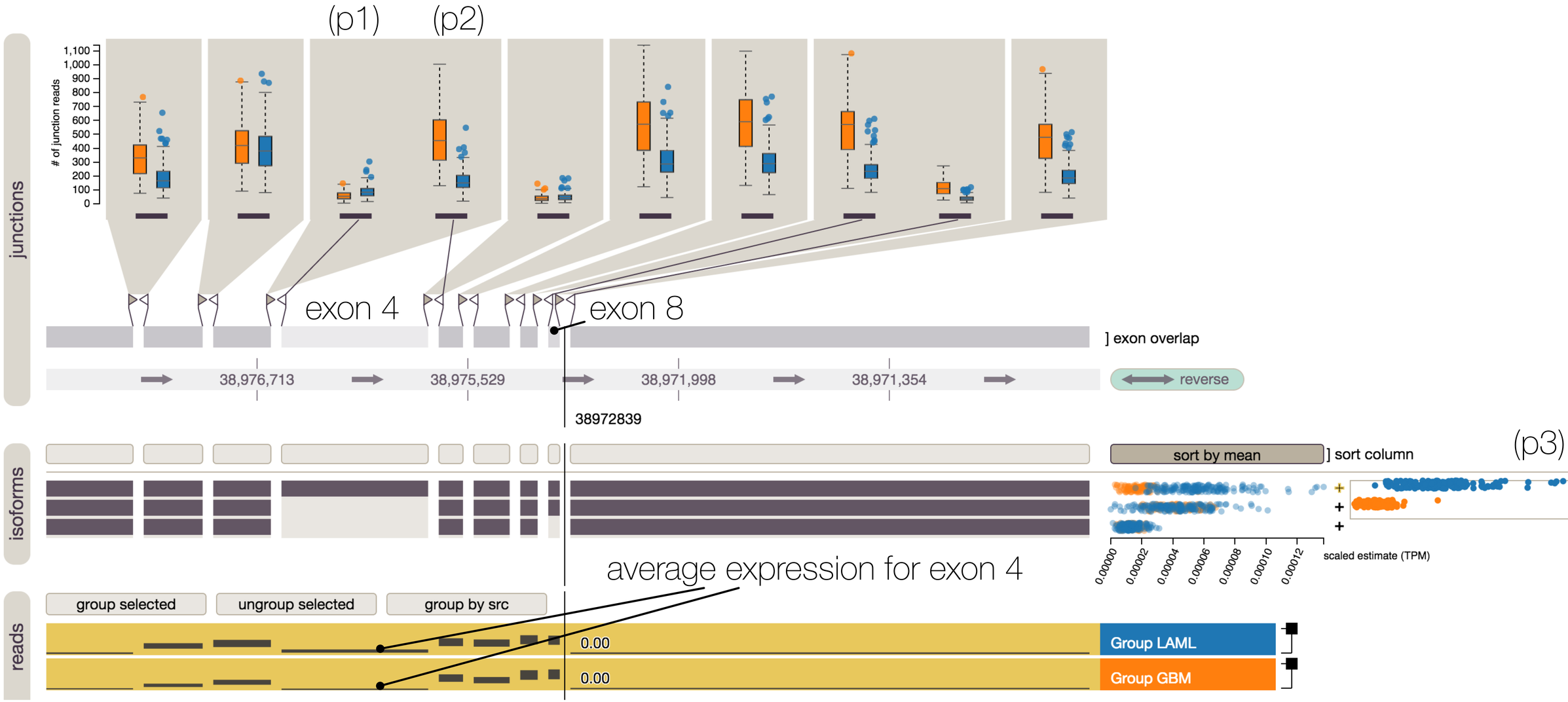
Junction View - Group Comparison



Junction View - Group Comparison



Case Study: Leukemia vs Glioblastoma



http://vials.io

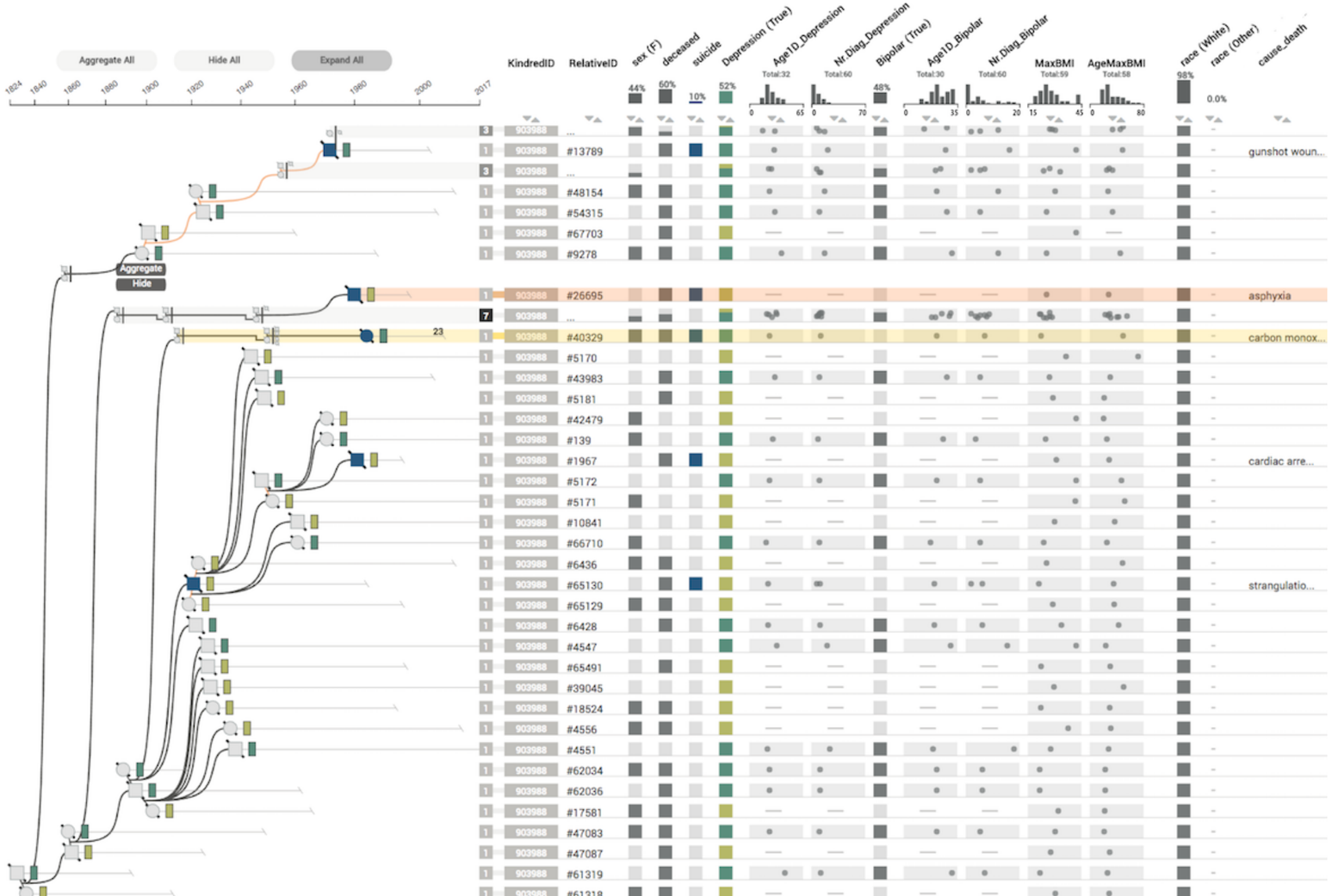
Lineage
Visualizing Clinical Data in Genealogy Graphs

Carolina Nobre

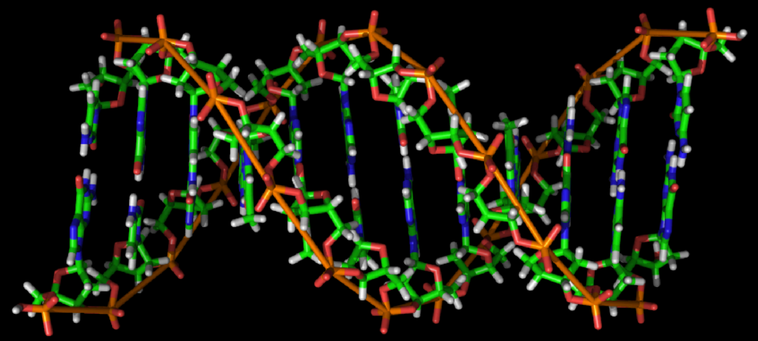
Nils Gehlenborg

Hilary Coon

Alexander Lex



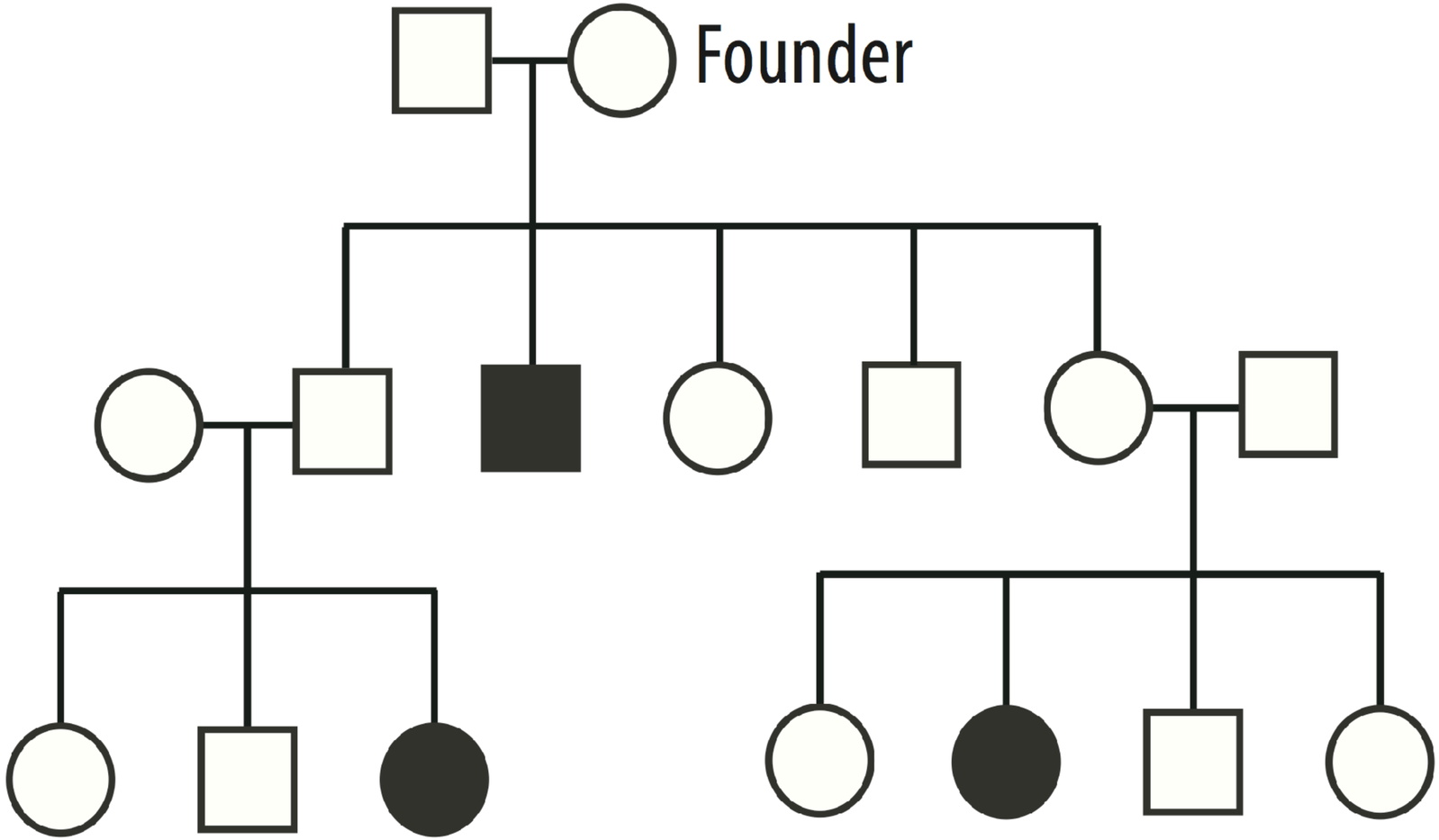
Motivation

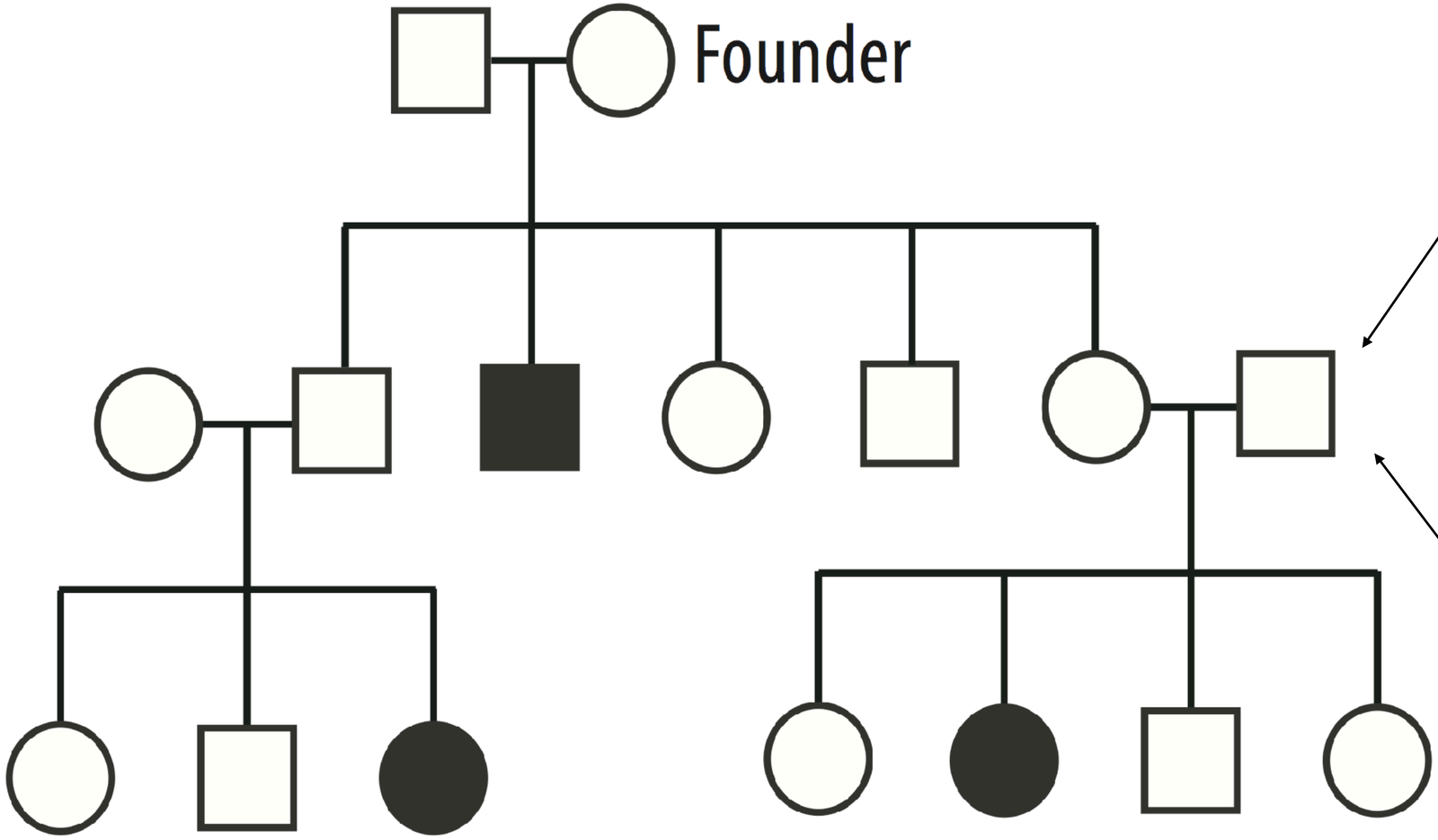


Understand Complex Psychiatric Conditions

Discover Genetic Risk Factors

Dataset: 118k people, 19k suicide cases, 550 families

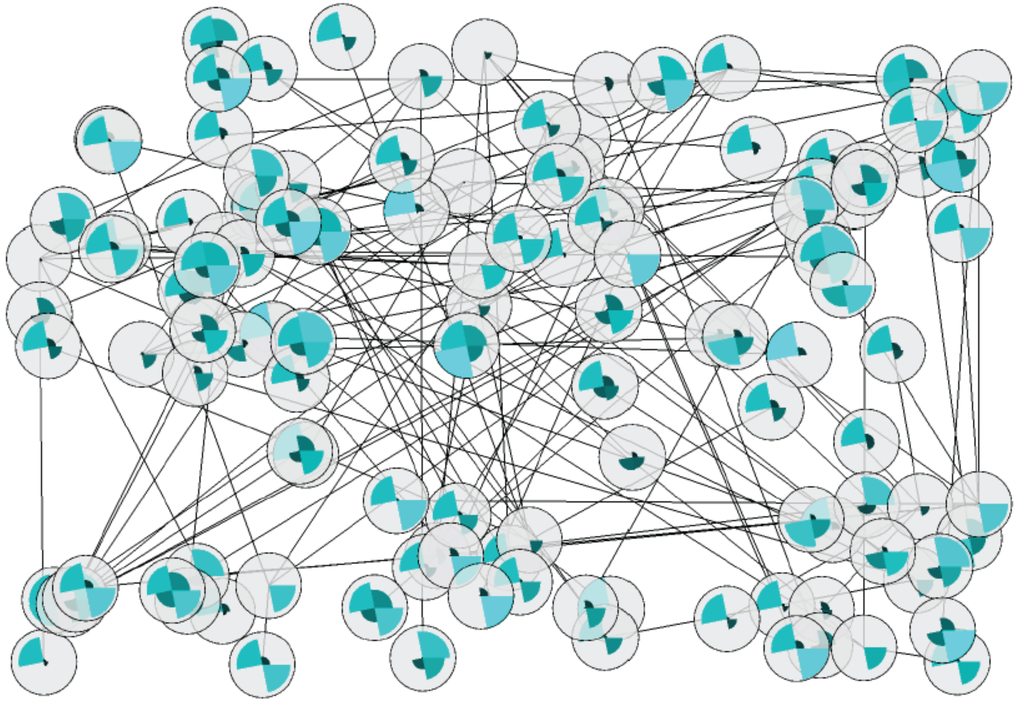

Founder



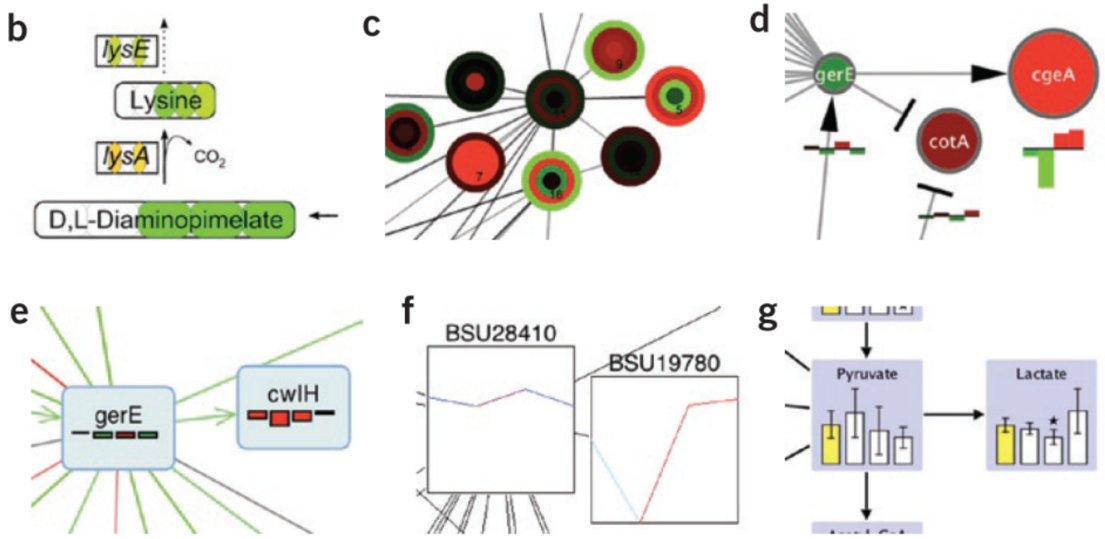
Age
Sex
Race
Bipolar
 # diagnosis bipolar
Depression
 # diagnosis depression
Asthma
 # diagnosis asthma
Obesity
Schizophrenia
Cause of Death
Weapon Used

Multivariate Attributes and Graphs

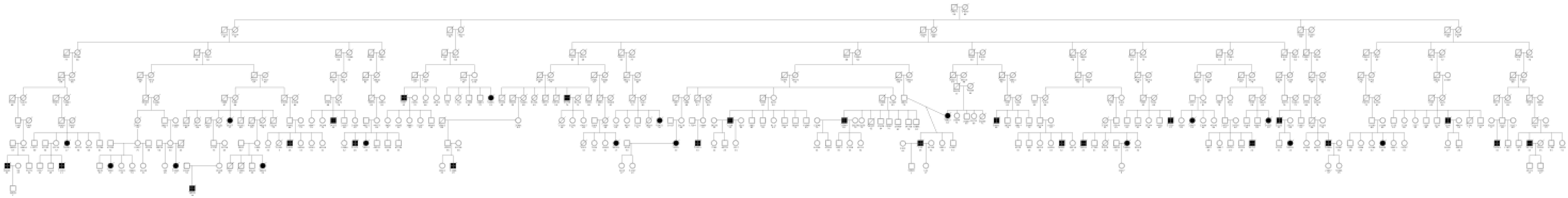
How can we deal with graphs that contain **rich attribute data**?



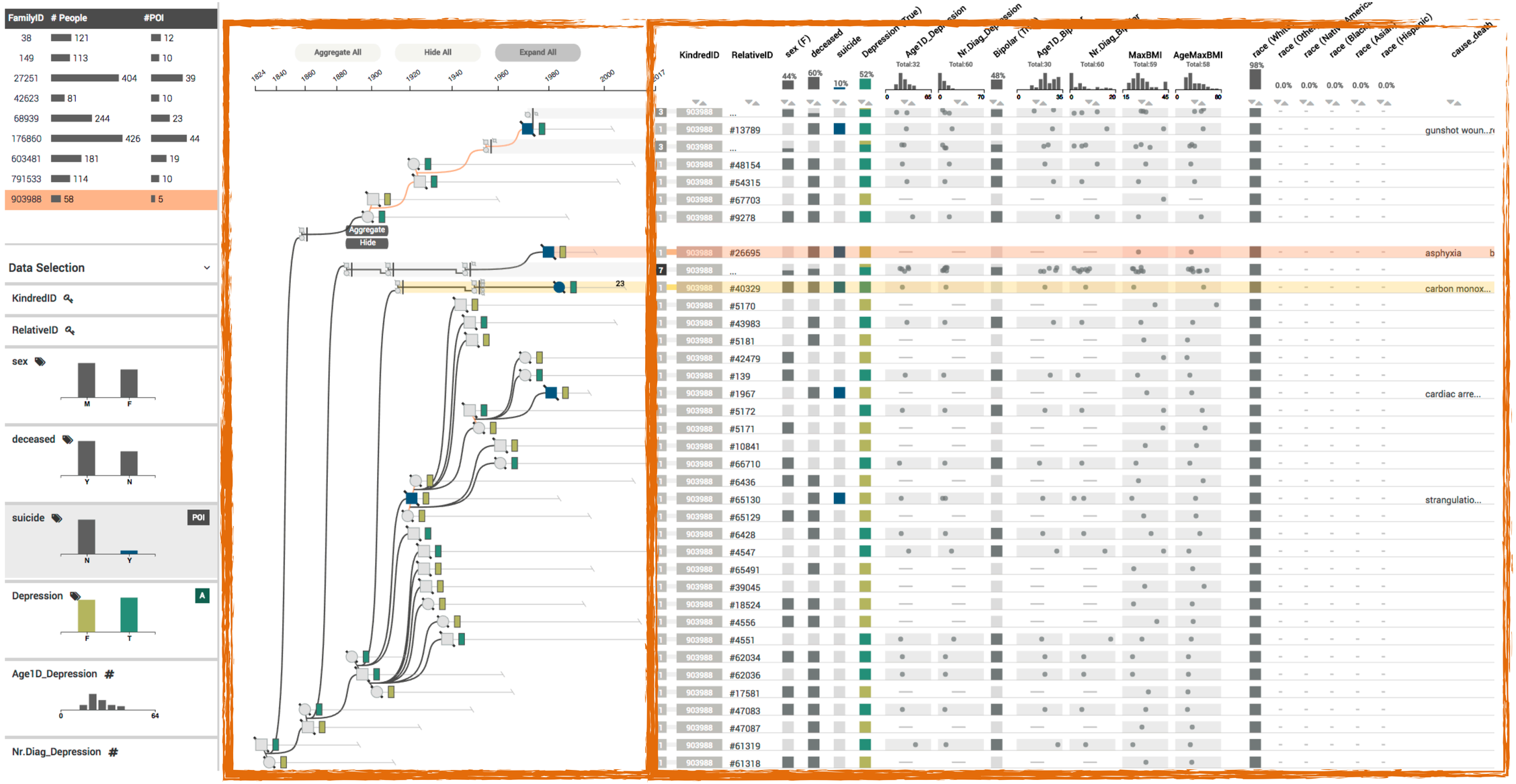
[McDonnel2009]



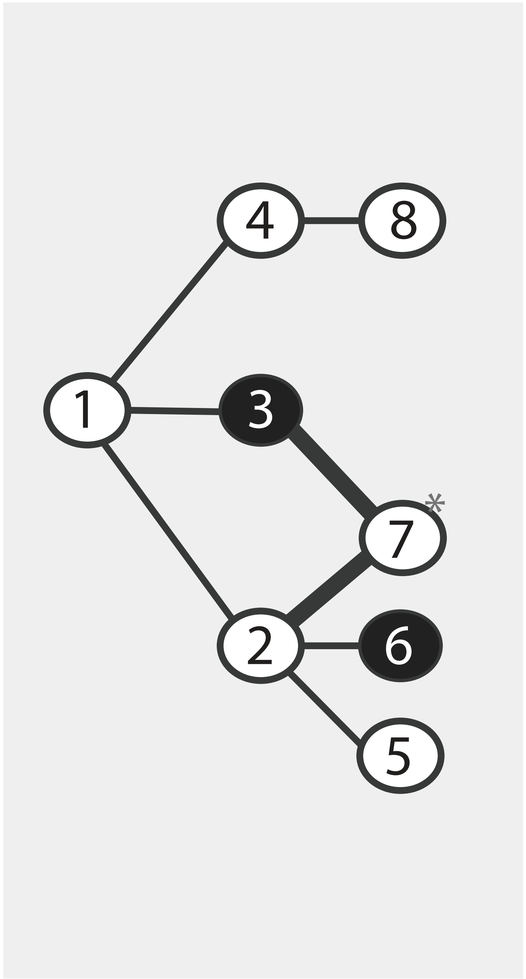
[Gehlenborg2010]



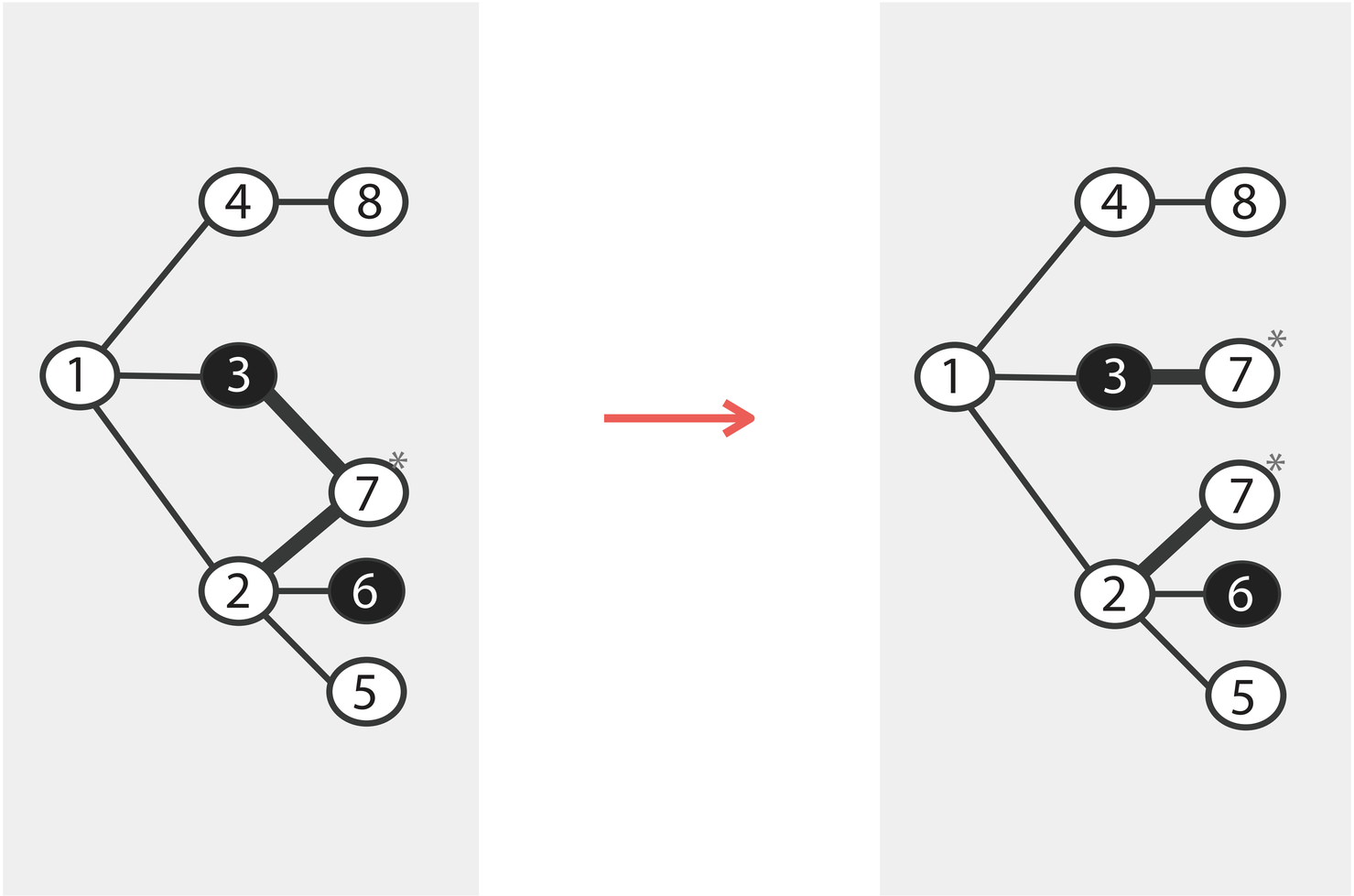
Genealogy with ~400 members rendered with Progeny


FamilyID # People #POI
38 121 12
149 113 10
27251 404 39
42623 81 10
68939 244 23
176860 426 44
603481 181 19
791533 114 10
903988 58 5
Data Selection
KindredID
RelativeID
sex
deceased
suicide
POI
Depression
A
Age1D_Depression #
Nr.Diag_Depression #
Aggregate All
Hide All
Expand All
Aggregate
Hide
KindredID
RelativeID
sex (F)
deceased
suicide
Depression (True)
Age1D_Depression
Nr.Diag_Depression
Bipolar (Ti
Age1D_Bip
Nr.Diag_Bip
MaxBMI
AgeMaxBMI
race (Whit
race (Othe
race (Nativ
race (Black
race (Asian
race (Hispanic)
cause_death
1. De-cycle and linearize graph
2. Plot attributes in table

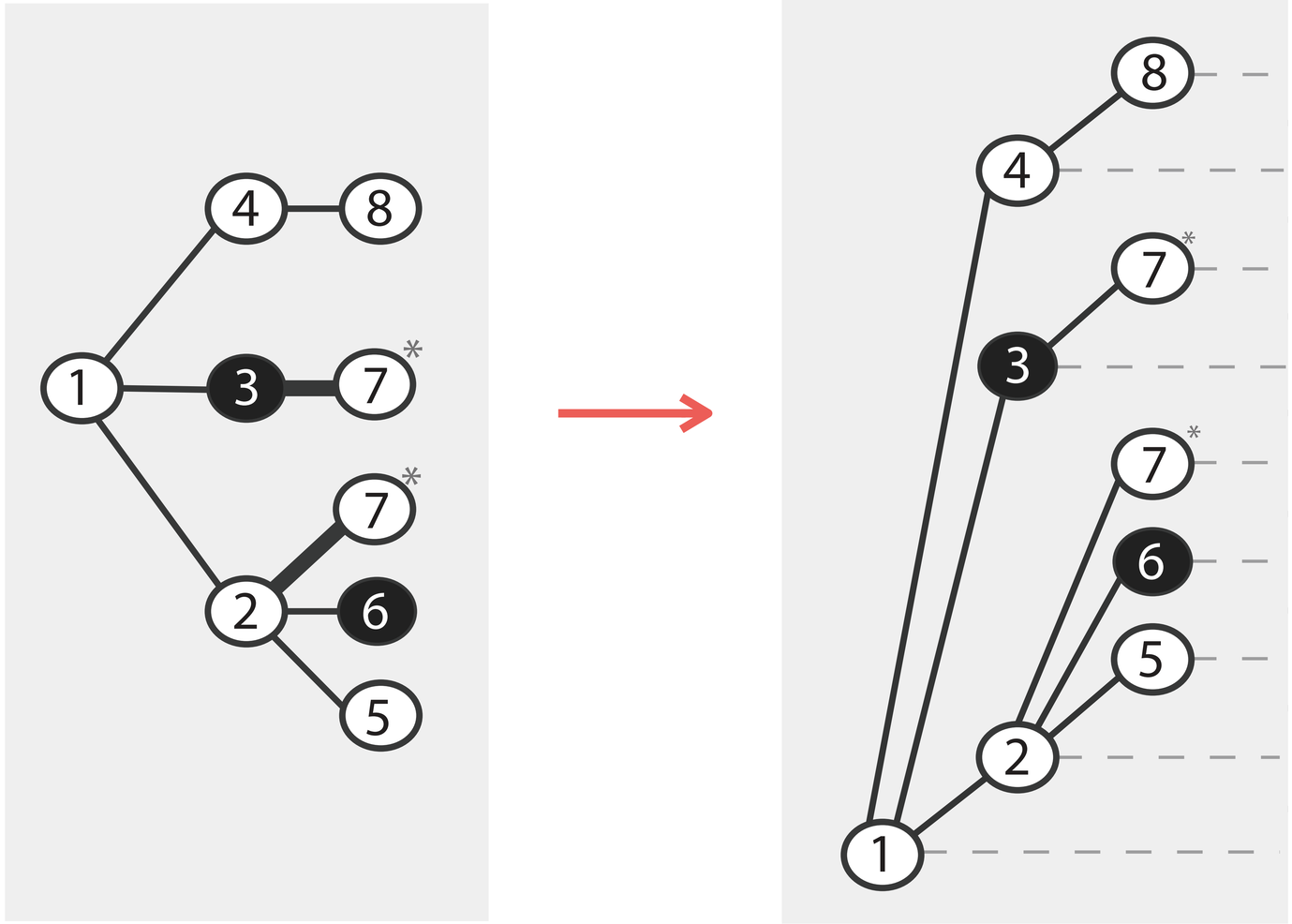
De-Cycling



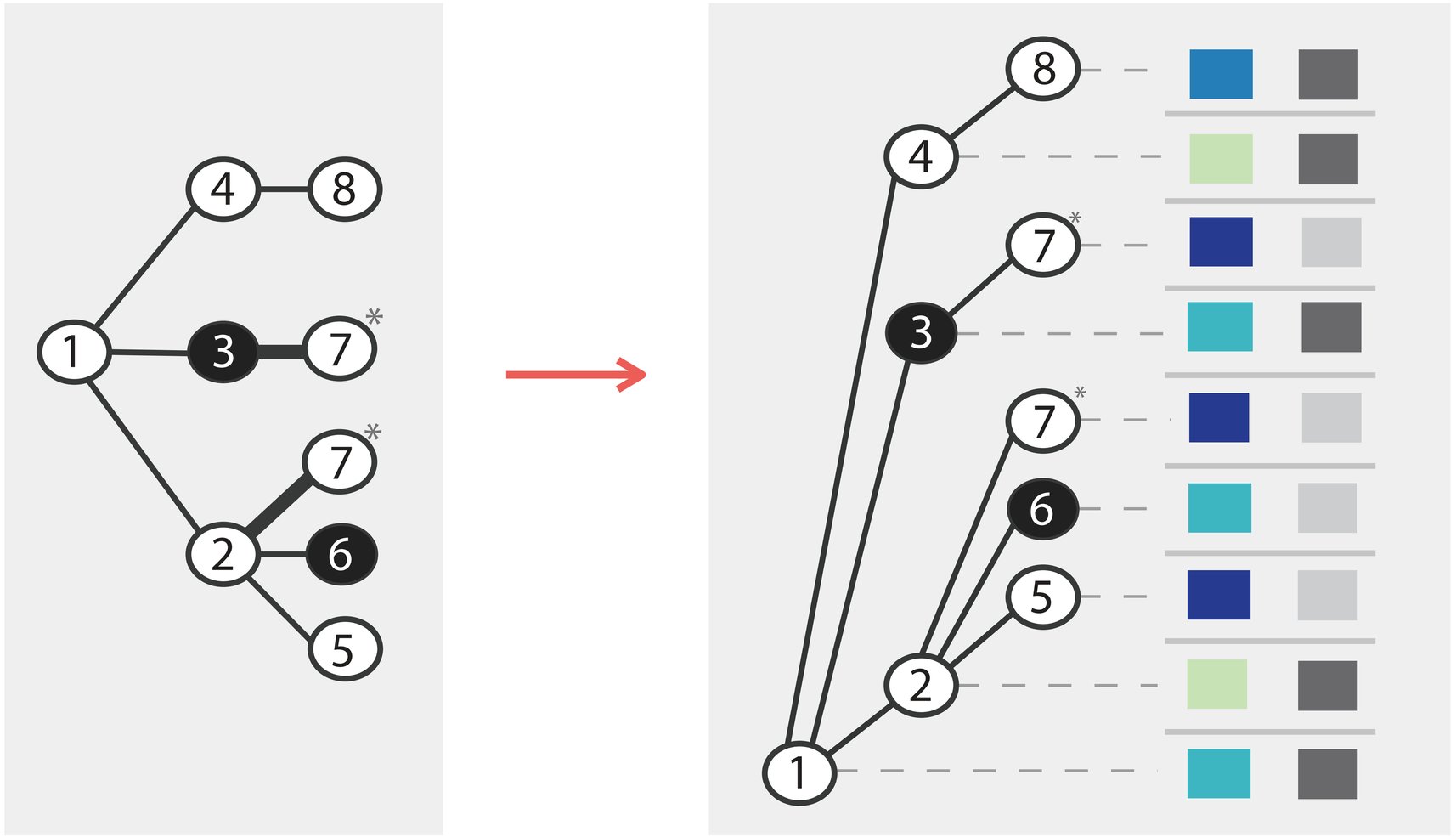
De-Cycling

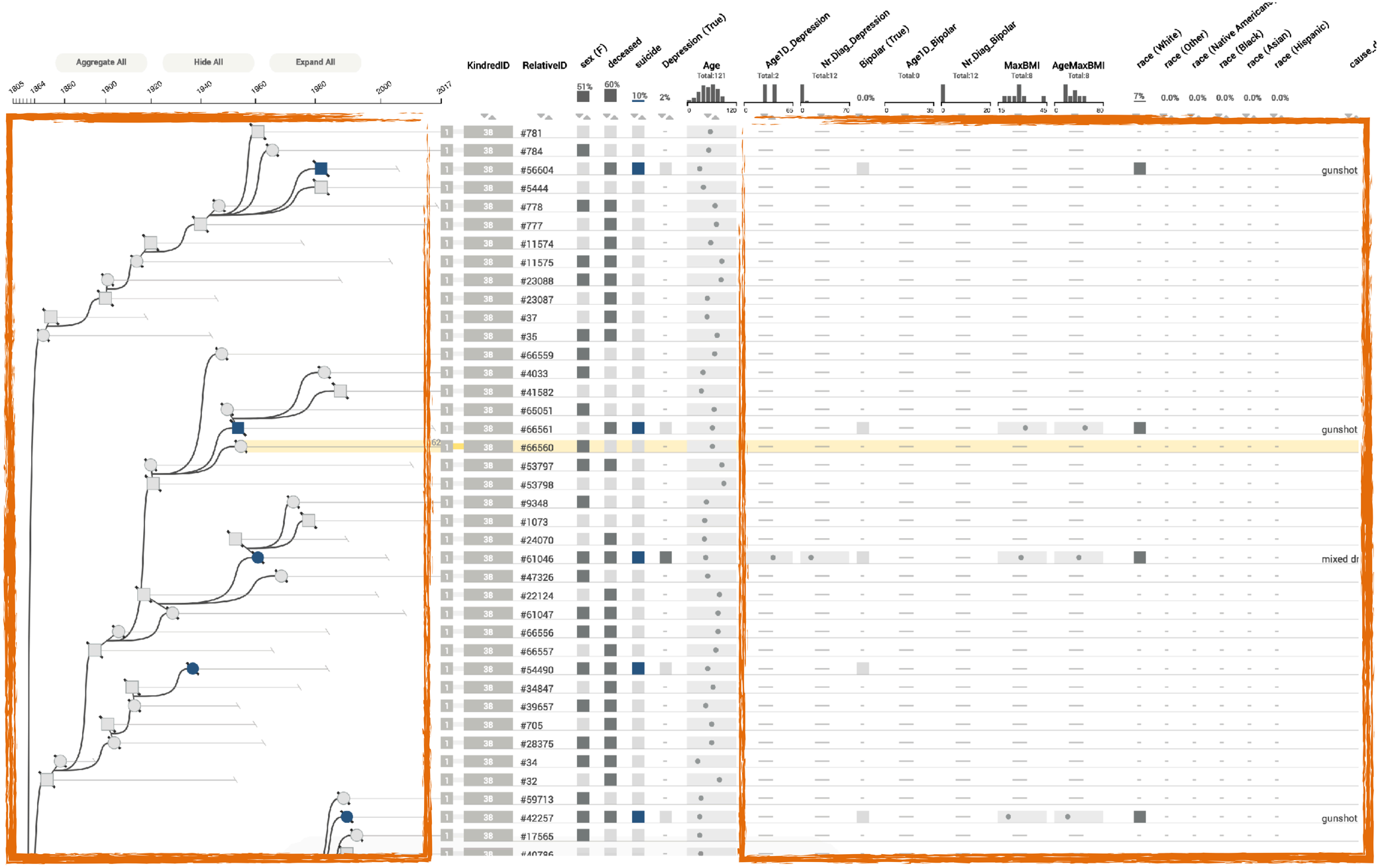


Linearization



Linearization

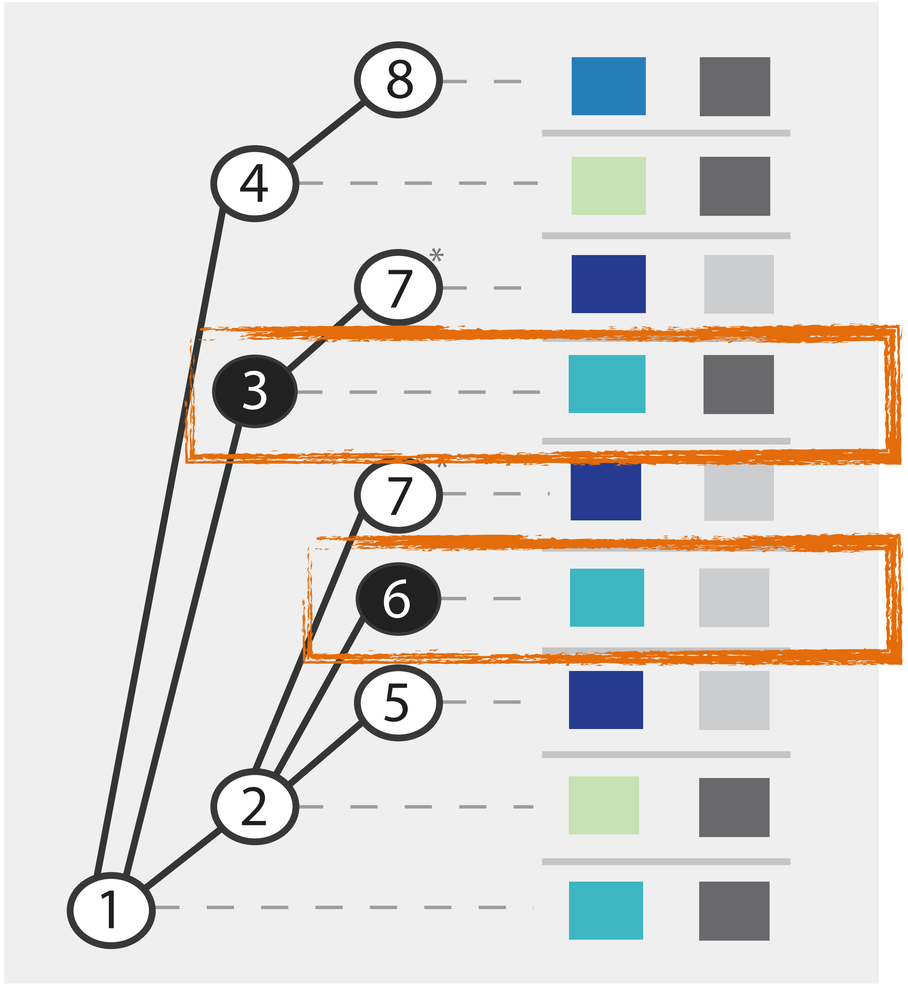




Can’t show many people

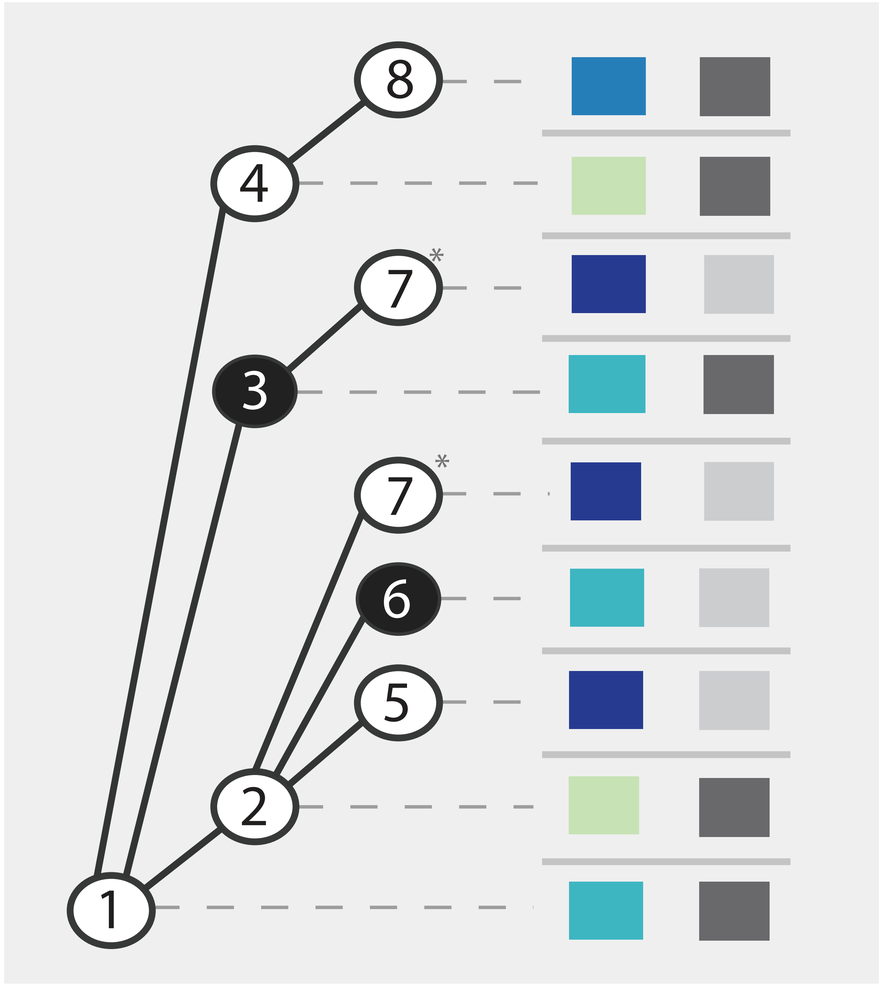
Lots of missing data

Aggregation

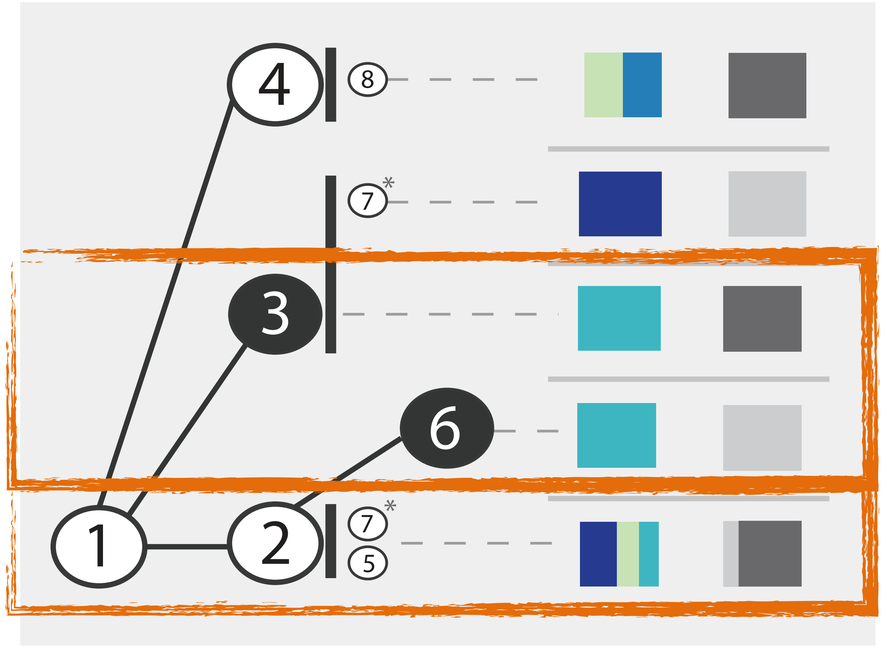


People of Interest

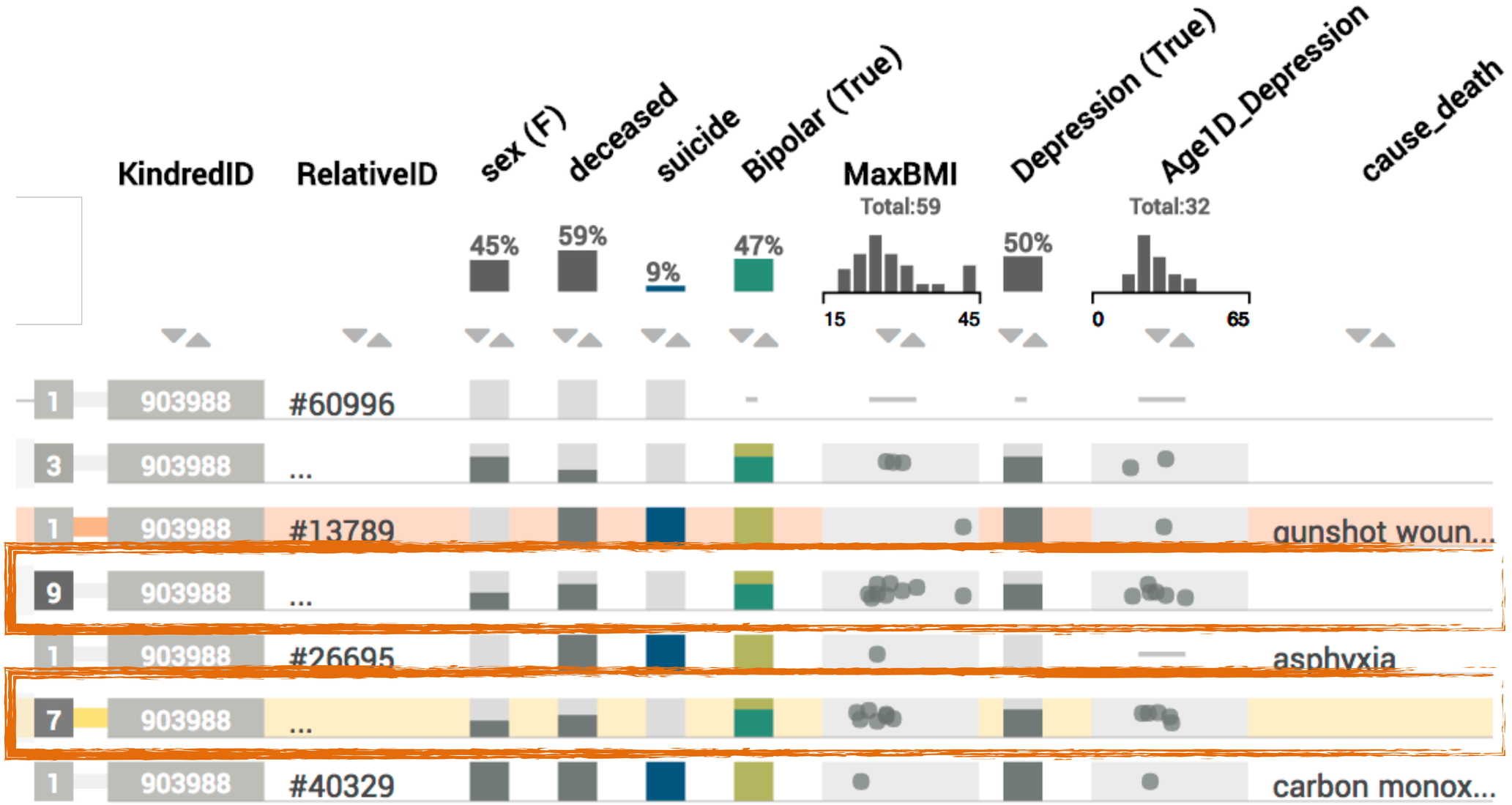
Aggregation



One row for every person of interest

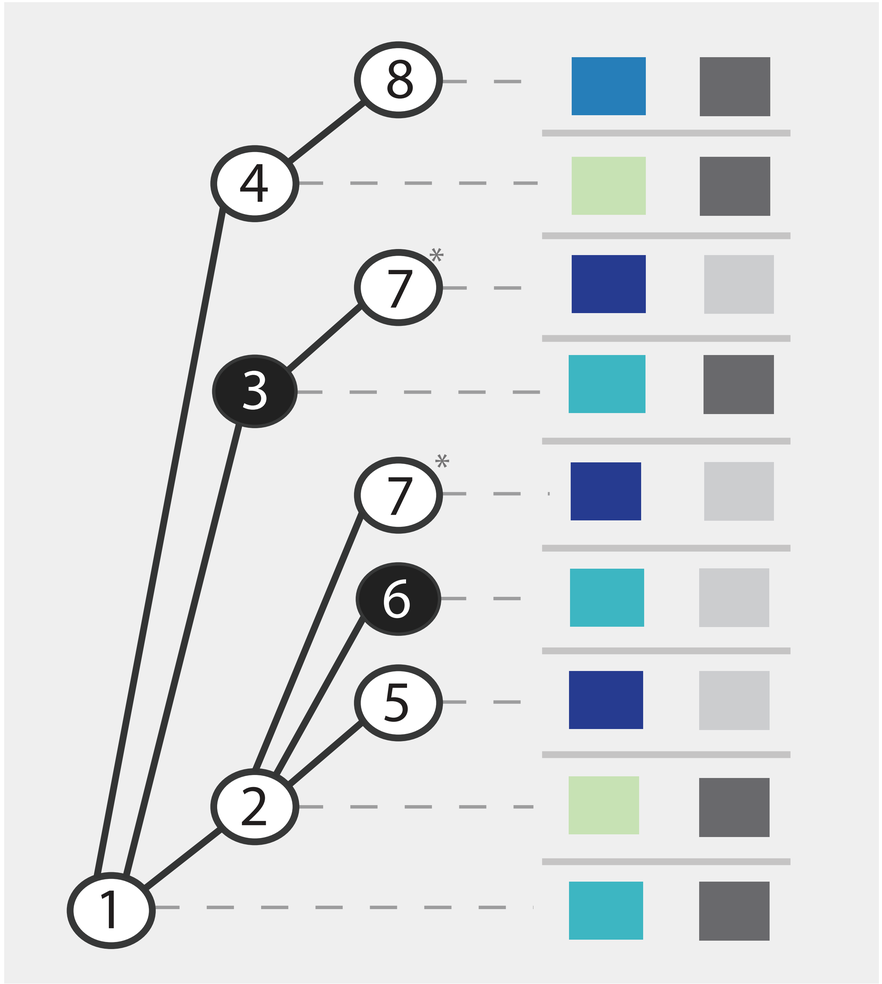


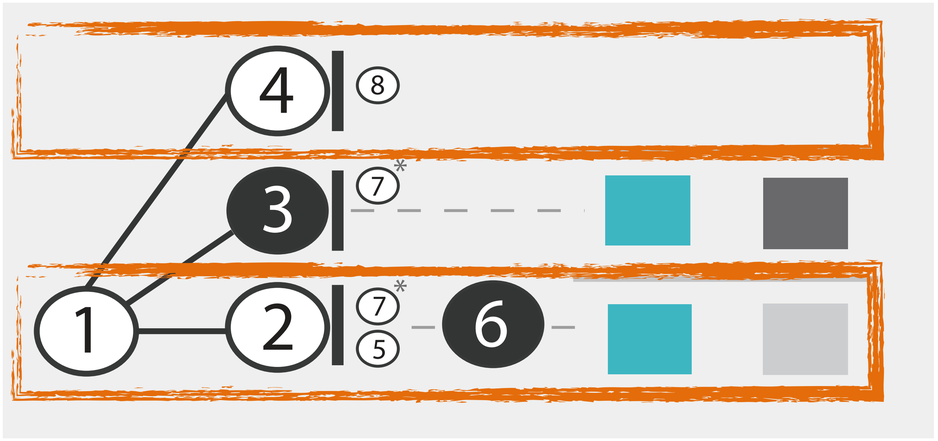
Others have to share a row



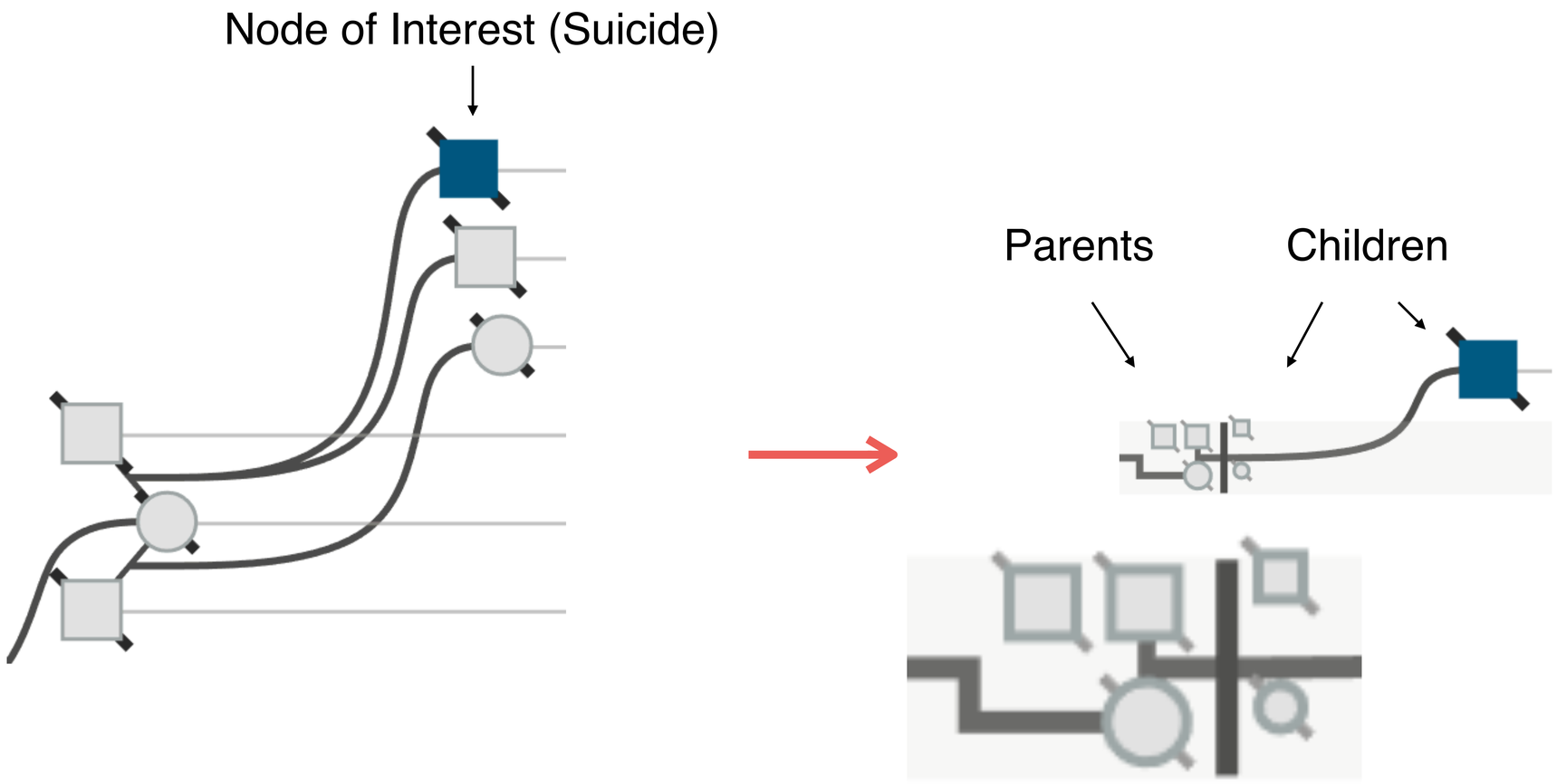
Aggregated Rows

More Aggressive: Hiding



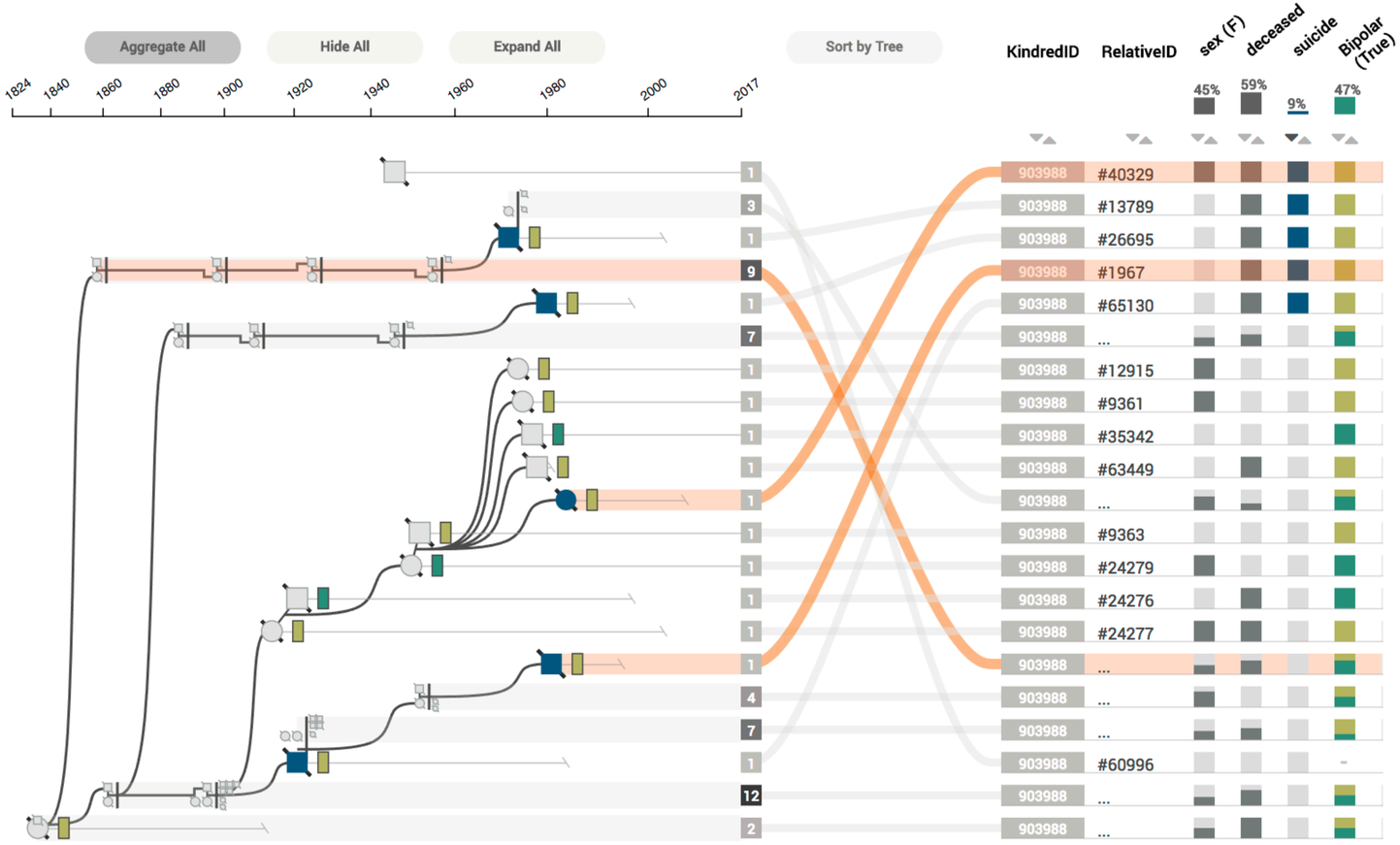


Implict Encoding of Family

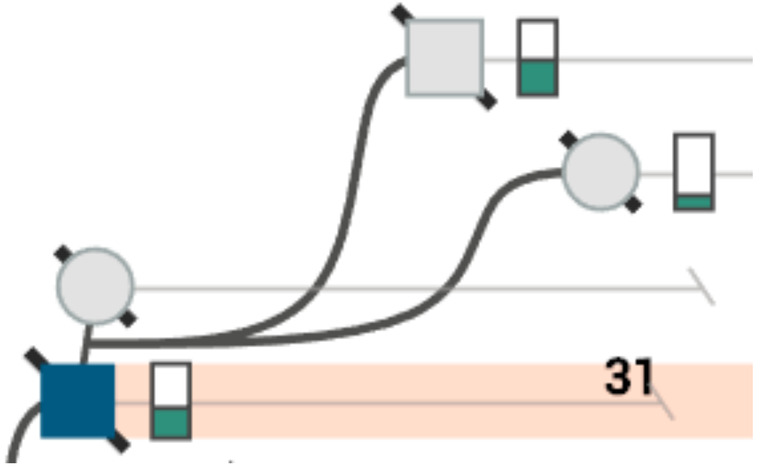


Find all people with a certain attribute

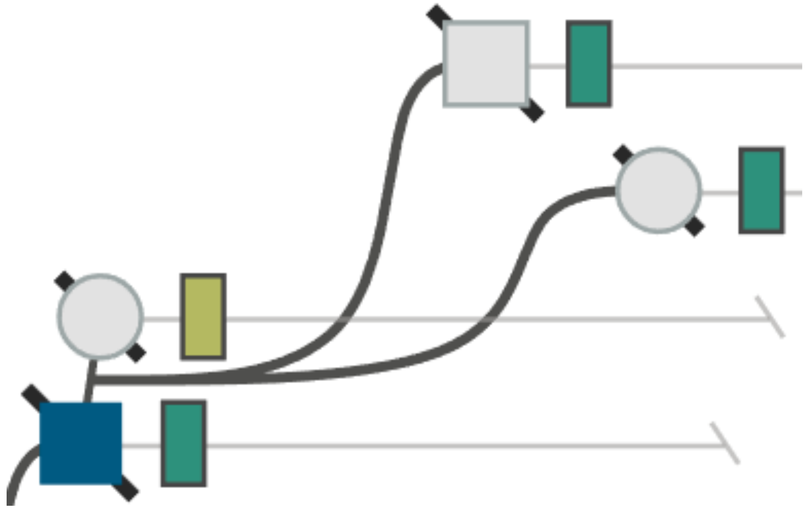
Sorting!



Node Attributes

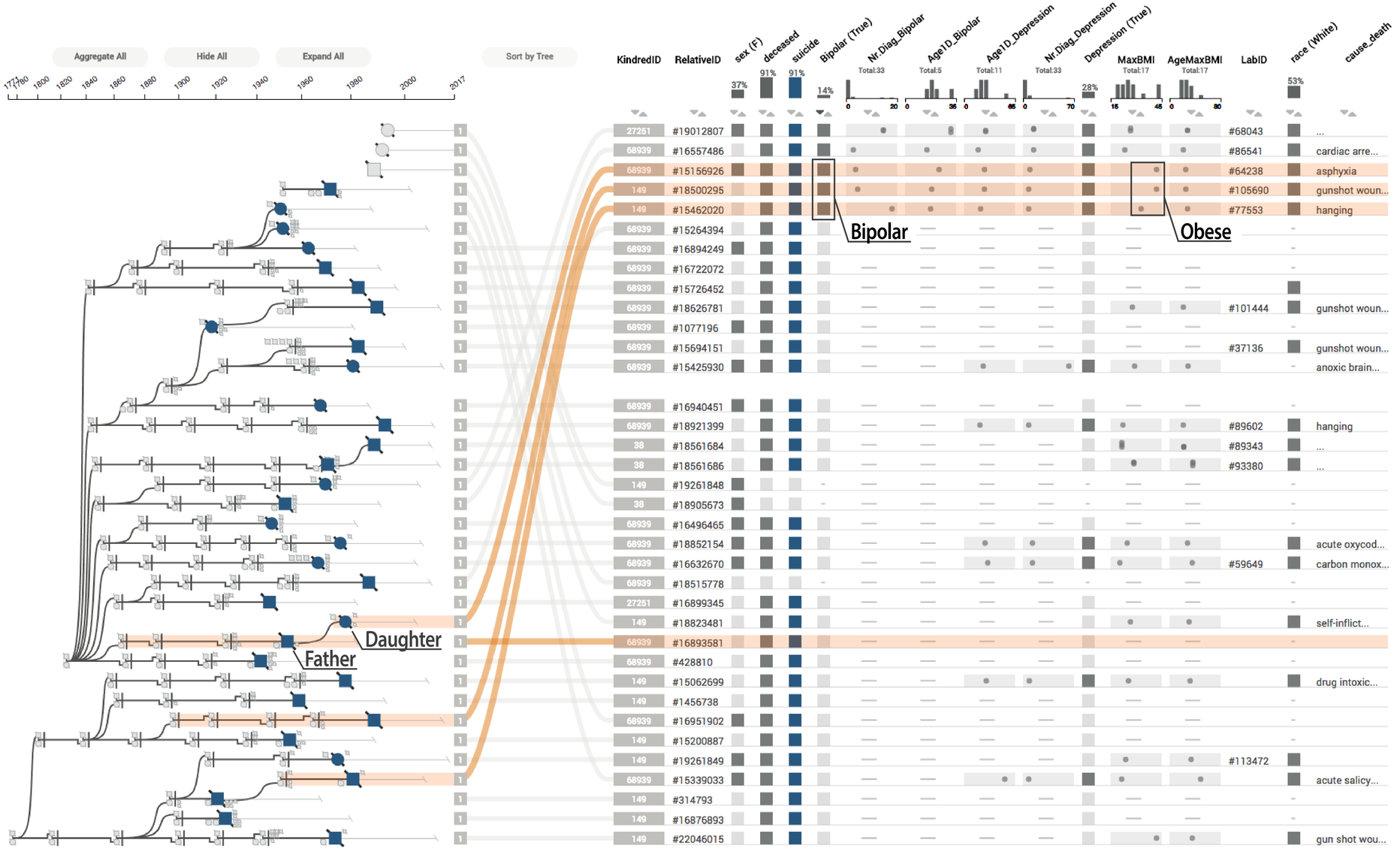


Numerical (Age)



Categorical (Depression)

Example


Aggregate All
Hide All
Expand All
Sort by Tree
1774
1780
1800
1820
1840
1860
1880
1900
1920
1940
1960
1980
2000
2017
Daughter
Father
KindredID
RelativeID
sex (F)
deceased
suicide
Bipolar (True)
Nr.Diag_Bipolar
Age1D_Bipolar
Age1D_Depression
Nr.Diag_Depression
Depression (True)
MaxBMI
AgeMaxBMI
LabID
race (White)
cause_death
37%
91%
91%
14%
Total:33
Total:5
Total:11
Total:33
28%
Total:17
Total:17
53%
Bipolar
Obese
27251 #19012807 #68043 ...
68939 #16557486 #86541 cardiac arre...
68939 #15156926 #64238 asphyxia
149 #18500295 #105690 gunshot woun...
149 #15462020 #77553 hanging
68939 #15264394
68939 #16894249
68939 #16722072
68939 #15726452
68939 #18626781 #101444 gunshot woun...
68939 #1077196
68939 #15694151 #37136 gunshot woun...
68939 #15425930 anoxic brain...
68939 #16940451
68939 #18921399 #89602 hanging
38 #18561684 #89343 ...
38 #18561686 #93380 ...
149 #19261848
38 #18905673
68939 #16496465
68939 #18852154 acute oxycod...
68939 #16632670 #59649 carbon monox...
68939 #18515778
27251 #16899345
149 #18823481 self-inflict...
68939 #16893581
68939 #428810
149 #15062699 drug intoxic...
149 #1456738
68939 #16951902
149 #15200887
149 #19261849 #113472
68939 #15339033 acute salicy...
149 #314793
149 #16876893
149 #22046015 gun shot wou...

Next Steps

Improve multi-family exploration

Find phenotype patterns across families

Add genetic data

Extend to other datasets
phylogenies, …

http://lineage.caleydoapp.org

Pathfinder: Visual Analysis of Paths in Graphs

[EuroVis '16]
Honorable Mention Award


Christian Partl


Samuel Gratzl

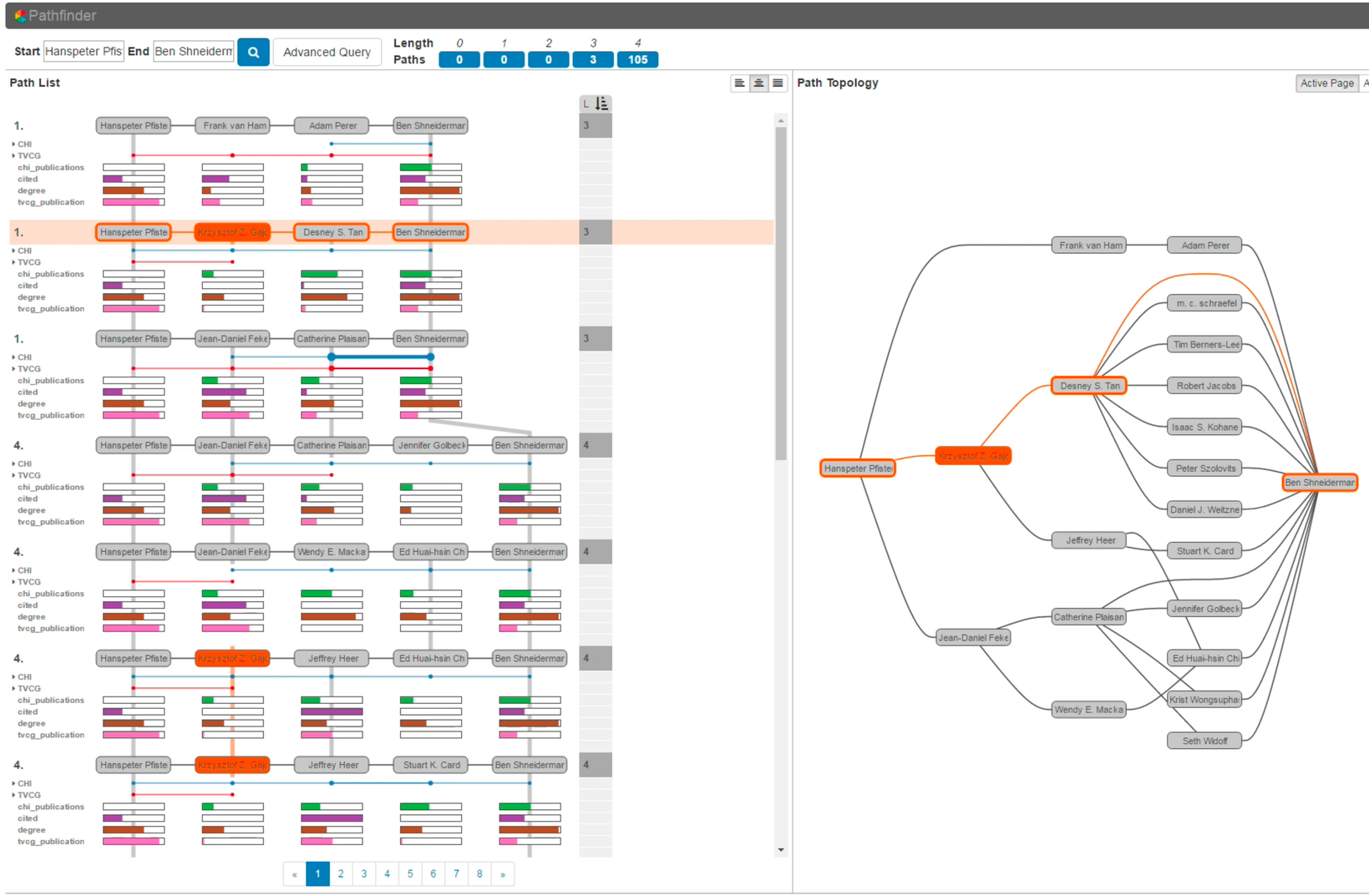

Marc Streit

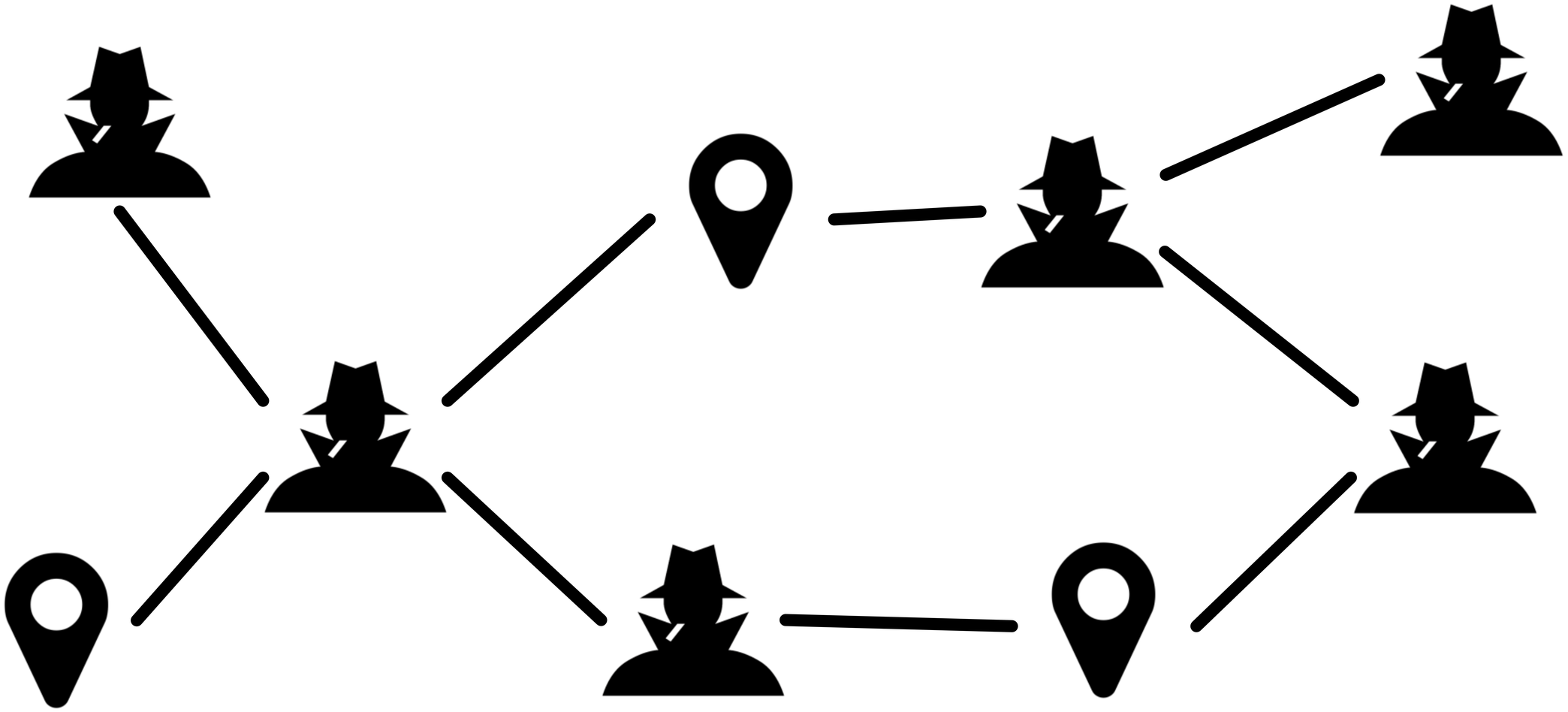

Anne Mai Wasserman


H. Pfister

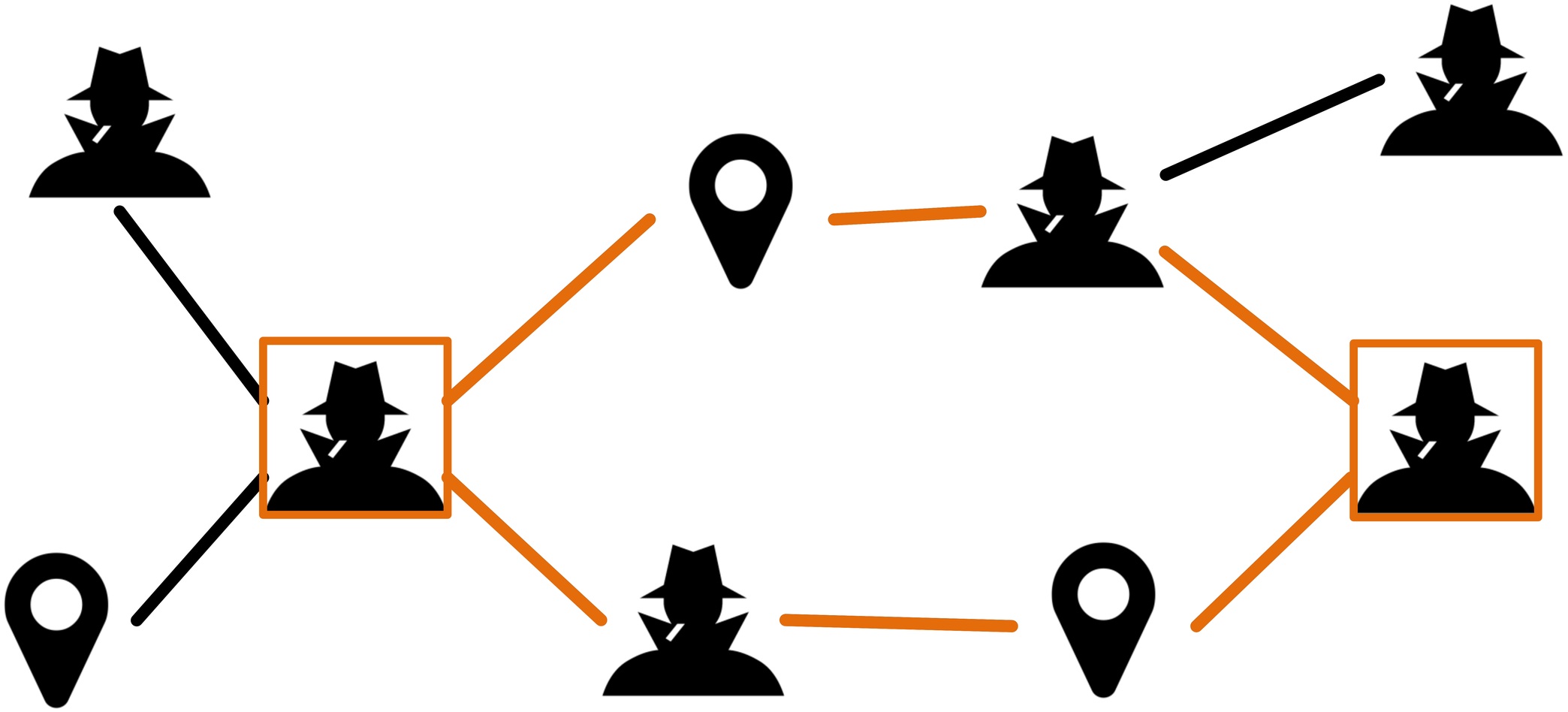

D. Schmalstieg


Alexander Lex

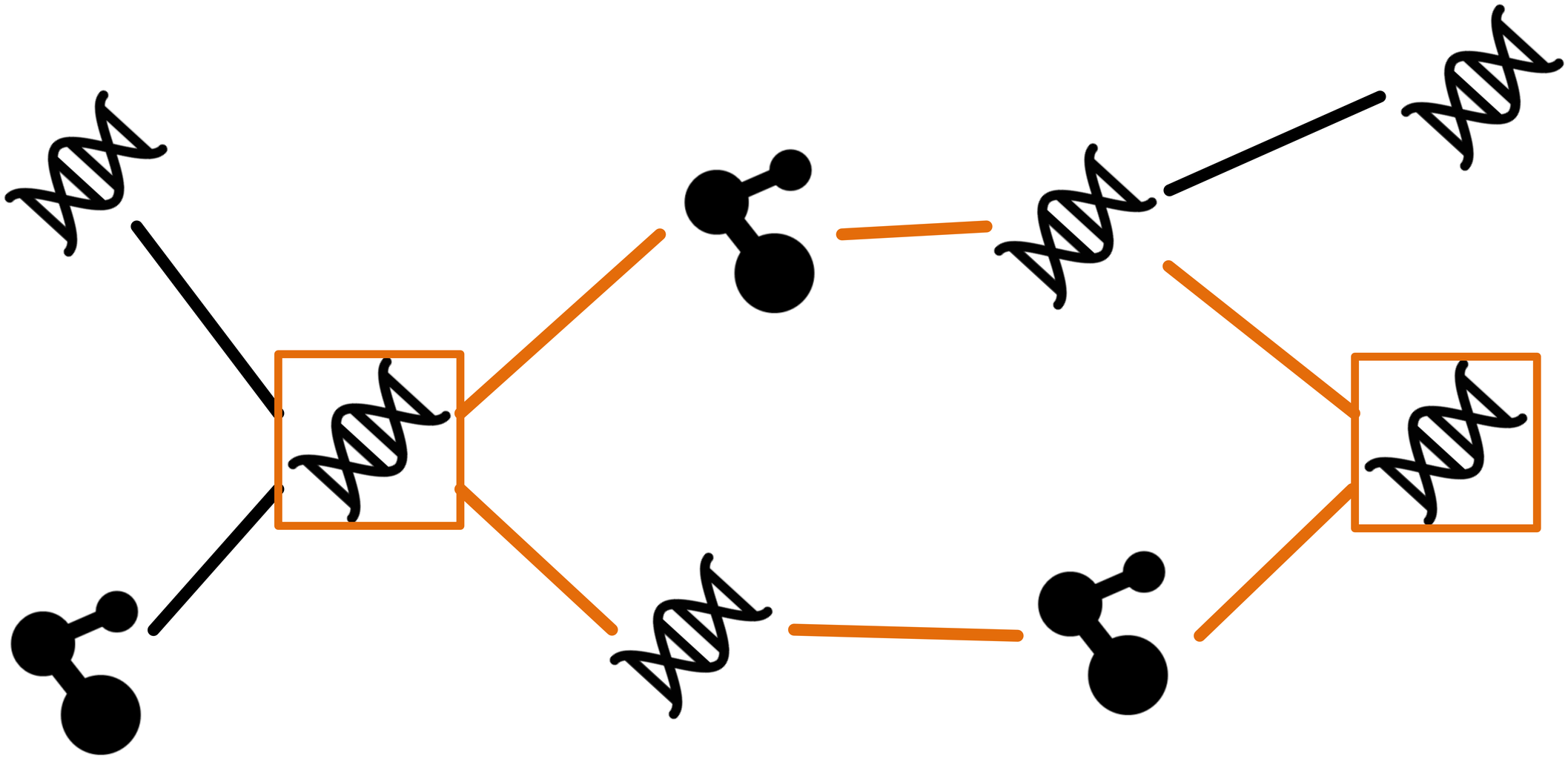




Intelligence Data: How are two suspects connected?



Intelligence Data: How are two suspects connected?



Biological Network: How do two genes interact?

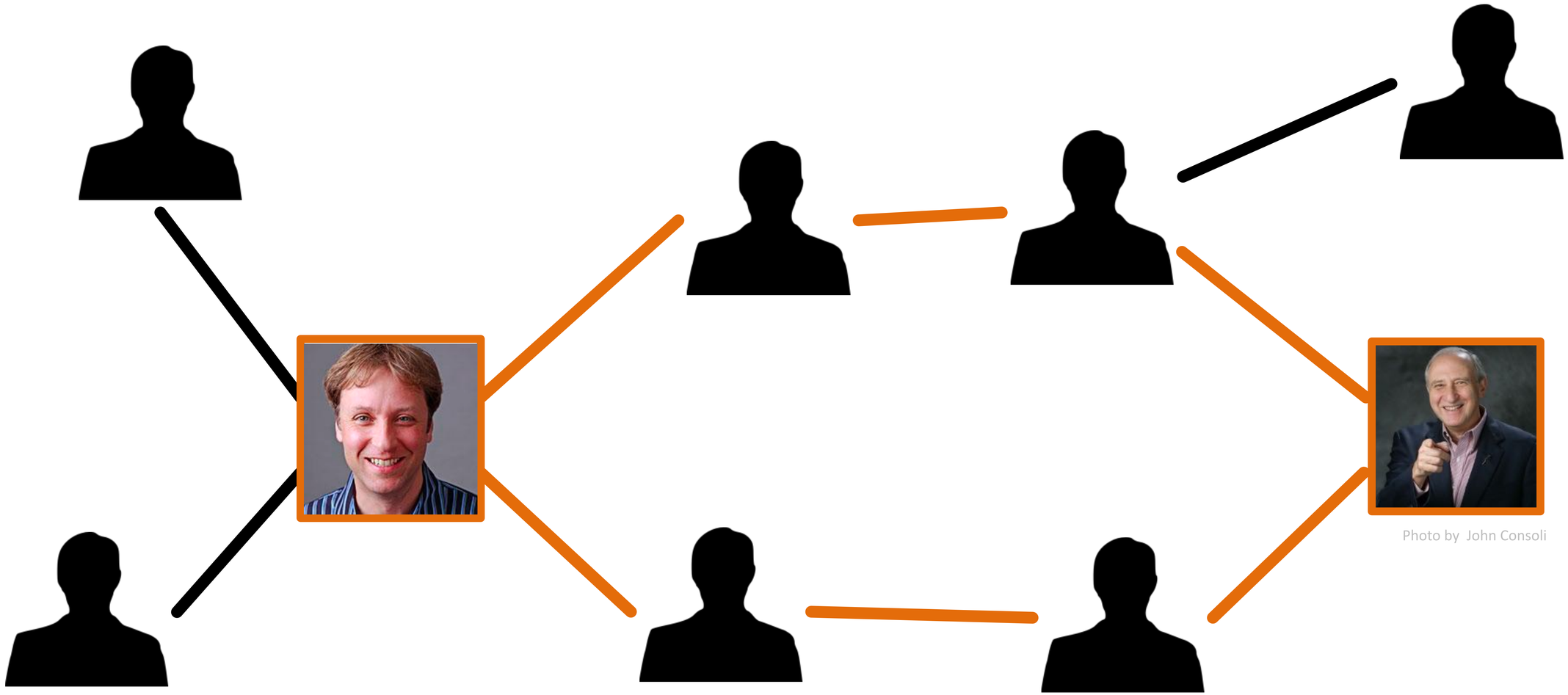


Photo by John Consoli

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

Challenge: Graph Size

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

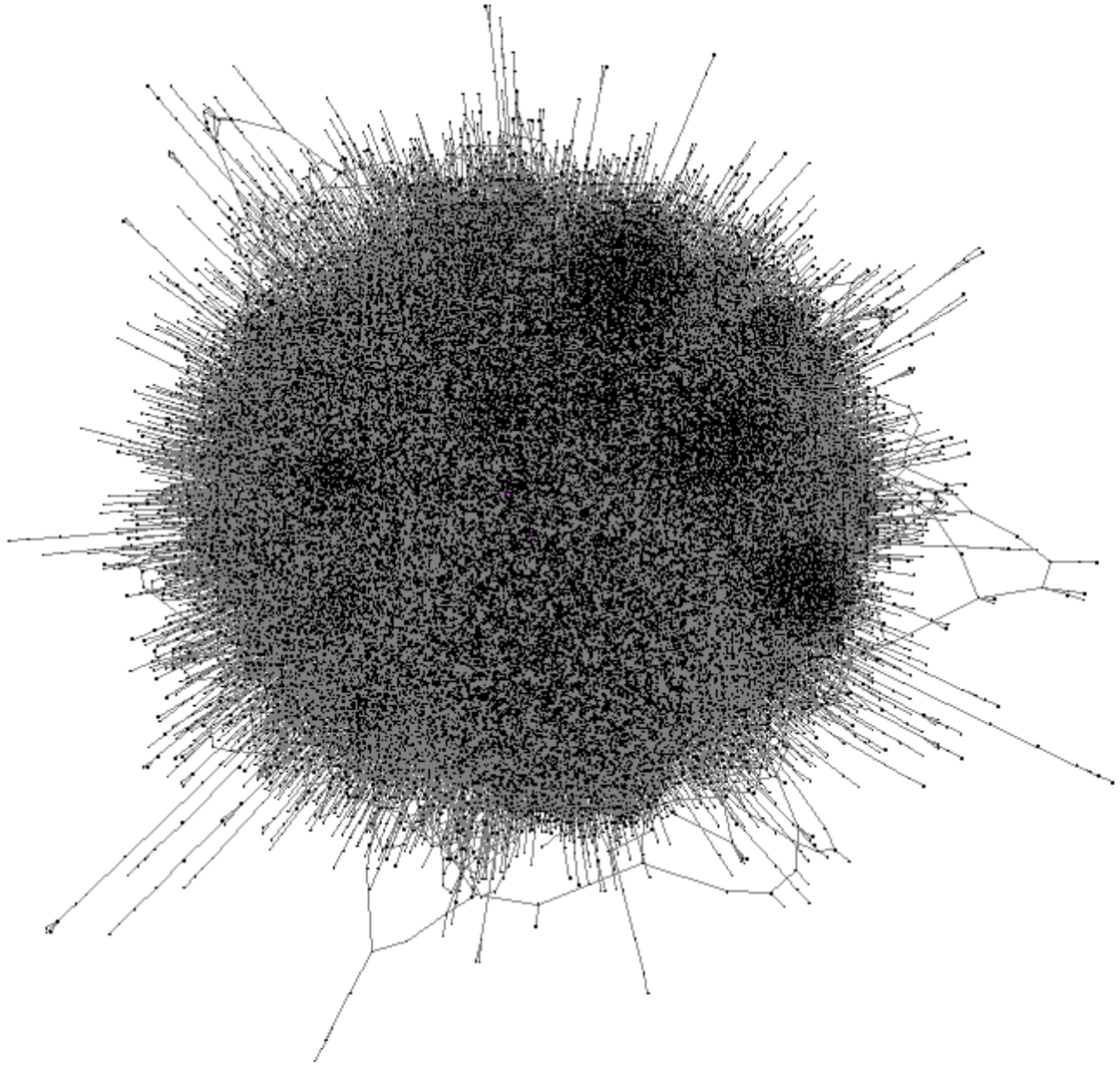
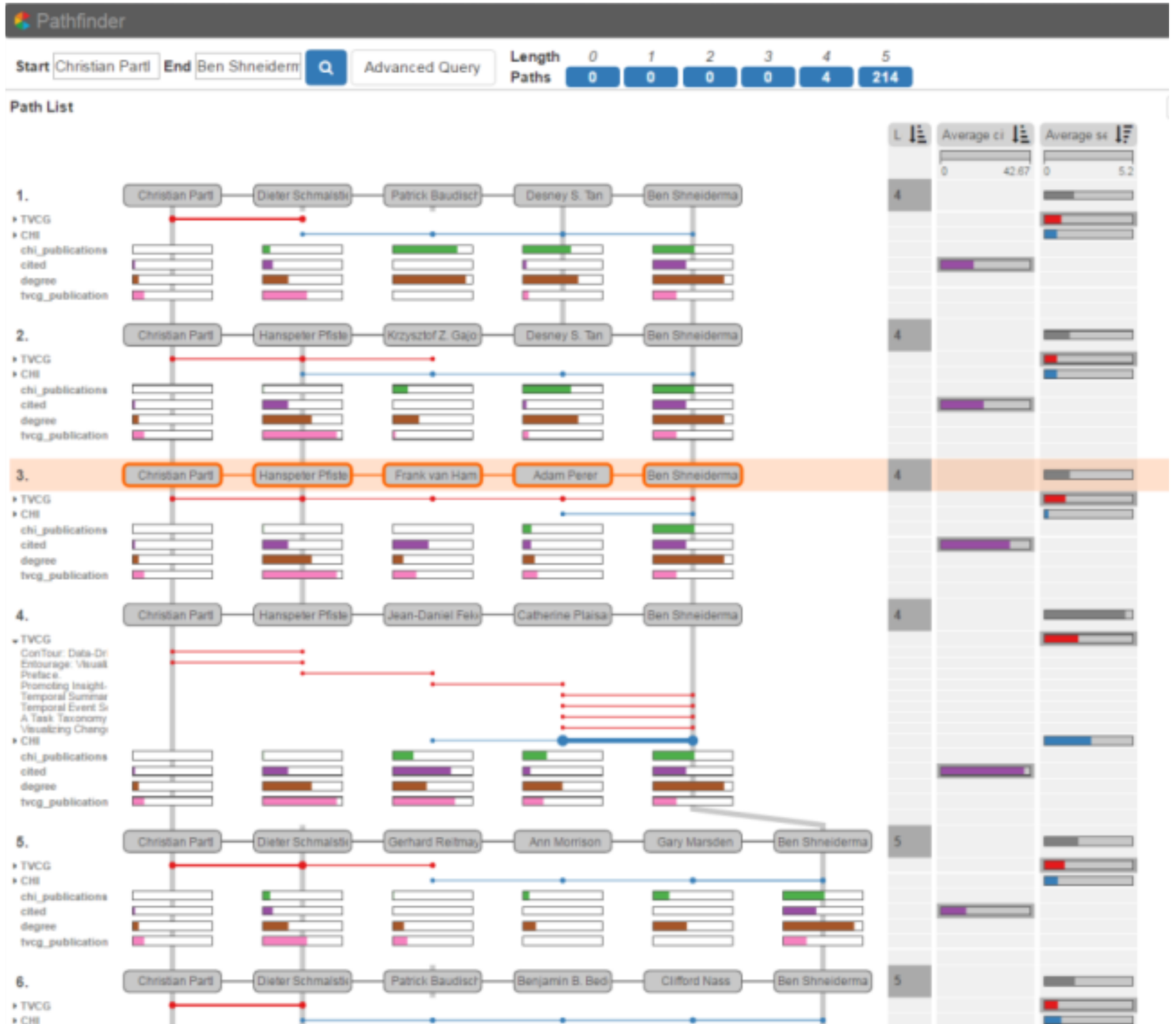


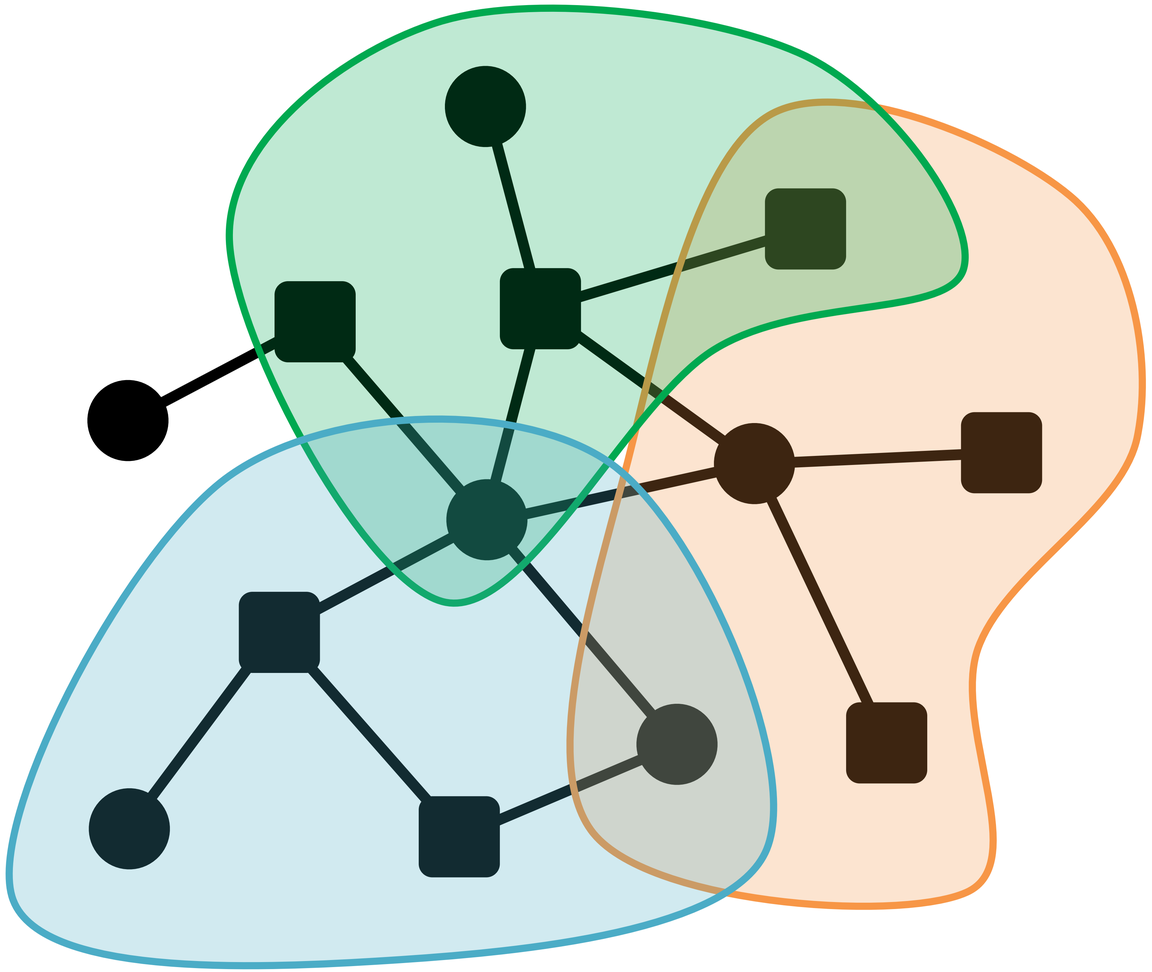
Image Source:
http://www.thenetworkthinkers.com/2013/03/big-data.html

Approach: (Path) Queries



The Data

Network Data



Nodes

Edges

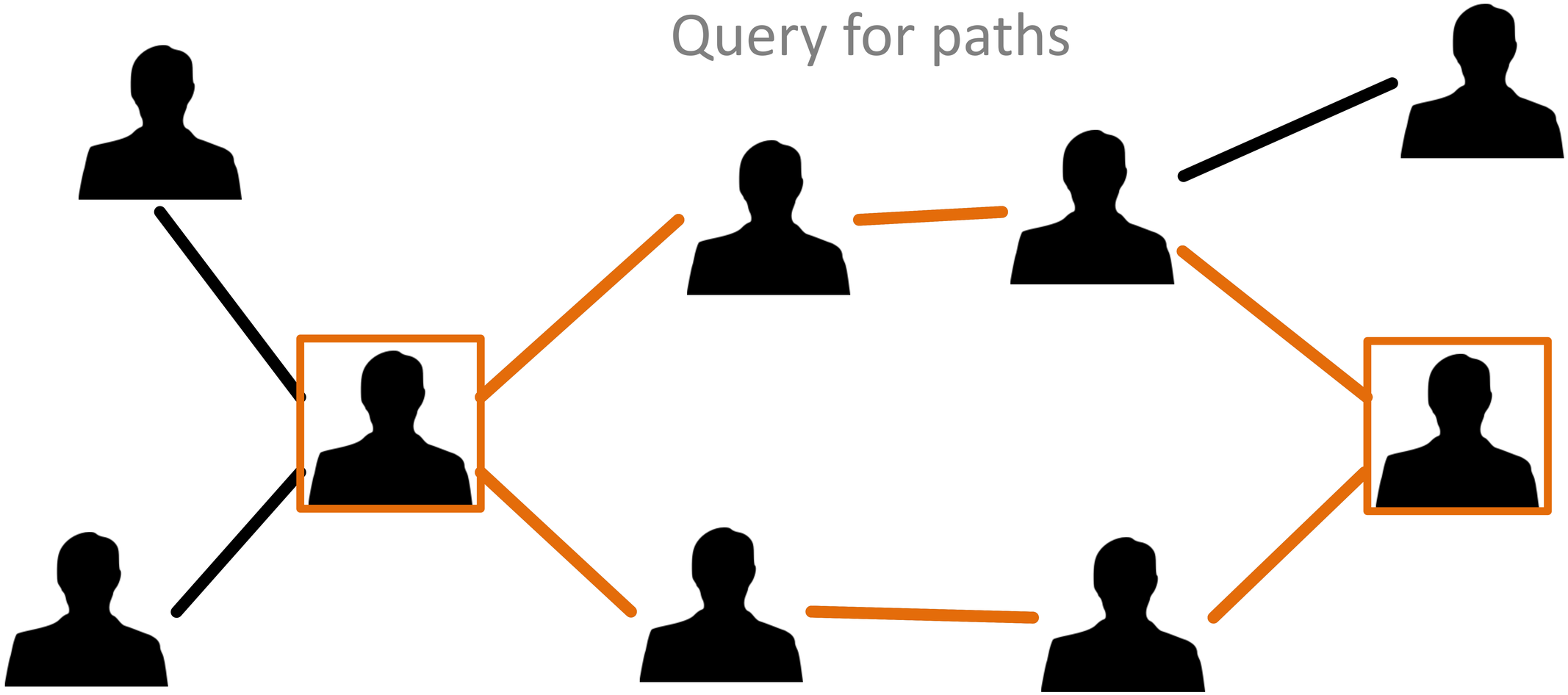
Attributes

Sets

The Approach

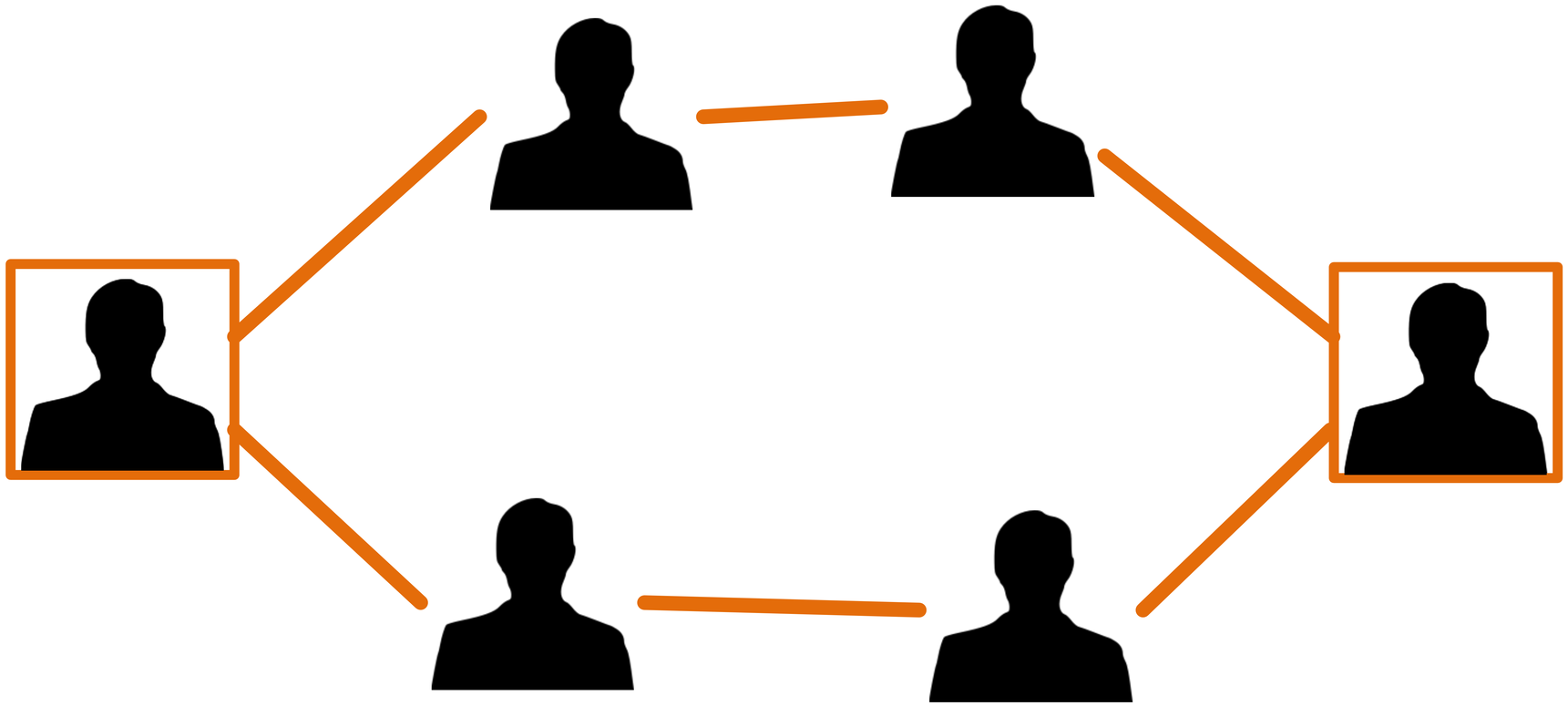
Pathfinder Approach

Query for paths



Pathfinder Approach

Shows node-edge diagram...

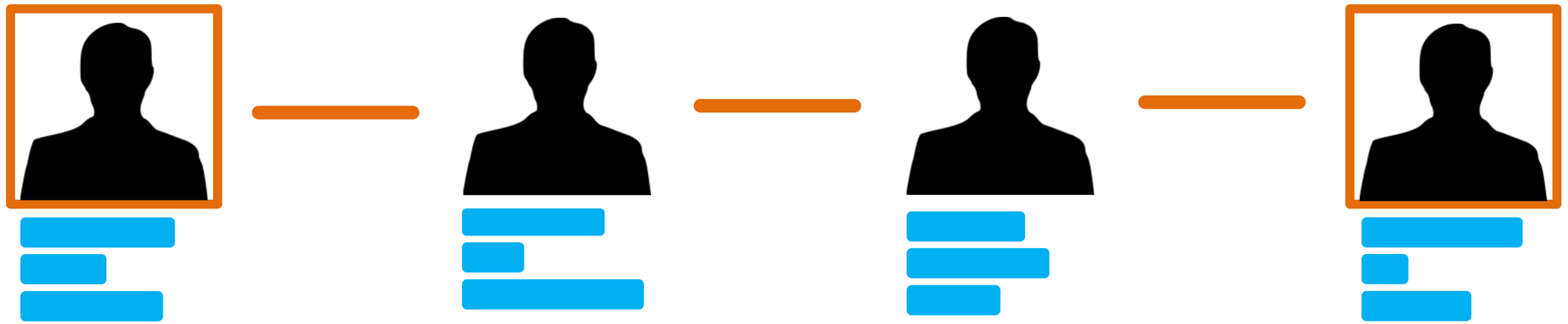


Pathfinder Approach

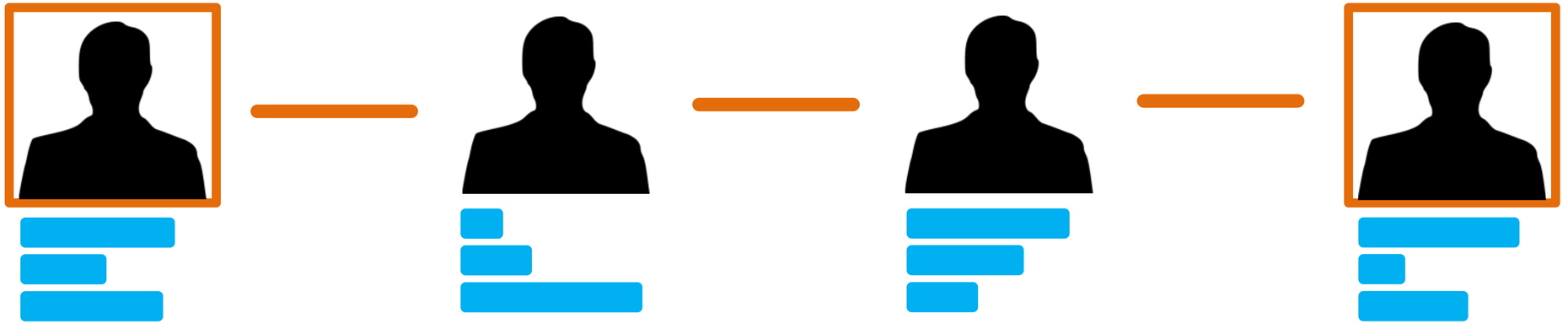
Update ranking to identify important paths

Path Score

1.

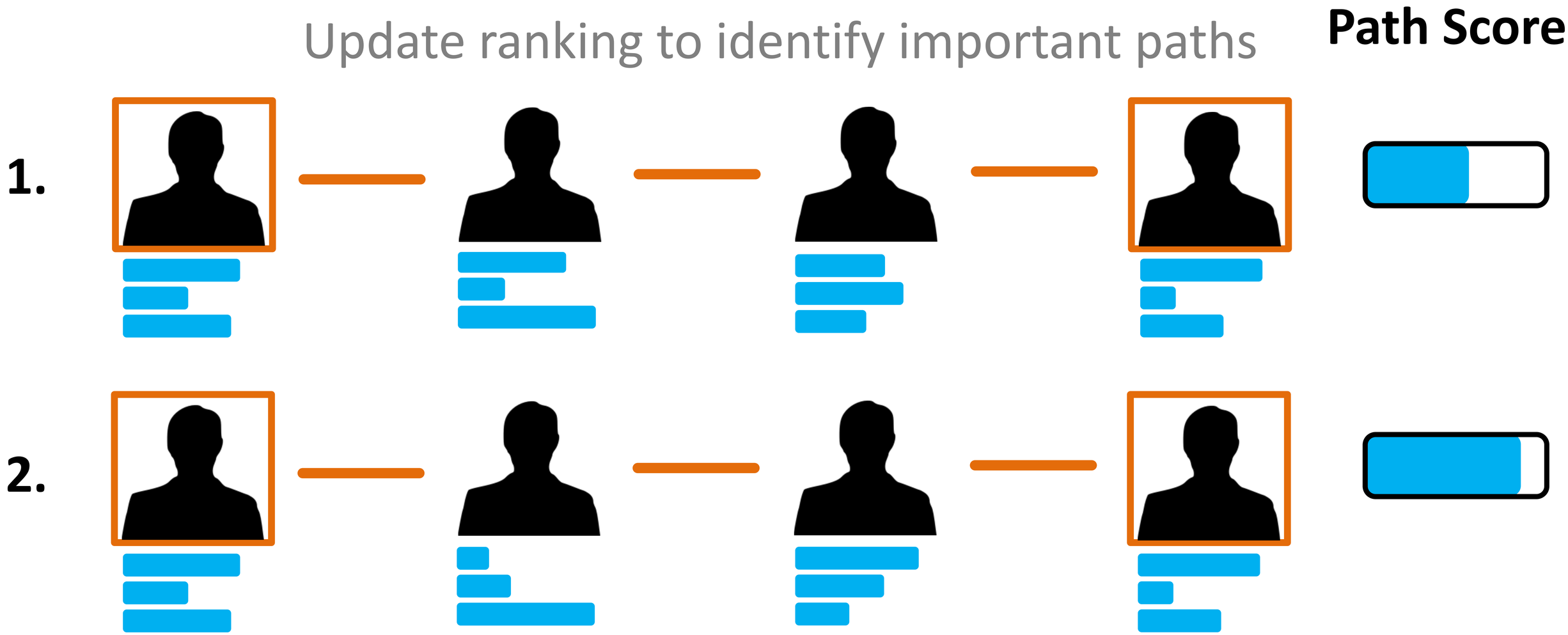


2.

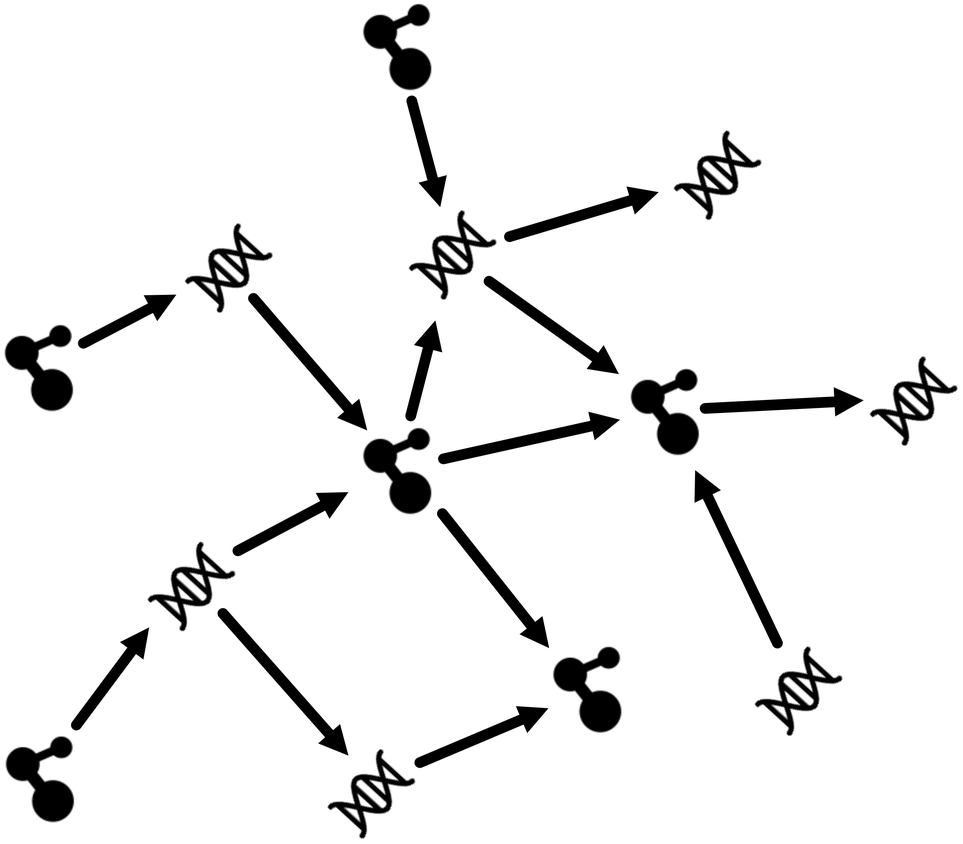


Pathfinder Approach

Update ranking to identify important paths

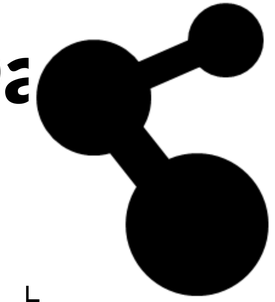


Biological Network



Generated from KEGG Pathway Data

Gene



Compound

11k Nodes, 71k Edges

Attributes

Gene Expression Data

Copy Number Data

Attributes

-

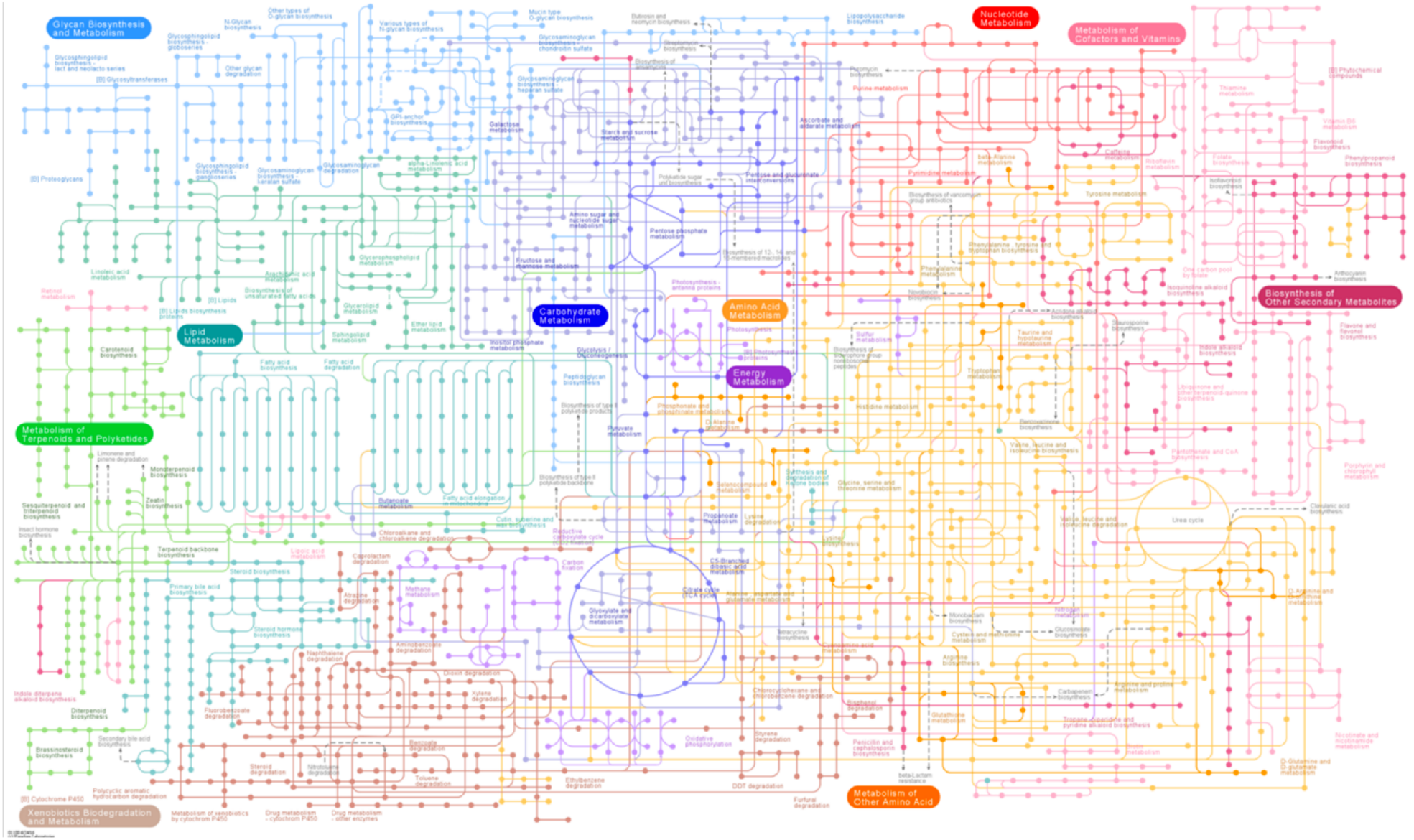
Sets

Biological Pathways

Sets

Biological Pathways

Example: KEGG Metabolism Overview



Analysis Questions

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

What are alternative routes from 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

Pathfinder

Start Hanspeter Pfis End Ben Shneiderm Advanced Query

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

Path List

1. Hanspeter Pfiste Frank van Ham 3
CHI
TVCG
chi_publications
cited
degree
tvcg_publication

1. Hanspeter Pfiste Krzysztof Z. Gajc Desney S. Tan Ben Shneidermar 3
CHI
TVCG
chi_publications
cited
degree
tvcg_publication

1. Hanspeter Pfiste Jean-Daniel Feke Catherine Plaisan Ben Shneidermar 3
CHI
TVCG
chi_publications
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tvcg_publication

4. Hanspeter Pfiste Jean-Daniel Feke Catherine Plaisan Jennifer Golbeck Ben Shneidermar 4
CHI
TVCG
chi_publications
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degree
tvcg_publication

4. Hanspeter Pfiste Jean-Daniel Feke Wendy E. Macka Ed Huai-hsin Ch Ben Shneidermar 4
CHI
TVCG
chi_publications
cited
degree
tvcg_publication

4. Hanspeter Pfiste Krzysztof Z. Gajc Jeffrey Heer Ed Huai-hsin Ch Ben Shneidermar 4
CHI
TVCG
chi_publications
cited
degree
tvcg_publication

4. Hanspeter Pfiste Krzysztof Z. Gajc Jeffrey Heer Stuart K. Card Ben Shneidermar 4
CHI
TVCG
chi_publications
cited
degree
tvcg_publication

« 1 2 3 4 5 6 7 8 »

Path Topology

Frank van Ham
Adam Perer
m. c. schraefel
Tim Berners-Lee
Desney S. Tan
Robert Jacobs
Isaac S. Kohane
Hanspeter Pfiste
Krzysztof Z. Gajc
Peter Szolovits
Ben Shneidermar
Daniel J. Weitzne
Jeffrey Heer
Stuart K. Card
Jennifer Golbeck
Catherine Plaisan
Jean-Daniel Feke
Ed Huai-hsin Chi
Krist Wongsupha
Wendy E. Macka
Seth Widoff

Path Statistics

Paths 108/108
Edges 196/196
Nodes 95/95 0 108

Author (95/95)
Ben Shneidermar
Hanspeter Pfister
Jean-Daniel Feke
Catherine Plaisar
Krzysztof Z. Gajo
Desney S. Tan
Krzysztof Gajos
Paul André
Adam Perer
Jacob O. Wobbro
Frank van Ham
Wendy E. Macka
Jeffrey Nichols
Juho Kim
Brad A. Myers
Sarita Yardi
Ed Huai-hsin Chi
Nam Wook Kim
Torsten Möller
m. c. schraefel
Erin Treacy Solov
Alan Borning

Sets 137/843 0 108

CHI (107/667)
Interacting with e
A Crowdsourced
Excentric Labelin
Predictability and
LifeFlow: visualizi
LifeFlow: visualizi
Aligning temporal
The challenges o
LifeLines: Visuali
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Scheduling on-of
Integrating statist
Touchstone: expl
Cobi: communitys
From slacktivism t
Demonstrational i
Improving the per
Frenzy: collabora
The many faces

TVCG (30/176)
Preface.
Promoting Insight
Evaluation of File
Temporal Summa
Temporal Event S
Visualizing Chang
A Task Taxonomy
Evaluation of Arte
Balancing Systen
"Search, Show C
Empirical Studies
Video Snapshots
MizBee: A Multisc
MulteeSum: A To
Overview Use in
Melange: Space
A Principled Way
What Makes a Vis
FacetMap: A Sca
SoccerStories: A
ConTour: Data-Dr
Entourage: Visua

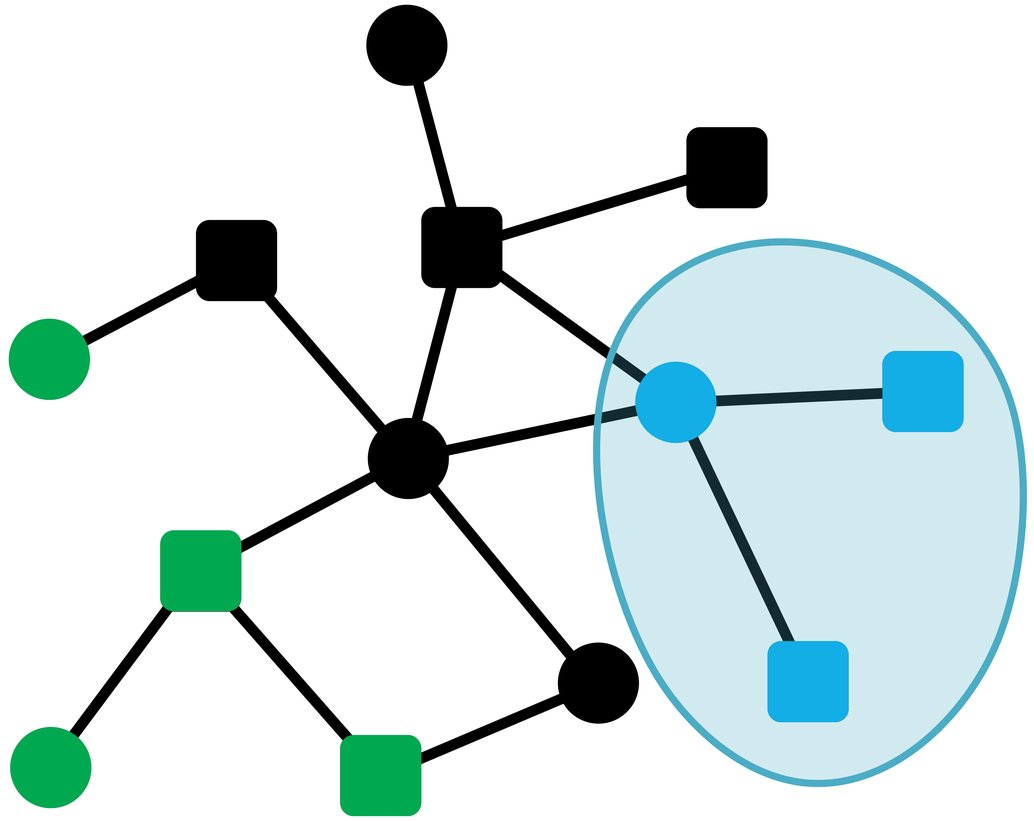
Path Query and Search

Query and Search

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

Start/end can be node lists

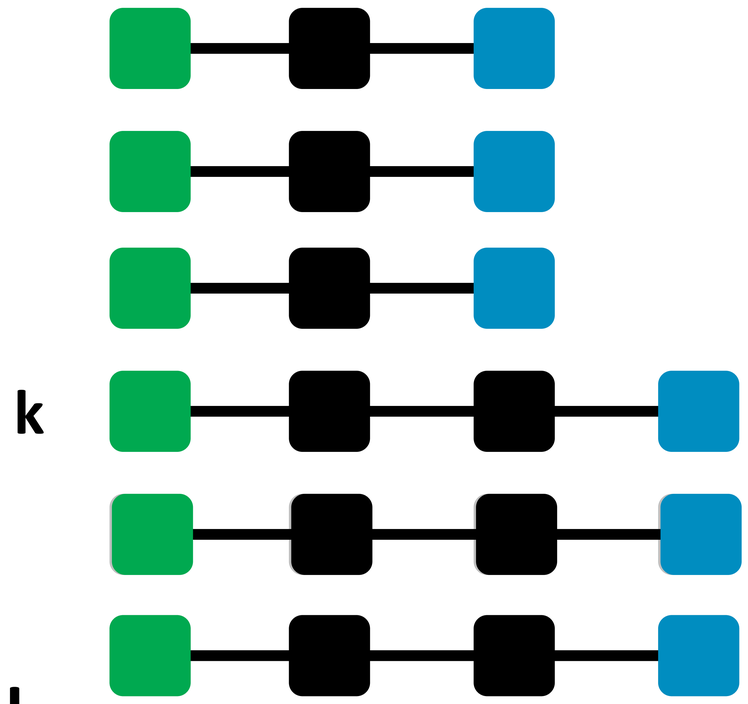
Start/end can be defined through set membership



Query and Search

Specify start and end

K-shortest path search



Continue until all path of length of k-th path are found

Pathfinder

Start End Advanced Query Length Paths

Path Statistics

Path List

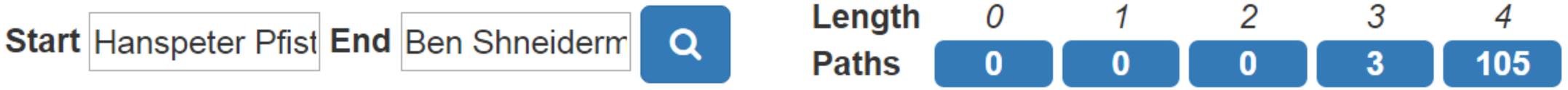
Path Topology Active Page All

Query Interface

« »

Query Interface

Simple



Advanced

Pathfinder

Start Hanspeter Pfis End Ben Shneiderm Advanced Query

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

Path List

1. Hanspeter Pfiste → Frank van Ham → Adam Perer → Ben Shneidermar (3)
1. Hanspeter Pfiste → Krzysztof Z. Gajc → Desney S. Tan → Ben Shneidermar (3)
1. Hanspeter Pfiste → Jean-Daniel Feke → Catherine Plaisan → Ben Shneidermar (3)
4. Hanspeter Pfiste → Jean-Daniel Feke → Catherine Plaisan → Jennifer Golbeck → Ben Shneidermar (4)
4. Hanspeter Pfiste → Jean-Daniel Feke → Wendy E. Macka → Ed Huai-hsin Ch → Ben Shneidermar (4)
4. Hanspeter Pfiste → Krzysztof Z. Gajc → Jeffrey Heer → Ed Huai-hsin Ch → Ben Shneidermar (4)
4. Hanspeter Pfiste → Krzysztof Z. Gajc → Jeffrey Heer → Stuart K. Card → Ben Shneidermar (4)

CHI
TVCG
chi_publications
cited
degree
tvcg_publication

« 1 2 3 4 5 6 7 8 »

Path Topology

Active Page | All

Path Statistics

Paths 108/108
Edges 196/196
Nodes 95/95 (0 – 108)

Author (95/95)
Ben Shneidermar
Hanspeter Pfister
Jean-Daniel Feke
Catherine Plaisar
Krzysztof Z. Gajos
Desney S. Tan
Krzysztof Gajos
Paul André
Adam Perer
Jacob O. Wobbro
Frank van Ham
Wendy E. Macka
Jeffrey Nichols
Juho Kim
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m. c. schraefel
Erin Treacy Solov
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Sets 137/843 (0 – 108)

CHI (107/667)
Interacting with e
A Crowdsourced
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LifeFlow: visualizi
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The challenges o
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Query Previews ir
'I hear the patter
Organization ove
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Video Snapshots
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MulteeSum: A To
Overview Use in
Melange: Space
A Principled Way
What Makes a Vis
FacetMap: A Sca
SoccerStories: A
ConTour: Data-Dr
Entourage: Visua

Path Topology View: Getting an Overview

Pathfinder

Start Hanspeter Pfis End Ben Shneiderm Advanced Query

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

Path List

1. Hanspeter Pfiste — Frank van Ham — Adam Perer — Ben Shneidermar (3)
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CHI
TVCG
chi_publications
cited
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tvcg_publication

« 1 2 3 4 5 6 7 8 »

Path Topology

Active Page | All

Path Topology View

Path Statistics

Paths 108/108
Edges 196/196
Nodes 95/95 (0 – 108)

Author (95/95)
Ben Shneidermar
Hanspeter Pfister
Jean-Daniel Feke
Catherine Plaisar
Krzysztof Z. Gajo
Desney S. Tan
Krzysztof Gajos
Paul André
Adam Perer
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Juho Kim
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'Search, Show Co
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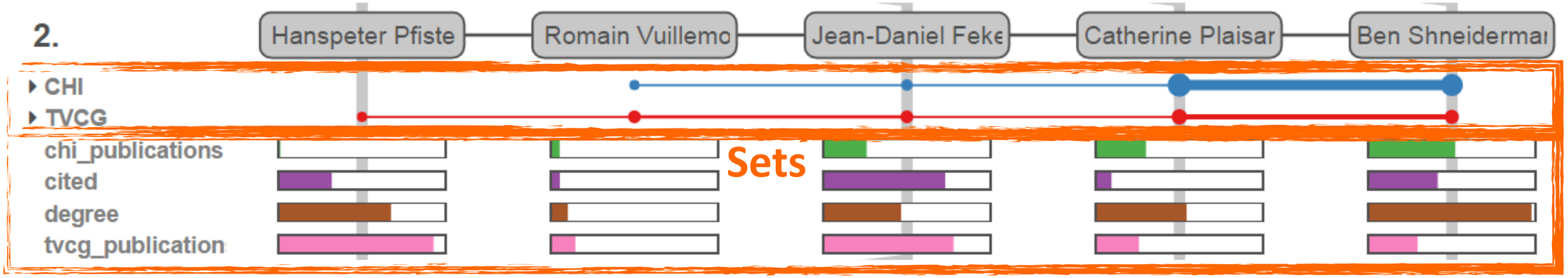
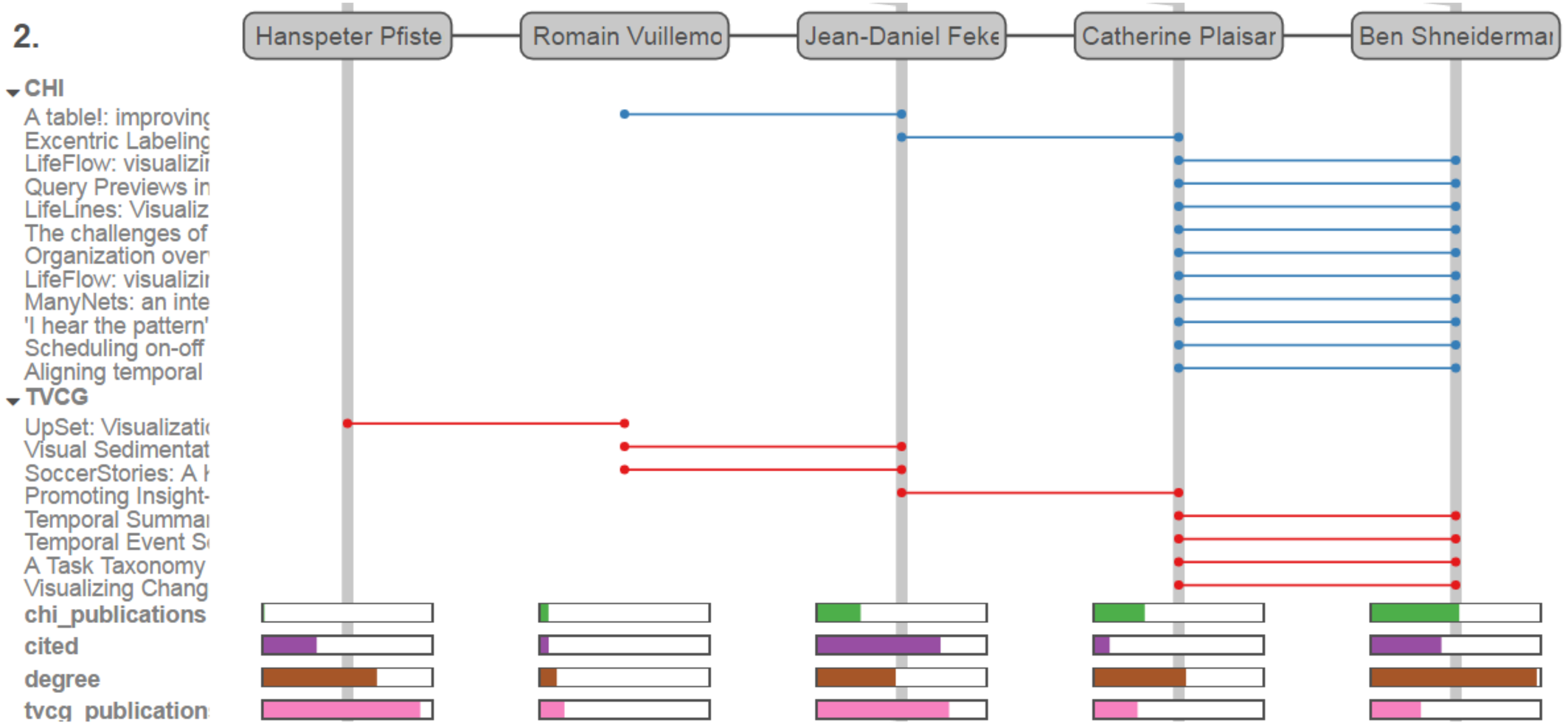
MizBee: A Multisc
MulteeSum: A To
Overview Use in M
Melange: Space
A Principled Way
What Makes a Vis
FacetMap: A Sca
SoccerStories: A
ConTour: Data-Dr
Entourage: Visua

Path List View: Investigating Paths in Detail

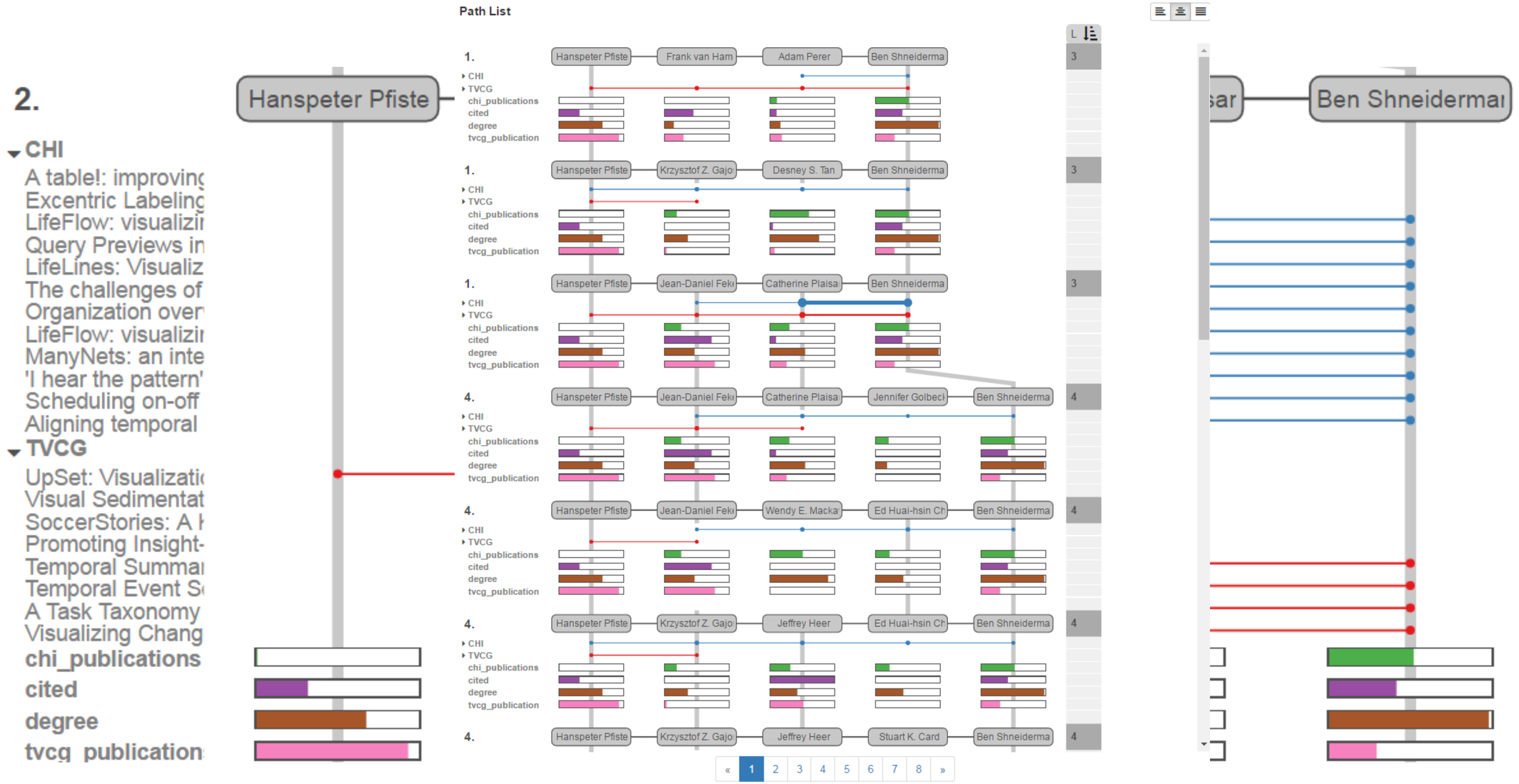
Path Representation

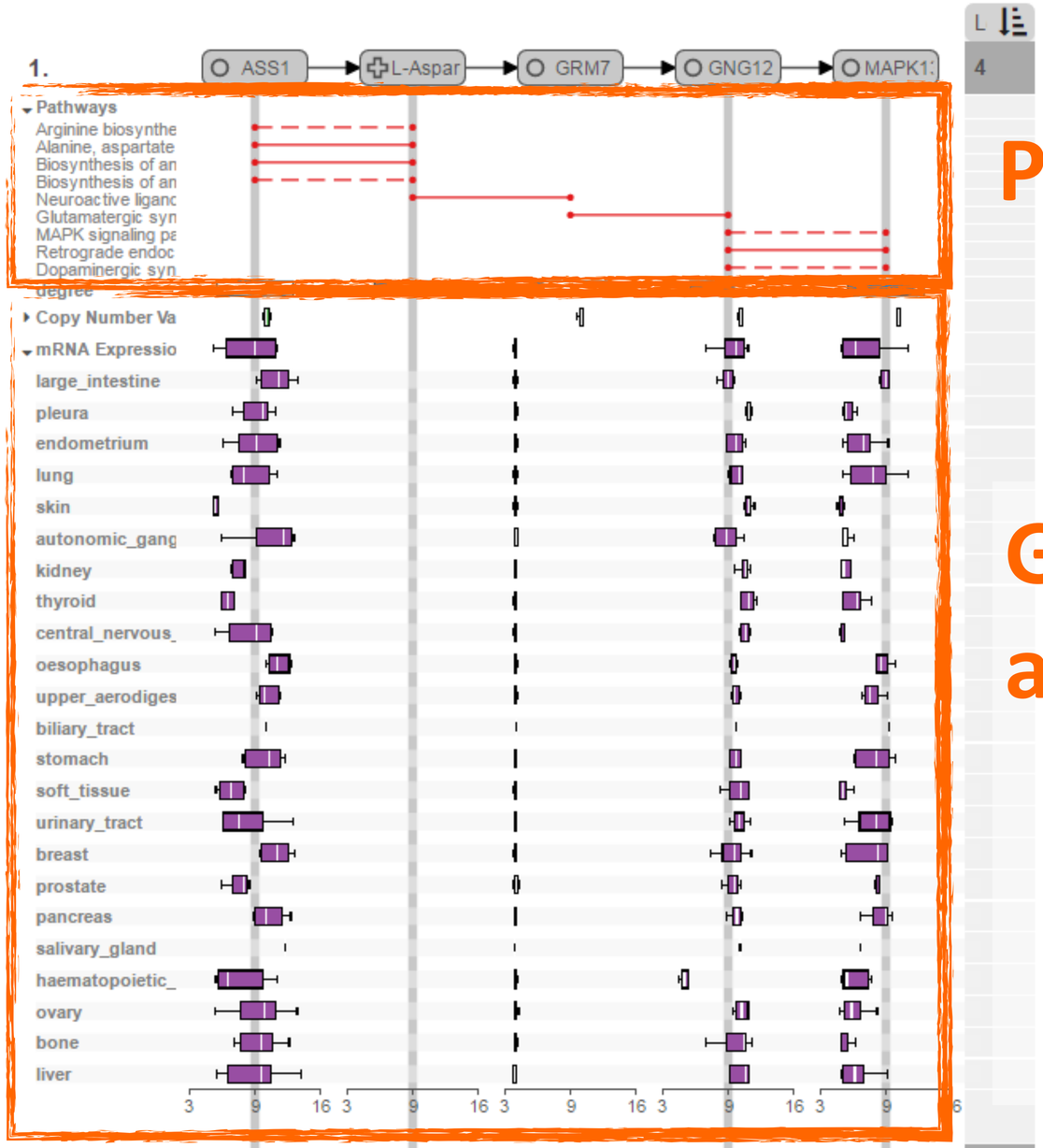


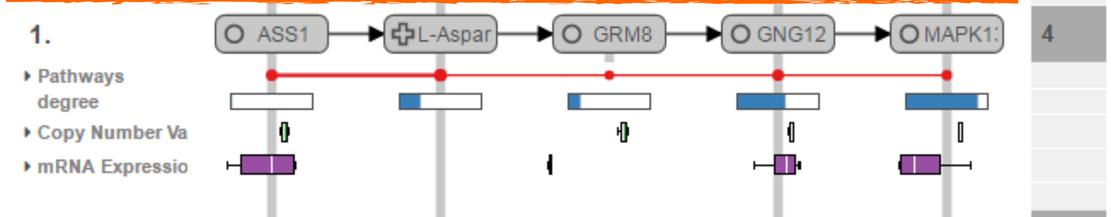
Path Representation



Path Representation



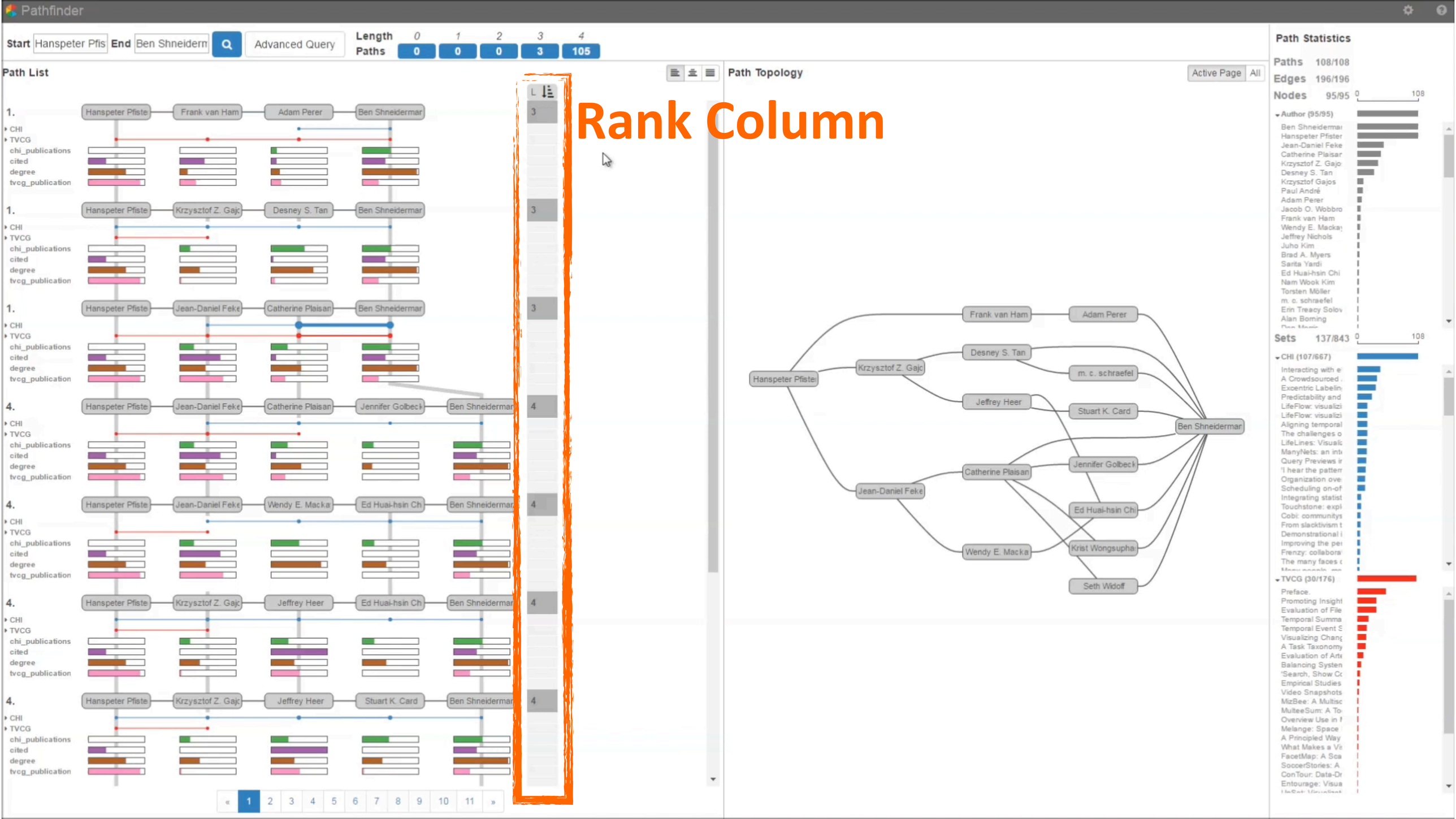




Pathways

Grouped Copy Number and Gene Expression Data

Path Ranking: Identifying Relevant Paths


Pathfinder
Start Hanspeter Pfis
End Ben Shneidern
Advanced Query
Length 0 1 2 3 4
Paths 0 0 0 3 105
Path List
Rank Column
Path Topology
Active Page
All
Path Statistics
Paths 108/108
Edges 196/196
Nodes 95/95
Sets 137/843
Hanspeter Pfiste
Frank van Ham
Adam Perer
Ben Shneiderman
Krzysztof Z. Gajc
Desney S. Tan
Jean-Daniel Fekete
Catherine Plaisant
Jennifer Golbeck
Wendy E. Mackay
Ed Huai-hsin Chi
Jeffrey Heer
Stuart K. Card
m. c. schraefel
Krist Wongsuphasawat
Seth Widoff
CHI
TVCG
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cited
degree
tvcg_publication

Pathfinder

Start Hanspeter Pfis End Ben Shneiderm Advanced Query

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

Path List

Average si

1. Hanspeter Pfiste Jean-Daniel Feke Catherine Plaisan Ben Shneidermar
2. Hanspeter Pfiste Romain Vuillemot Jean-Daniel Feke Catherine Plaisan Ben Shneidermar
2. Hanspeter Pfiste Jean-Daniel Feke Petra Isenberg Catherine Plaisan Ben Shneidermar
4. Hanspeter Pfiste Krzysztof Z. Gajc Mary Czerwinsk Desney S. Tan Ben Shneidermar
4. Hanspeter Pfiste Jean-Daniel Feke Enrico Bertini Catherine Plaisan Ben Shneidermar
4. Hanspeter Pfiste Tamara Munzner Heidi Lam Catherine Plaisan Ben Shneidermar
7. Hanspeter Pfiste Torsten Möller Jean-Daniel Feke Catherine Plaisan Ben Shneidermar

CHI
TVCG
chi_publications
cited
degree
tvcg_publication

« 1 2 3 4 5 6 7 8 9 10 11 »

Rank by Average Set Connection Strength
Rank by Journal Set Connection Strength

Path Topology

Active Page All

Path Statistics

Paths 108/108
Edges 196/196
Nodes 95/95 0 108

Author (95/95)
Ben Shneiderma
Hanspeter Pfister
Jean-Daniel Feke
Catherine Plaisar
Krzysztof Z. Gajo
Desney S. Tan
Krzysztof Gajos
Paul André
Adam Perer
Jacob O. Wobbro
Frank van Ham
Wendy E. Macka
Jeffrey Nichols
Juho Kim
Brad A. Myers
Sarita Yardi
Ed Huai-hsin Chi
Nam Wook Kim
Torsten Möller
m. c. schraefel
Erin Treacy Solov
Alan Borning

Sets 137/843 0 108

CHI (107/667)
Interacting with e
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Scheduling on-of
Integrating statist
Touchstone: expl
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Improving the per
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TVCG (30/176)
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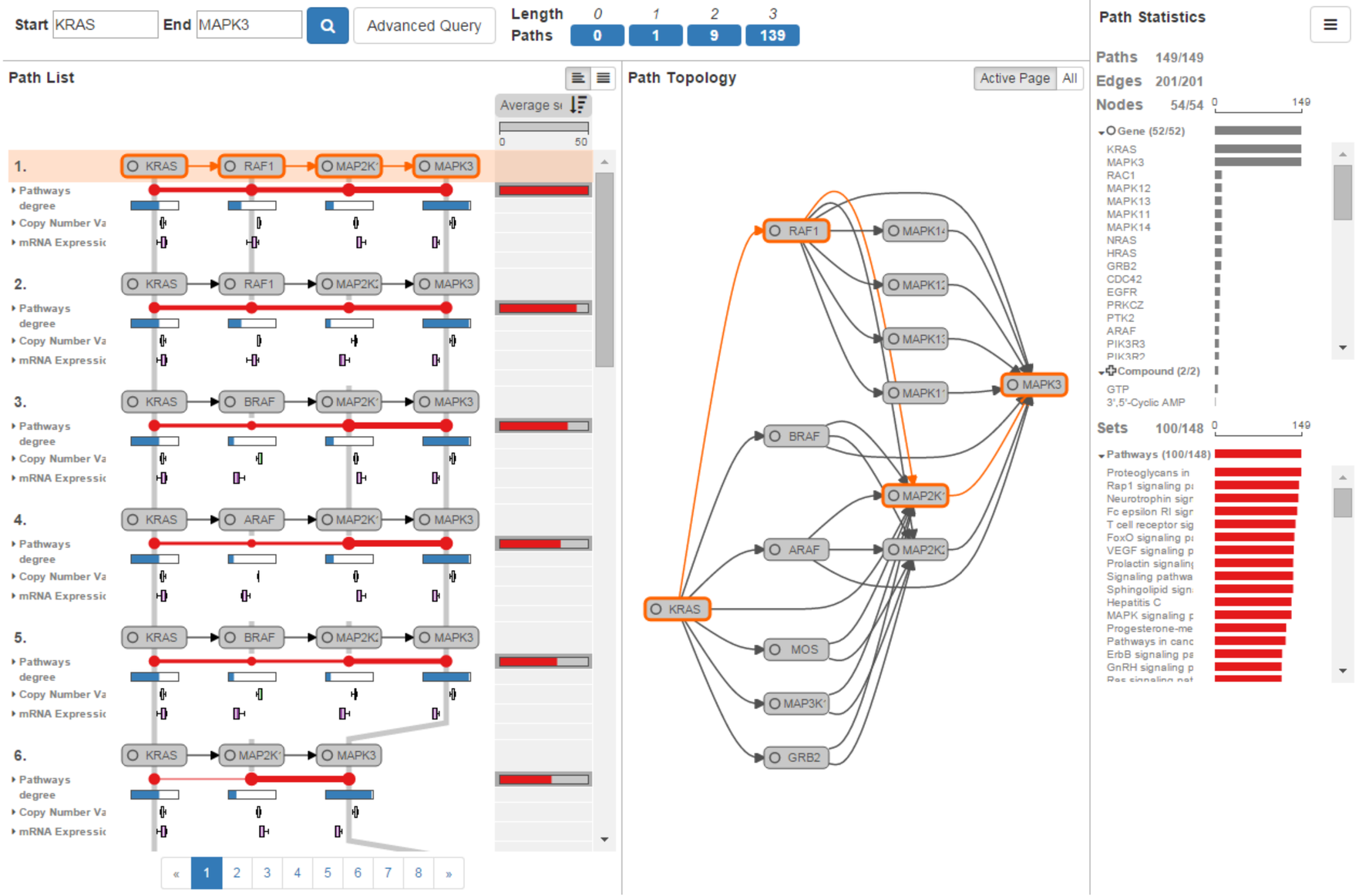
Melange: Space
A Principled Way
What Makes a Vi
FacetMap: A Sca
SoccerStories: A
ConTour: Data-Dr
Entourage: Visua

Case Study: Biological Network

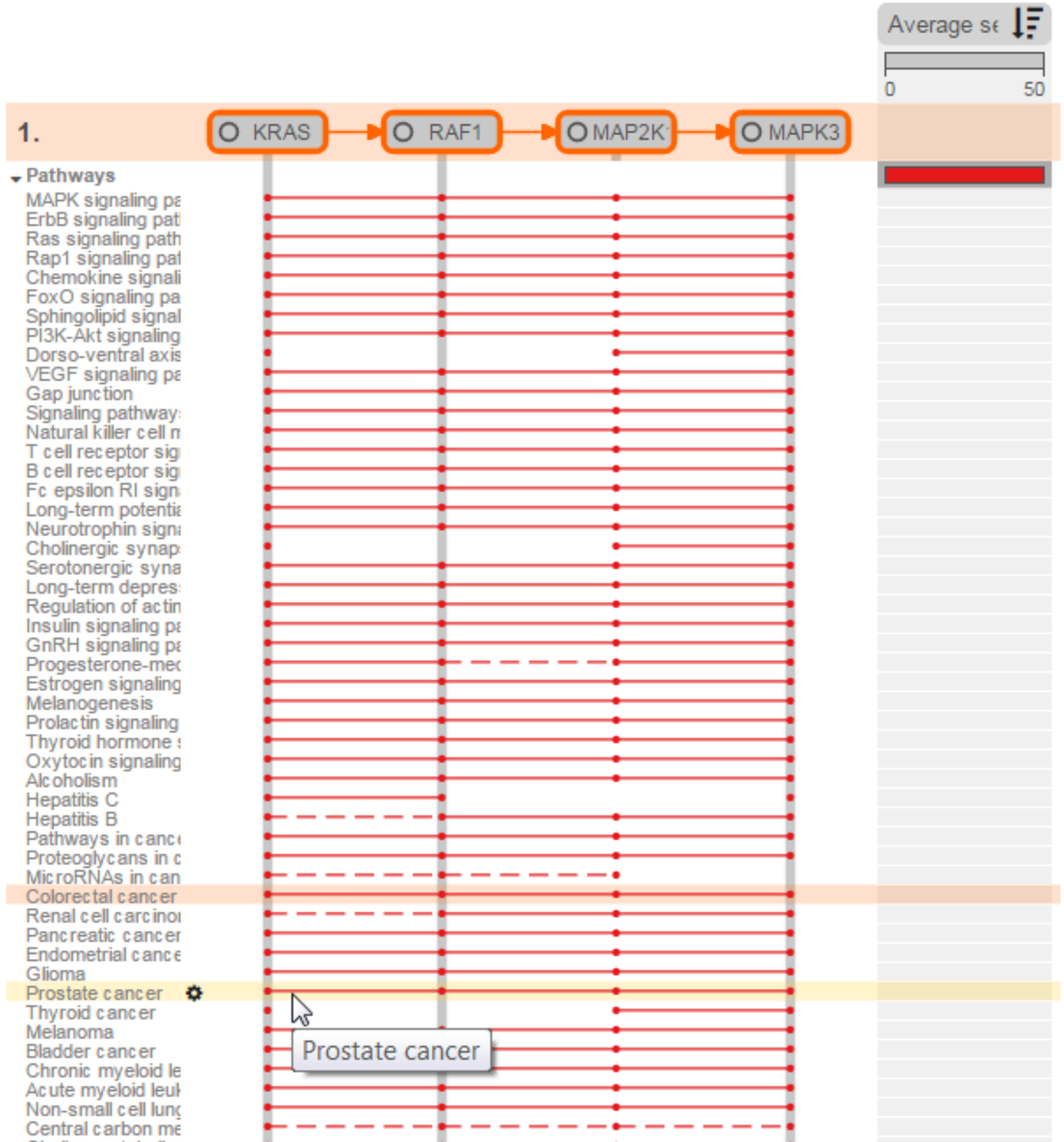
ERK-MAPK signaling cascade



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.

http://pathfinder.caleydoapp.org

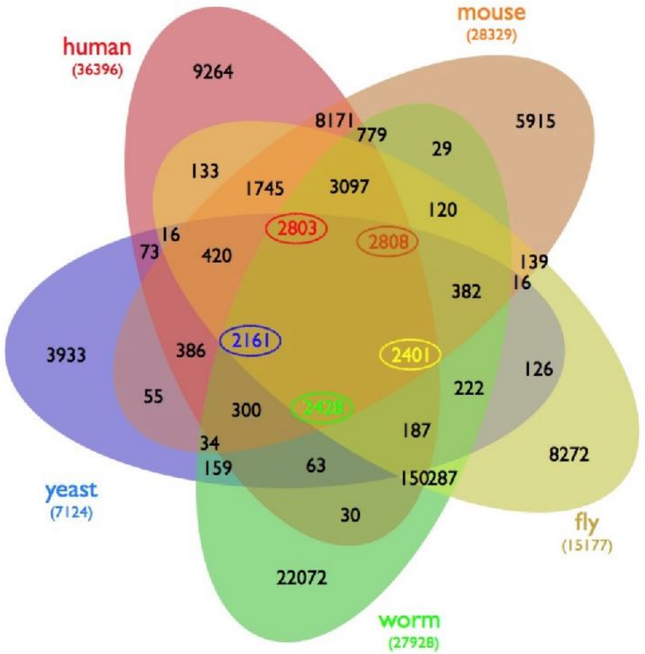
Visualization Design Strategies

1. Encoding channel primacy
2. Show relationships explicitly
3. Use queries
4. User color sparingly
5. Enable annotation / provenance

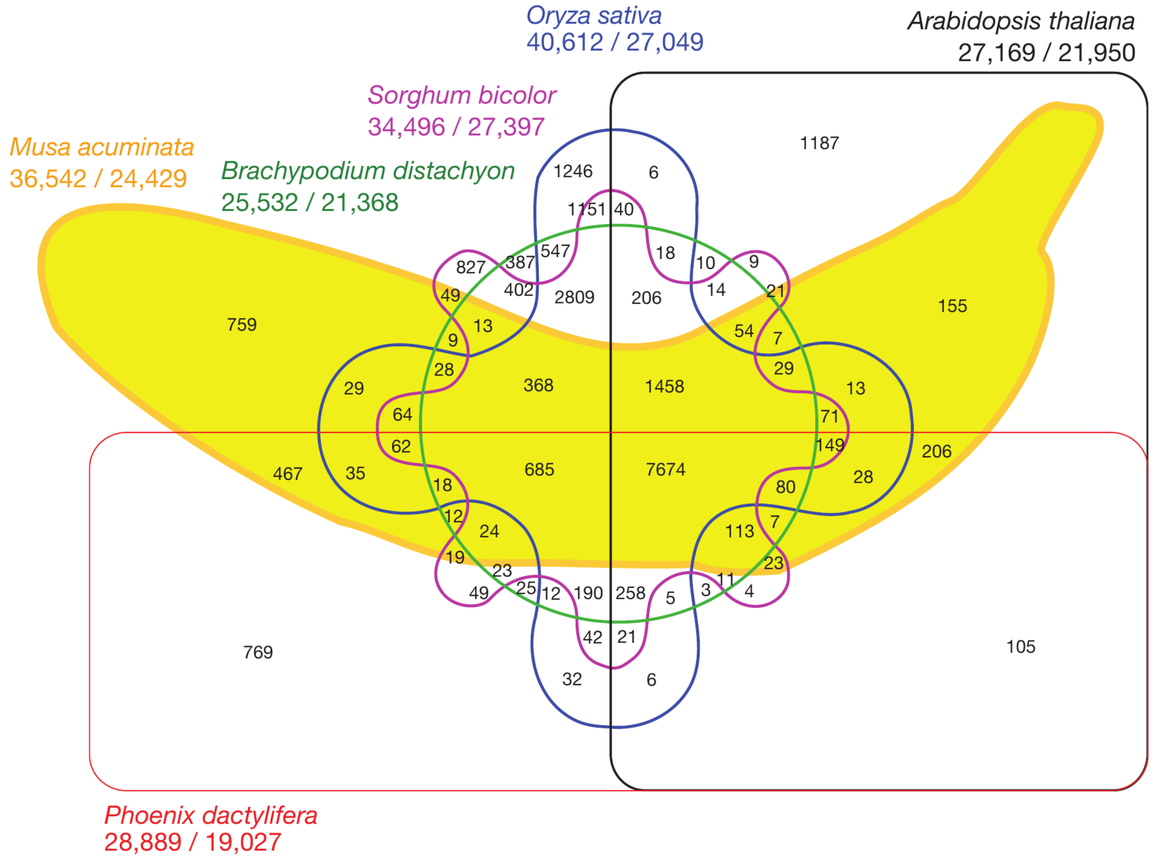
1. Encoding Channel Primacy

Most important data is assigned most powerful encoding channel (position)

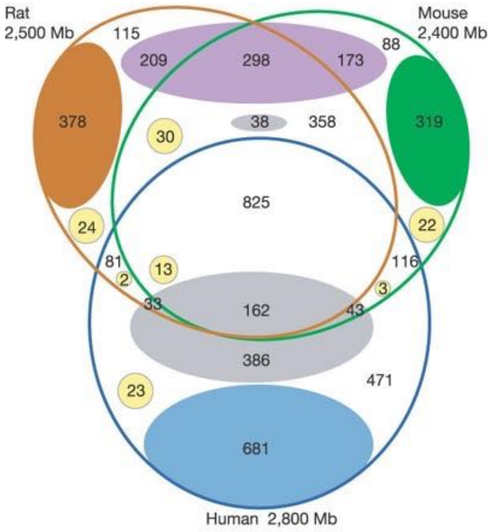
Example: Set Visualization



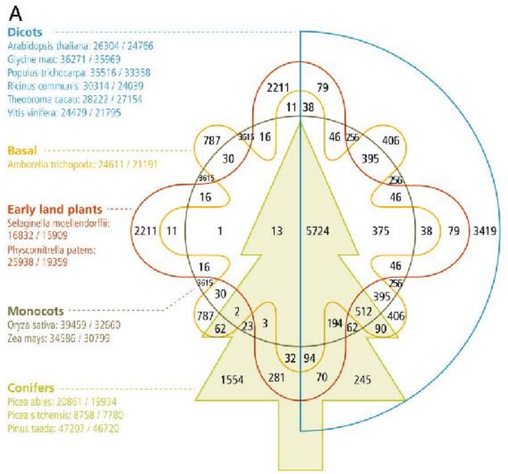
[Wiles et al., BMC Systems Biology]



[D'Hont et al., Nature, 2012]

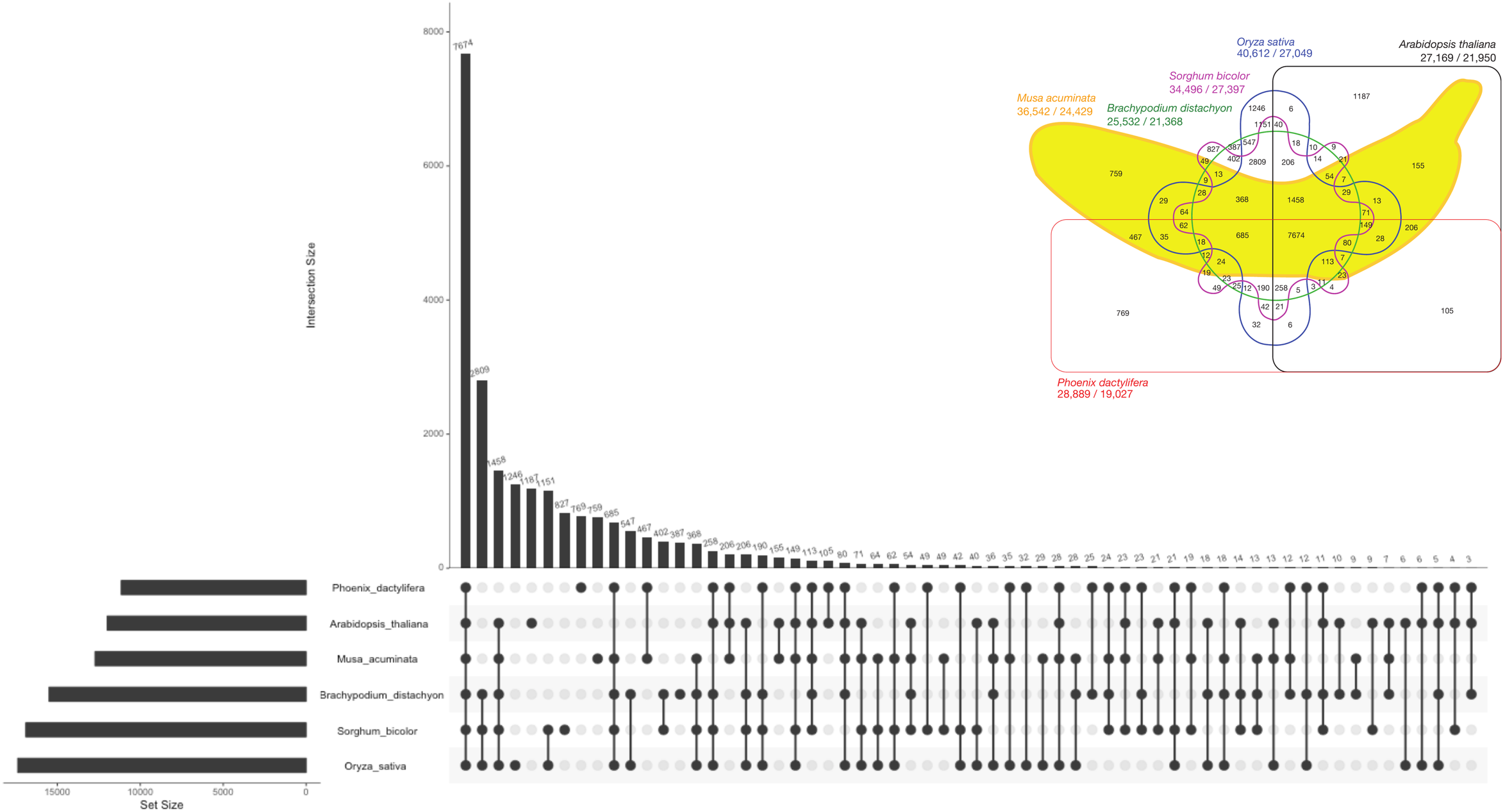


[Gibbs et al., Nature, 2004]



[Neale et al., BMC Genome Biology, 2014]

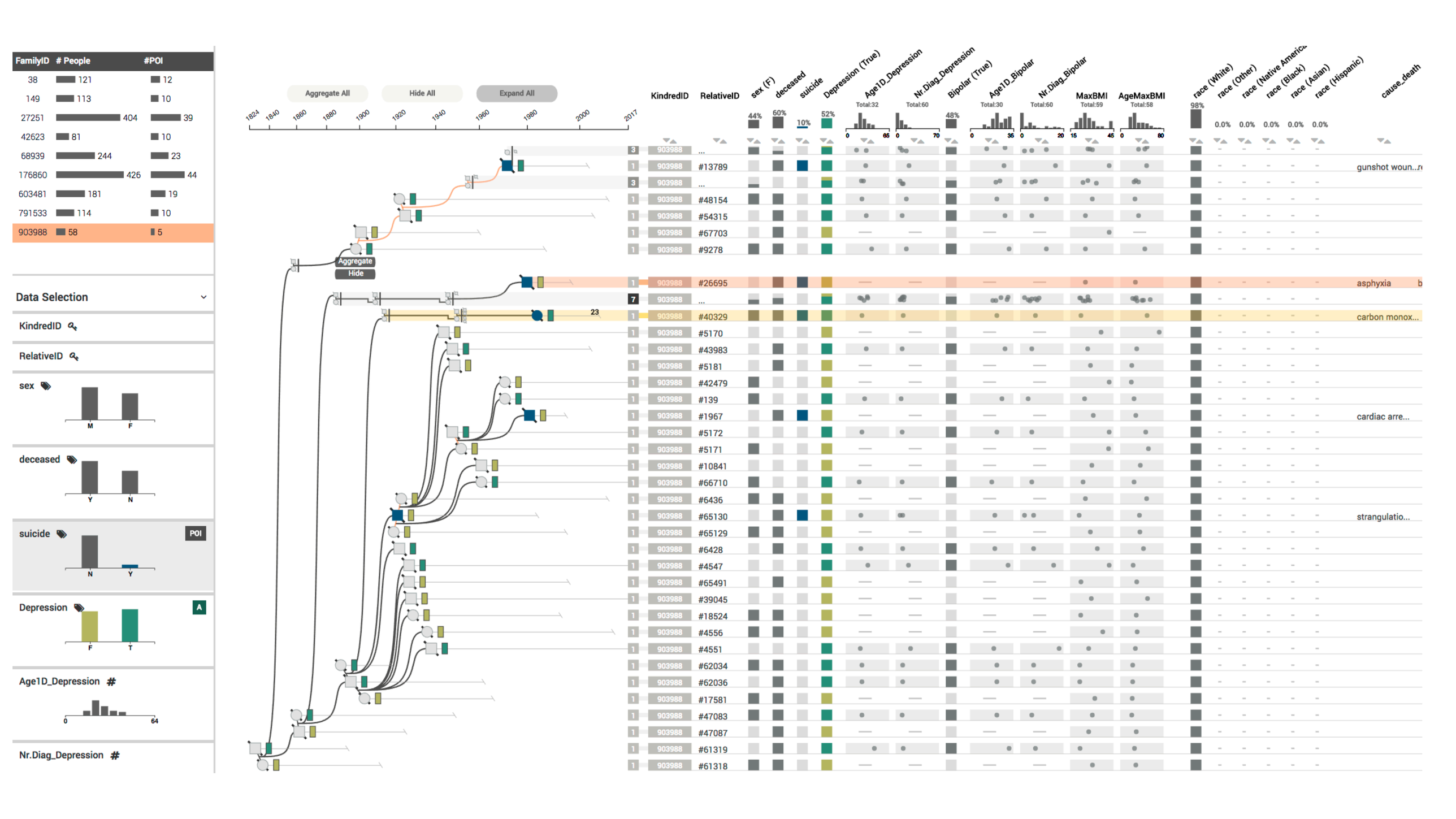
The Banana Chart Redesigned



2. Show relationships explicitly

Don't use highlighting to connect different views

Use smart layouts (position) or connectivity


FamilyID # People #POI
38 121 12
149 113 10
27251 404 39
42623 81 10
68939 244 23
176860 426 44
603481 181 19
791533 114 10
903988 58 5
Aggregate All
Hide All
Expand All
1824 1840 1860 1880 1900 1920 1940 1960 1980 2000 2017
Data Selection
KindredID
RelativeID
sex
M F
deceased
Y N
suicide
POI
N Y
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A
F T
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Nr.Diag_Depression #
Aggregate
Hide
23
KindredID RelativeID sex (F) deceased suicide Depression (True) Age1D_Depression Nr.Diag_Depression Bipolar (True) Age1D_Bipolar Nr.Diag_Bipolar MaxBMI AgeMaxBMI race (White) race (Other) race (Native Americ... race (Black) race (Asian) race (Hispanic) cause_death
44% 60% 10% 52% 48% 98%
Total:32 Total:60 Total:30 Total:60 Total:59 Total:58
0 65 0 70 0 35 0 20 15 45 0 80
0.0% 0.0% 0.0% 0.0% 0.0%
3 903988 ...
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1 903988 #48154
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1 903988 #65491
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1 903988 #18524
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1 903988 #62034
1 903988 #62036
1 903988 #17581
1 903988 #47083
1 903988 #47087
1 903988 #61319
1 903988 #61318

3. Use queries

especially for big data

Pathfinder

Start Hanspeter Pfis End Ben Shneiderm Advanced Query

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

Path List

1. Hanspeter Pfiste → Frank van Ham → Adam Perer → Ben Shneidermar (3)
1. Hanspeter Pfiste → Krzysztof Z. Gajc → Desney S. Tan → Ben Shneidermar (3)
1. Hanspeter Pfiste → Jean-Daniel Feke → Catherine Plaisan → Ben Shneidermar (3)
4. Hanspeter Pfiste → Jean-Daniel Feke → Catherine Plaisan → Jennifer Golbeck → Ben Shneidermar (4)
4. Hanspeter Pfiste → Jean-Daniel Feke → Wendy E. Macka → Ed Huai-hsin Ch → Ben Shneidermar (4)
4. Hanspeter Pfiste → Krzysztof Z. Gajc → Jeffrey Heer → Ed Huai-hsin Ch → Ben Shneidermar (4)
4. Hanspeter Pfiste → Krzysztof Z. Gajc → Jeffrey Heer → Stuart K. Card → Ben Shneidermar (4)

CHI
TVCG
chi_publications
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degree
tvcg_publication

« 1 2 3 4 5 6 7 8 »

Path Topology

Active Page | All

Path Statistics

Paths 108/108
Edges 196/196
Nodes 95/95 (0 – 108)

Author (95/95)
Ben Shneidermar
Hanspeter Pfister
Jean-Daniel Feke
Catherine Plaisar
Krzysztof Z. Gajos
Desney S. Tan
Krzysztof Gajos
Paul André
Adam Perer
Jacob O. Wobbro
Frank van Ham
Wendy E. Macka
Jeffrey Nichols
Juho Kim
Brad A. Myers
Sarita Yardi
Ed Huai-hsin Chi
Nam Wook Kim
Torsten Möller
m. c. schraefel
Erin Treacy Solov
Alan Borning

Sets 137/843 (0 – 108)

CHI (107/667)
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A Crowdsourced
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Predictability and
LifeFlow: visualizi
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Aligning temporal
The challenges o
LifeLines: Visuali
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Query Previews ir
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Organization ove
Scheduling on-of
Integrating statist
Touchstone: expl
Cobi: communitys
From slacktivism t
Demonstrational i
Improving the per
Frenzy: collabora
The many faces o

TVCG (30/176)
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Temporal Event S
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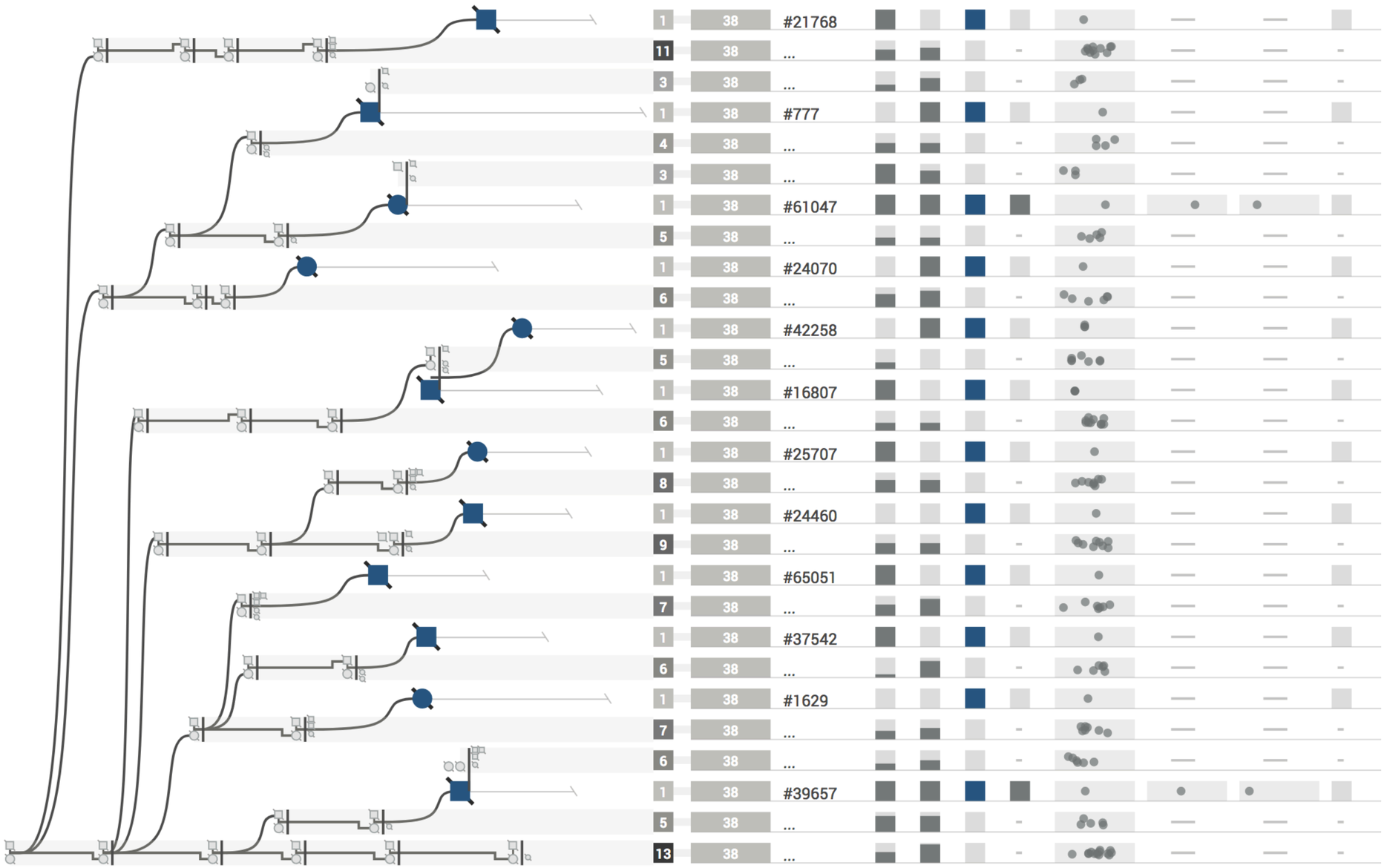
Balancing Systen
'Search, Show Co
Empirical Studies
Video Snapshots
MizBee: A Multisc
MulteeSum: A To
Overview Use in
Melange: Space
A Principled Way
What Makes a Vis
FacetMap: A Sca
SoccerStories: A
ConTour: Data-Dr
Entourage: Visua

4. User color sparingly

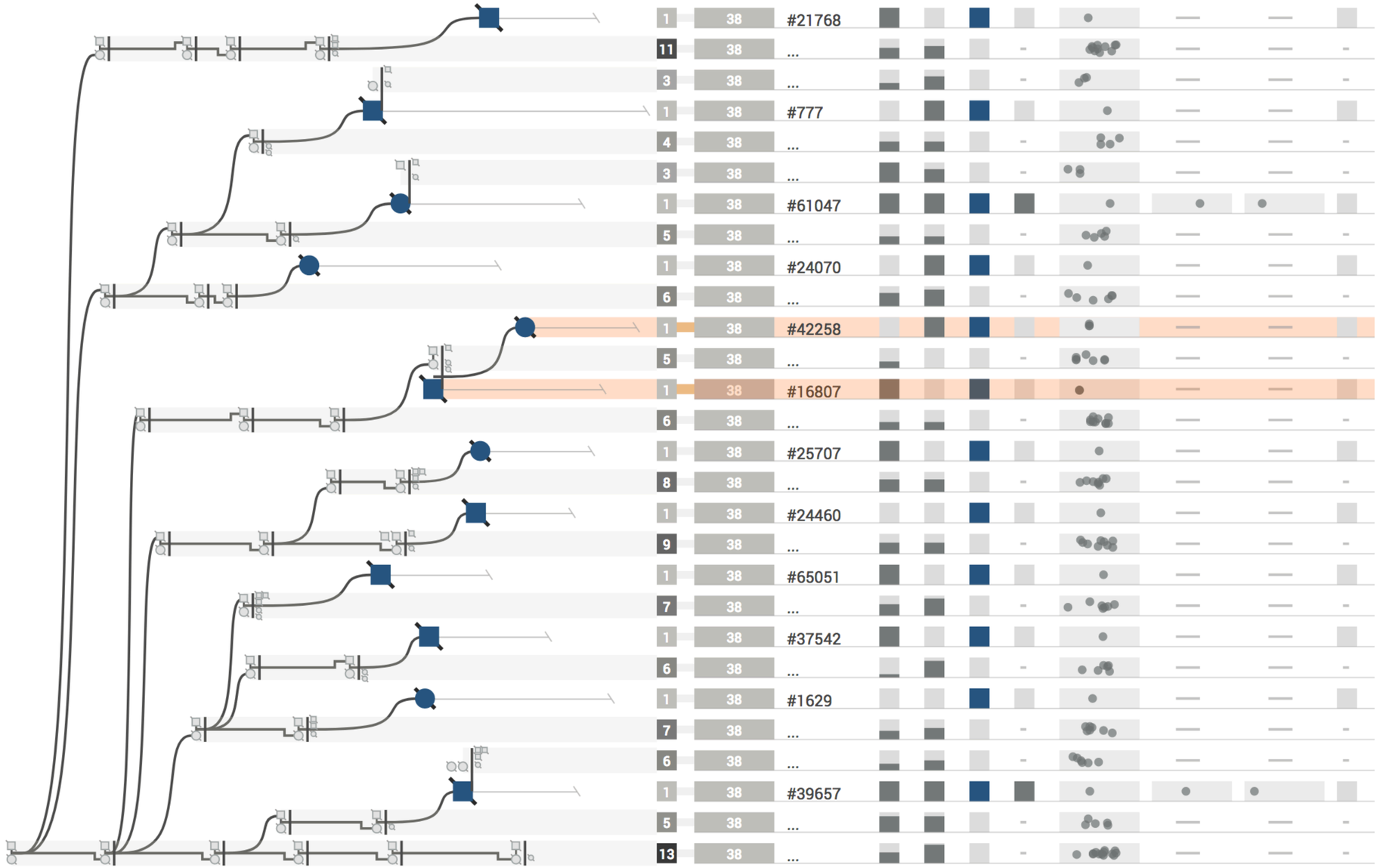
Limit use to encode data

Primarily use it to highlight items of interest

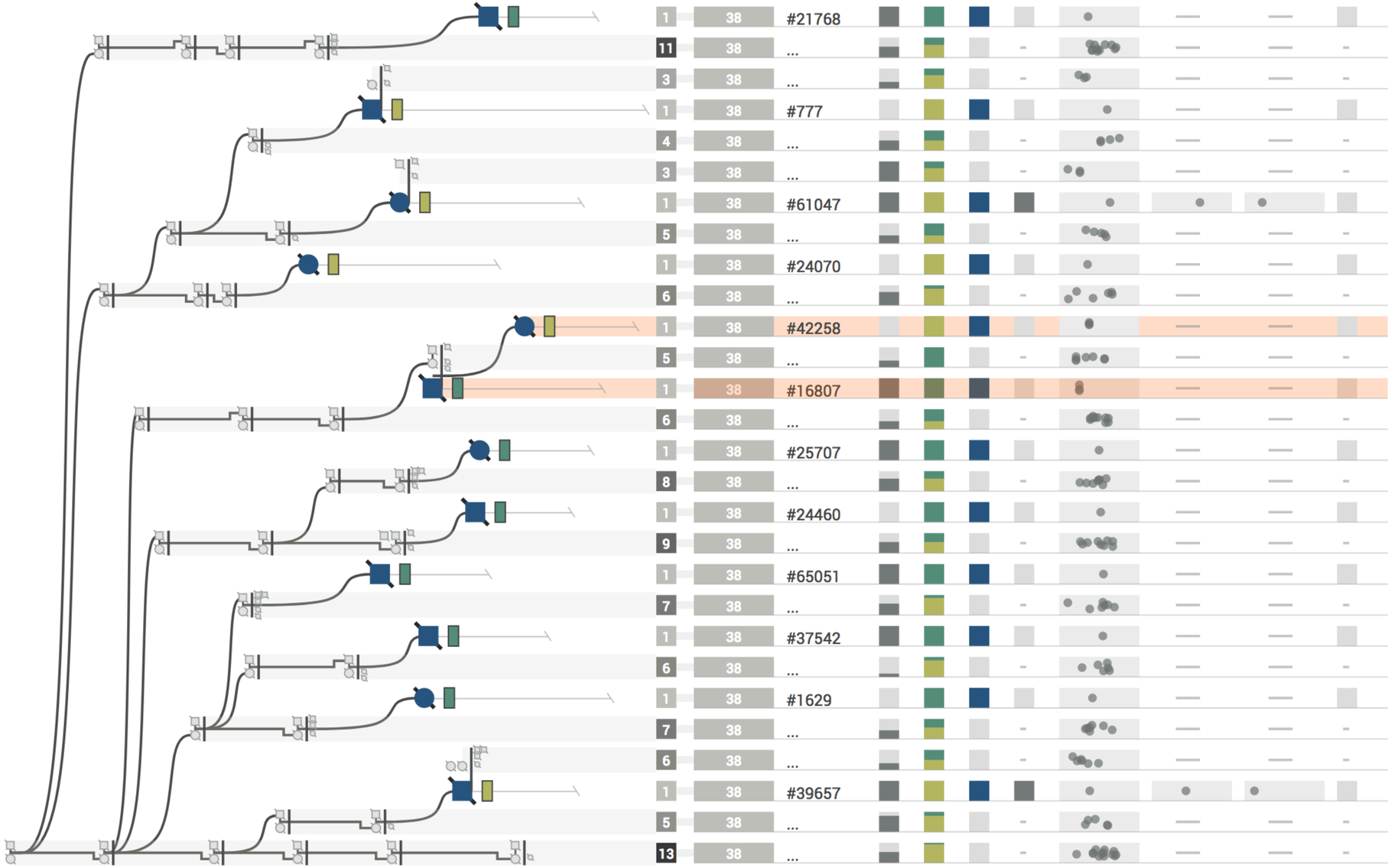
Pop out effect!



Only one color for primary attribute (suicide, blue)



Another color for highlights, to emphasize parent-child relationship (orange)

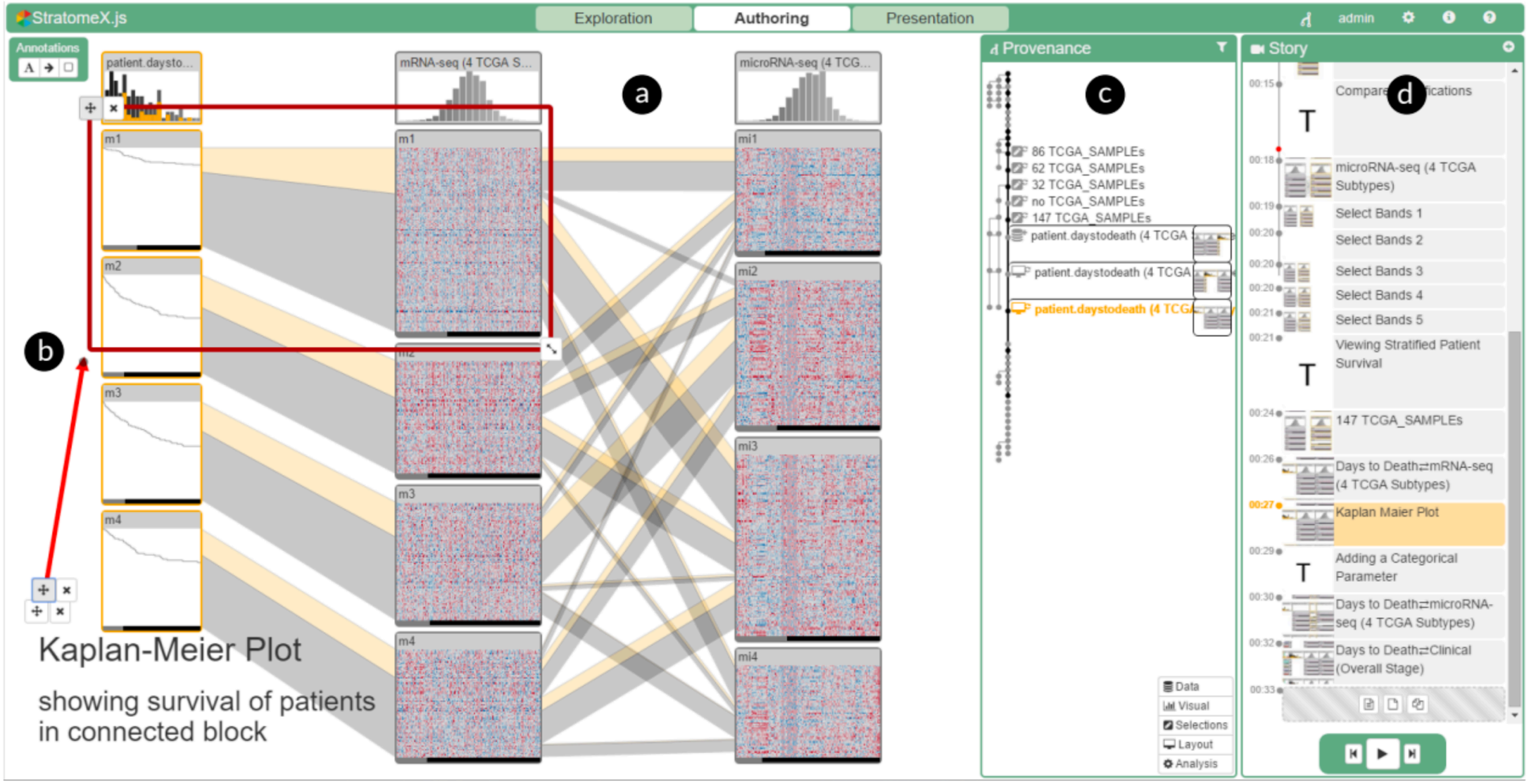


Adding a color for an additional attribute (deceased yes/no, green)

5. Enable annotation / provenance

What did you see / think when looking at this visualization?

How did I get here? Can I go back?


StratomeX.js
Exploration
Authoring
Presentation
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Annotations
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microRNA-seq (4 TCG...
m1
m2
m3
m4
mi1
mi2
mi3
mi4
a
b
c
d
Provenance
86 TCGA_SAMPLEs
62 TCGA_SAMPLEs
32 TCGA_SAMPLEs
no TCGA_SAMPLEs
147 TCGA_SAMPLEs
patient.daystodeath (4 TCGA
patient.daystodeath (4 TCGA
patient.daystodeath (4 TCGA
Data
Visual
Selections
Layout
Analysis
Story
00:15
Compare Classifications
00:18
microRNA-seq (4 TCGA Subtypes)
00:19
Select Bands 1
00:20
Select Bands 2
00:20
Select Bands 3
00:20
Select Bands 4
00:21
Select Bands 5
00:21
Viewing Stratified Patient Survival
00:24
147 TCGA_SAMPLEs
00:26
Days to Death⇄mRNA-seq (4 TCGA Subtypes)
00:27
Kaplan Maier Plot
00:29
Adding a Categorical Parameter
00:30
Days to Death⇄microRNA-seq (4 TCGA Subtypes)
00:32
Days to Death⇄Clinical (Overall Stage)
00:33
Kaplan-Meier Plot
showing survival of patients in connected block

We’re hiring PostDocs and accept PhD Students!

visualization design lab

Miriah Meyer

Alexander Lex

Alexander Lex
@alexander_lex
http://alexander-lex.net

THE UNIVERSITY OF UTAH

Visualizing Biological Data: Pathway Graphs, Genealogies, and Alternative Splicing

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