

Biological Information Visualization

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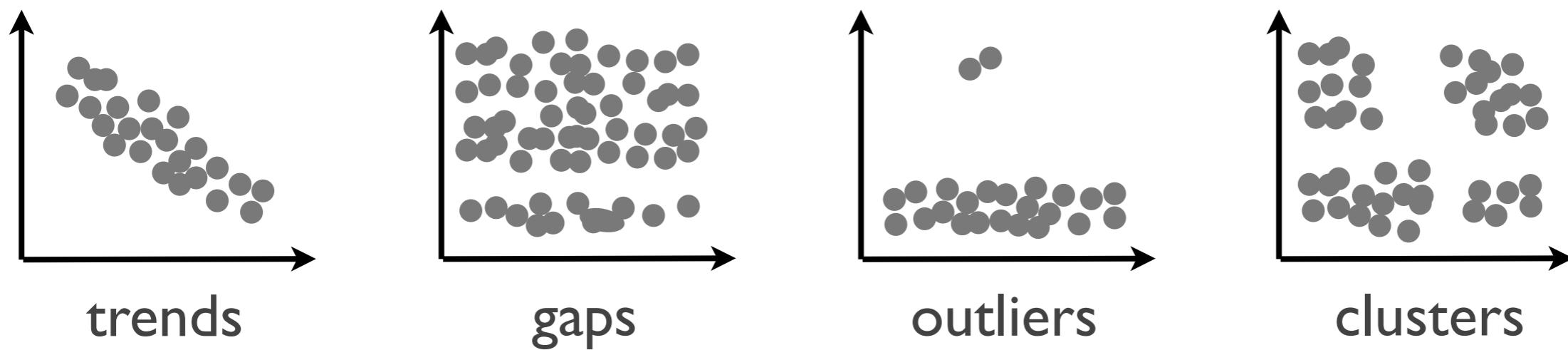
Harvard Medical School & Broad Institute

Part 2

Methods for Biological Data

Nils Gehlenborg

Exploration: Hypothesis Generation



In biology, most data visualization problems are related to exploratory analysis.

Exploration

Exploration: Hypothesis Generation

- Visualization for exploration is an “Exploratory Data Analysis” technique (Tukey 1977). Statistical graphics such as box plots and scatter plots are early examples.
- When there is a specific question that can easily be determined algorithmically (“What is the highest value?”), then visualization is usually not the right tool.
- When it is not clear what should be asked or when the answer can not be summarized easily (“What is the distribution of the values?”), then visualization is an excellent choice.
- **Visualization for exploration is challenging because the data sets are getting bigger and more heterogeneous.**

Exploration: Information Seeking Mantra

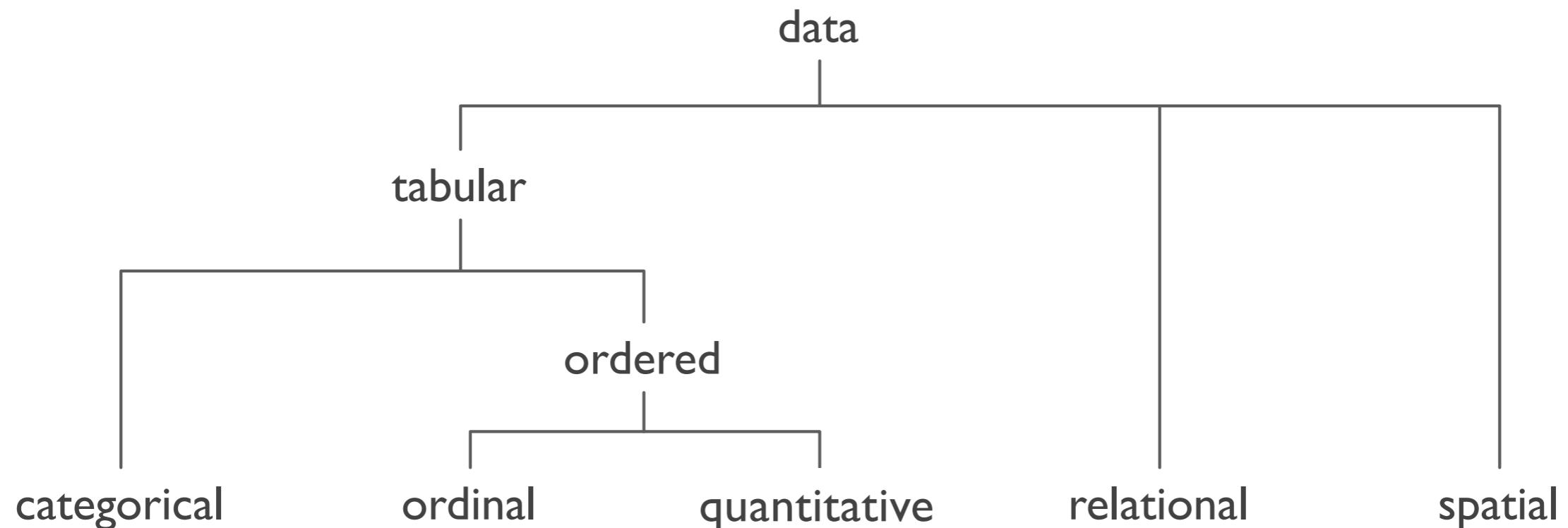
- In explorative settings the user is normally dealing with large amounts of data.
- Impossible to grasp everything at once.
- Solution: Make visualizations **interactive** to support the user in exploring subsets of the data at different resolutions.
- Ben Shneiderman's **Information Seeking Mantra**:
 - Overview first, zoom and filter, then details on demand.
- Keim-Mansmann-Thomas **Visual Analytics Mantra**:
 - Analyze first, show the important, zoom, filter and analyze further, details on demand

Biological Data

Biological Data Types

- Experimental data and knowledge (including meta data)
- Detail and overview
 - example: 3D structure of a protein versus metabolome map of an organism
- Complex relationships
 - example: gene expression data, protein-DNA interactions, sequence motifs

Exercise: Biological Data Types



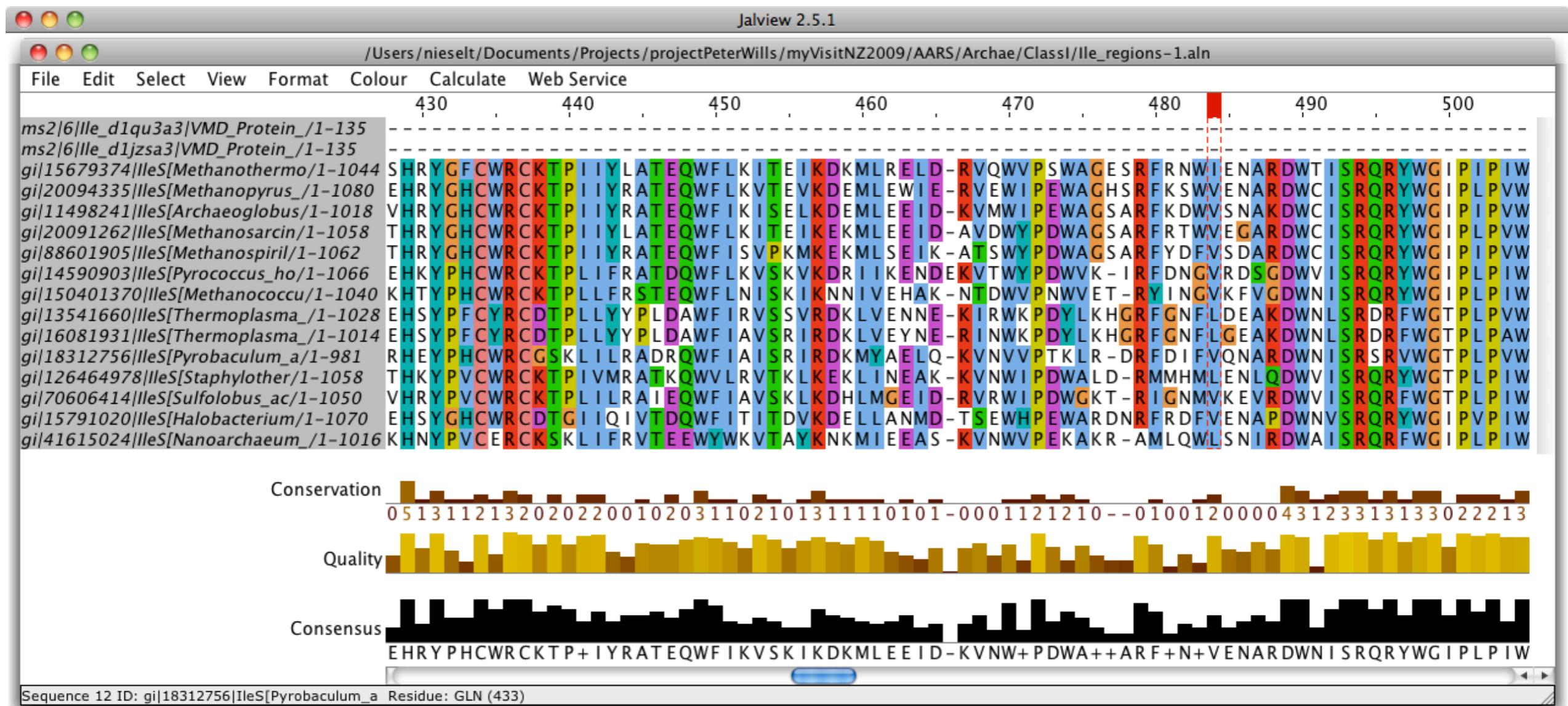
apples	small	10 inches	trees	intrinsic position
oranges	medium	13 inches	networks	
bananas	large	18.5 inches		

Exercise: Biological Data Types

G T A C G G G G G C T C G C T G C T A C T * A C G A A G T T A * G G G T T T T * C A G A T T T C T

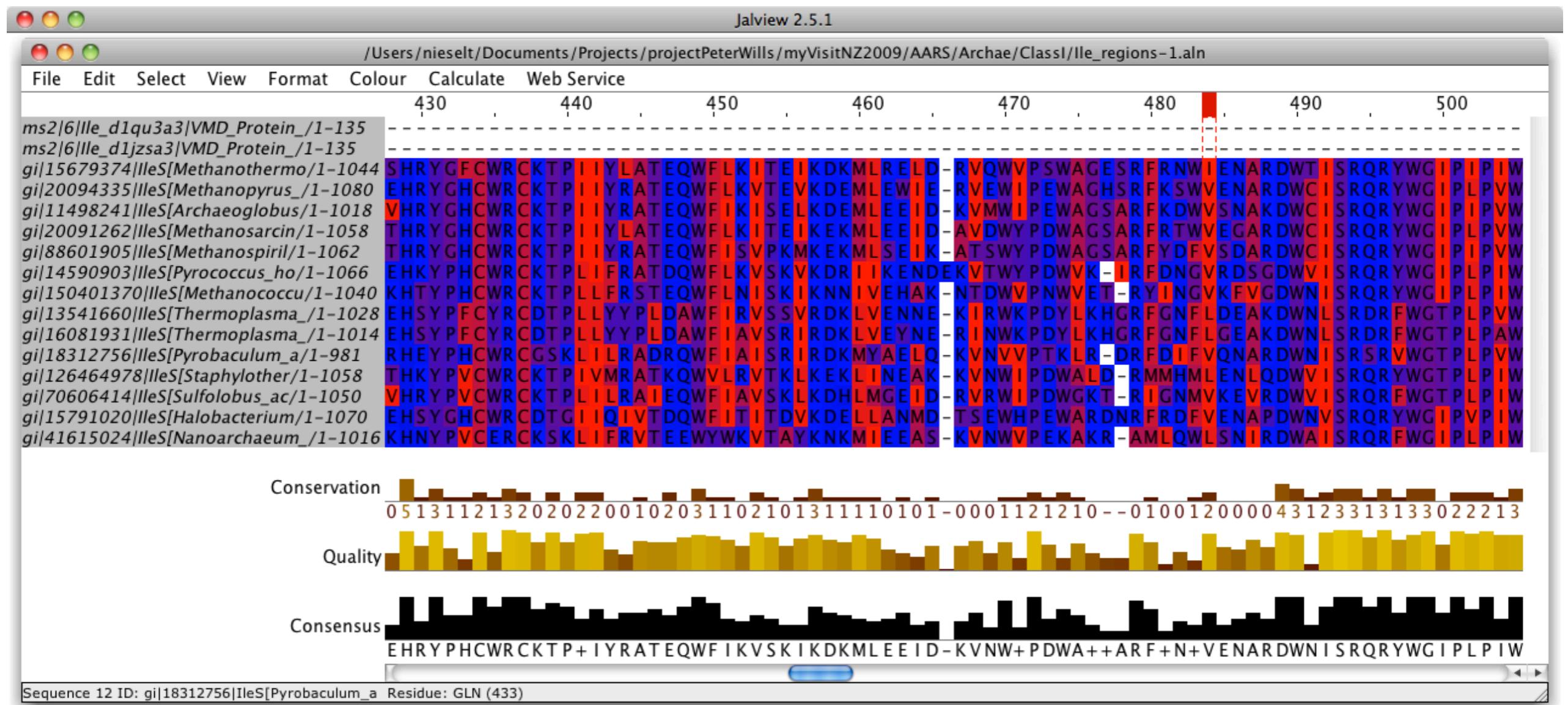
DNA sequence

Exercise: Biological Data Types



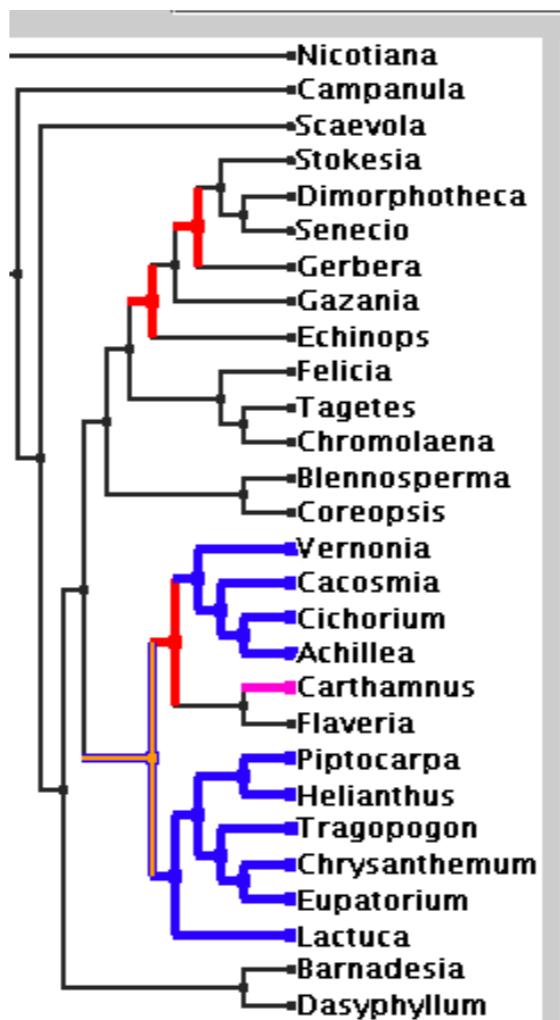
multiple sequence alignment

Exercise: Biological Data Types



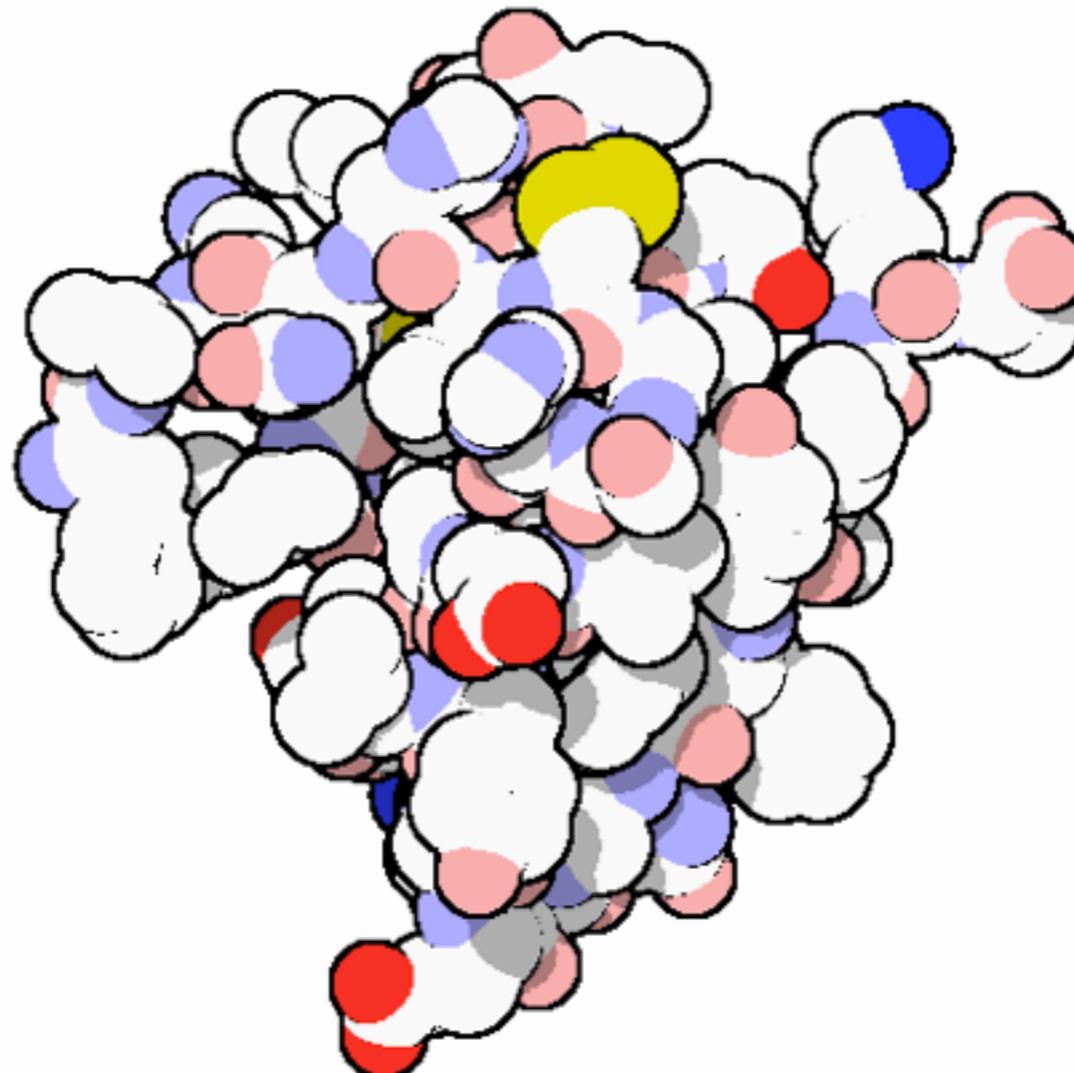
multiple sequence alignment

Exercise: Biological Data Types



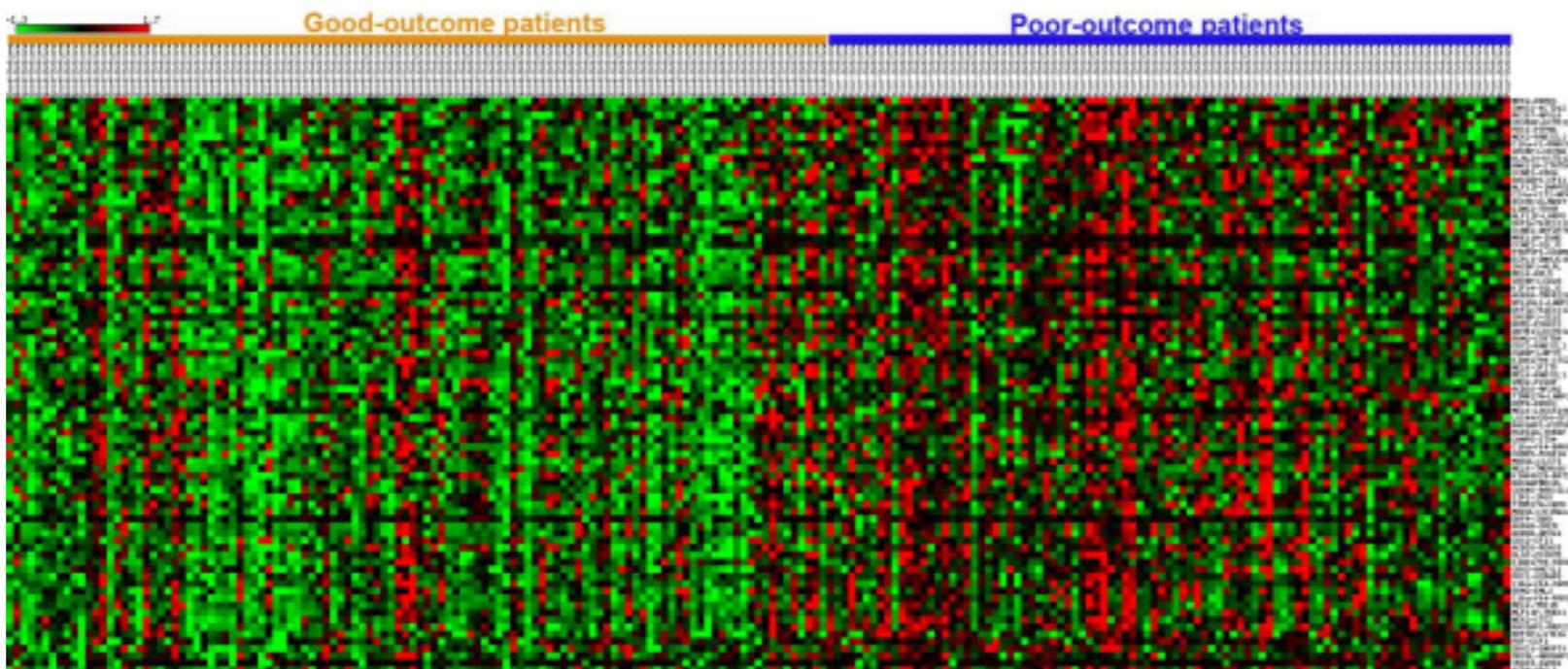
phylogeny

Exercise: Biological Data Types



protein structure

Exercise: Biological Data Types



gene expression data

Overview: Biological Data Types

Sequences

genes, alignments, genomes

Multivariate Data

gene and protein expression levels, metabolite concentrations

Interactions

protein interactions, gene regulation, metabolic pathways

Sequences

Sequences: Genes

NM_000546 gattggggtttcccctccatgtgctcaagactggcgctaaaagttttagcttctcaaaagtctagac

NP_000537 MEEPQSDPSVEPPLSQETFSDLWKLLPENNVLSPLPSQAMDDILMLSPDDIEQWFTEDPGPDEAPRMPEAA



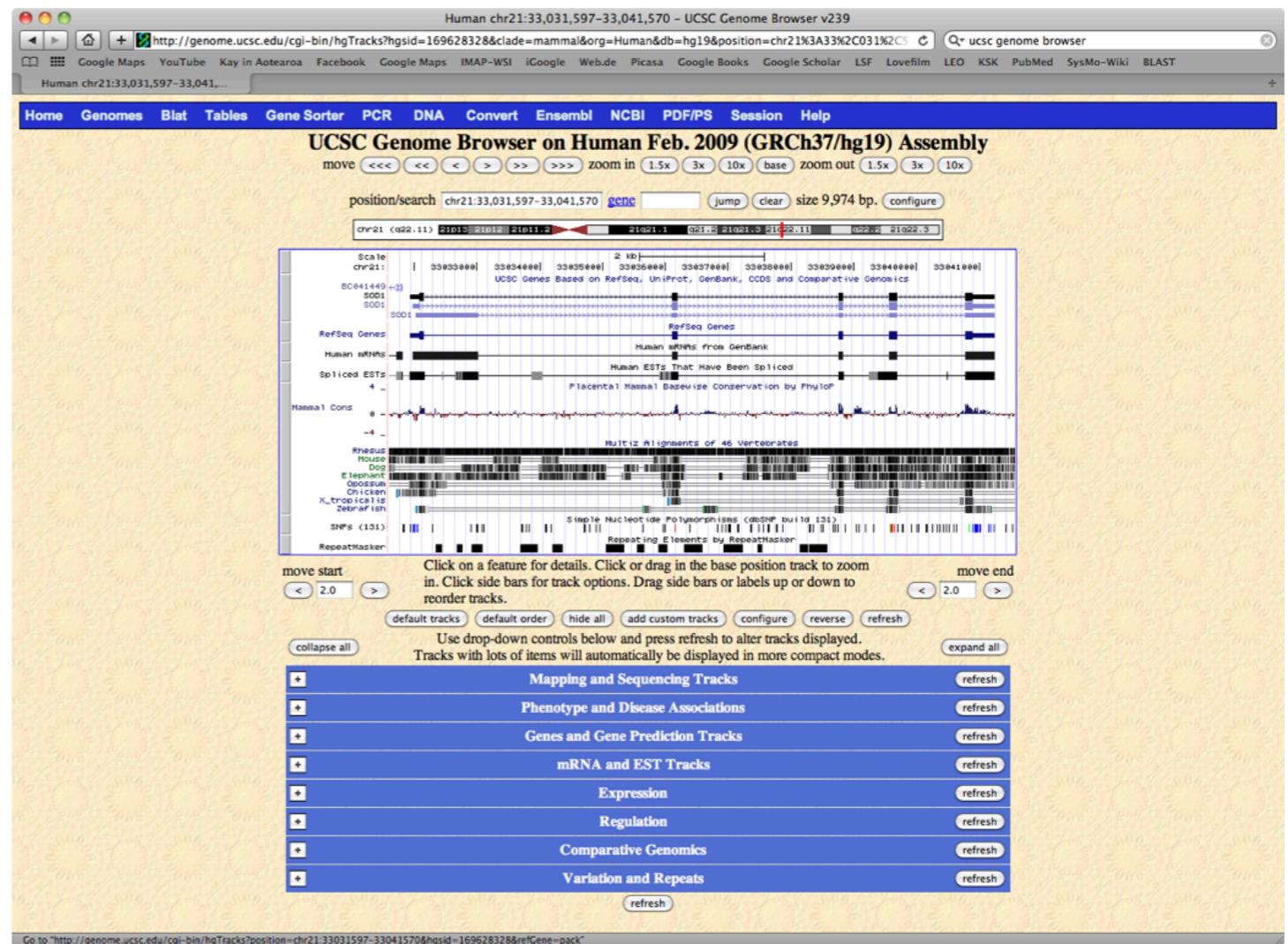
Sequences: Genomes

Genome Browsers

- display genomic data in a “position-centric” view
- genome serves as reference for positions
- usually track-based
- varying levels of interactivity
- browsing vs exploration
- web-browser-based or desktop applications

Sequences: UCSC Genome Browser

- most commonly used browser
- supports basically any data type that can be mapped to the genome
- “classic implementation”: images are rendered on the server and embedded in the webpage



Sequences: UCSC Genome Browser

“squished”



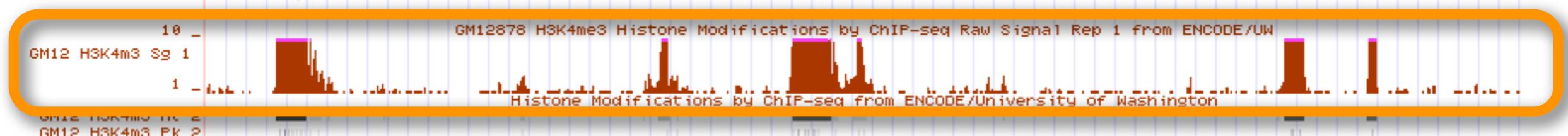
“dense”



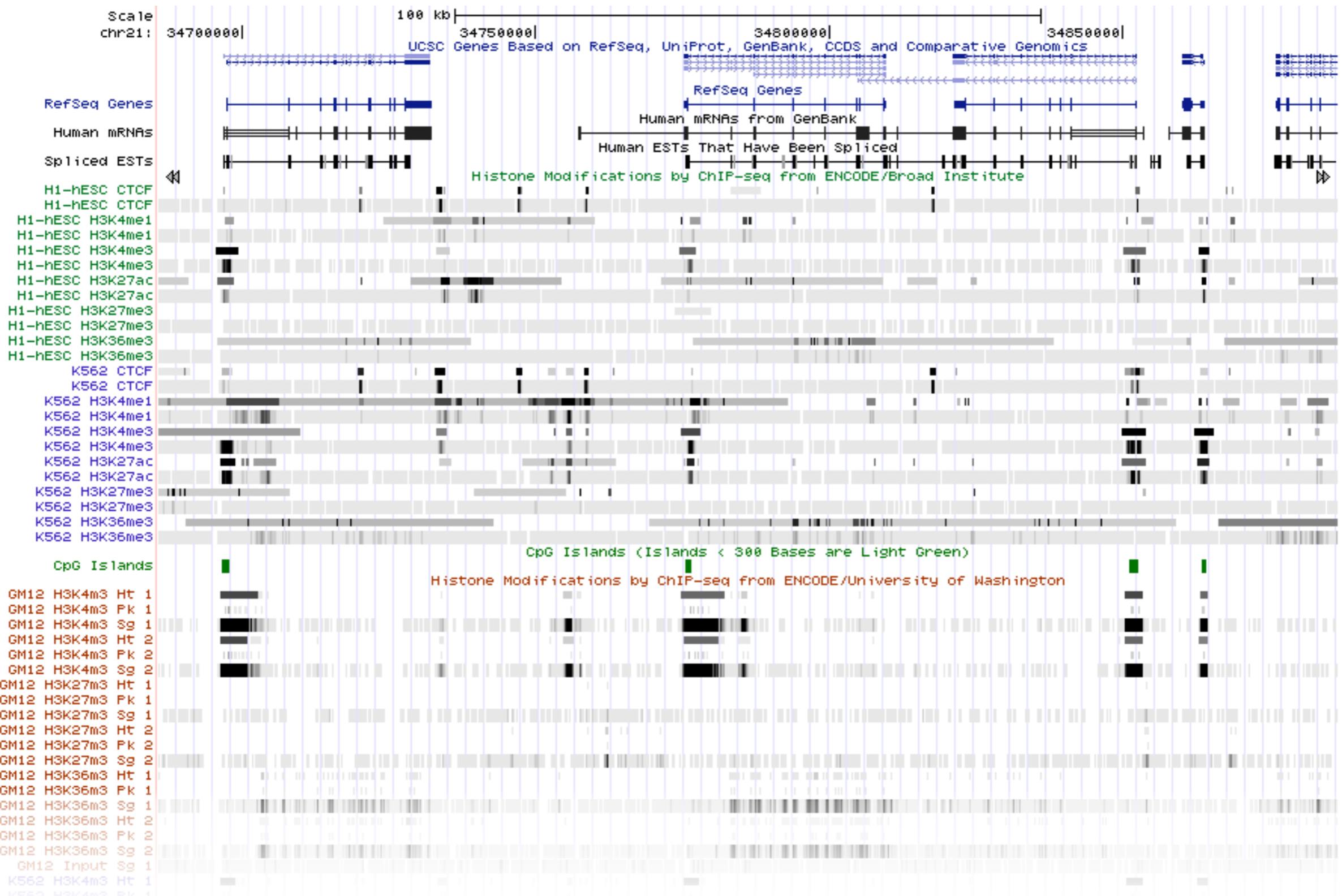
“packed”



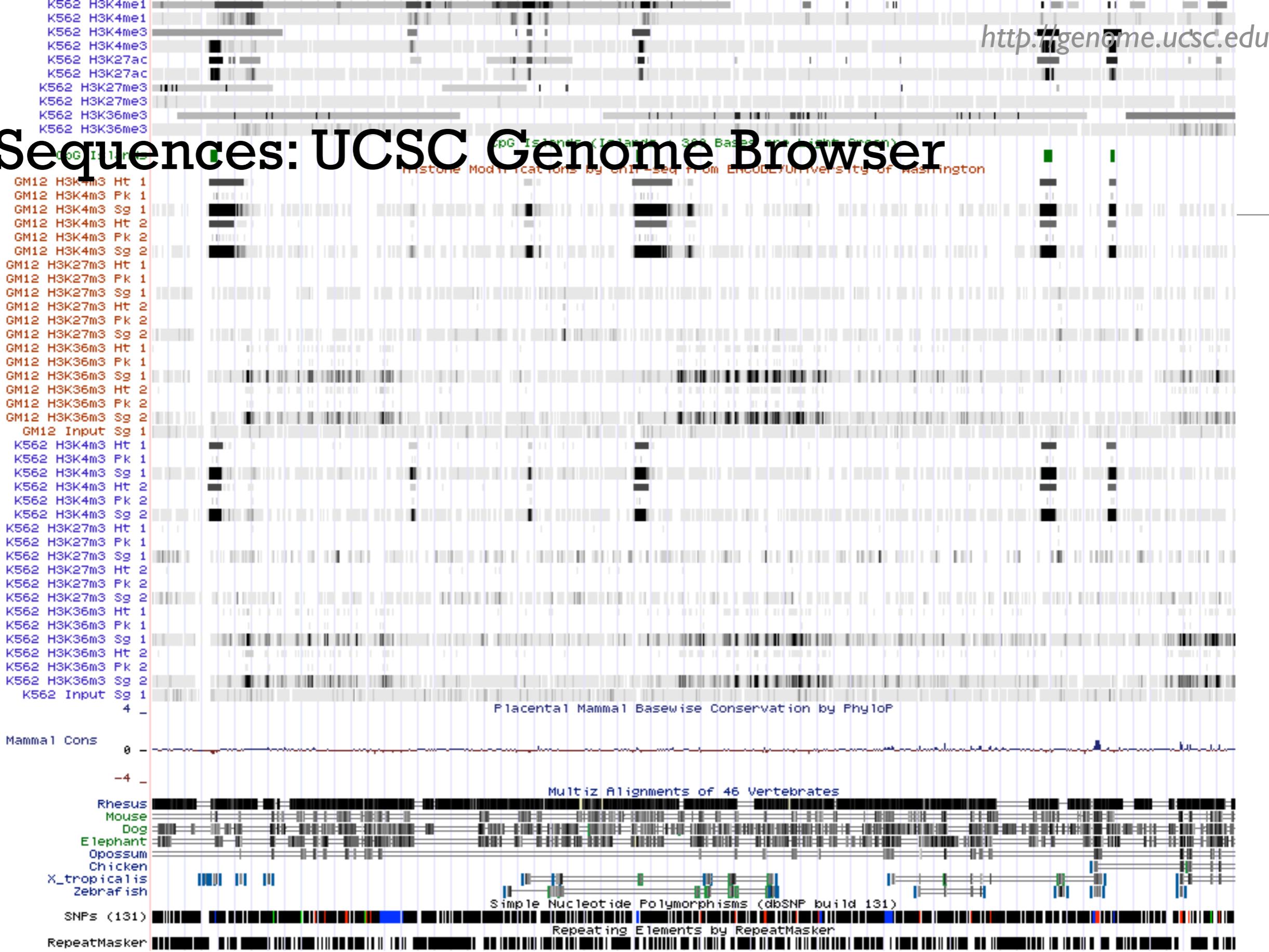
“full”



Sequences: UCSC Genome Browser

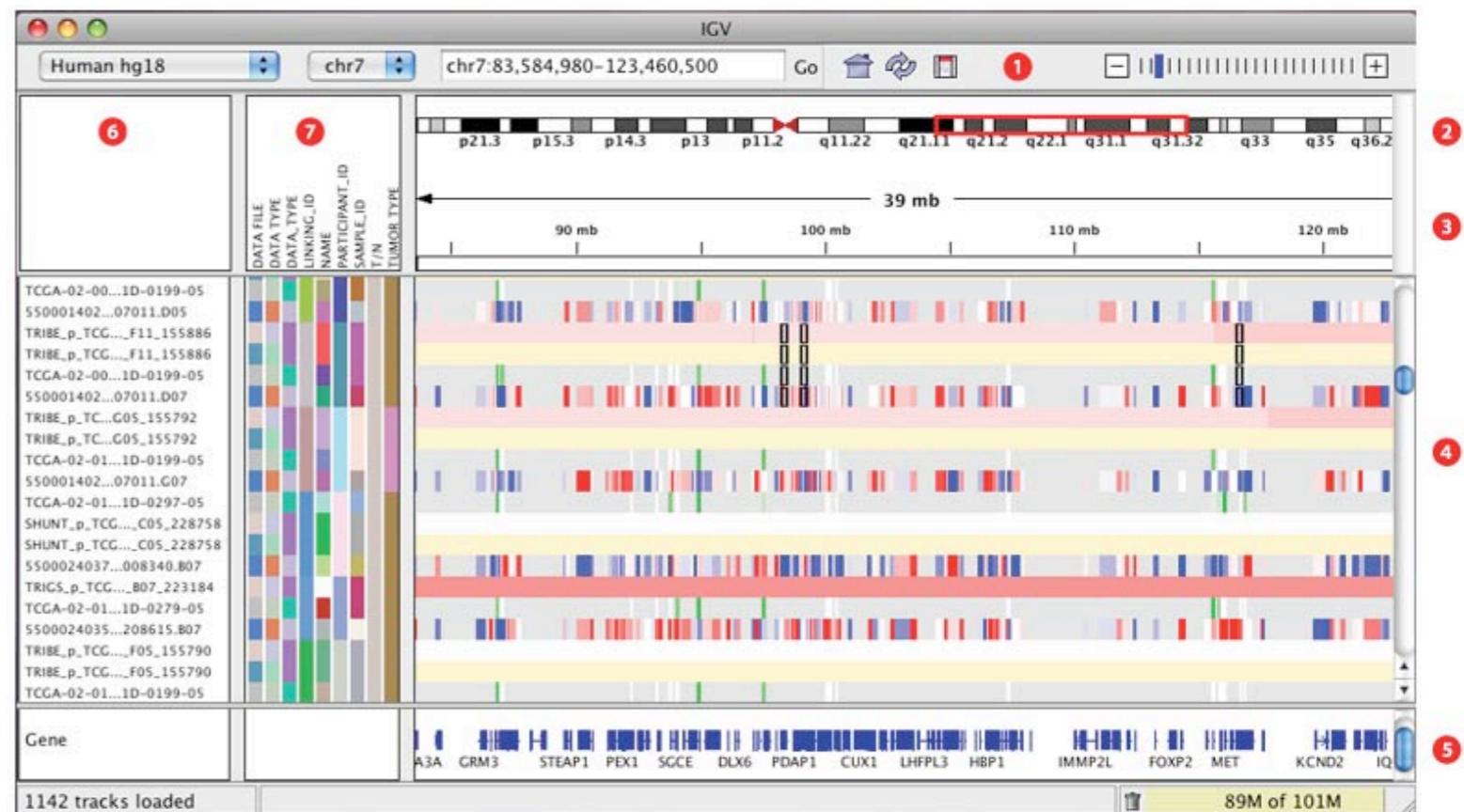


Sequences: UCSC Genome Browser

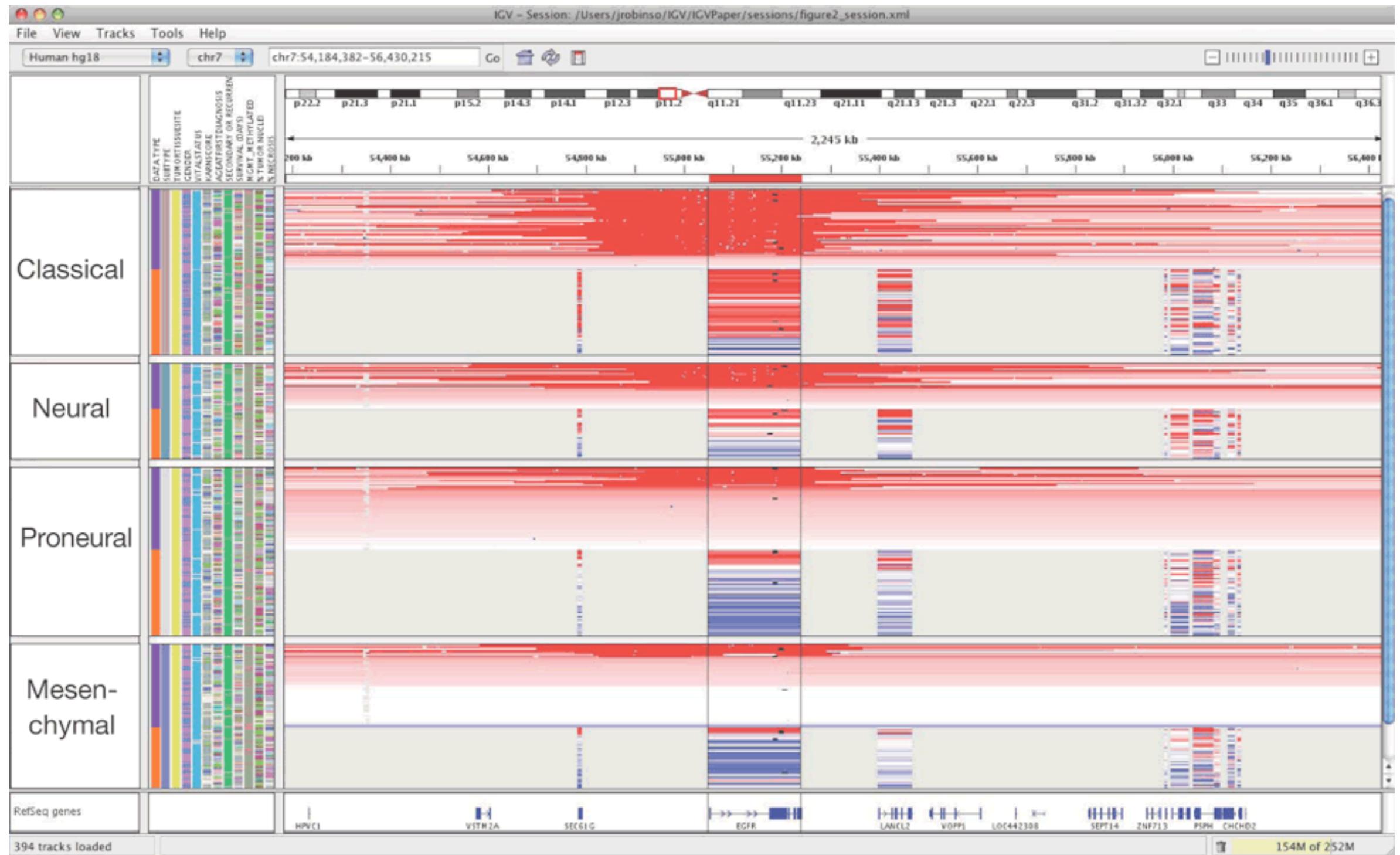


Sequences: Integrative Genomics Viewer (IGV)

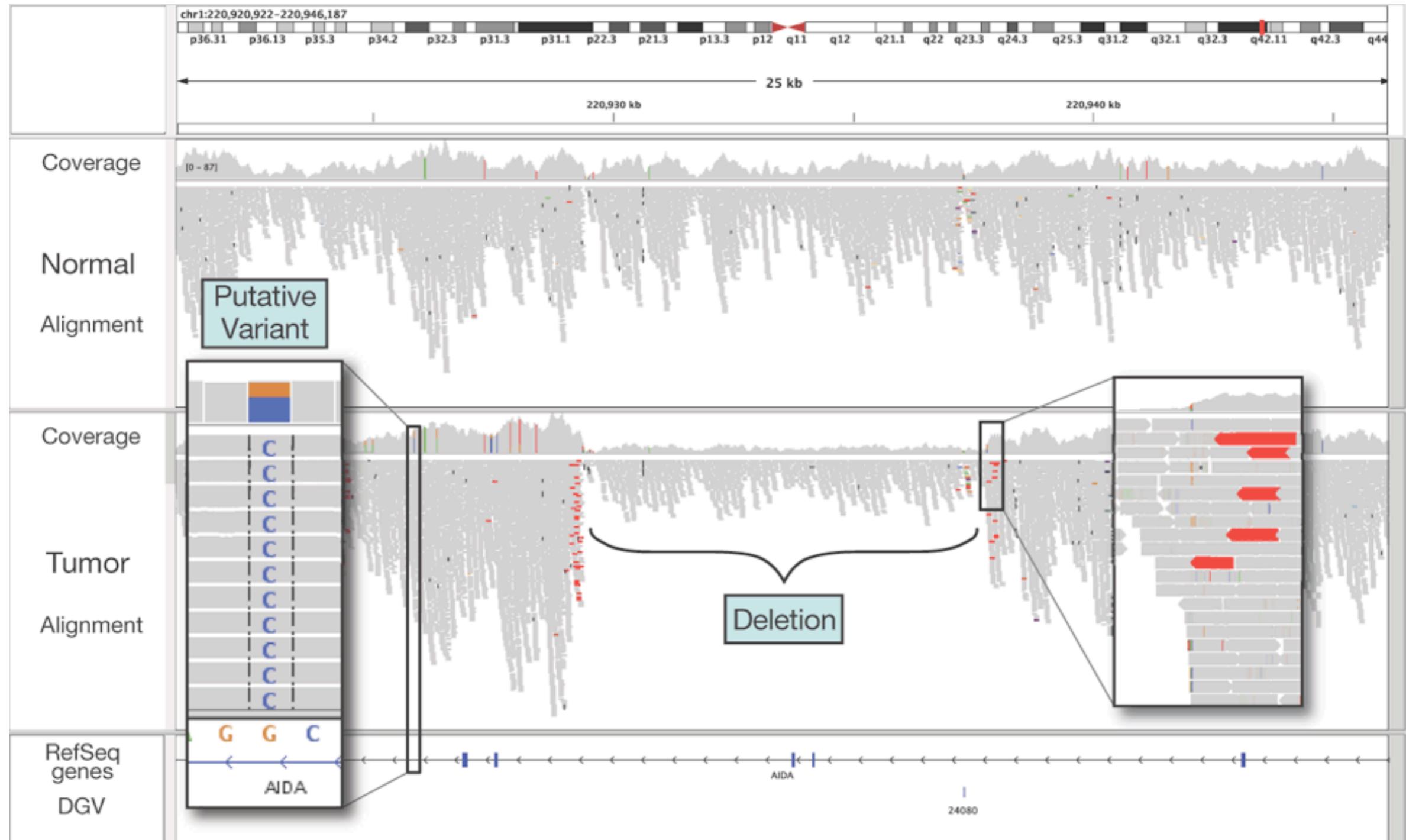
- visualization tool for interactive exploration of large, integrated datasets.
- supports a wide variety of data types including sequence alignments, expression data, copy number variation, RNA-seq, annotations



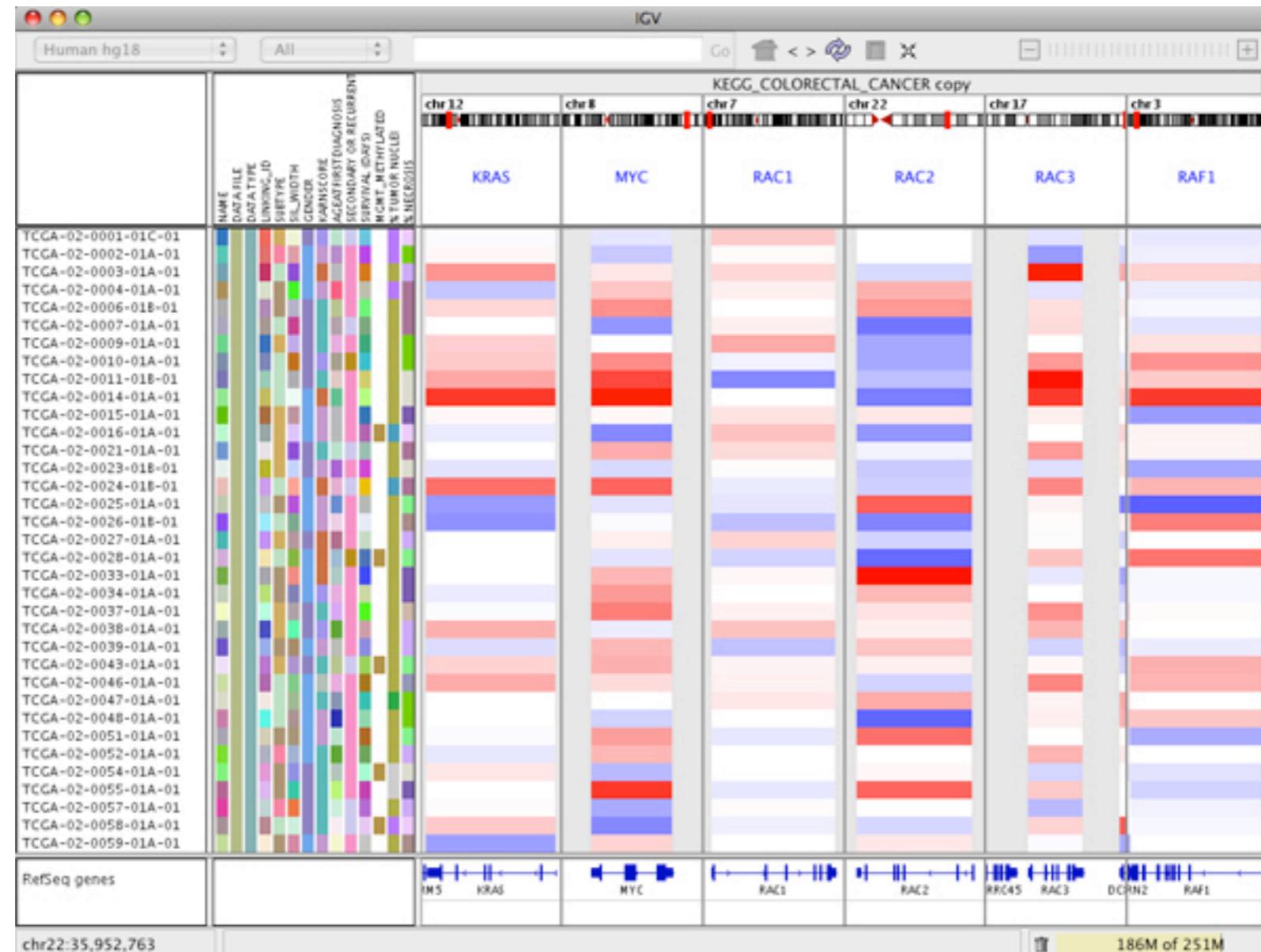
Sequences: Integrative Genomics Viewer (IGV)



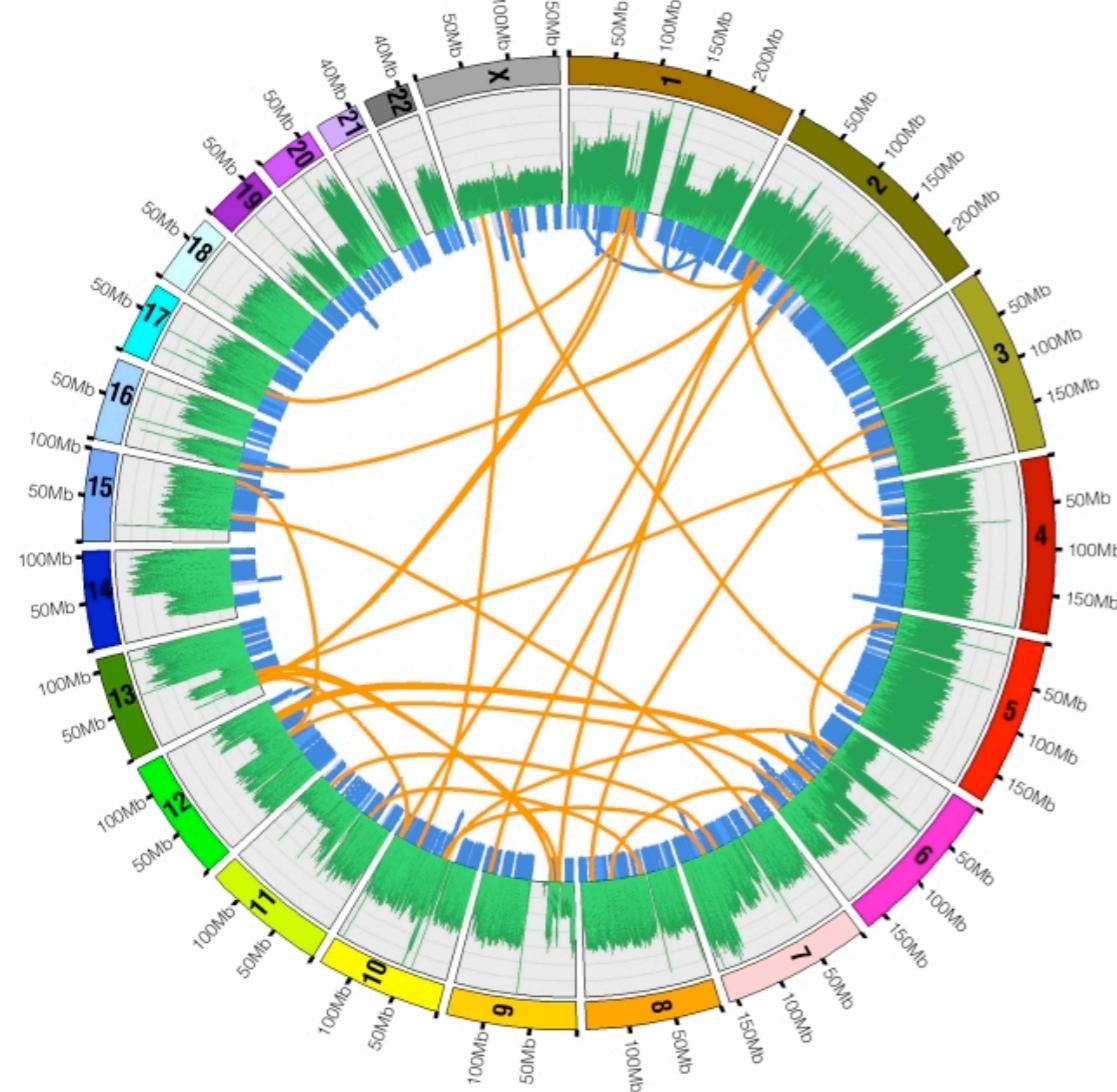
Sequences: Integrative Genomics Viewer (IGV)



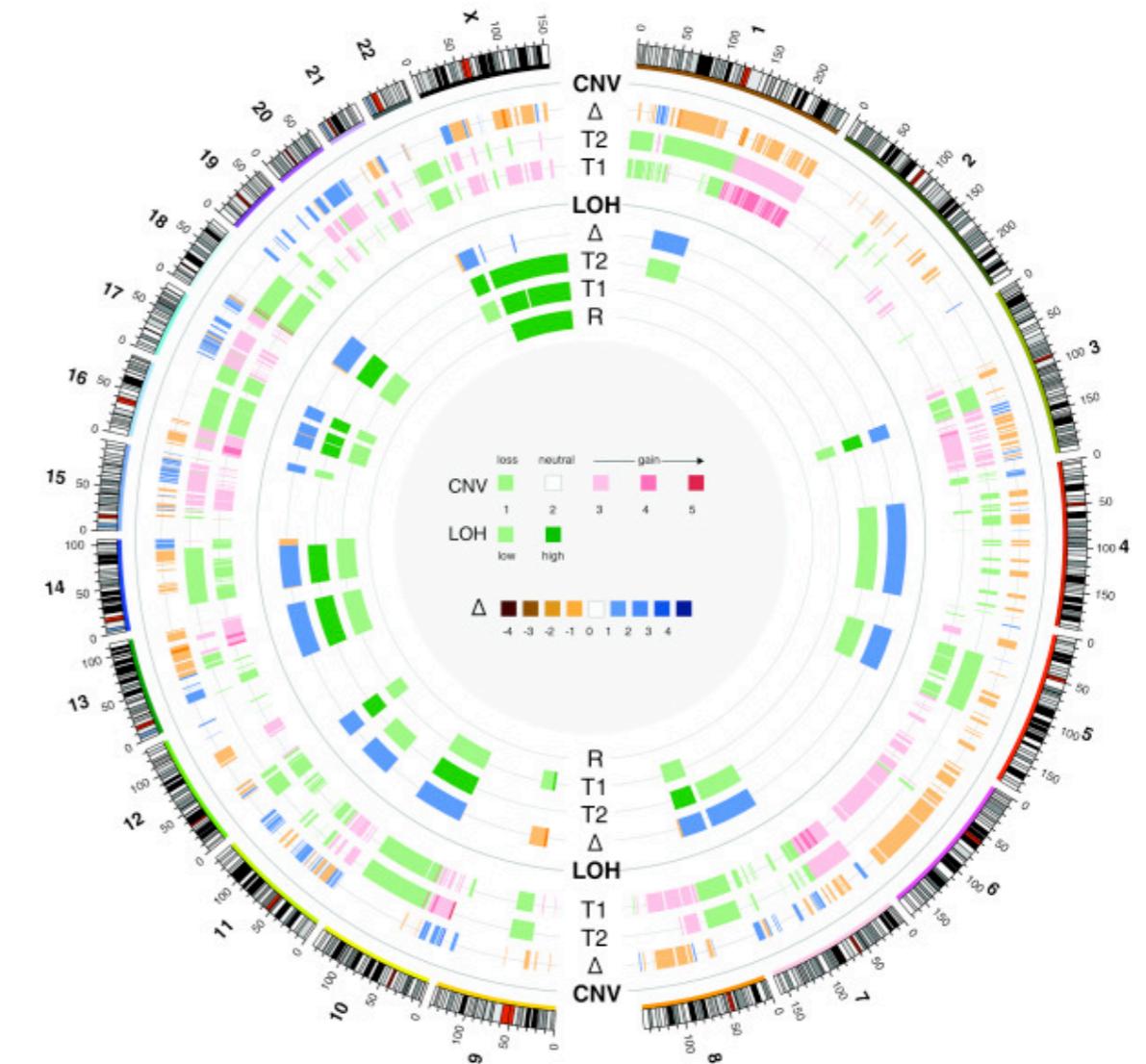
Sequences: Integrative Genomics Viewer (IGV)



Sequences: Circos

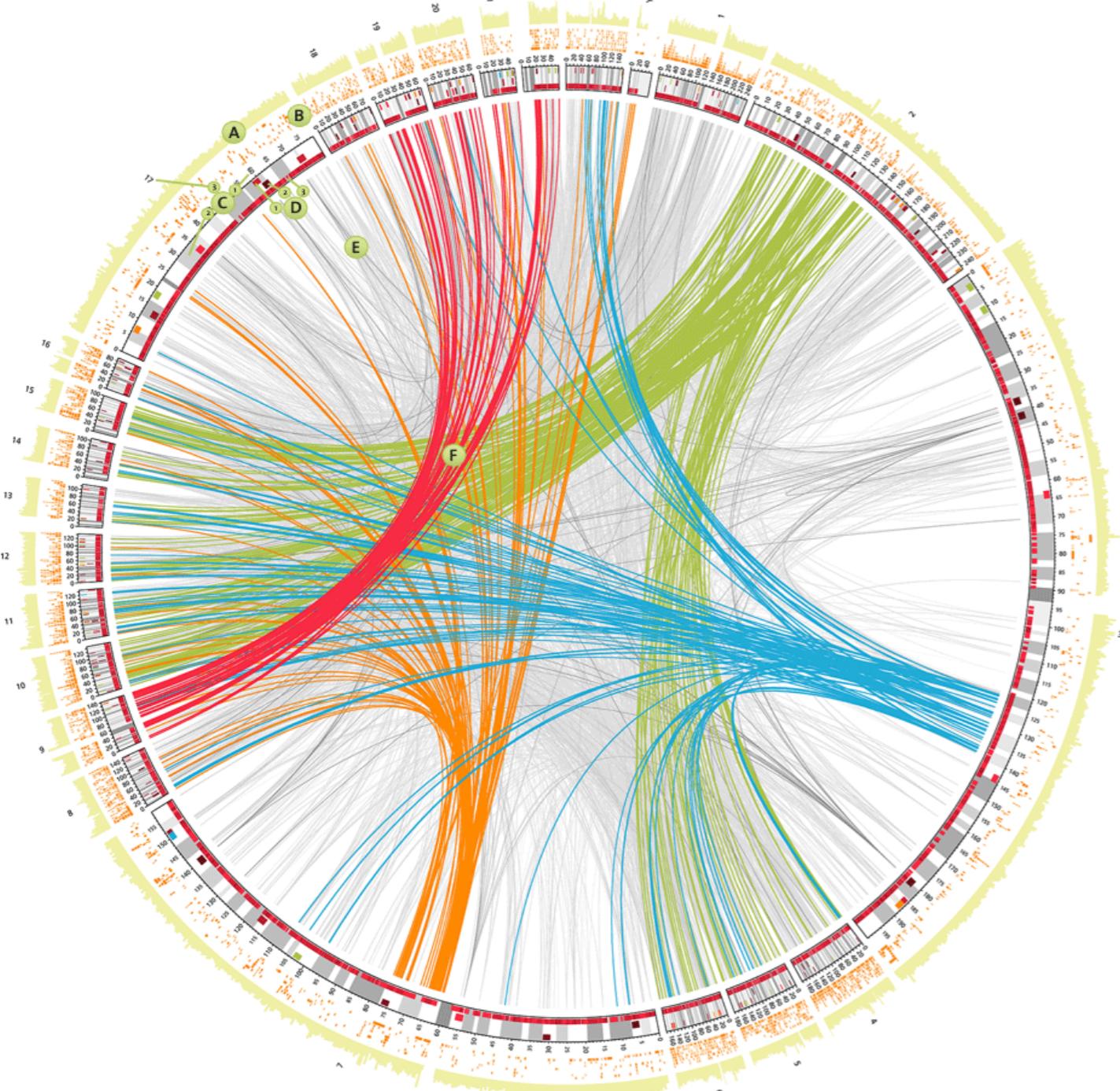


Clark et al. 2009, PLoS Genetics



Jones et al. 2010, Genome Biology

Sequences: Circos



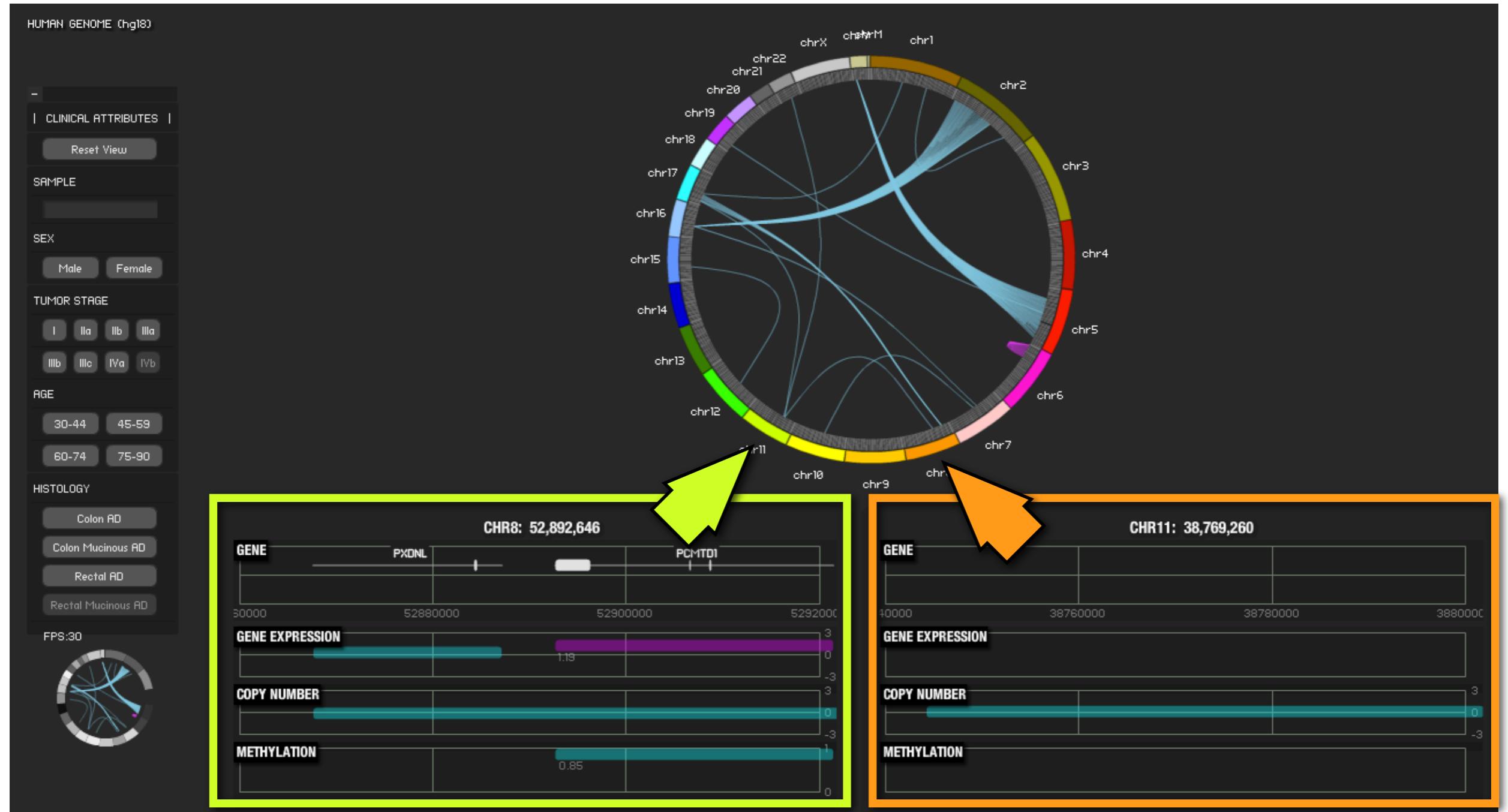
Sequences: Circos



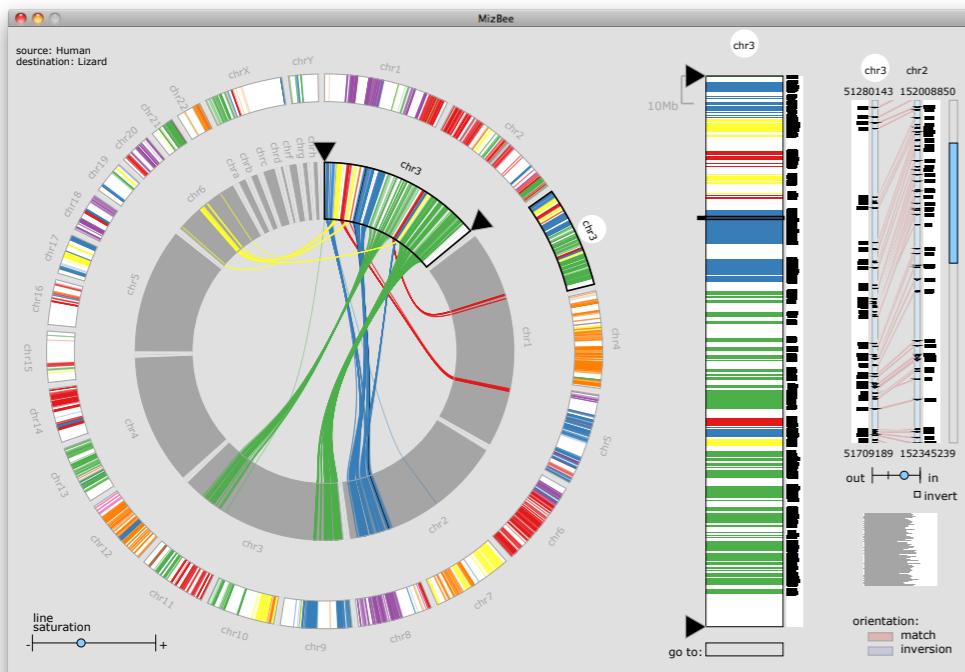
Sequences: Seqeyes



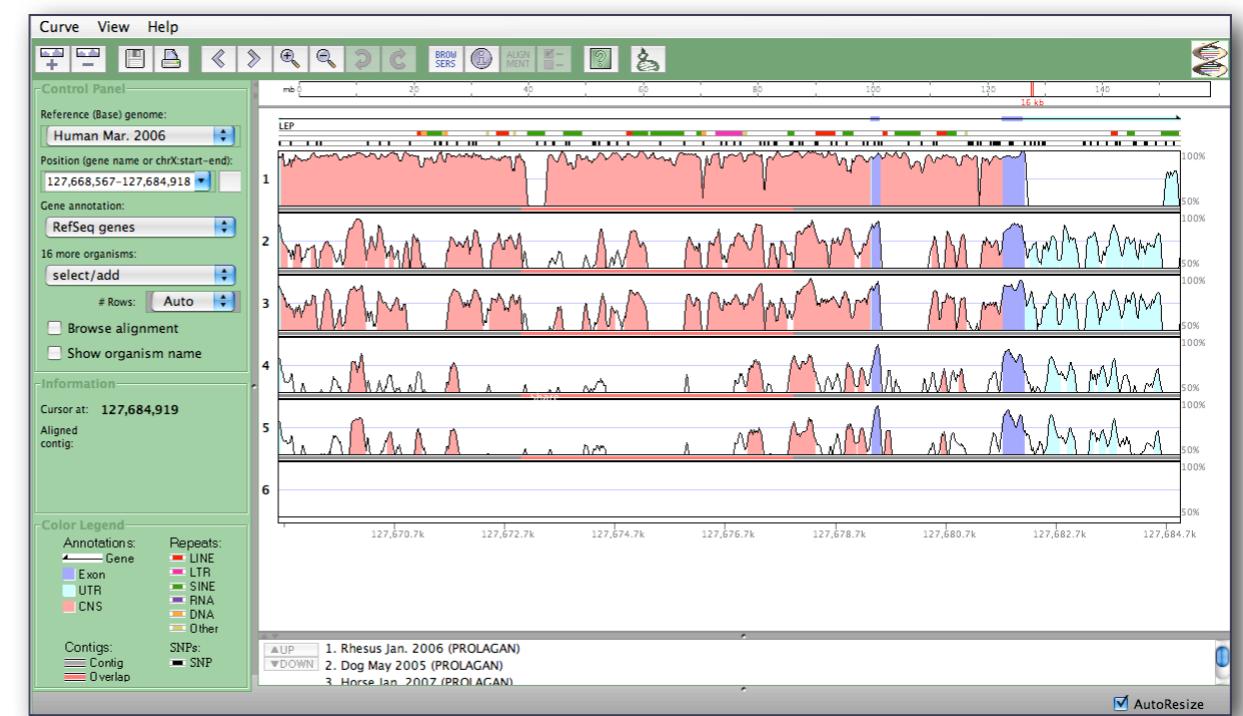
Sequences: Seqeyes



Sequences: Comparative Genomics

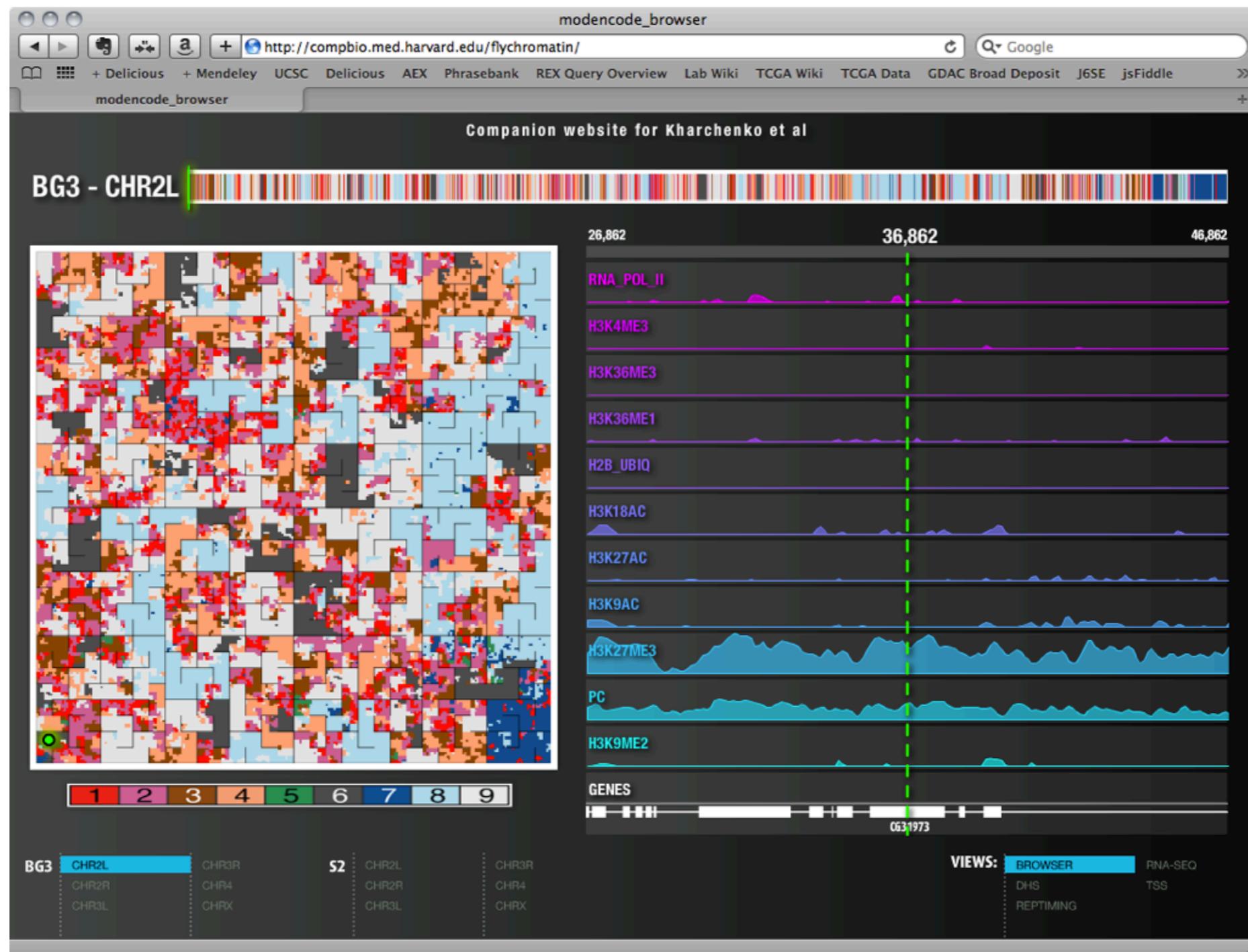


<http://www.mizbee.org>

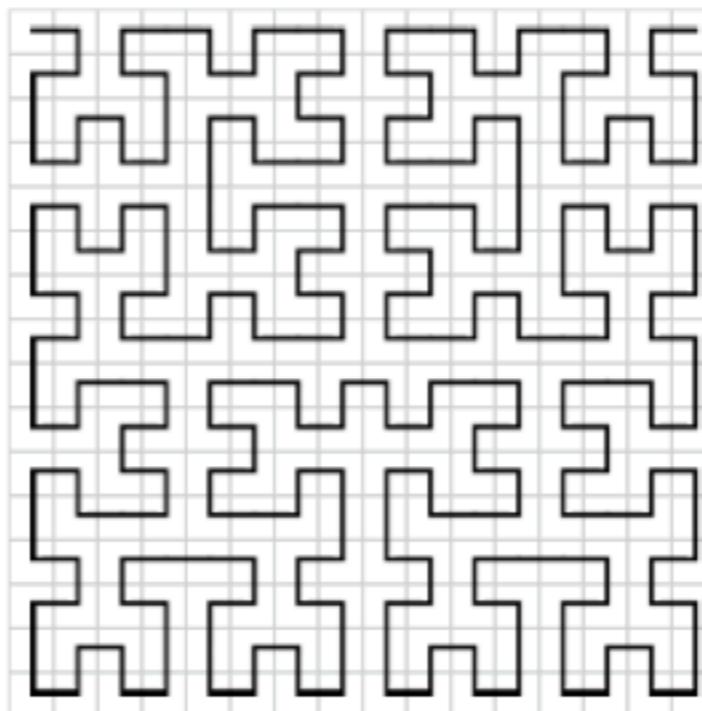


<http://genome.lbl.gov/vista>

Sequences: Epigenomics



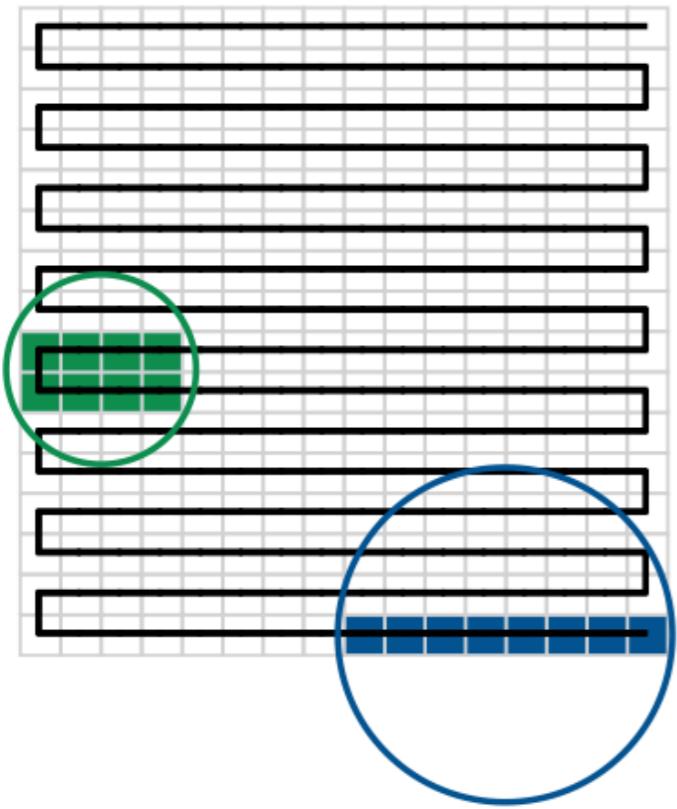
Space-Filling Curves: Hilbert Curve



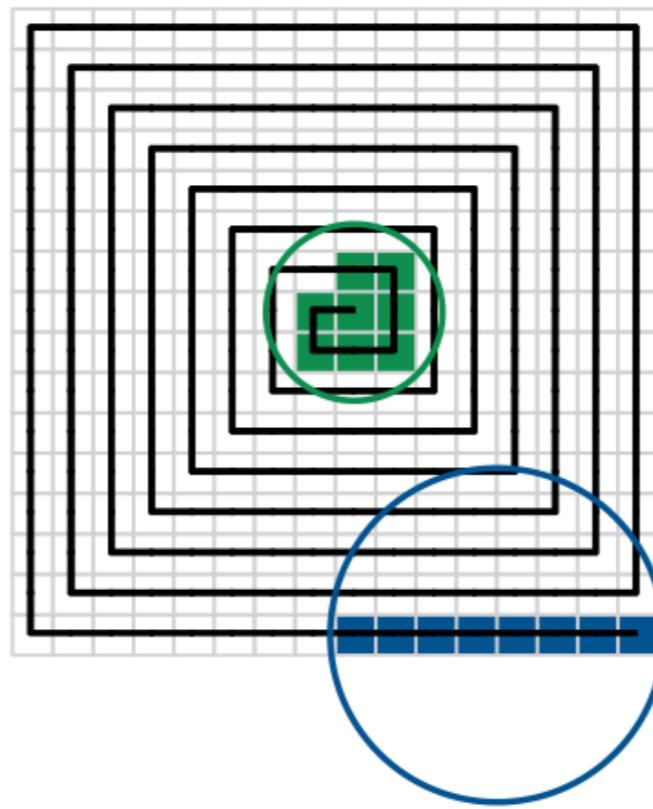
Hilbert Curve

1D sequence mapped onto 2D grid

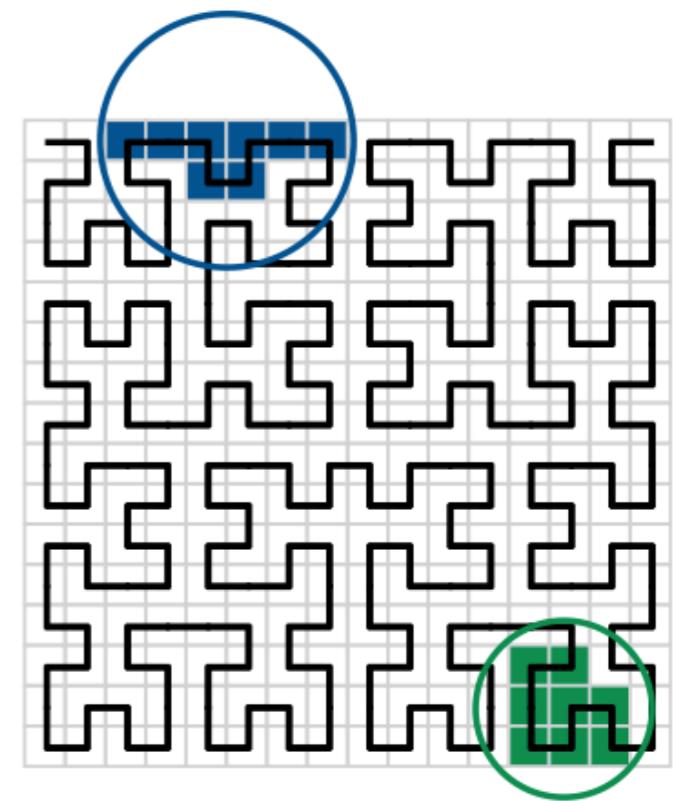
Space-Filling Curves: Locality



Zig-Zag Curve



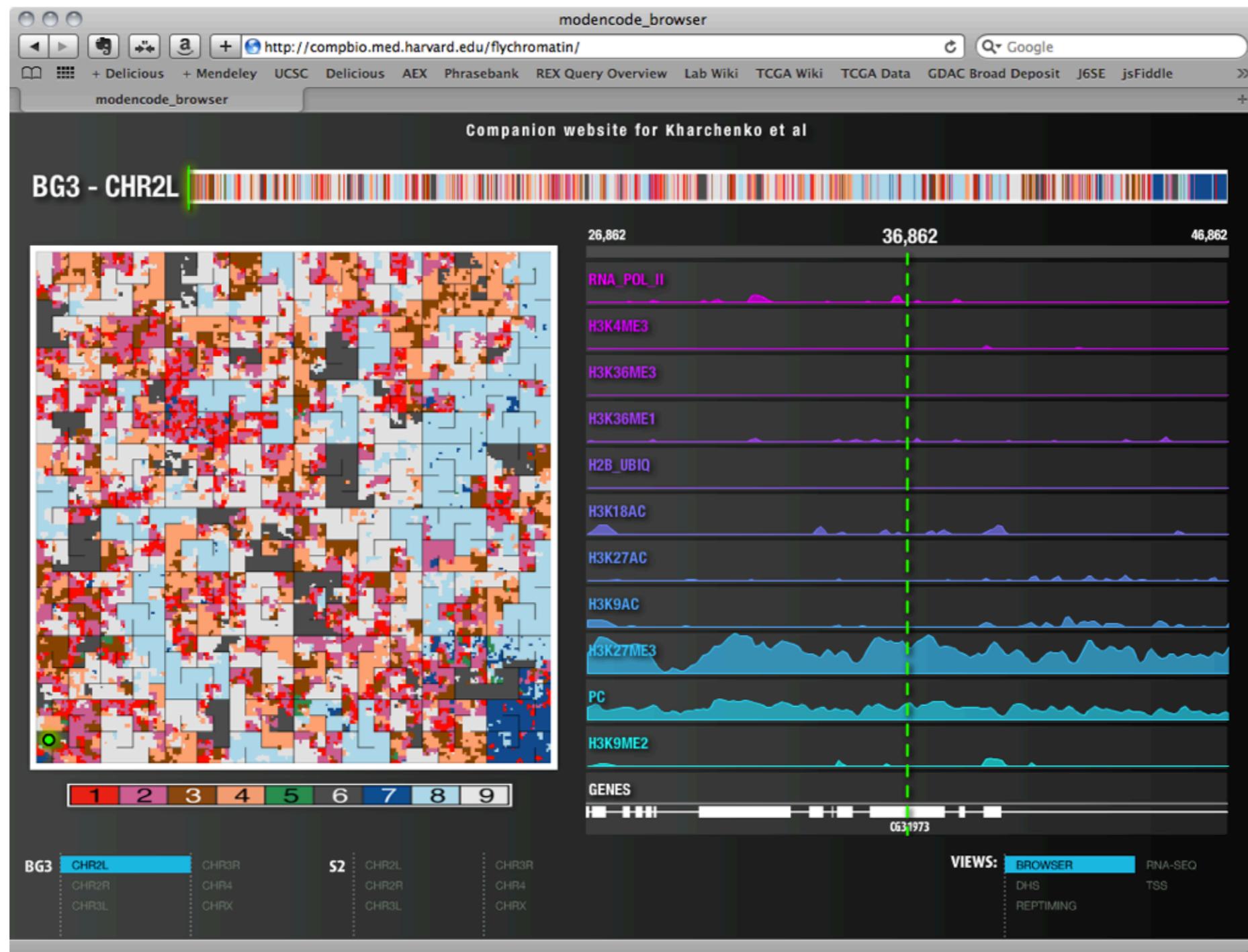
Spiral Curve



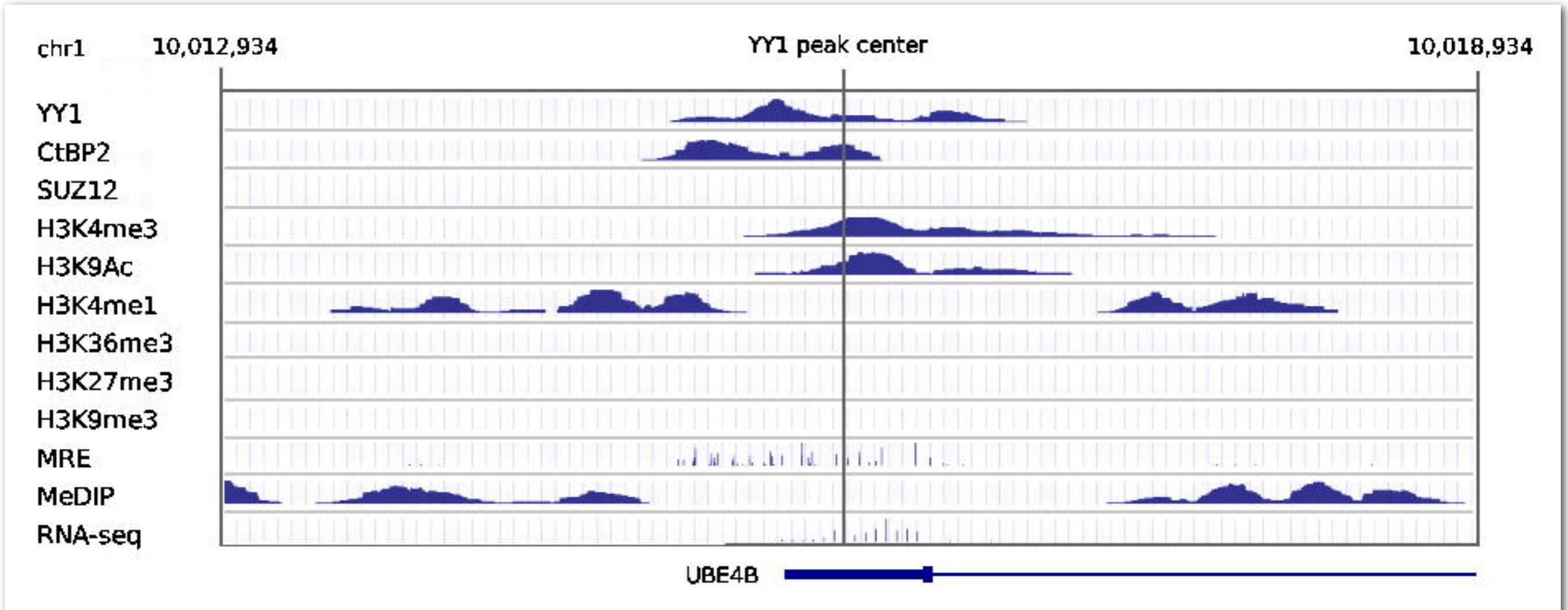
Hilbert Curve

Better locality: Subsequences are more compact and therefore easier to perceive and select.

Sequences: Epigenomics

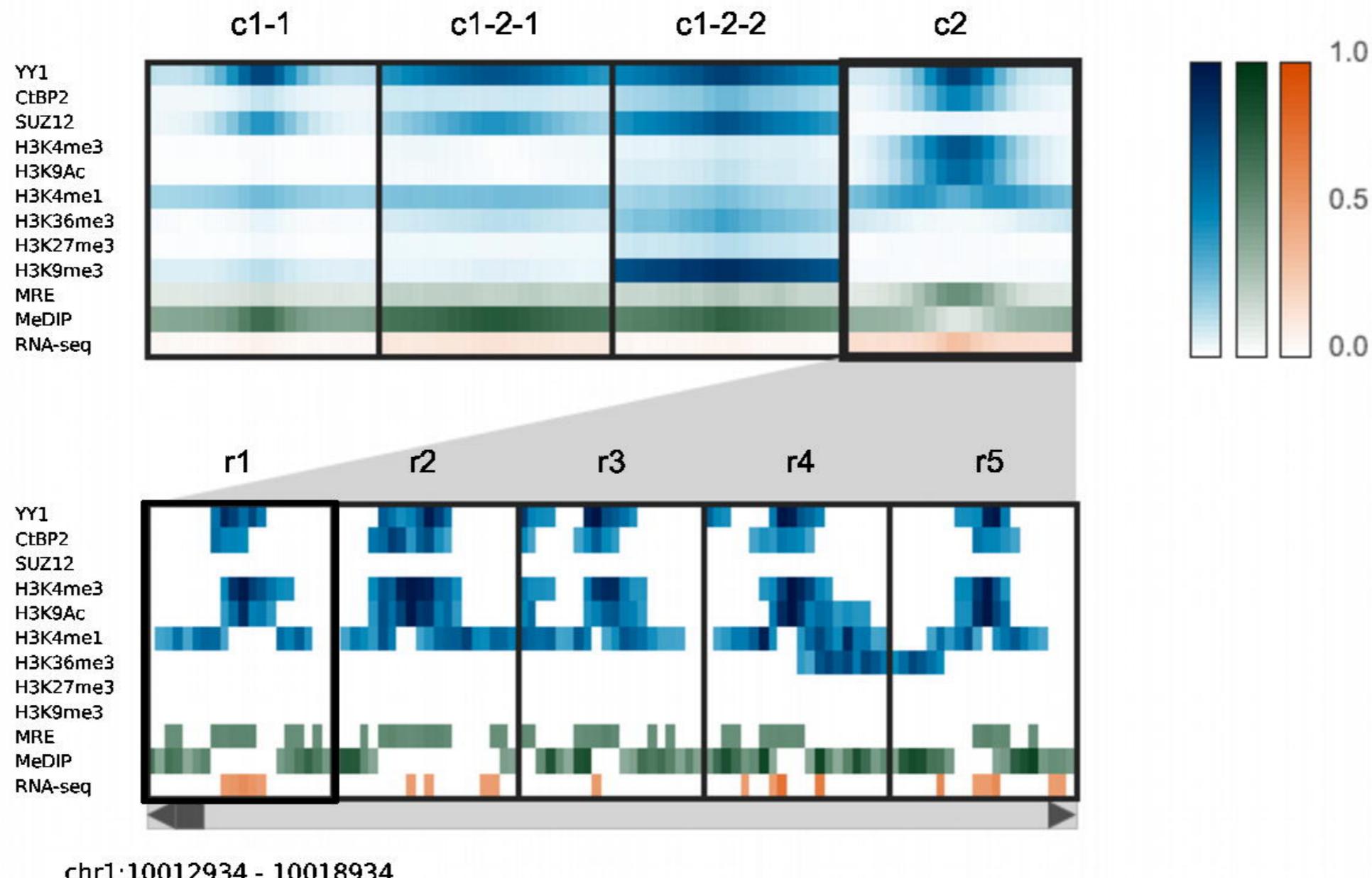


Sequences: Epigenomics



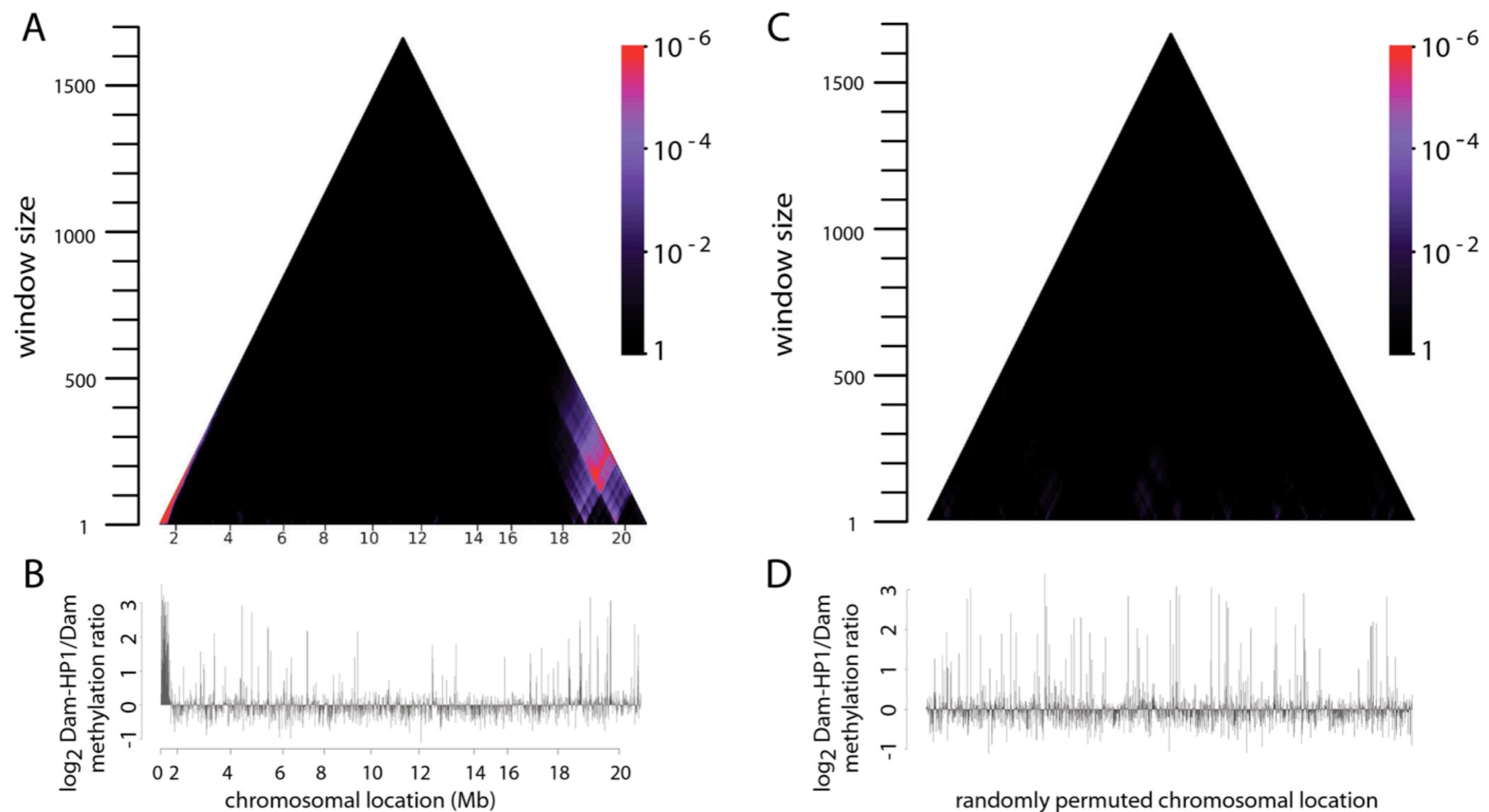
Sequences: Epigenomics

Spark Profile Summaries



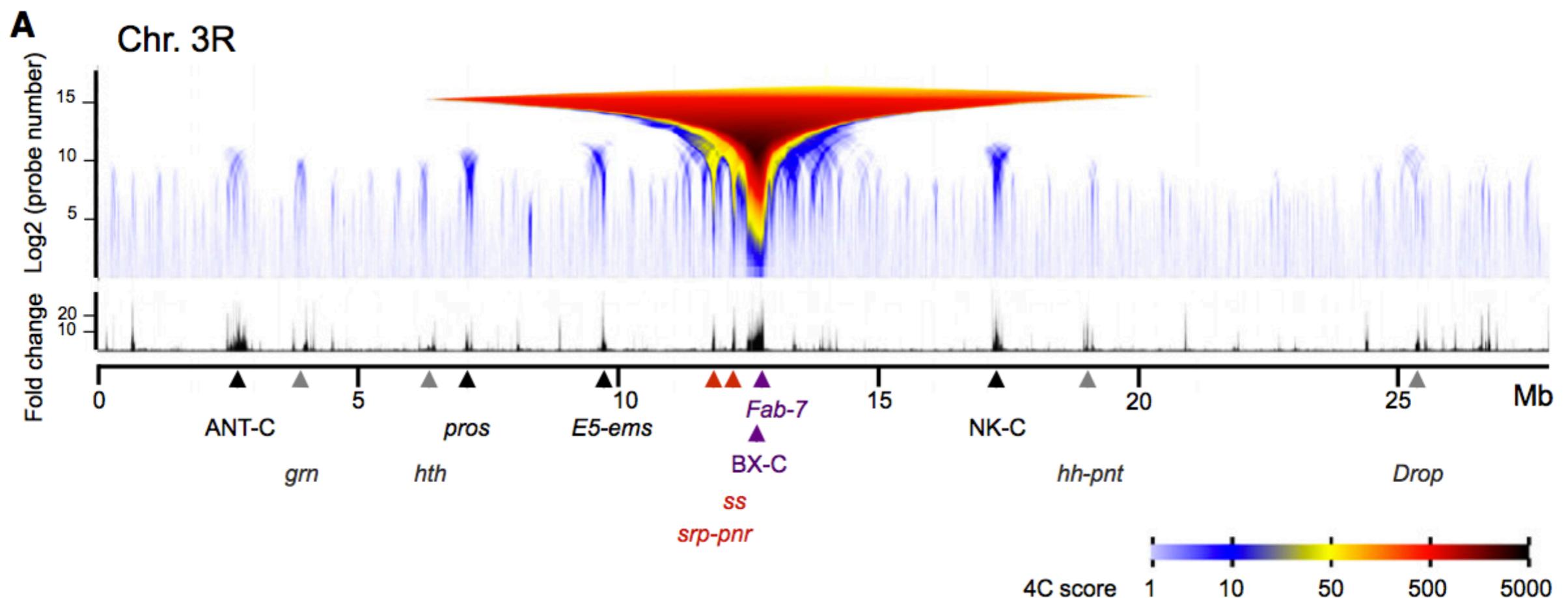
Sequences: Epigenomics

Domainogram

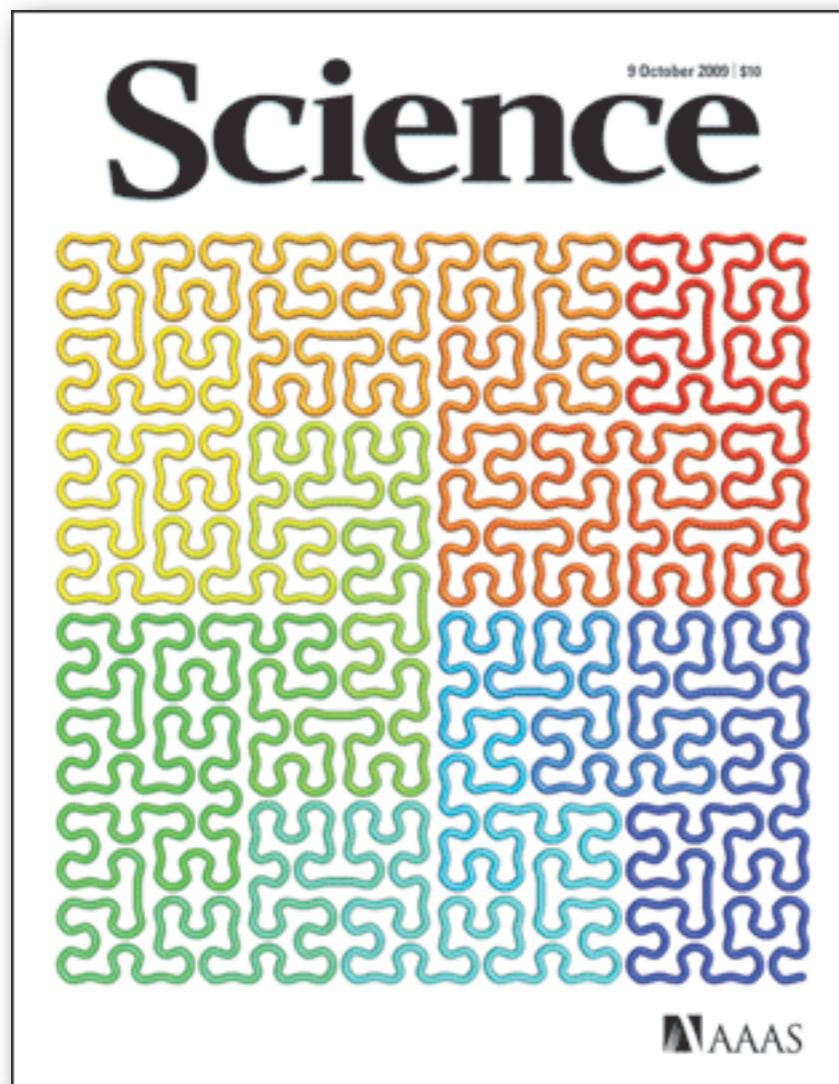


Sequences: Epigenomics

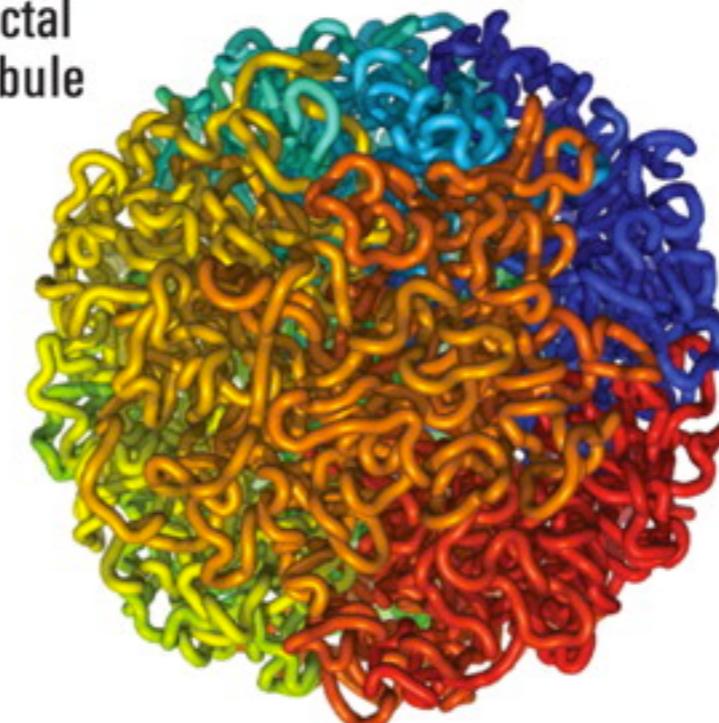
Domainogram



Sequences: 3D Genome Structure



Fractal
globule

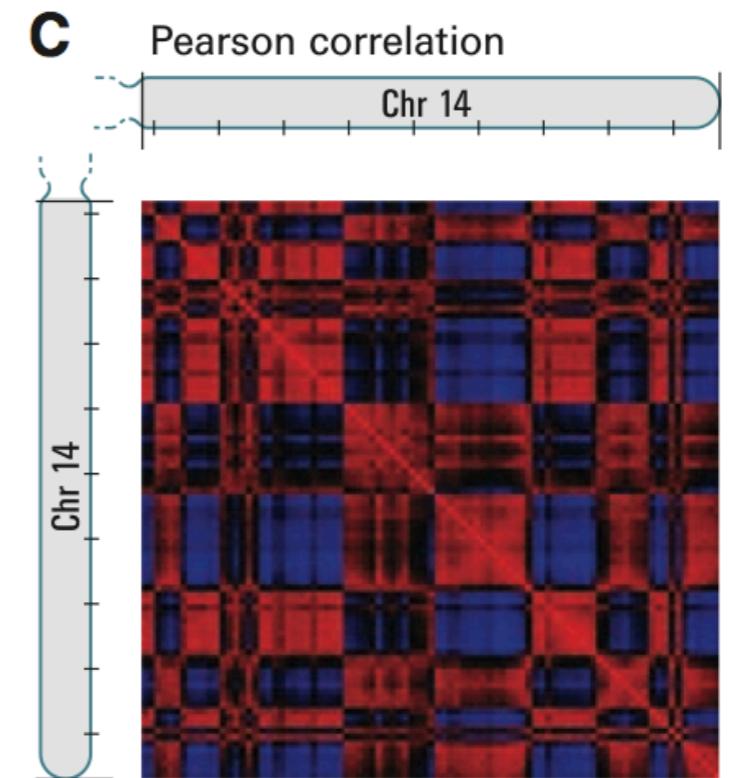
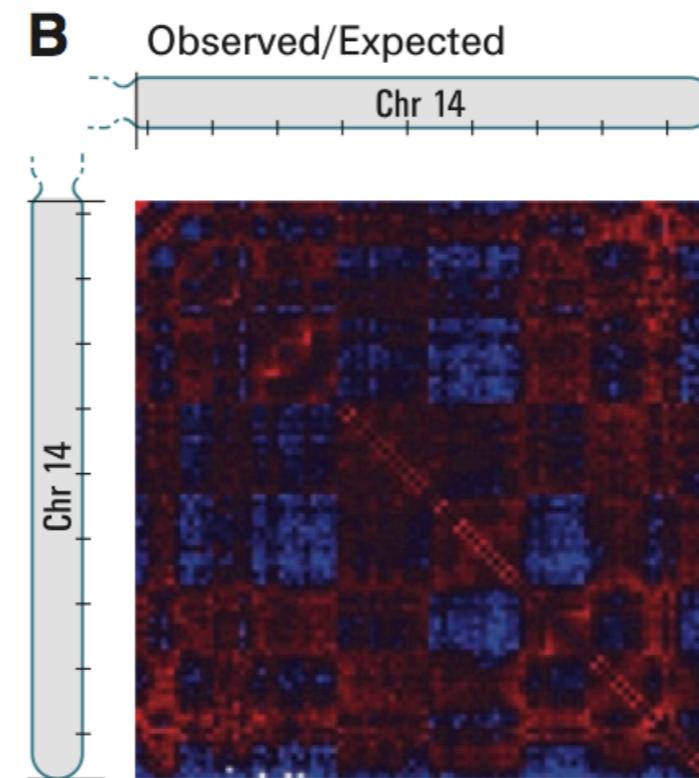
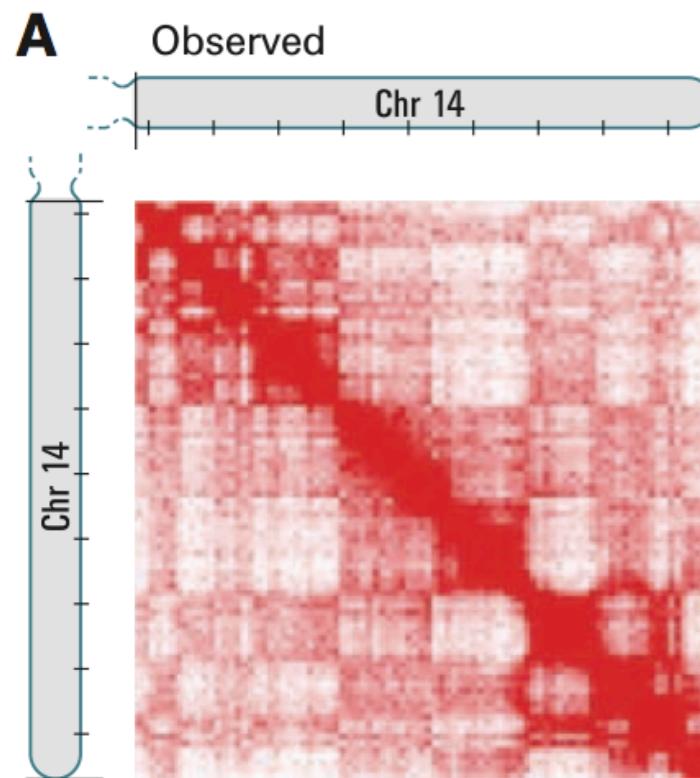


Cross-section view



Sequences: 3D Genome Structure

Contact Probability Map



Conveys Uncertainty!

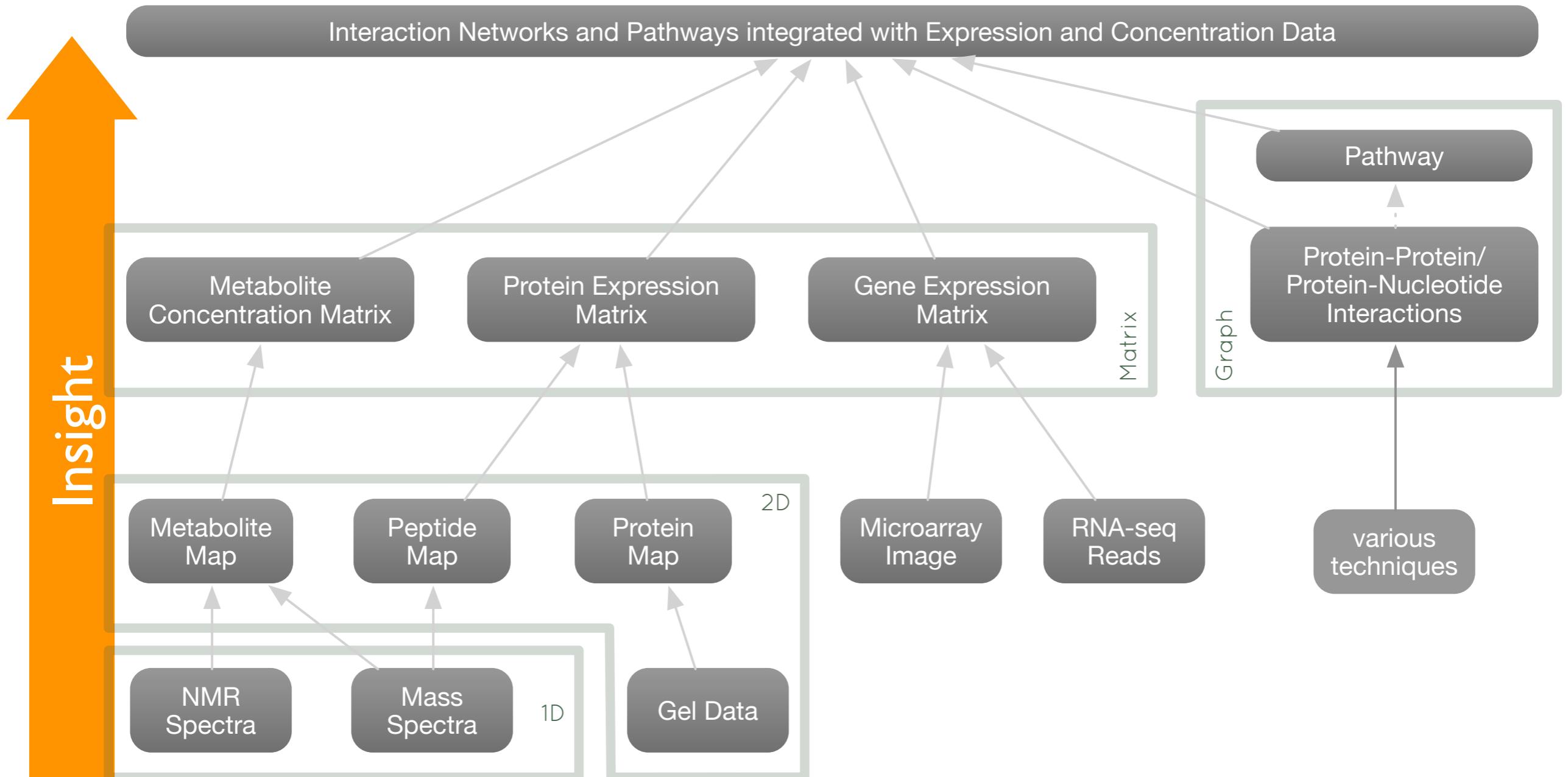
Multivariate Data

Multivariate Data

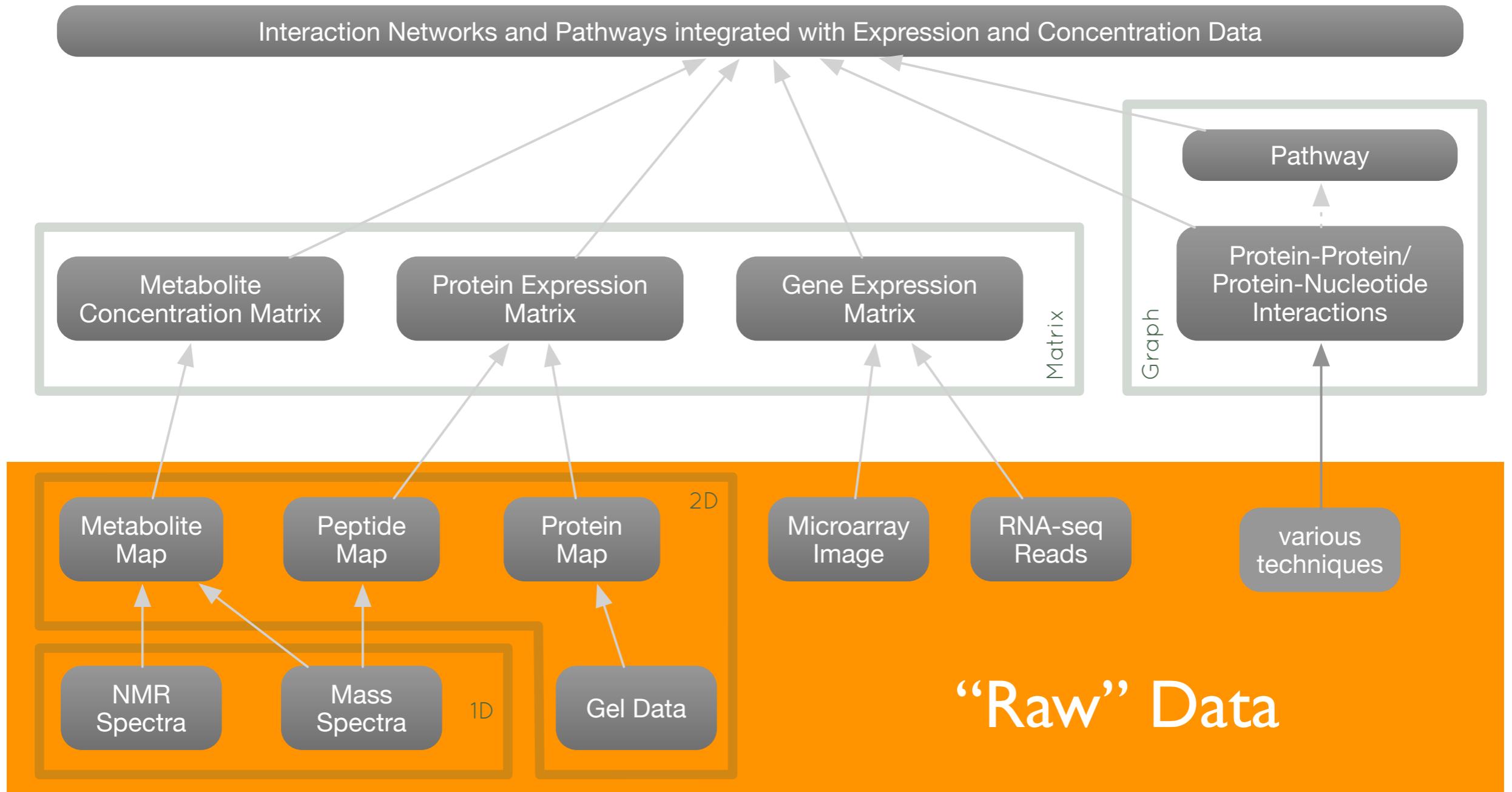
- typical “omics” data: transcriptomics, proteomics, metabolomics
- expression/concentration levels of many biological entities (transcripts, proteins, etc.) across many different conditions/time points
- entity levels measured per sample on a “genome-wide” scale
- often entities are not measured directly



Multivariate Data



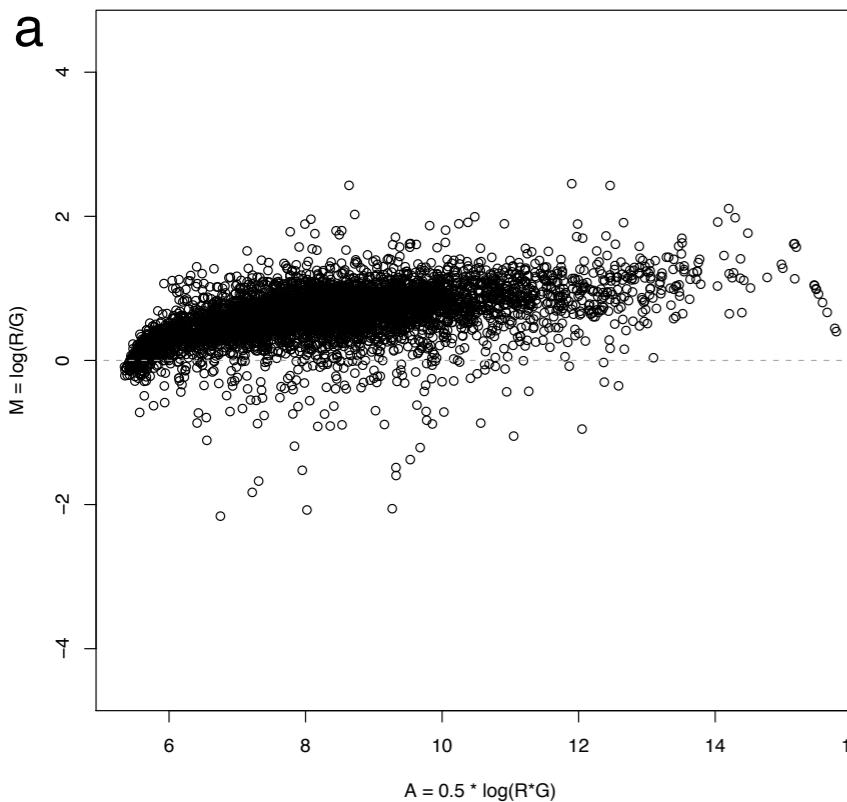
Multivariate Data: “Raw” Data



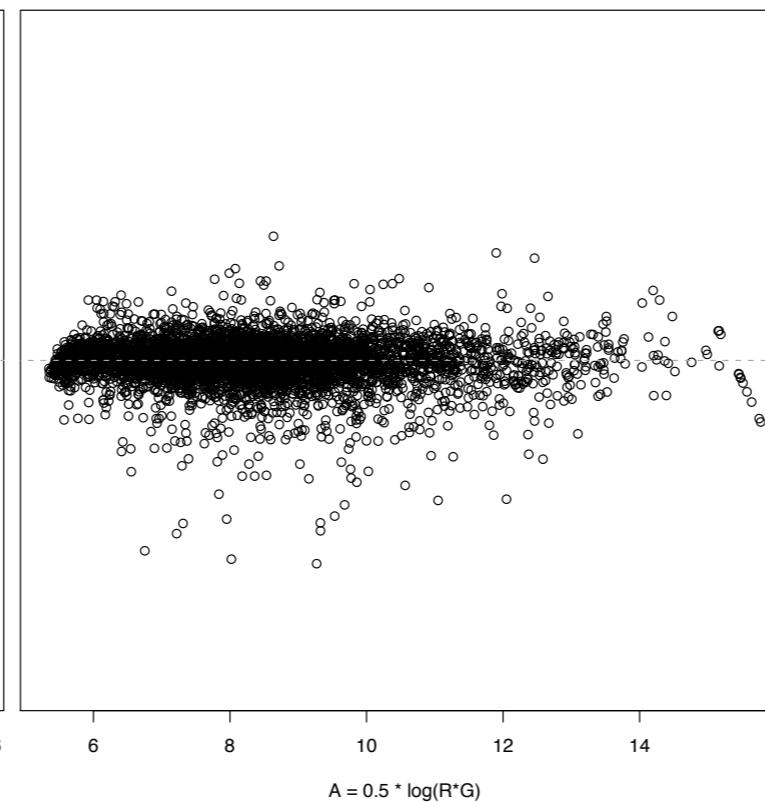
Multivariate Data: Transcriptomics

MA Plot: 1 array

before normalization

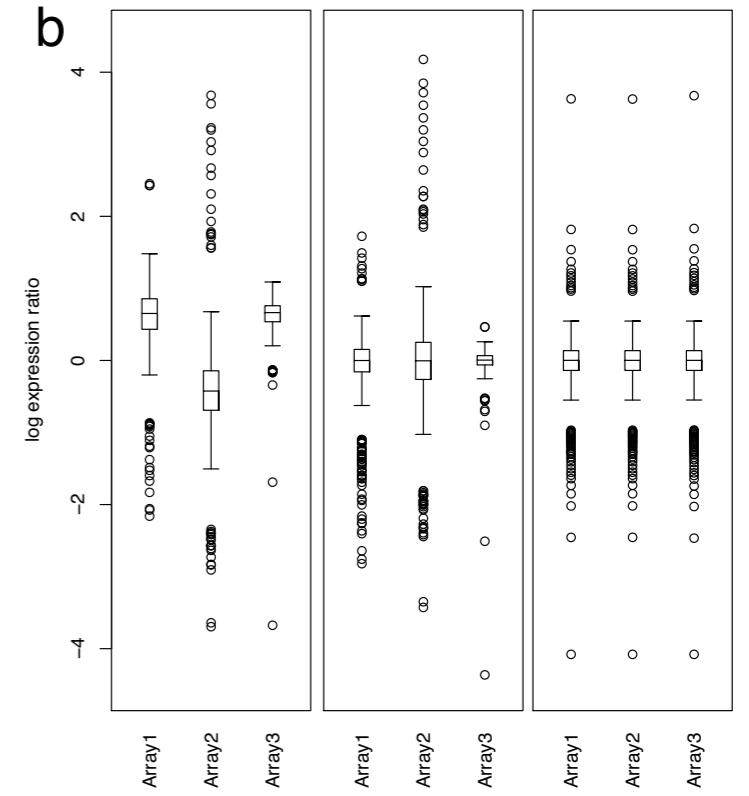


after normalization



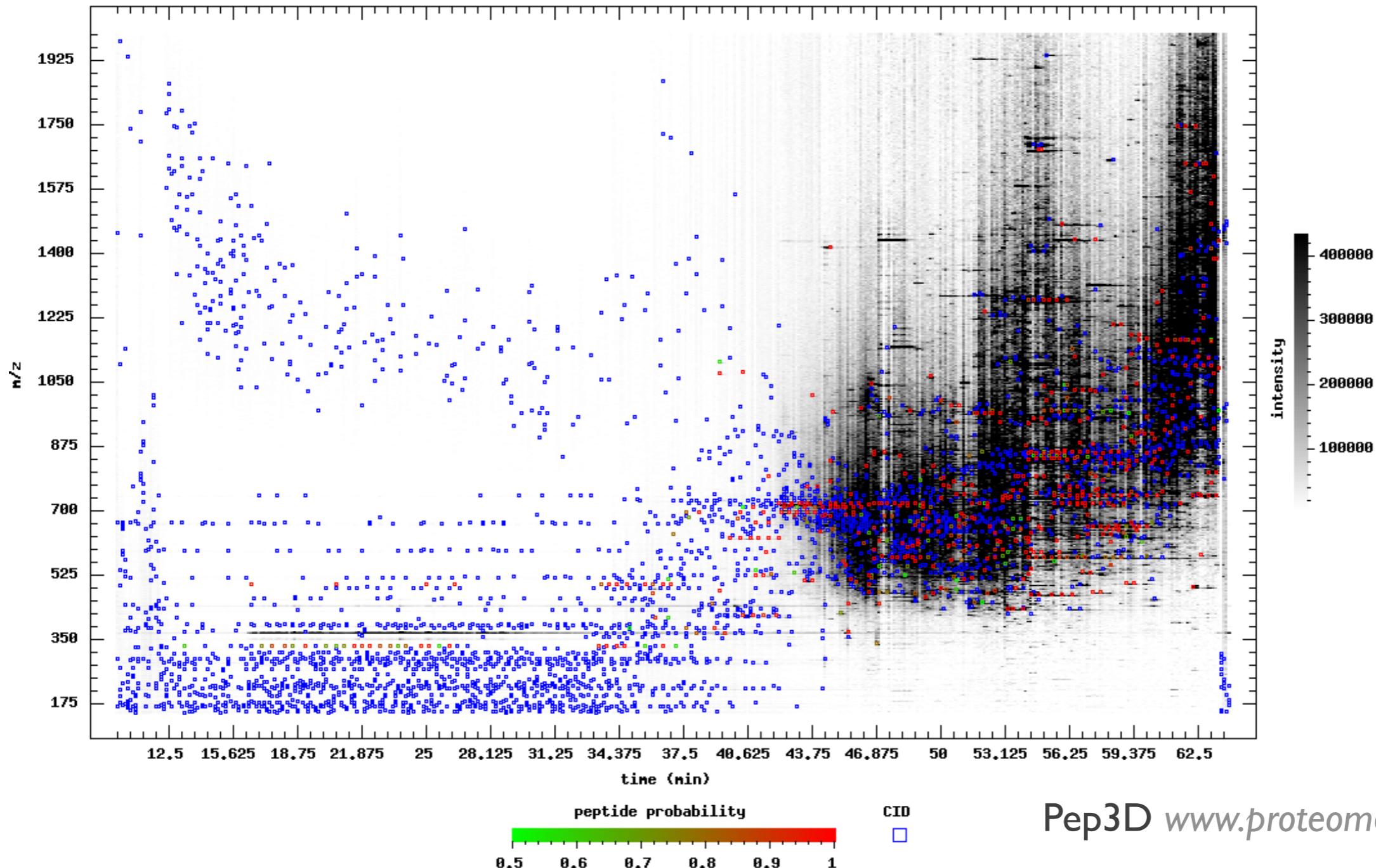
Box Plot: 3 arrays

1 2 3

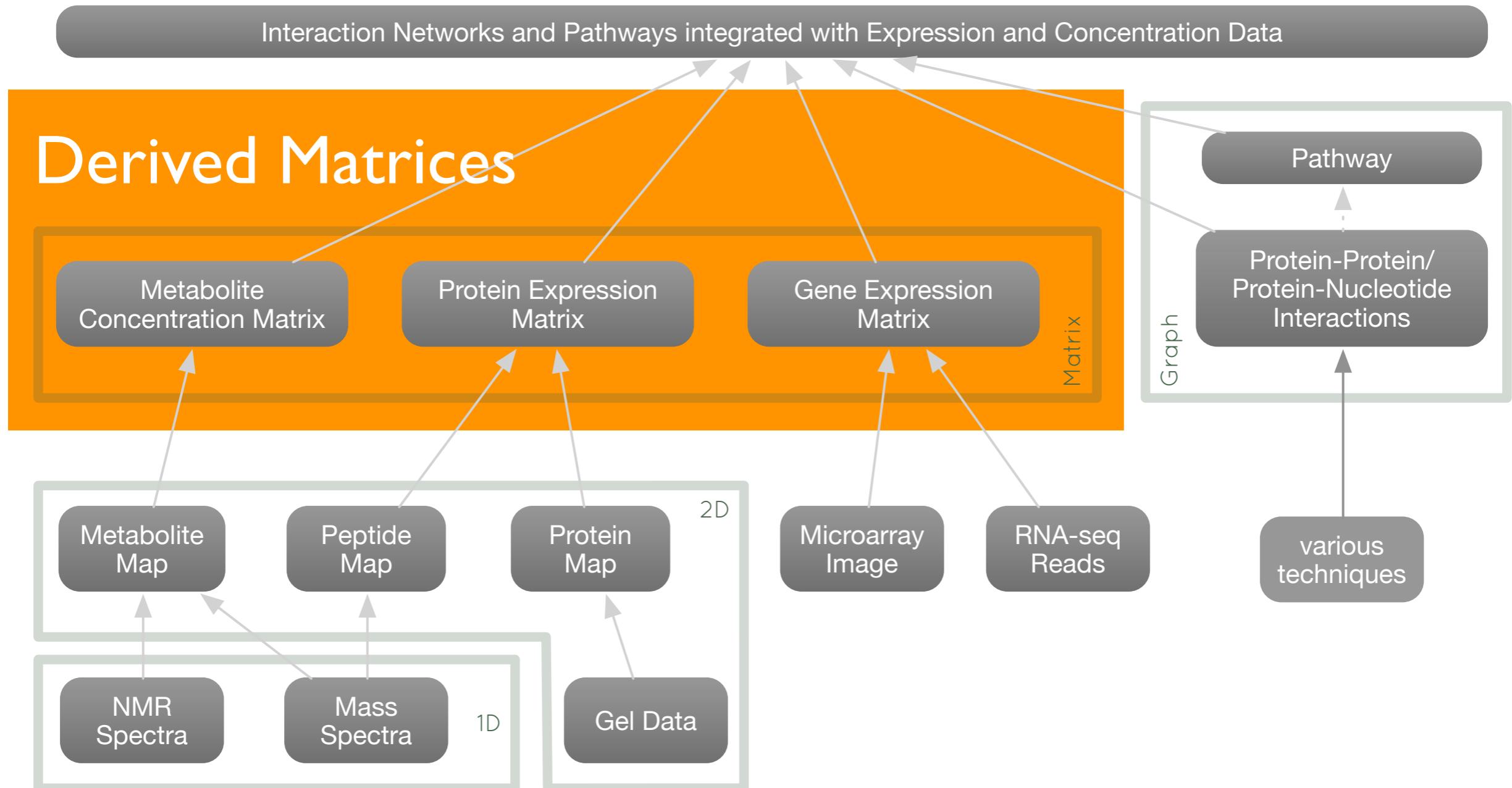


- 1 = before normalization
- 2 = after within-array normalization
- 3 = after between-array normalization

Multivariate Data: LC-MS/MS Proteomics

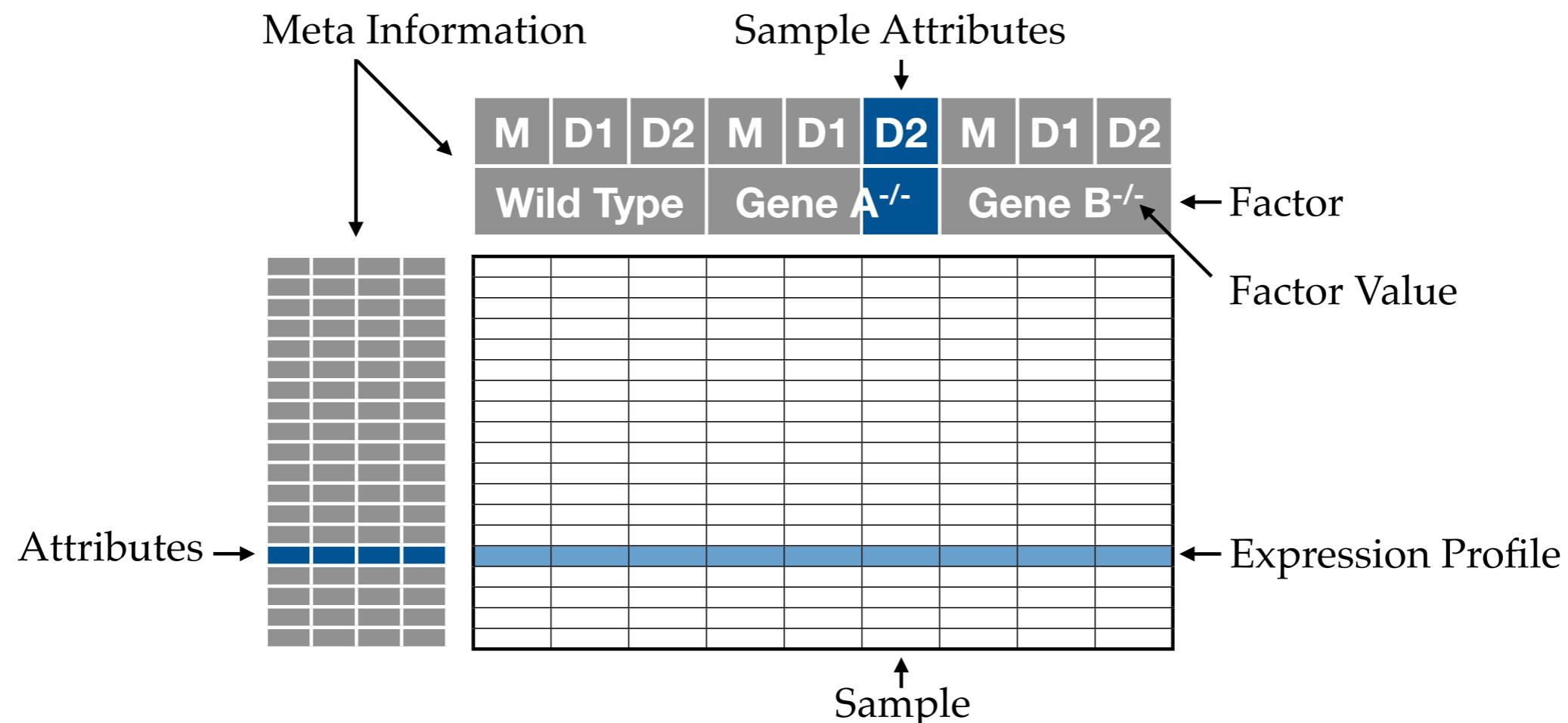


Multivariate Data: Derived Matrices



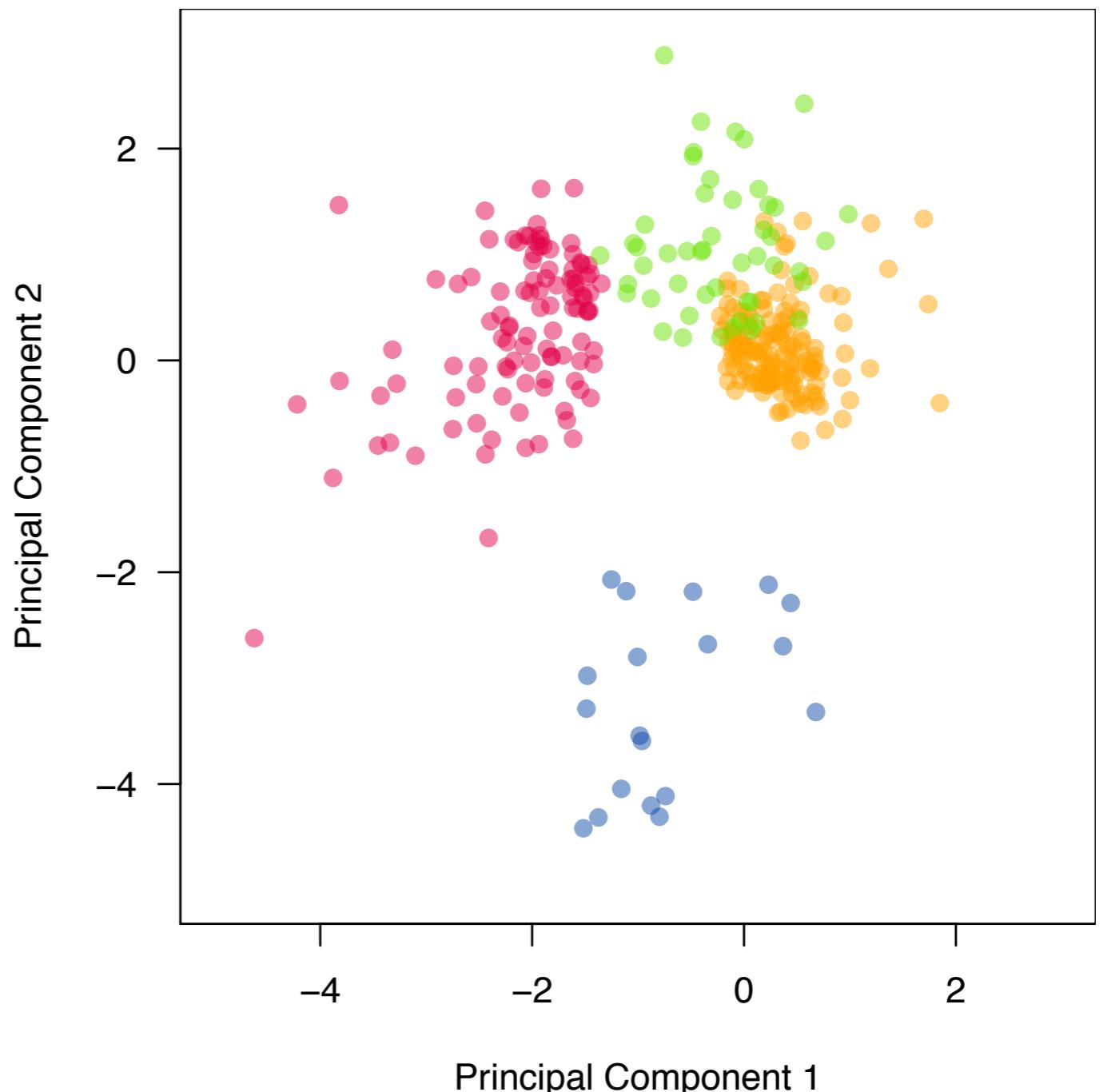
Multivariate Data: Derived Matrices

- matrices of multi-dimensional vectors
- usually abundance profiles, e.g. transcript or protein levels, metabolite concentrations



Multivariate Data: Derived Matrices

Scatter Plot



Multivariate Data: Derived Matrices

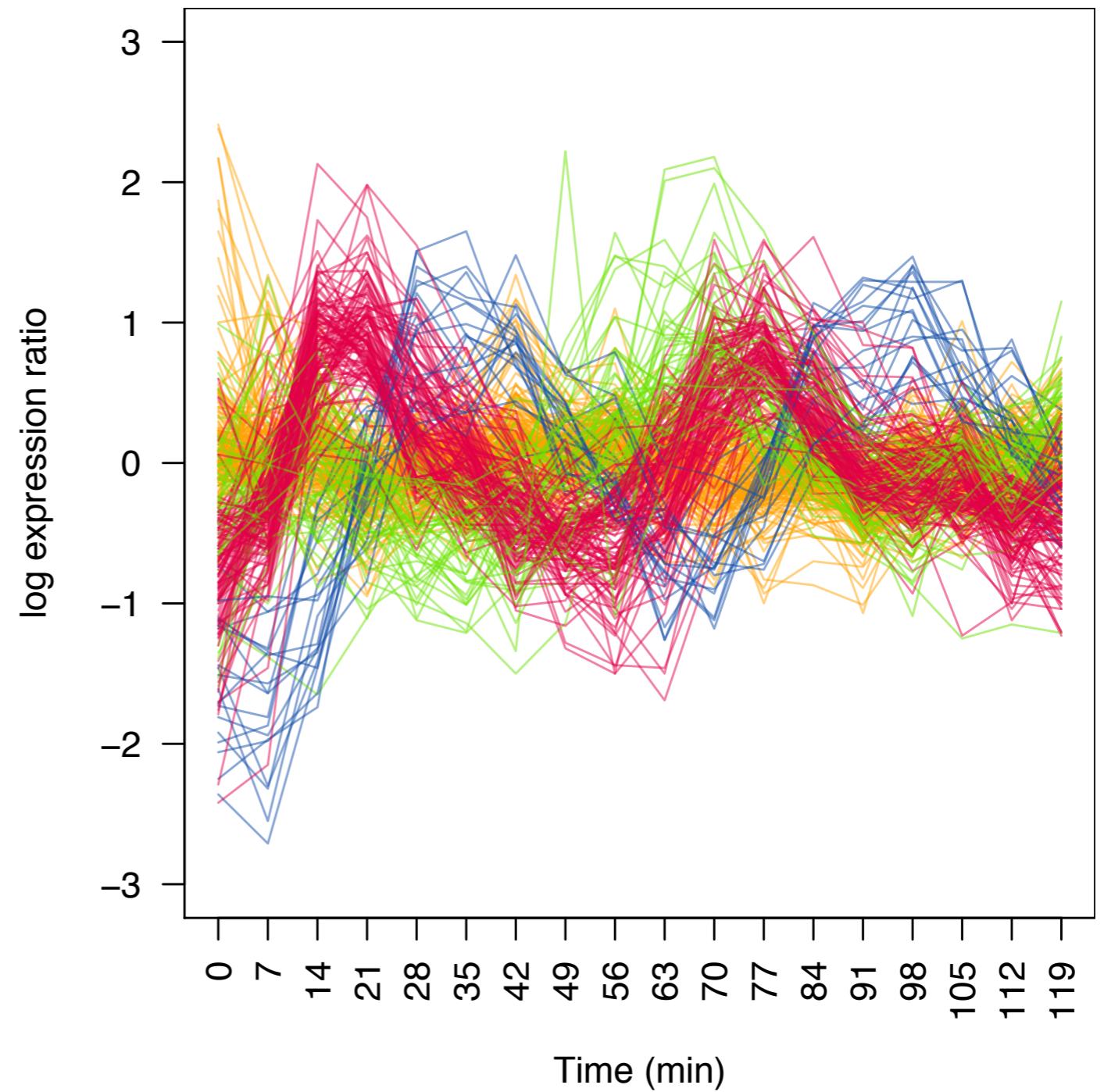
Multivariate Data: Derived Matrices

- Scatter Plots and Dimensionality Reduction

- used to visualize high-dimensional profiles as projections in lower-dimensional spaces (usually 2D, sometimes also 3D ...)
- there is always a loss of information in the process, goal is to minimize the loss of information
- many different algorithms: Principal Components Analysis (PCA), Multi-Dimensional Scaling (MDS), Isomap, etc.
- **Pros** - good choice to get an idea about the overall structure of the whole data set: clusters, outliers, gaps in the data
- **Cons** - because of the dimensionality reduction the original profiles are not accessible in the visualization

Multivariate Data: Derived Matrices

Profile Plot a.k.a.
Parallel Coordinates



Multivariate Data: Derived Matrices

- Profile Plot/Parallel Coordinate Plots

- Pros

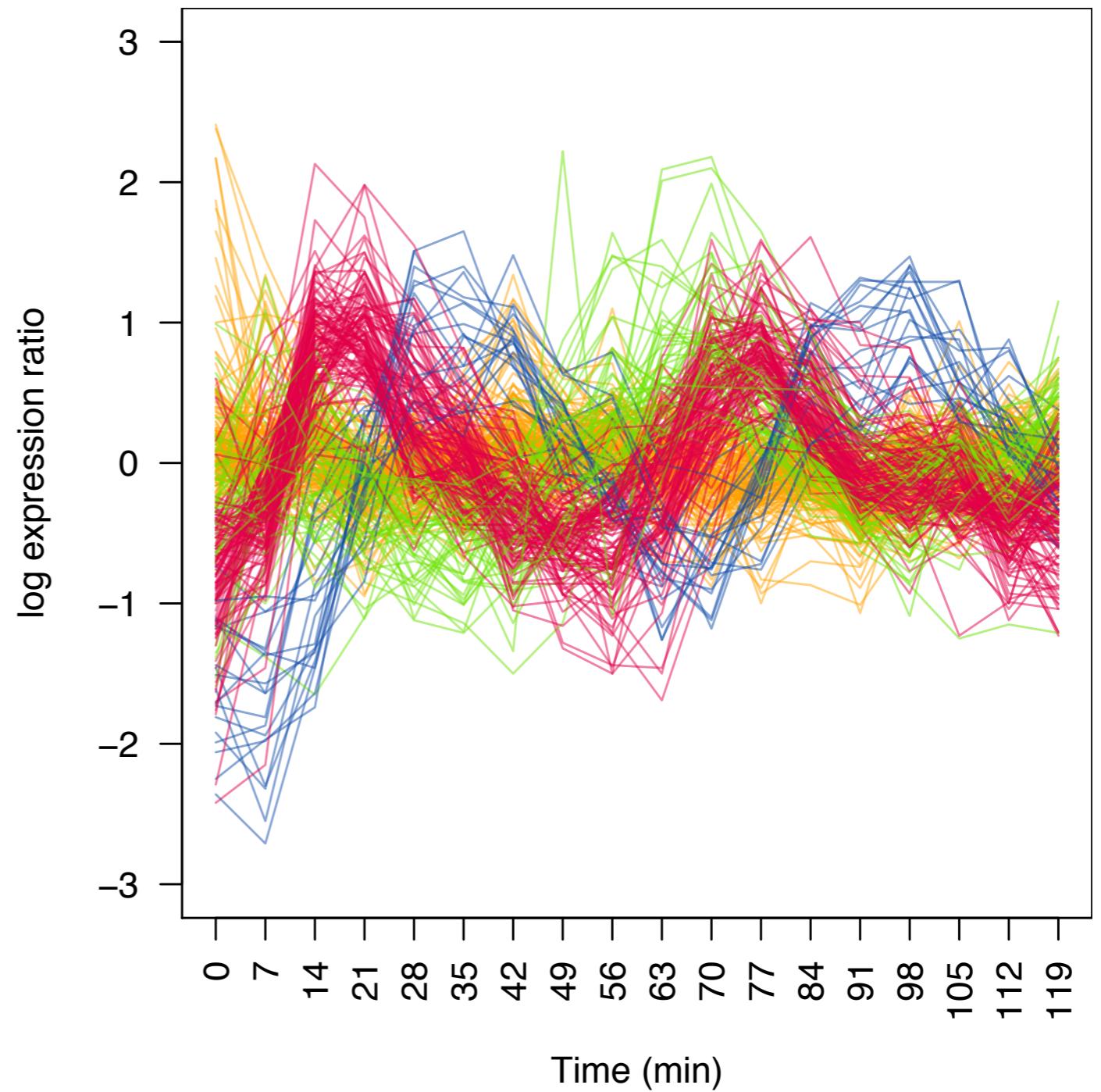
- encoding by position: profiles easy to read
- color-coding of expression profiles (groups) very efficient

- Cons

- overplotting
- grows horizontally with every additional sample

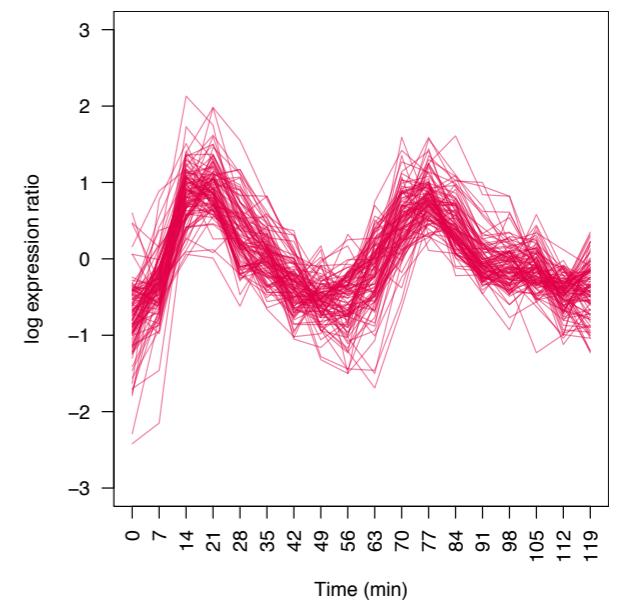
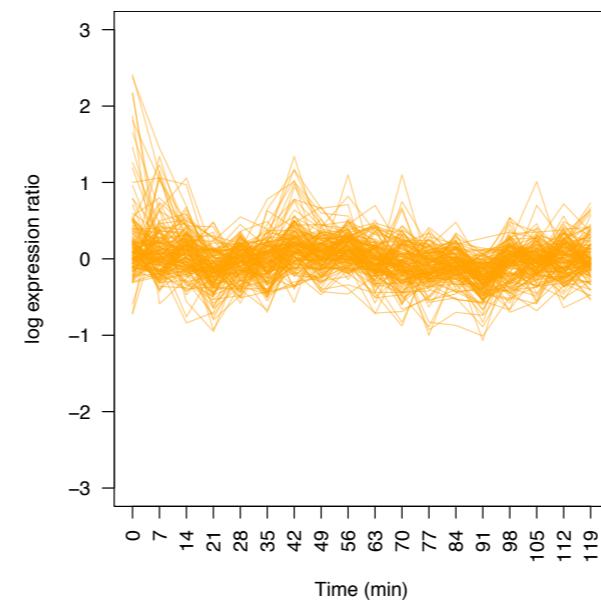
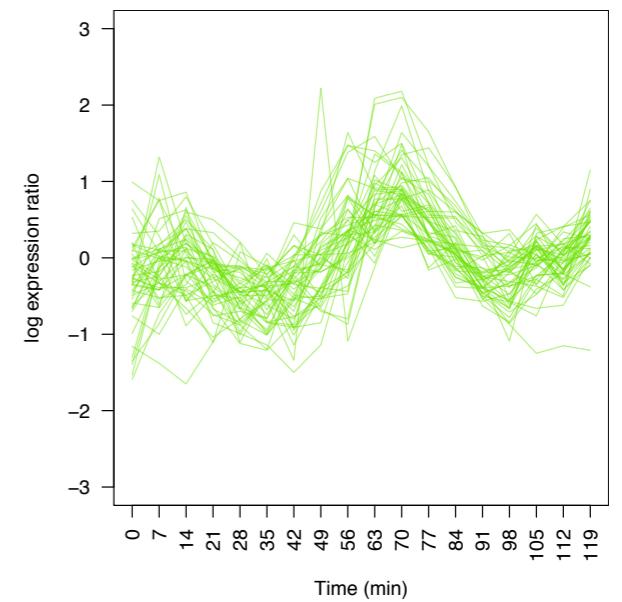
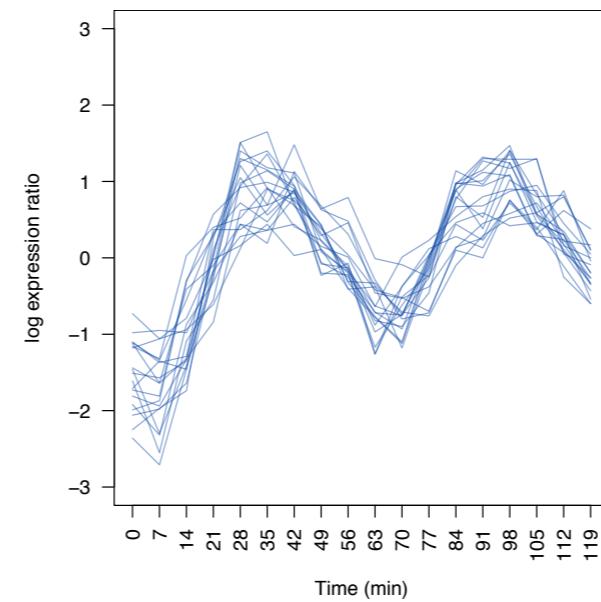
Multivariate Data: Derived Matrices

Profile Plot a.k.a.
Parallel Coordinates



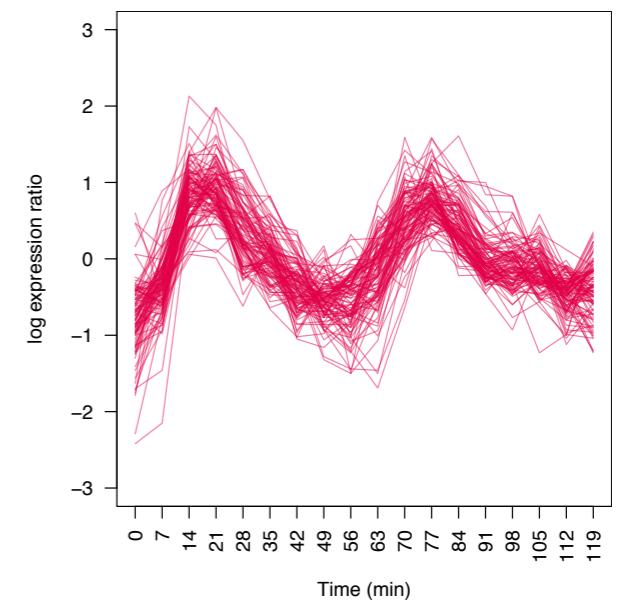
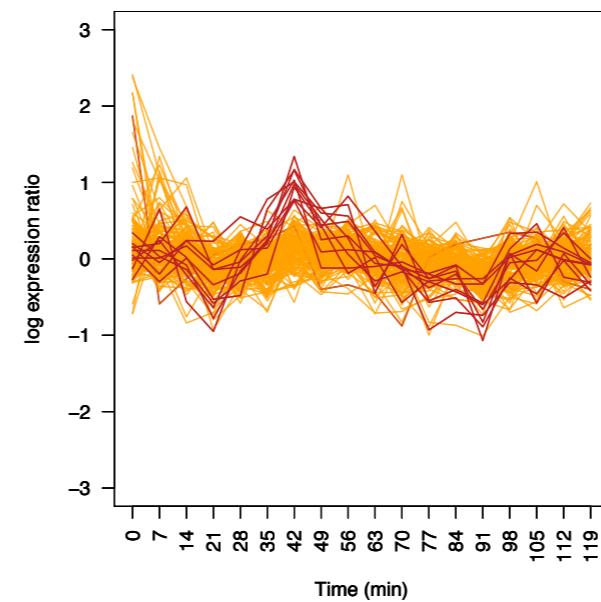
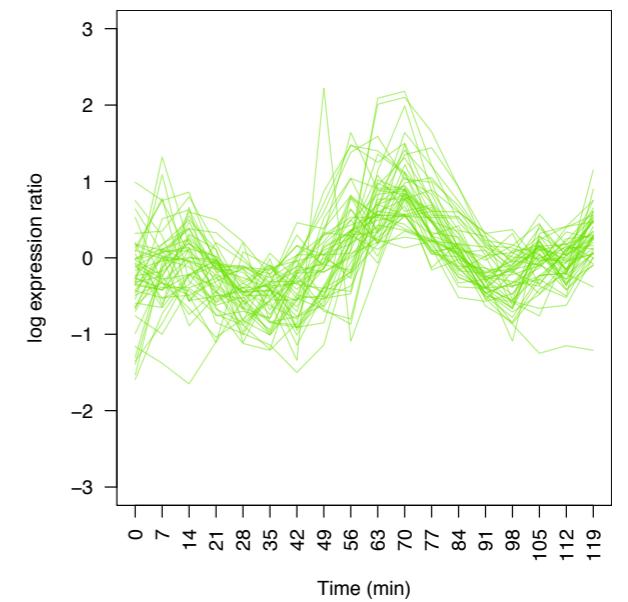
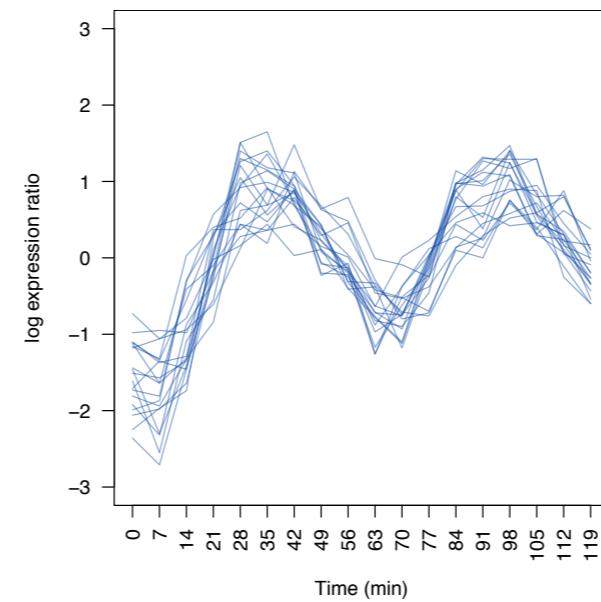
Multivariate Data: Derived Matrices

Profile Plot a.k.a.
Parallel Coordinates



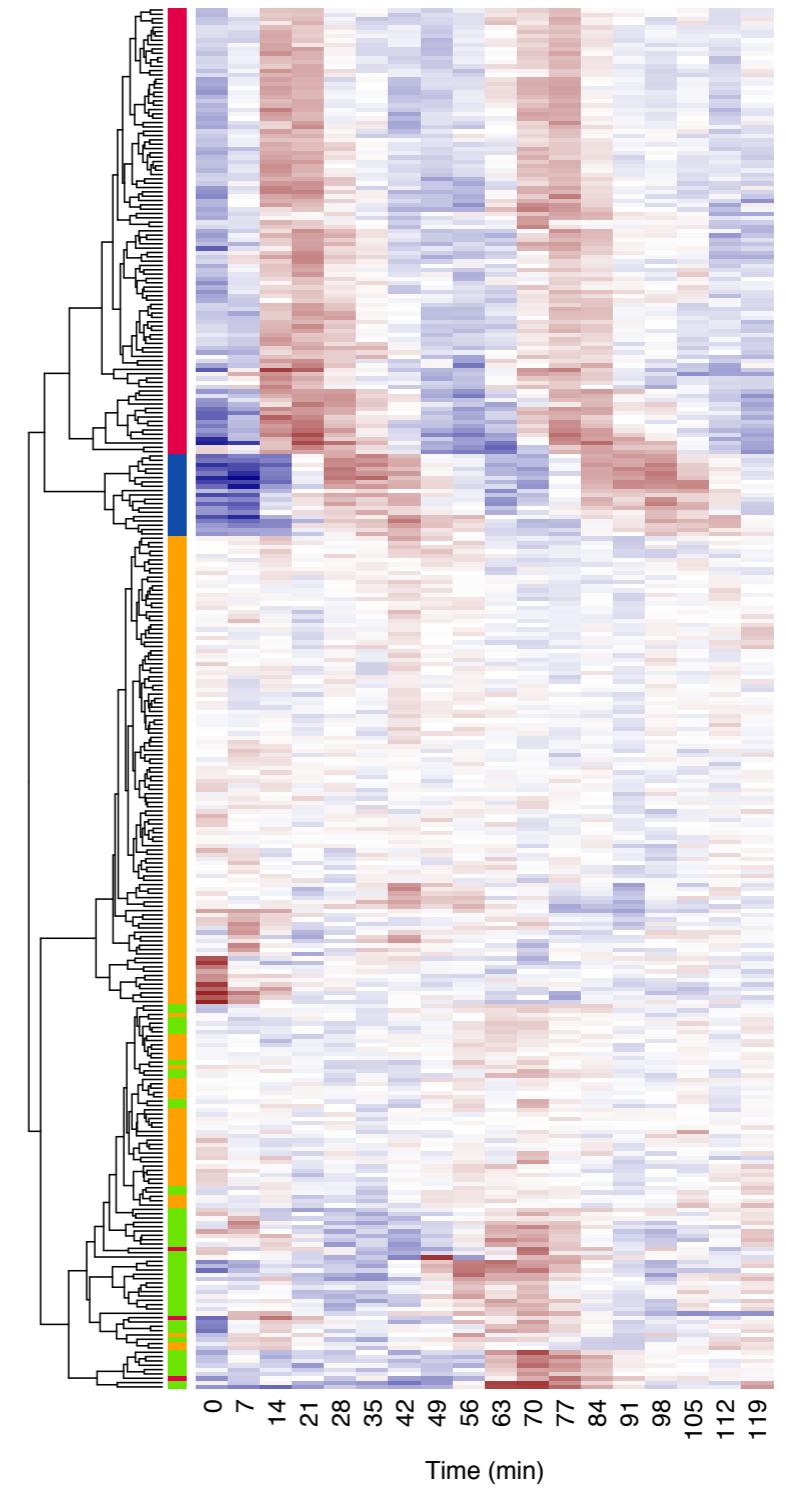
Multivariate Data: Derived Matrices

Profile Plot a.k.a.
Parallel Coordinates



Multivariate Data: Derived Matrices

Heat Map with Dendrogram



Multivariate Data: Derived Matrices

- Heatmap

- Pros

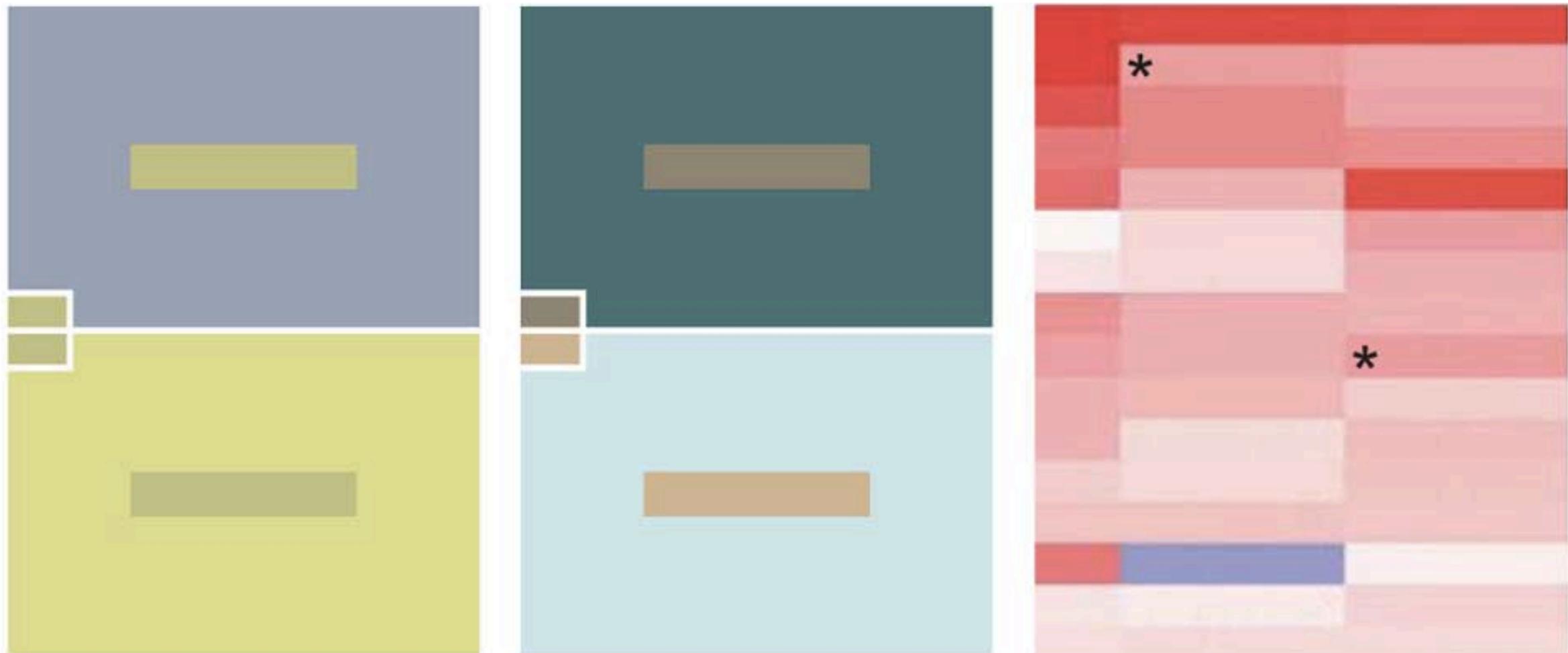
- no overplotting, yet a very dense information display
- can be combined with dendrogram and additional information can be encoded in further columns or in the height of rows

- Cons

- only qualitative interpretation possible due to color coding
- grows horizontally with every additional sample and grows vertically with every additional profile

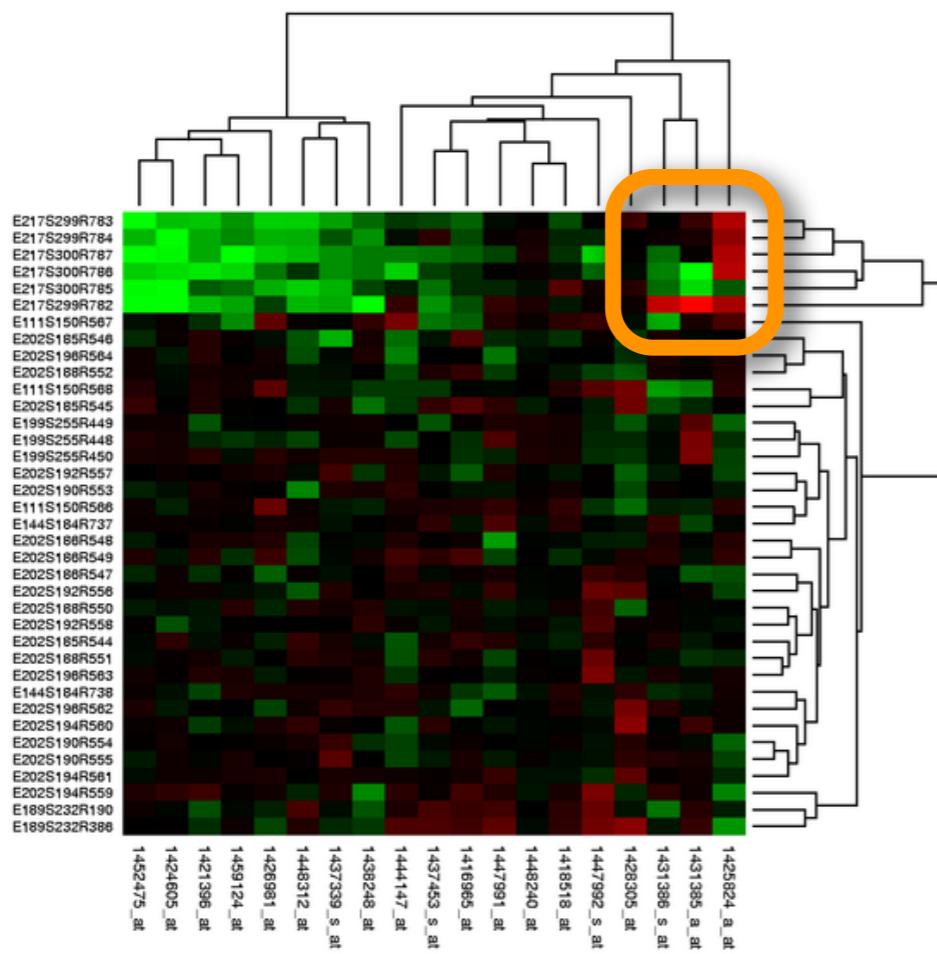
Color Pitfall: Relativity

Color is a relative medium and context matters

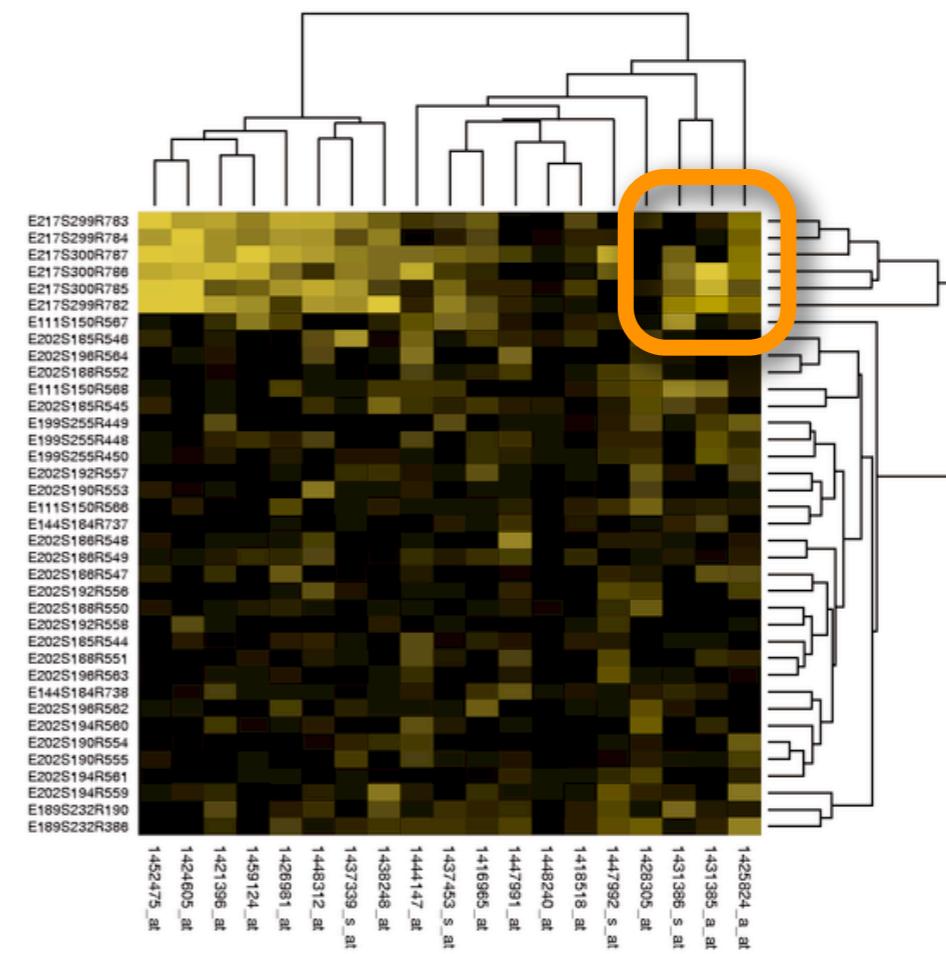


Color Pitfall: Color Blindness

Bad color mapping!



Normal Vision

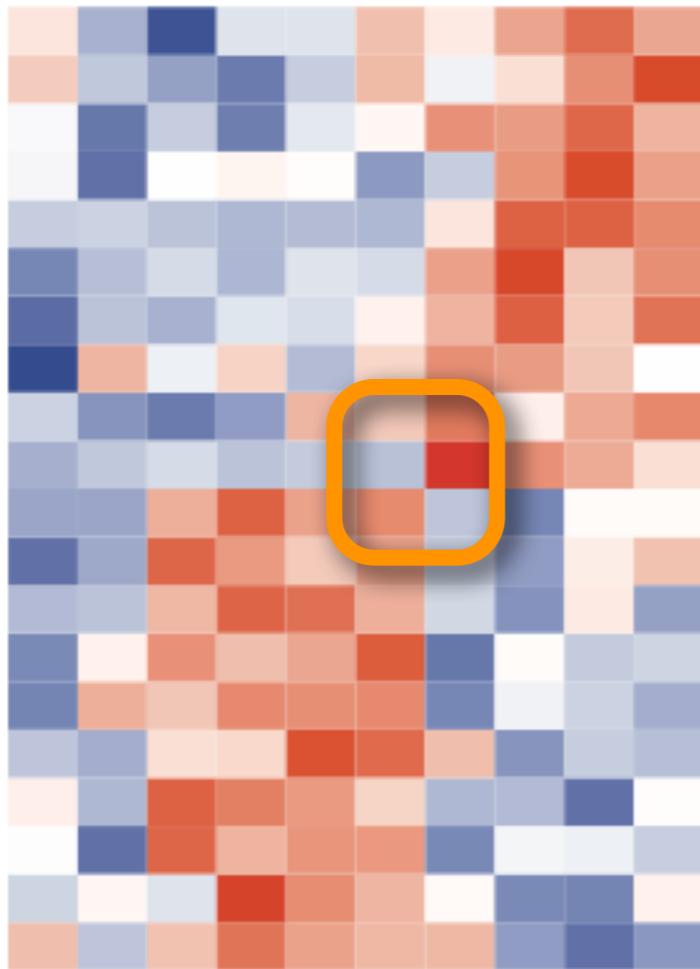


Deutanope Vision
("Red-Green Blindness")

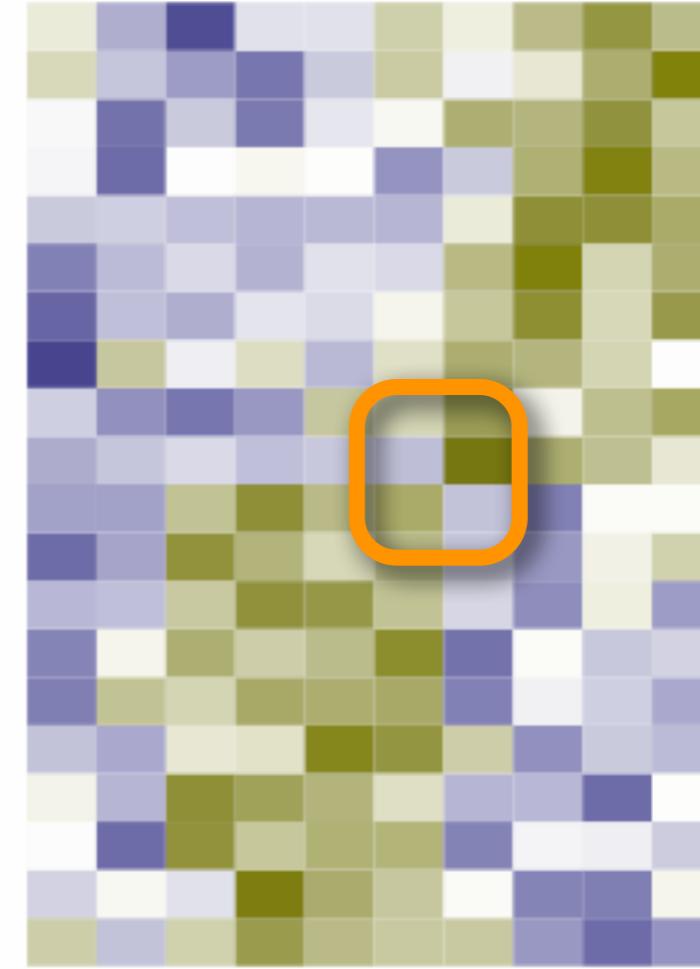
~ 7% of male population affected

Color Pitfall: Color Blindness

Good color mapping!



Normal Vision

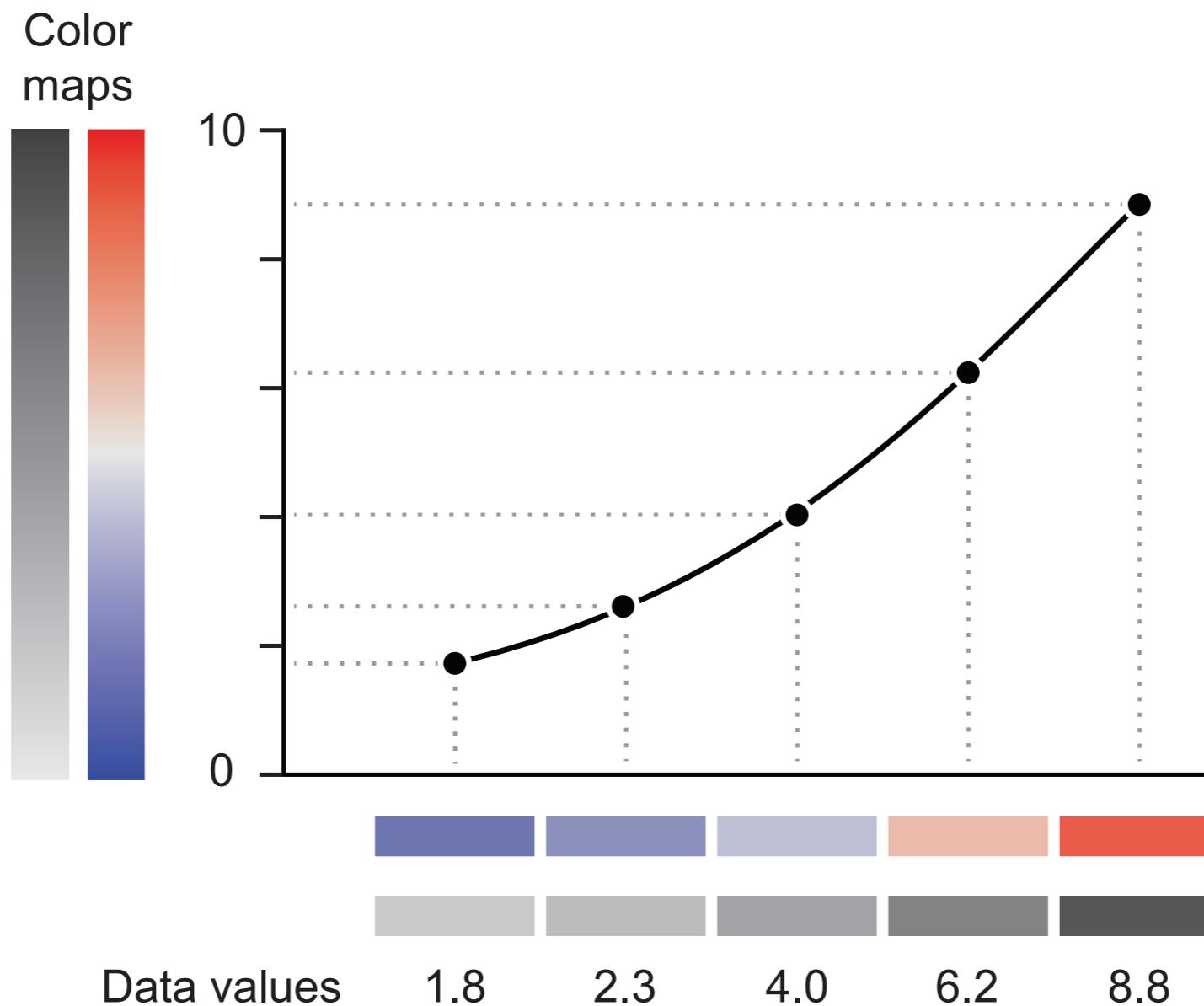


Deutanope Vision
("Red-Green Blindness")

~ 7% of male population affected

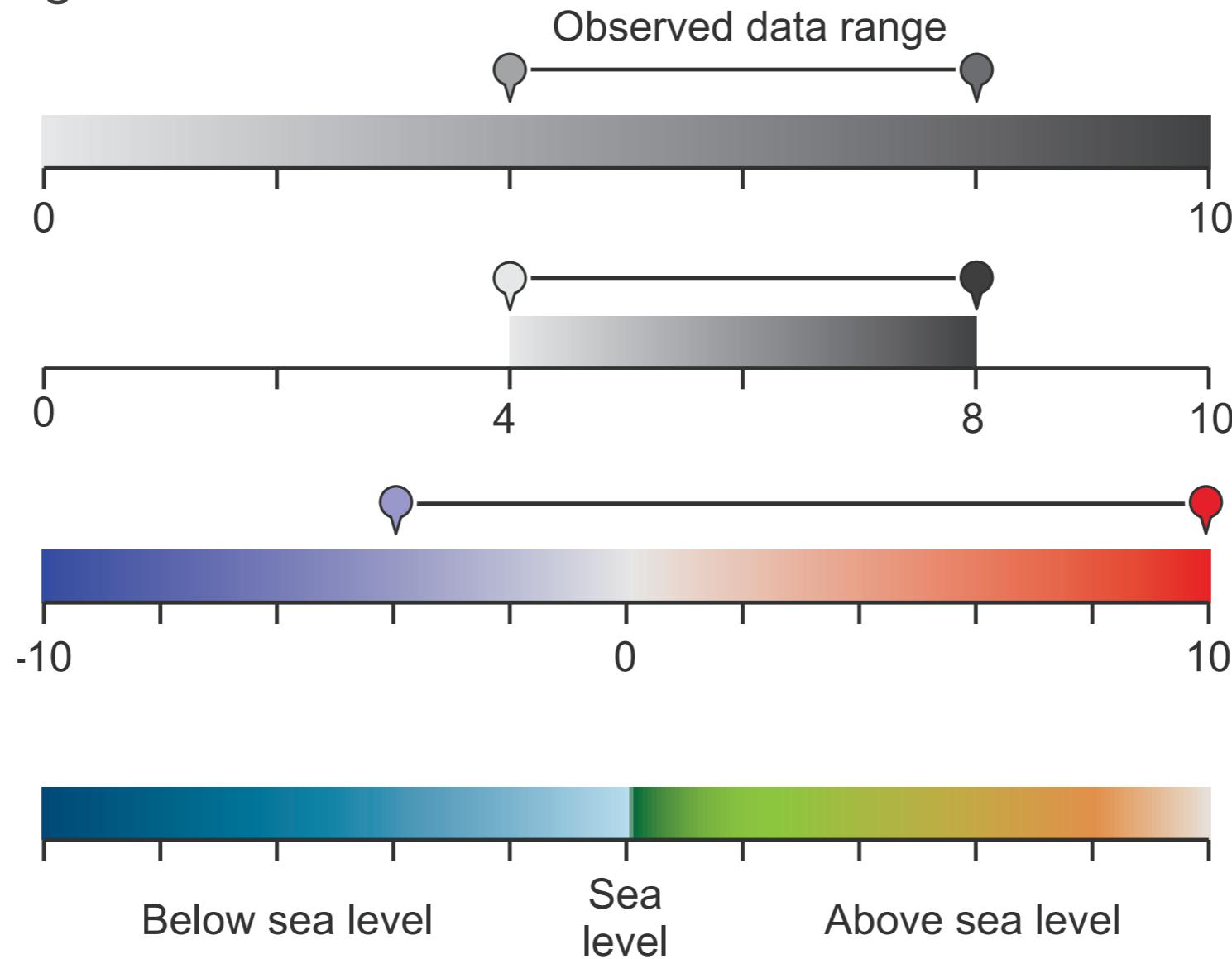
Color Pitfall: Color Mapping

Bad color mapping!



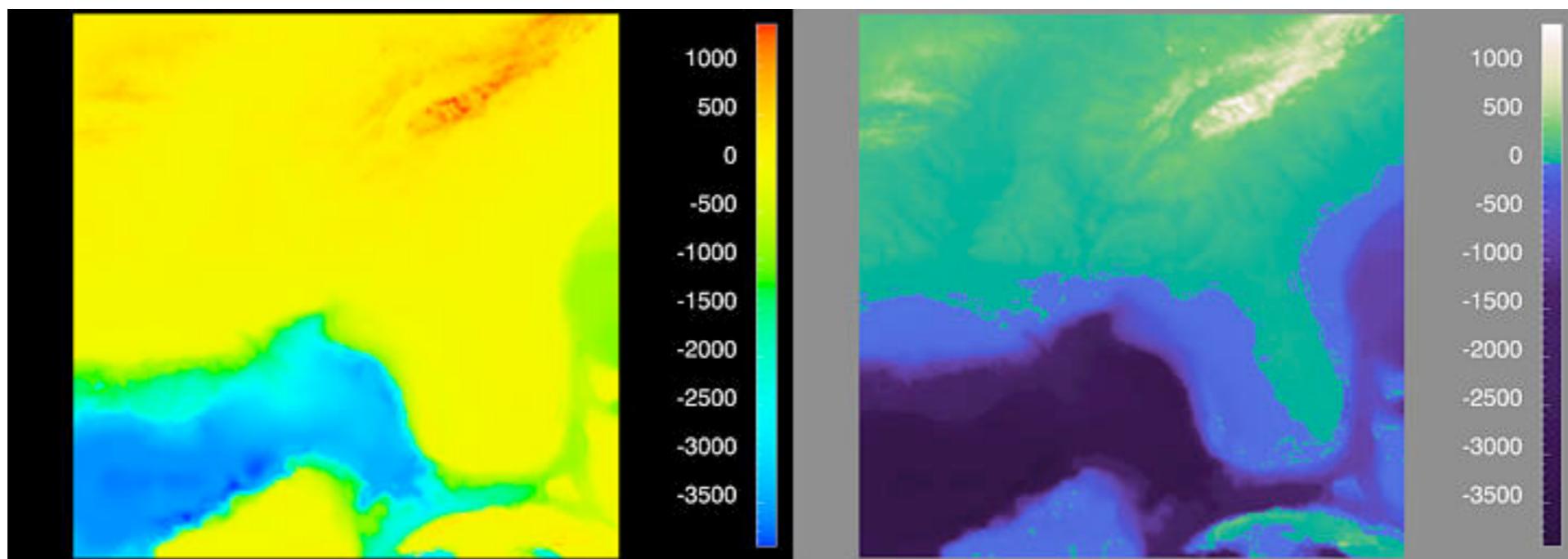
Color Pitfall: Color Mapping

Good color mapping!



Color Pitfall: Rainbow Color Map

Southeastern United States and Gulf of Mexico

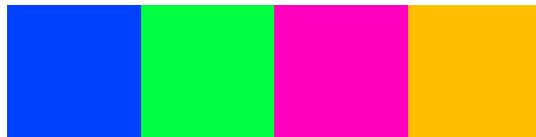


Problems:

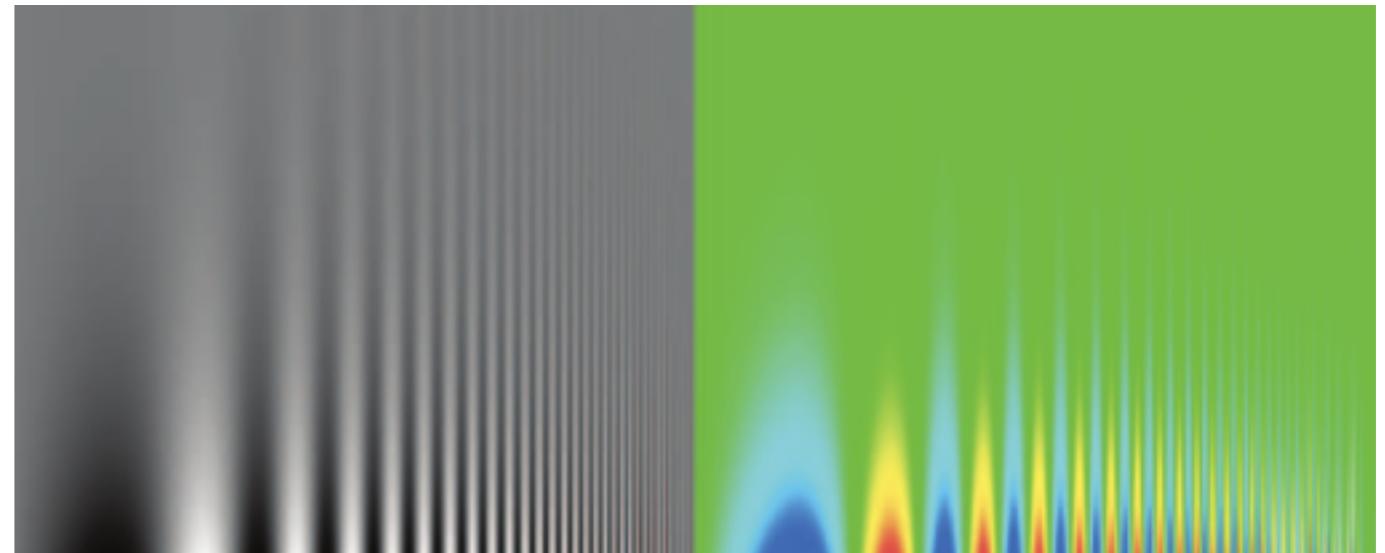
- zero crossing not explicit
- lack of ordering of colors makes it hard to interpret the map

Color Pitfall: Rainbow Color Map

hard to order



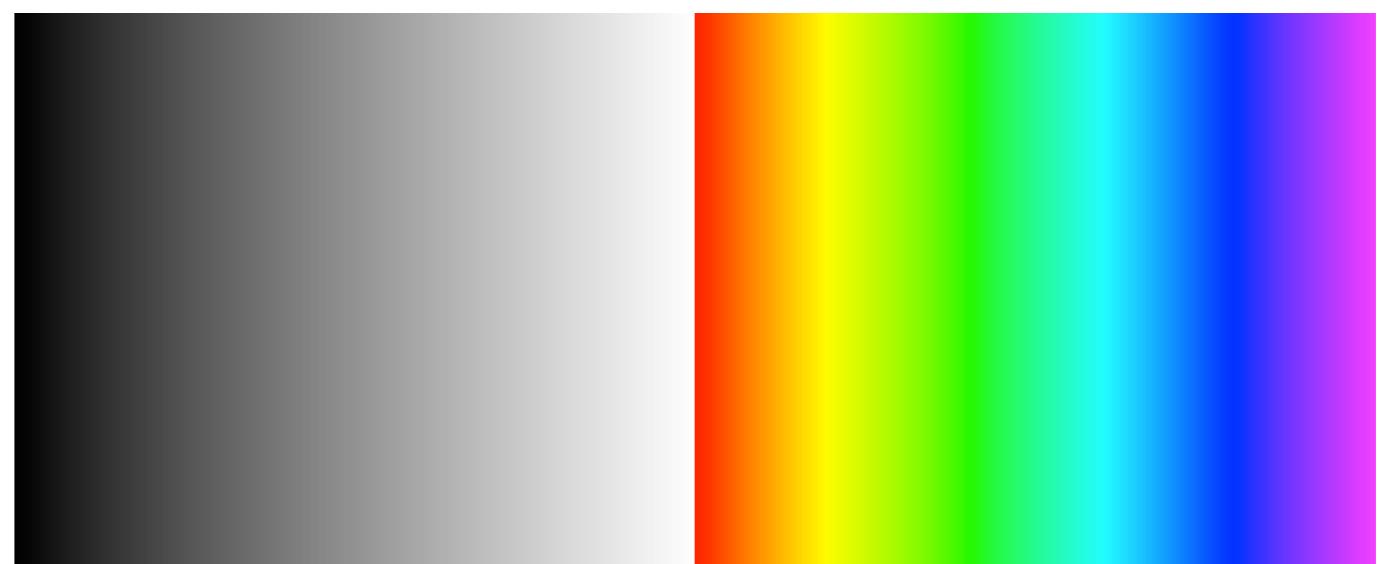
lower resolution



easy to order

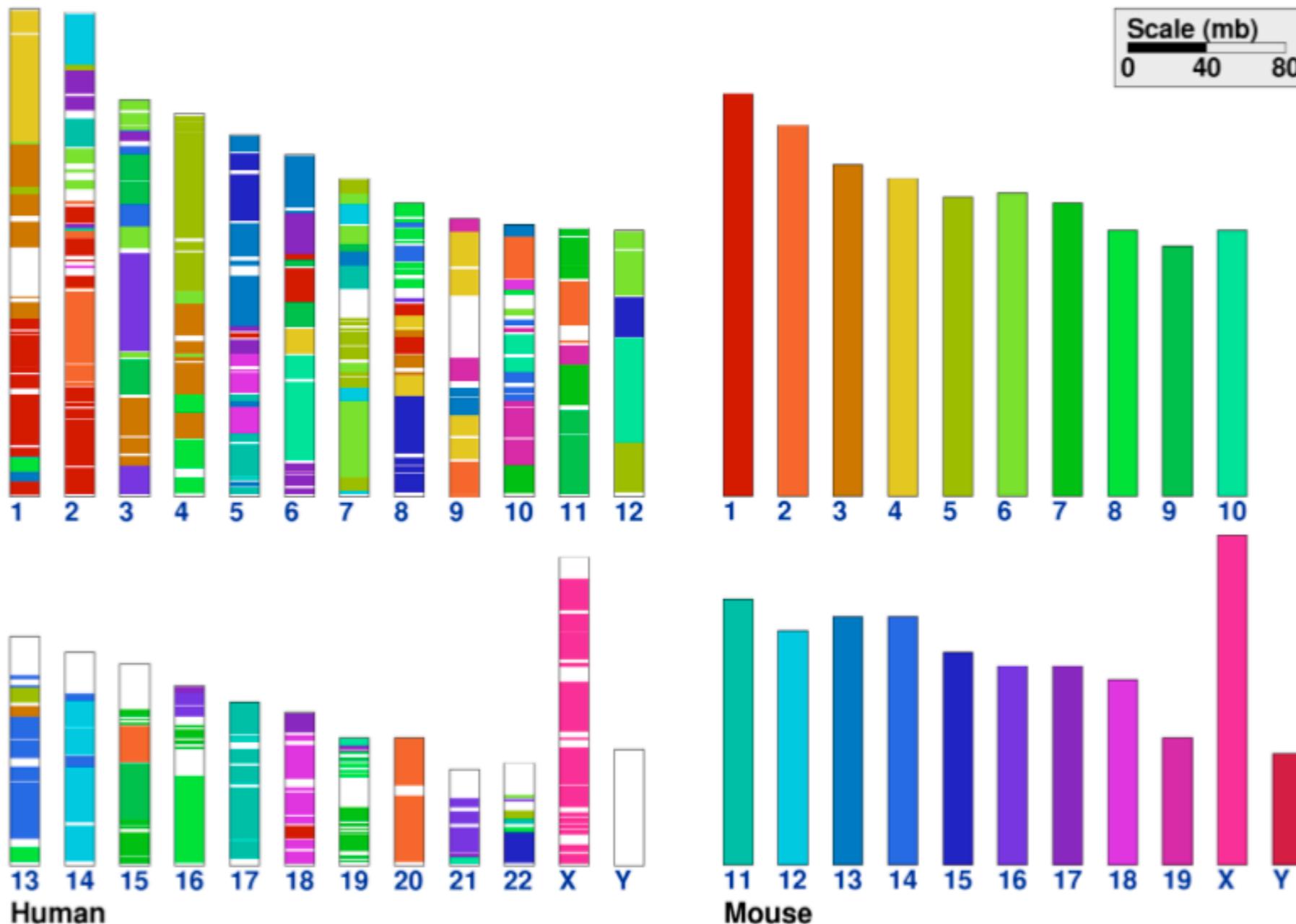


creates artifacts



Color Pitfall: Discriminability

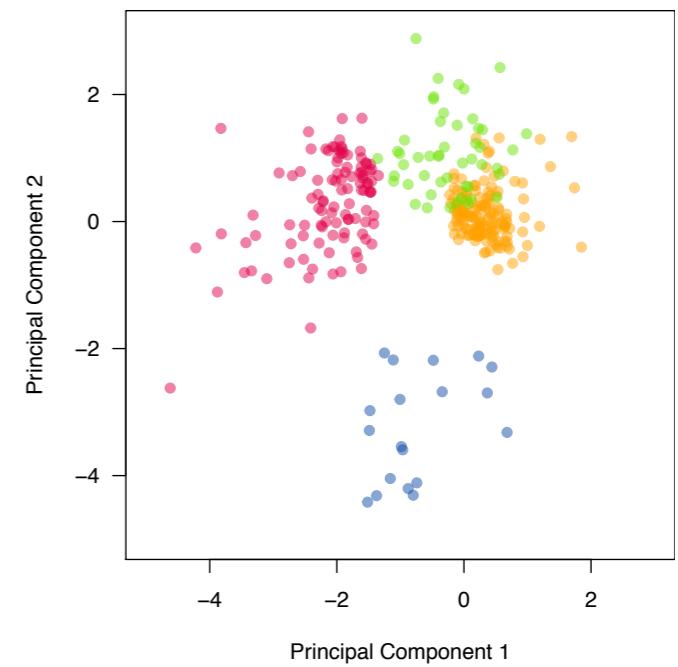
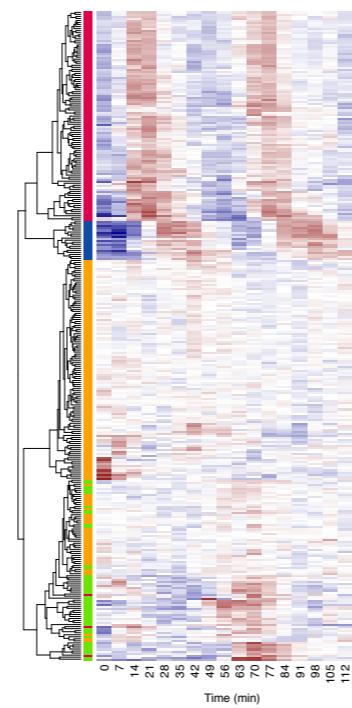
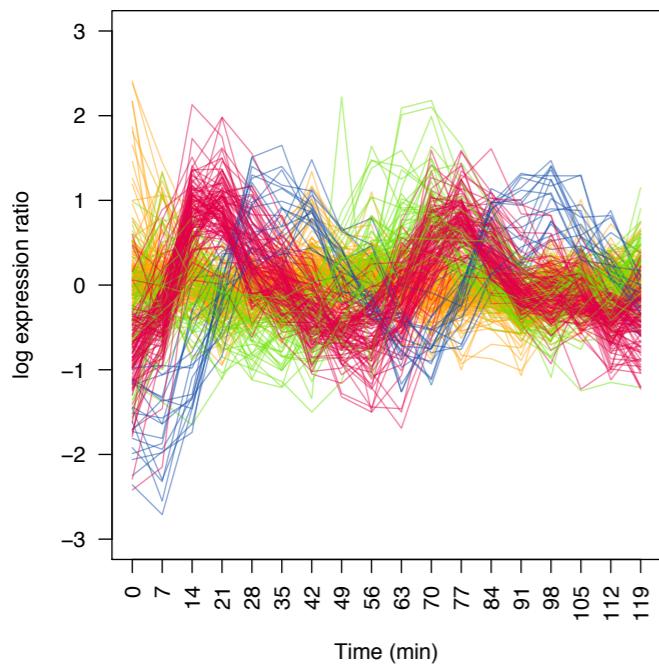
Only 6-12 colors are visually discernable



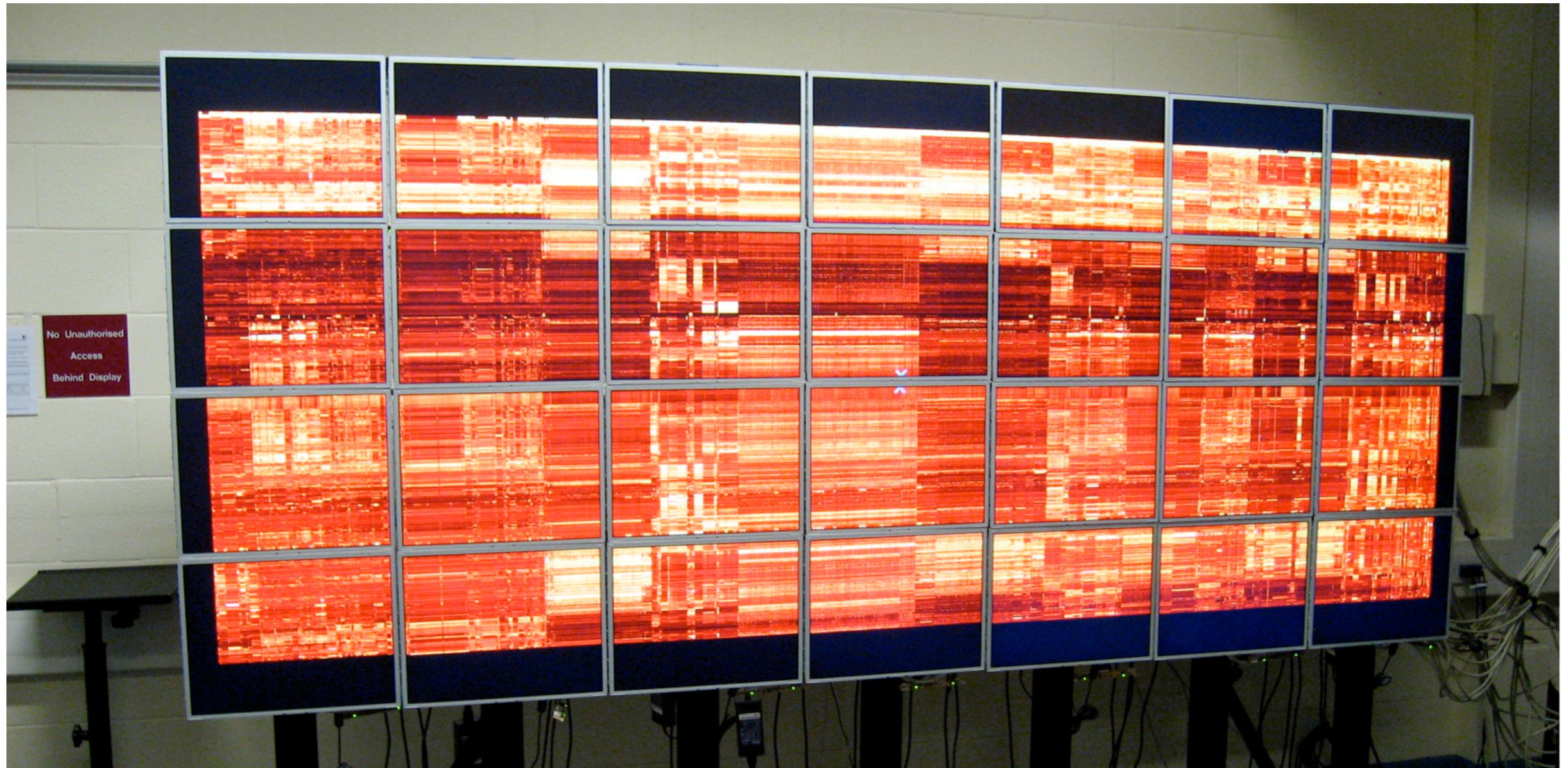
Multivariate Data: Summary

few, high-res

many, low-res



Problem: Very Large Expression Matrices



Power Wall (7x4 screens = 11,200x4,800), University of Leeds

1000 transcripts, 5372 samples

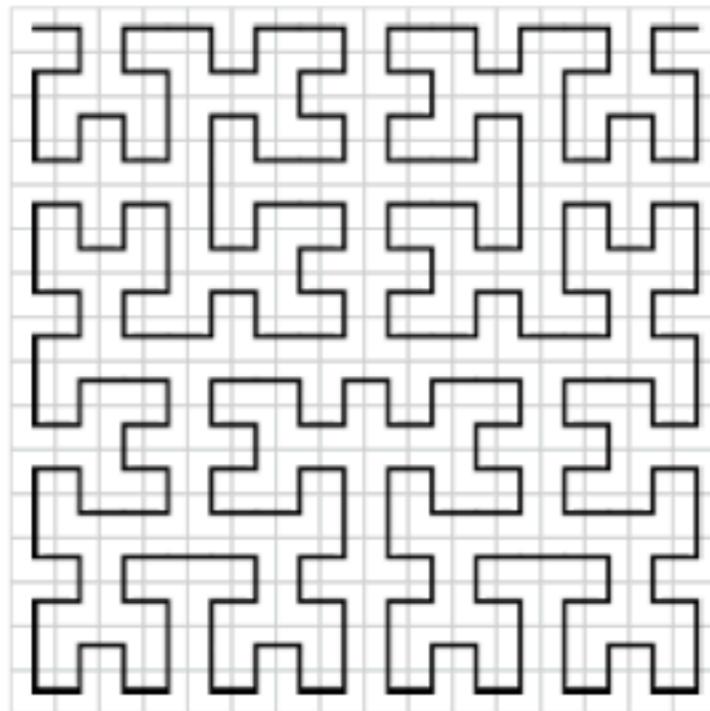
Very Large Expression Matrices: Space Maps

1 gene, 213 samples



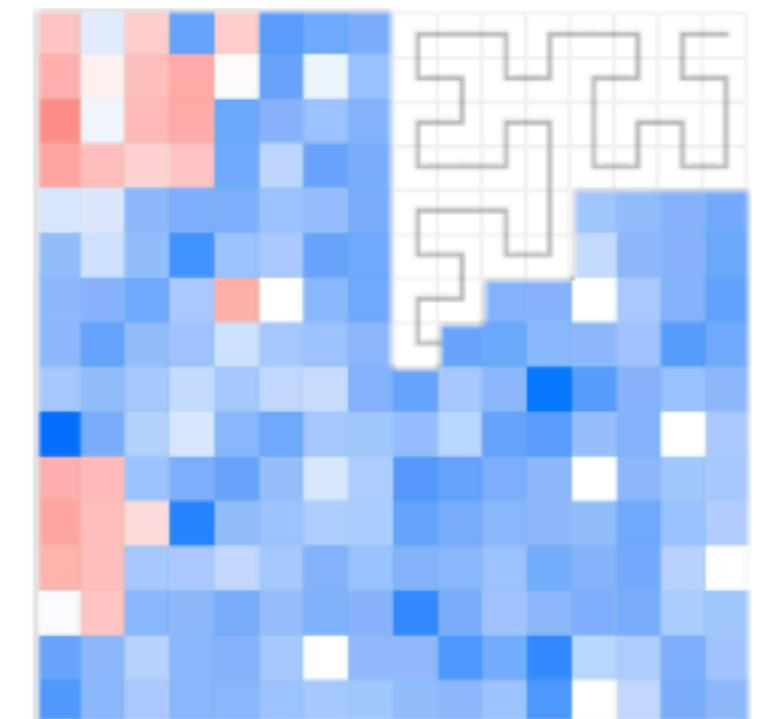
assume samples ordered

Hilbert Curve

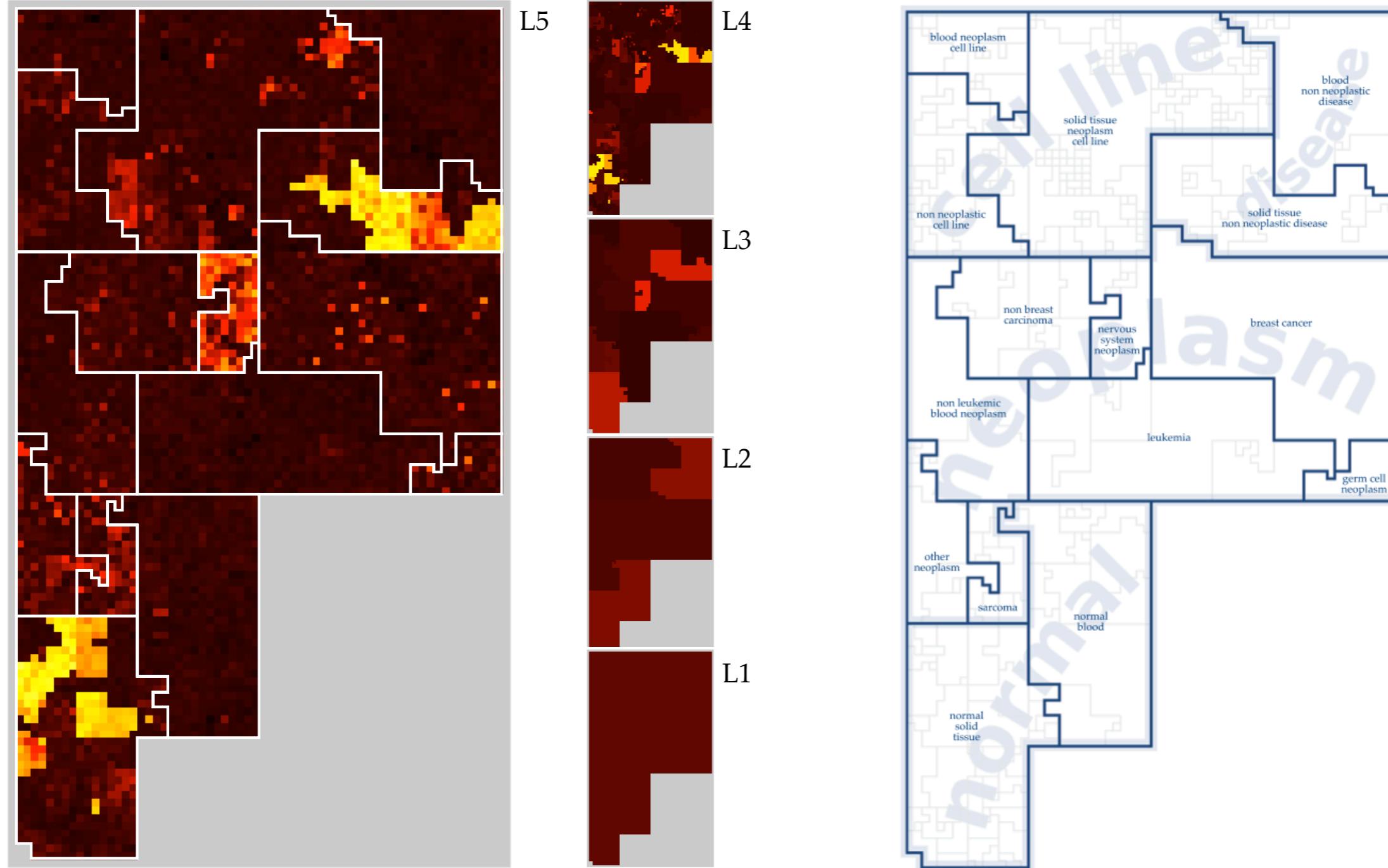


16 × 16 grid

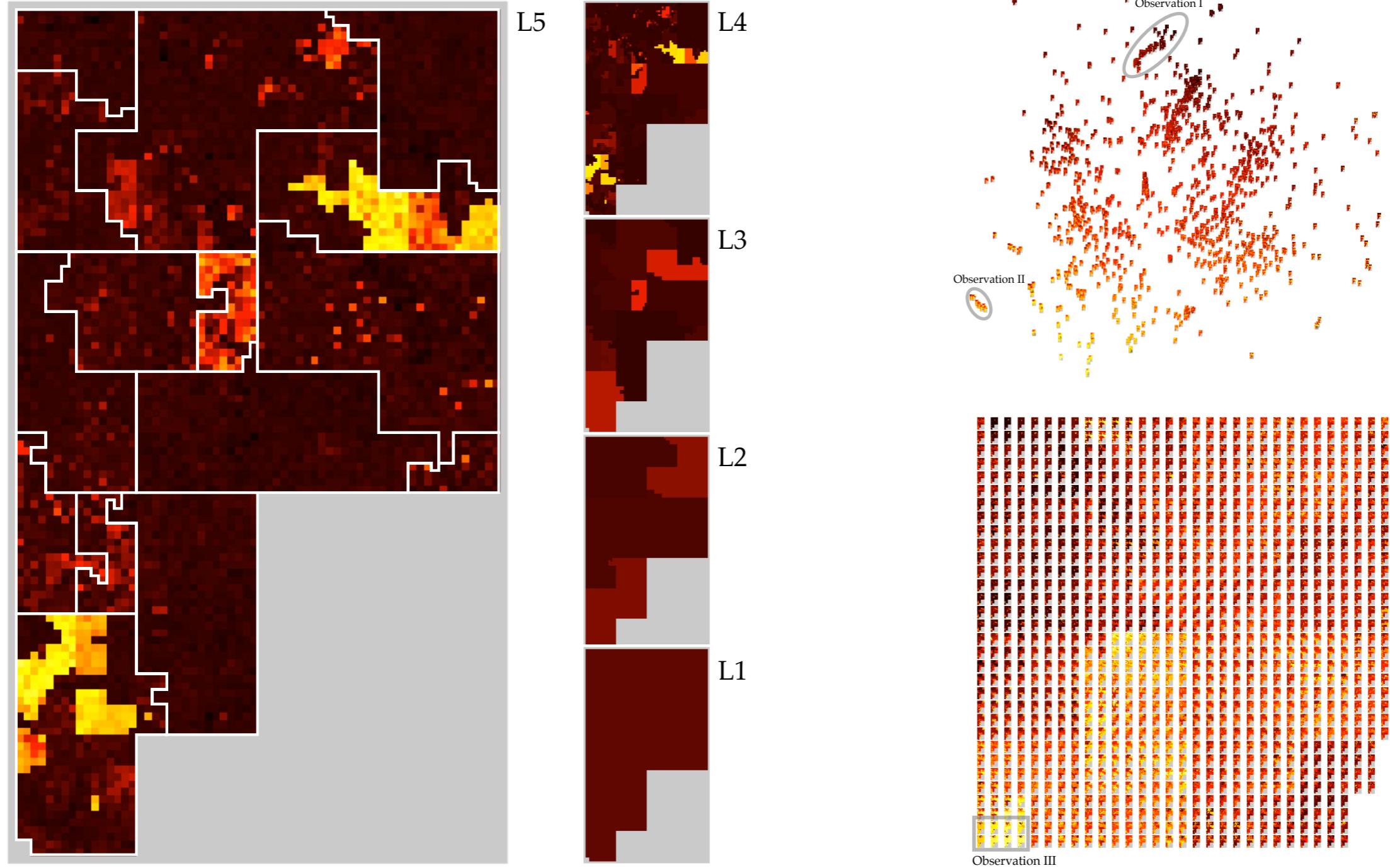
down up
0



Very Large Expression Matrices: Space Maps

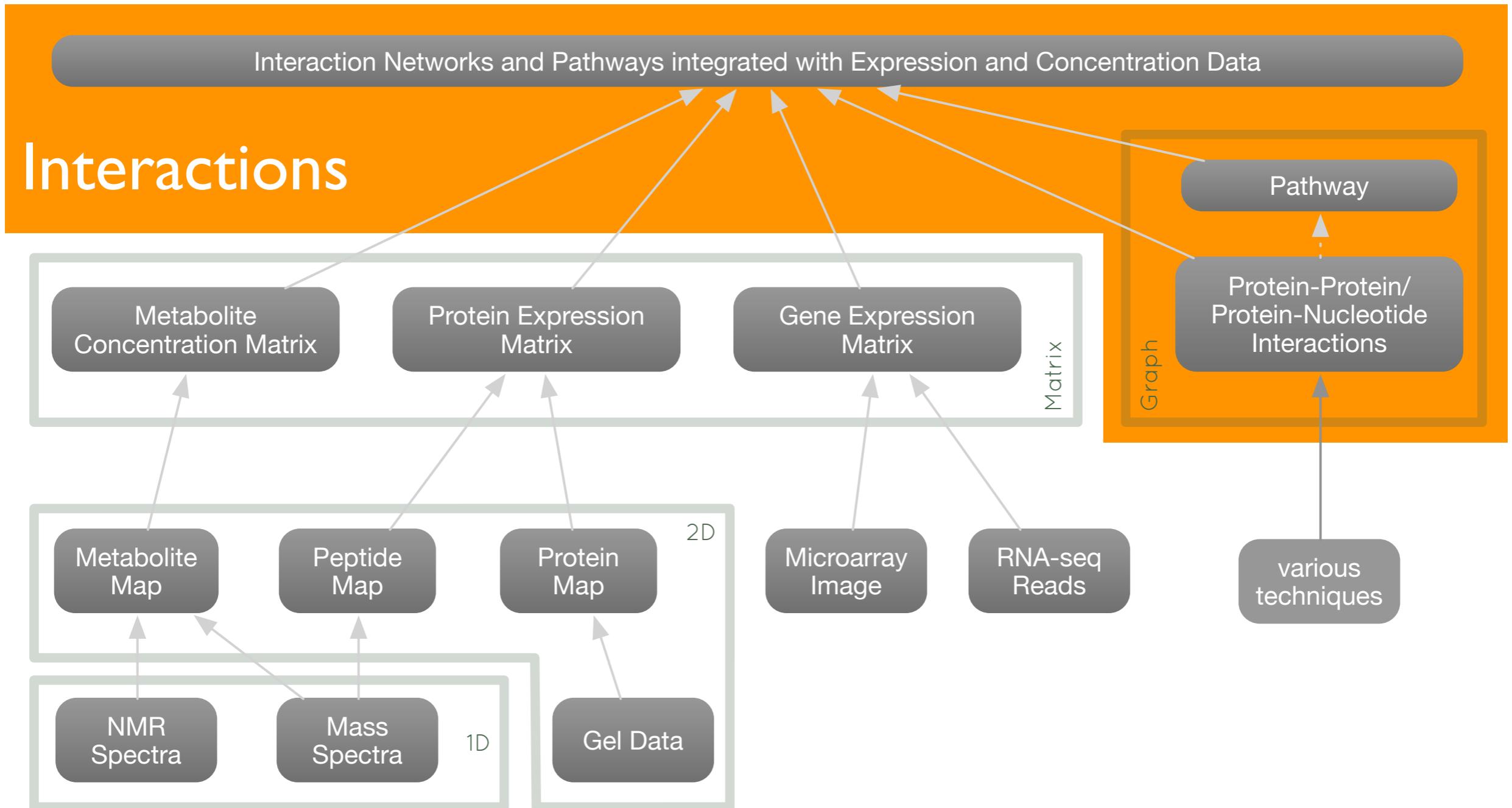


Very Large Expression Matrices: Space Maps



Interactions

Interactions



Interactions

- **Data-derived** **Focus: Exploration**

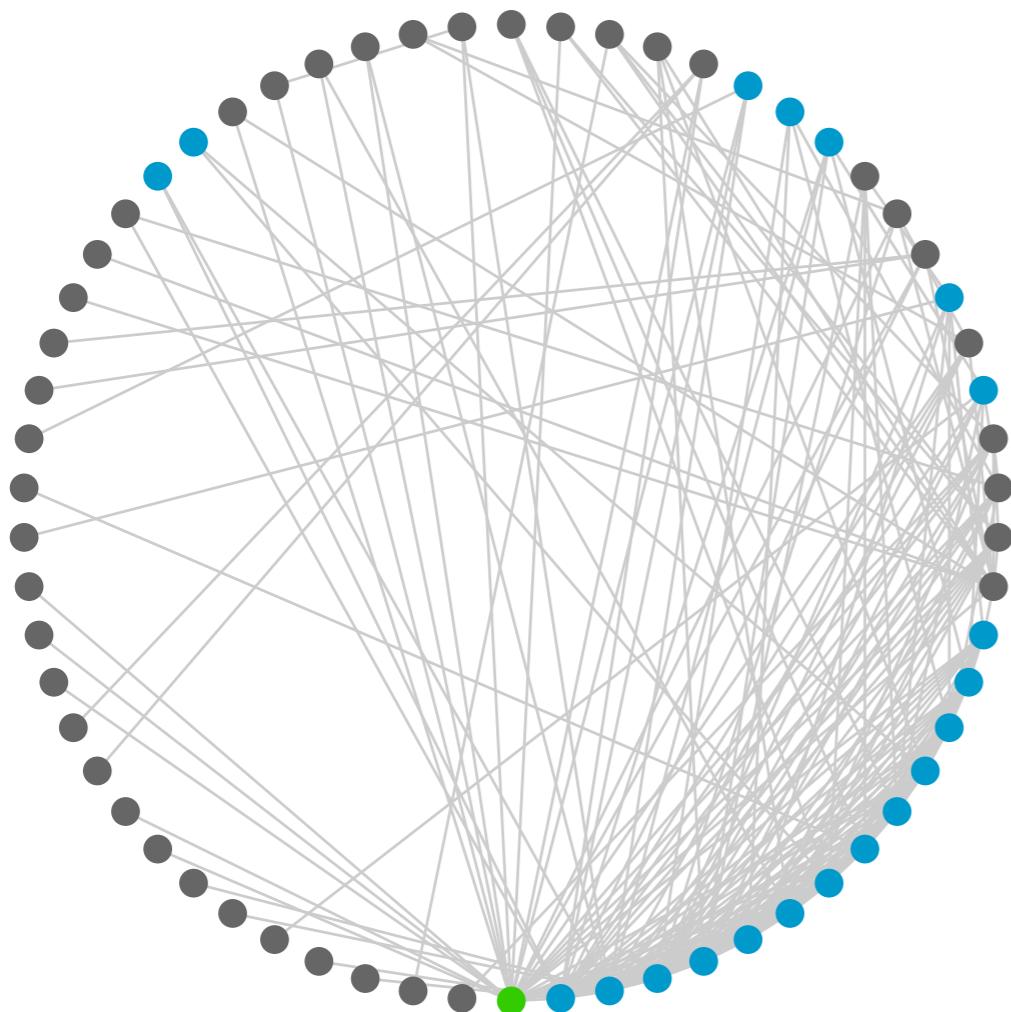
- protein-protein interaction or protein-DNA interaction networks derived from Chromatin Immuno Precipitation (ChIP) or Yeast-2-Hybrid (Y2H) measurements
- gene regulatory networks inferred from gene expression data
- correlation networks derived from gene expression data

- **Knowledge-derived** **Focus: Communication**

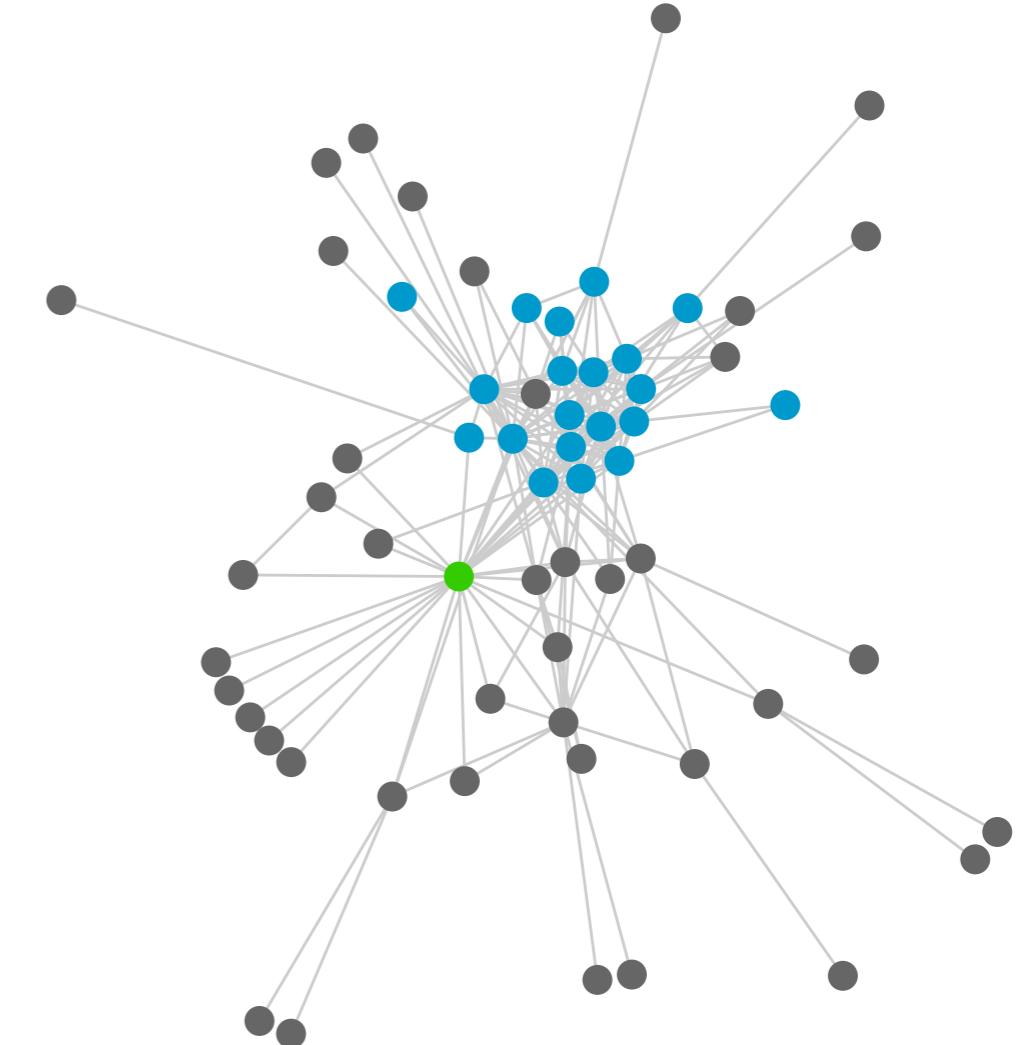
- biochemical pathway maps
- other curated networks derived from the literature

- **Combination of networks and multivariate data**

Interactions: Node-Link Diagrams



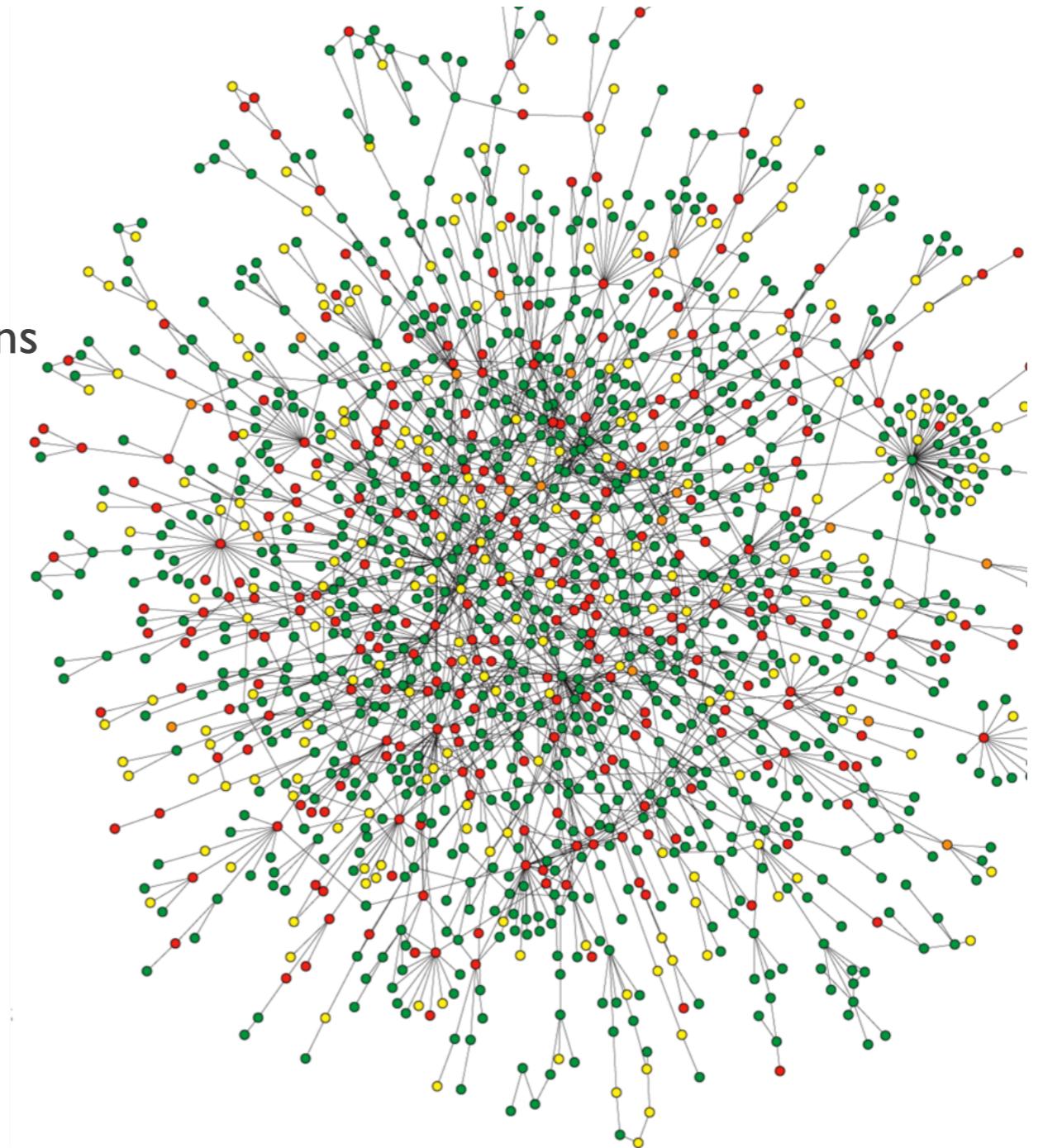
Circular Layout

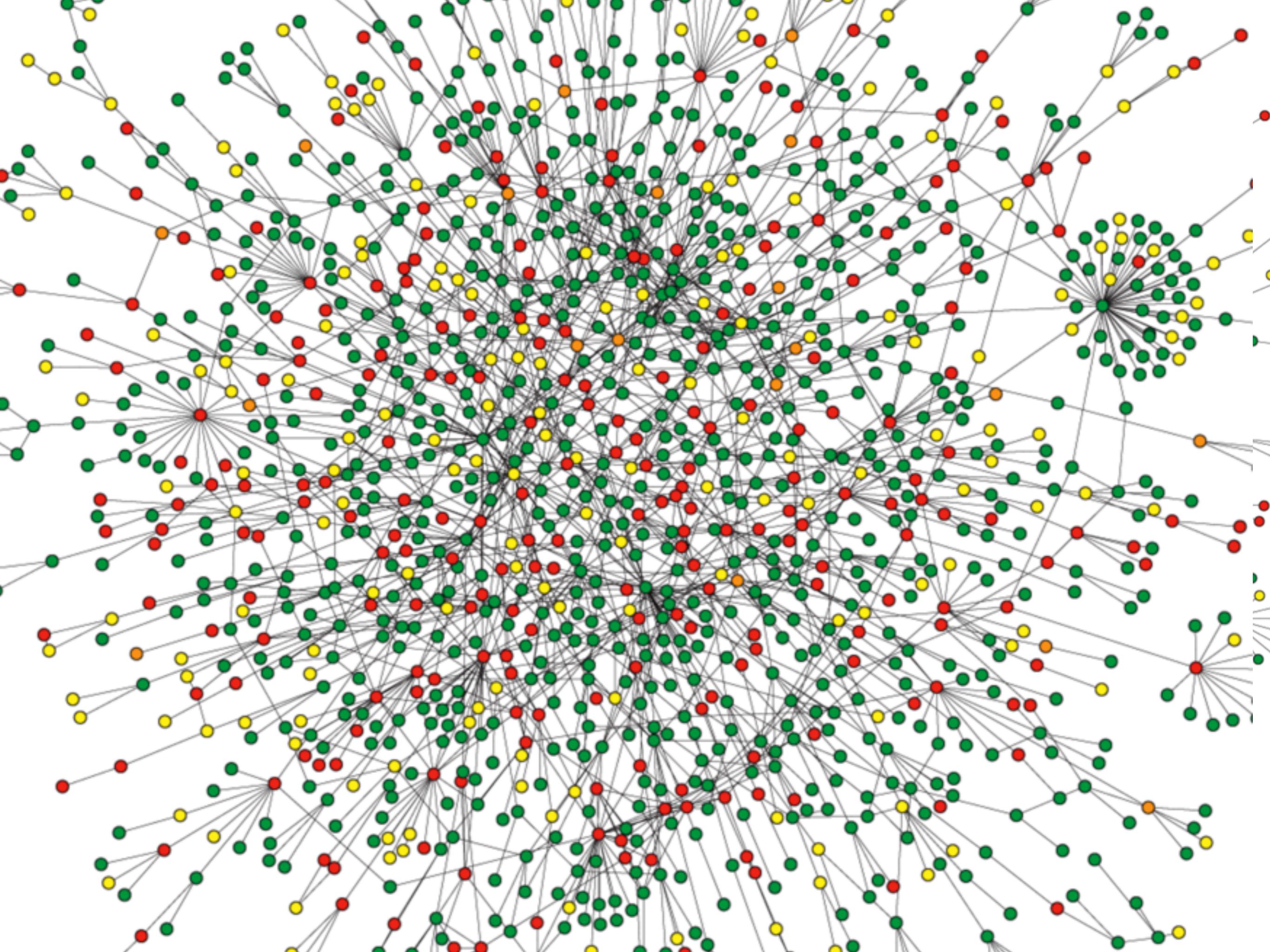


Force-directed Layout

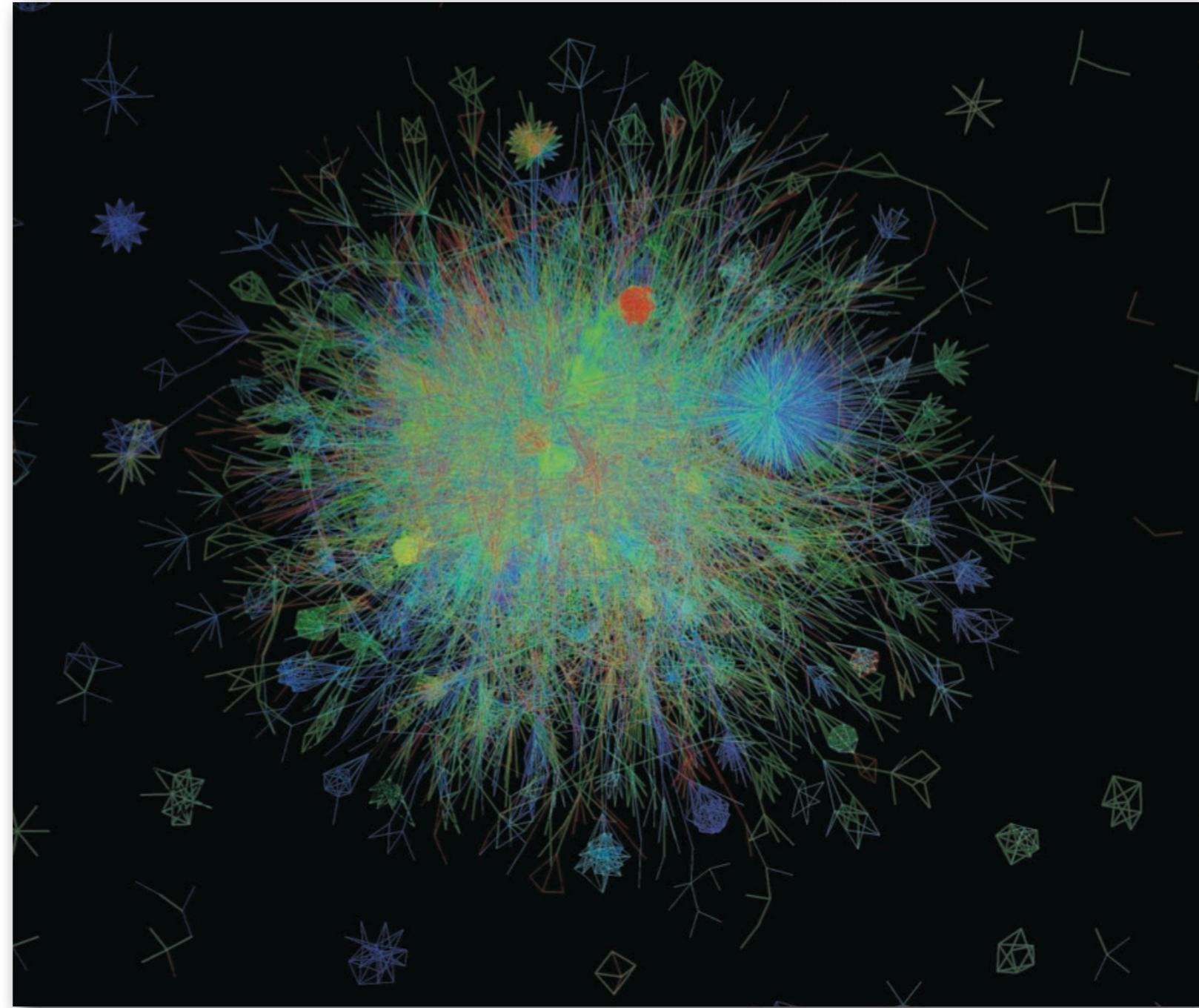
Yeast Protein-Protein Interaction Network

- This network shows the largest connected component of the yeast interactome as determined by Yeast-2-Hybrid
- This component contains 78% of all proteins
- Nodes are color-coded by the effect of a knock-out mutant:
 - Red: lethal
 - Green: non-lethal
 - Orange: slow growth
 - Yellow: unknown
- Hubs are often colored red!

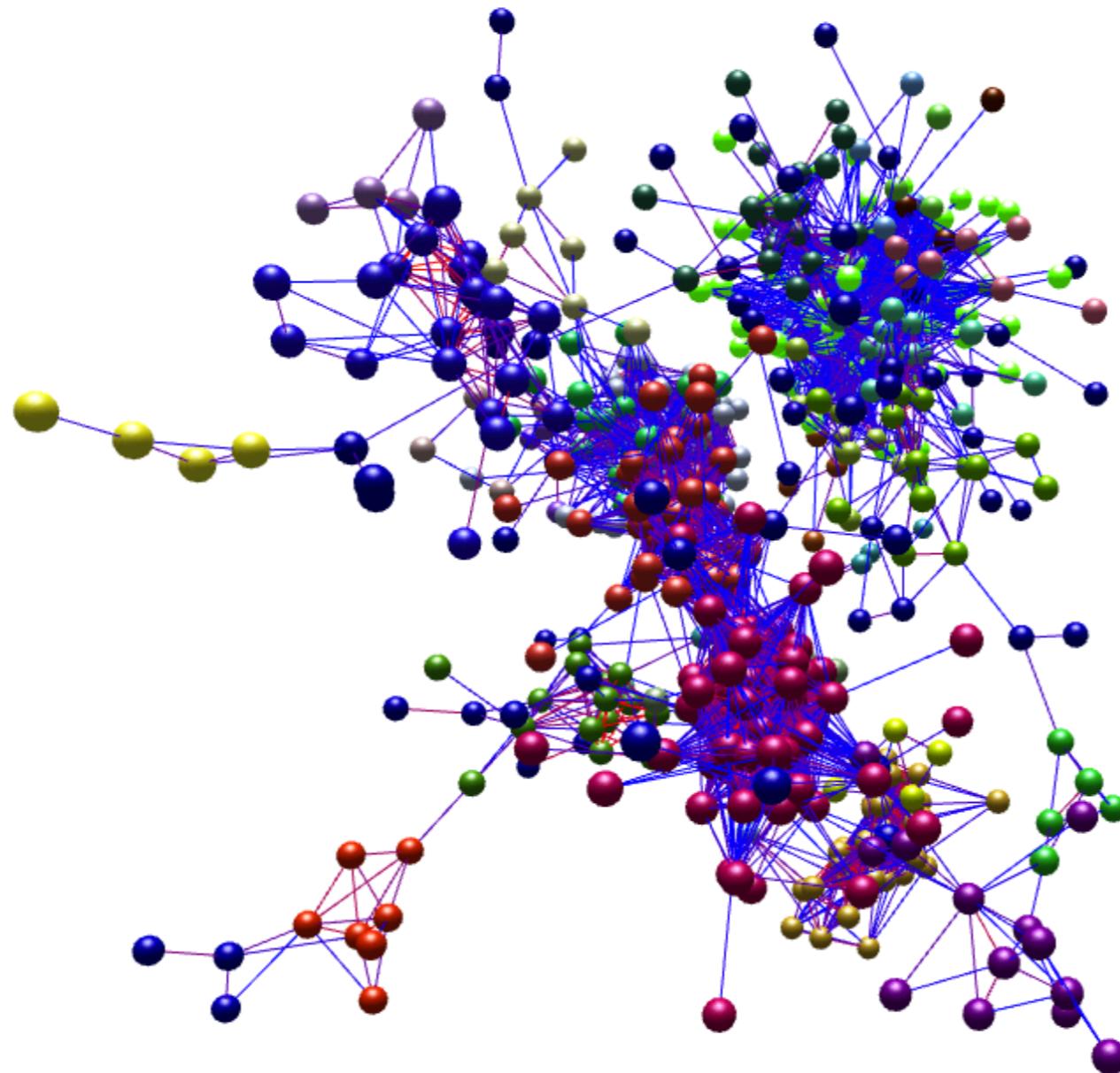




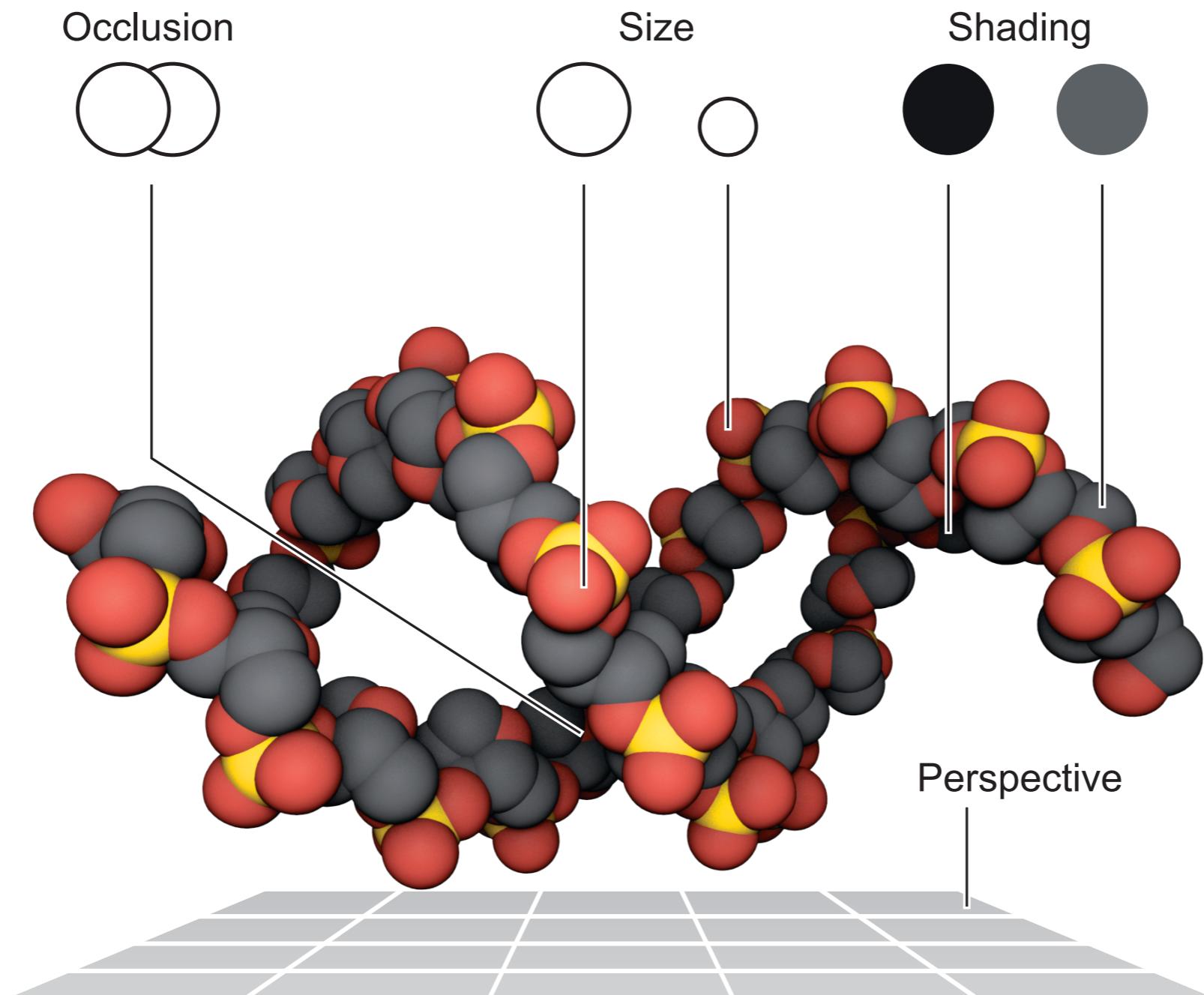
Interactions: Hairballs, Ridiculograms et al.



Interactions: 3D Network Representation



3D: Depth Cues

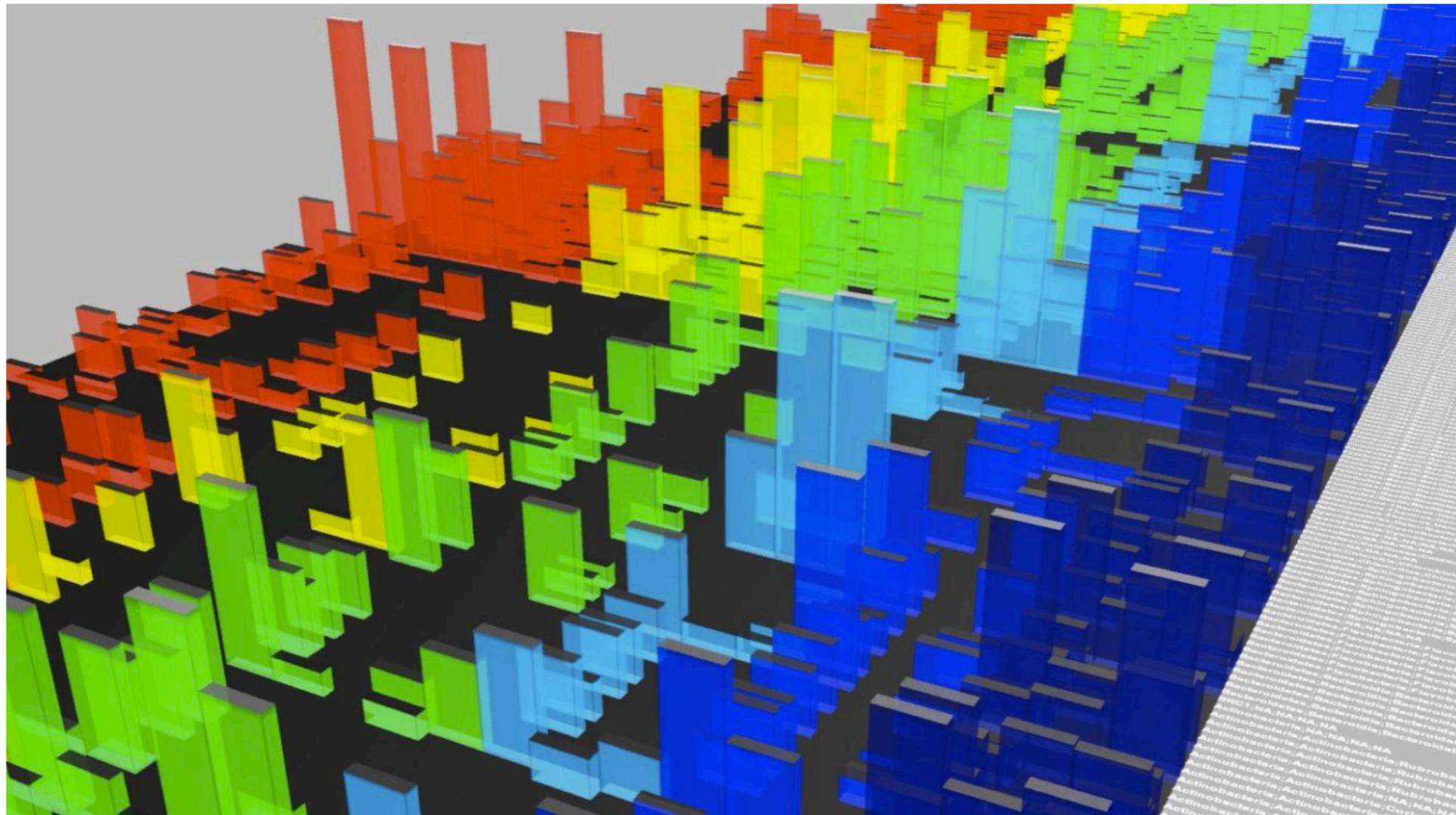


3D Representations

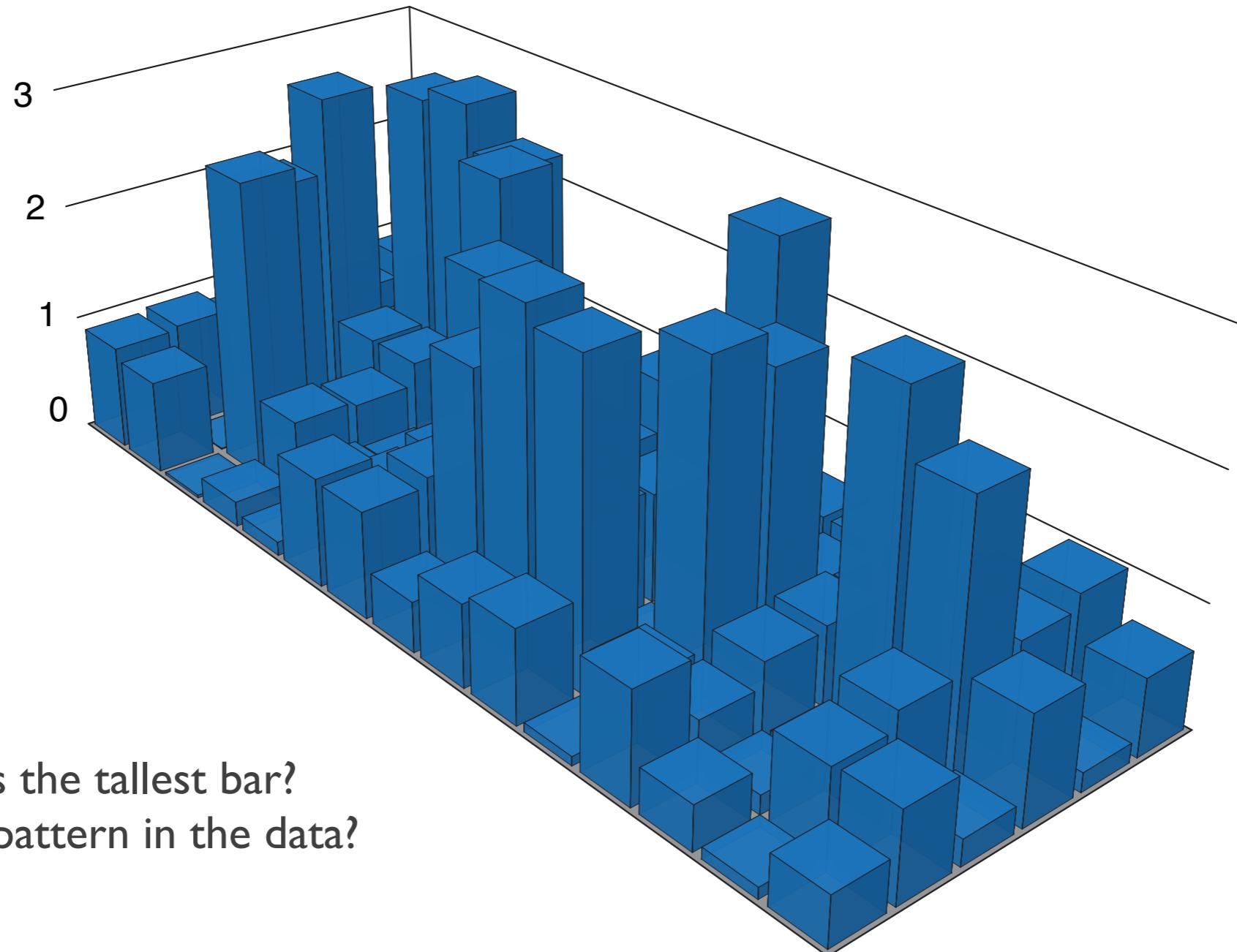
- generally we only see the surfaces of objects in our world
- how we see the world in 3D:
 - rapid eye-movement
 - head and body movements
 - depth cues
- (often) legitimate for 3D spatial data, difficult to justify for abstract data

3D Pitfall: Perspective

- **perspective distortion:** interferes with size channel encoding
- **shading:** interferes with color, lightness, and saturation channel encodings

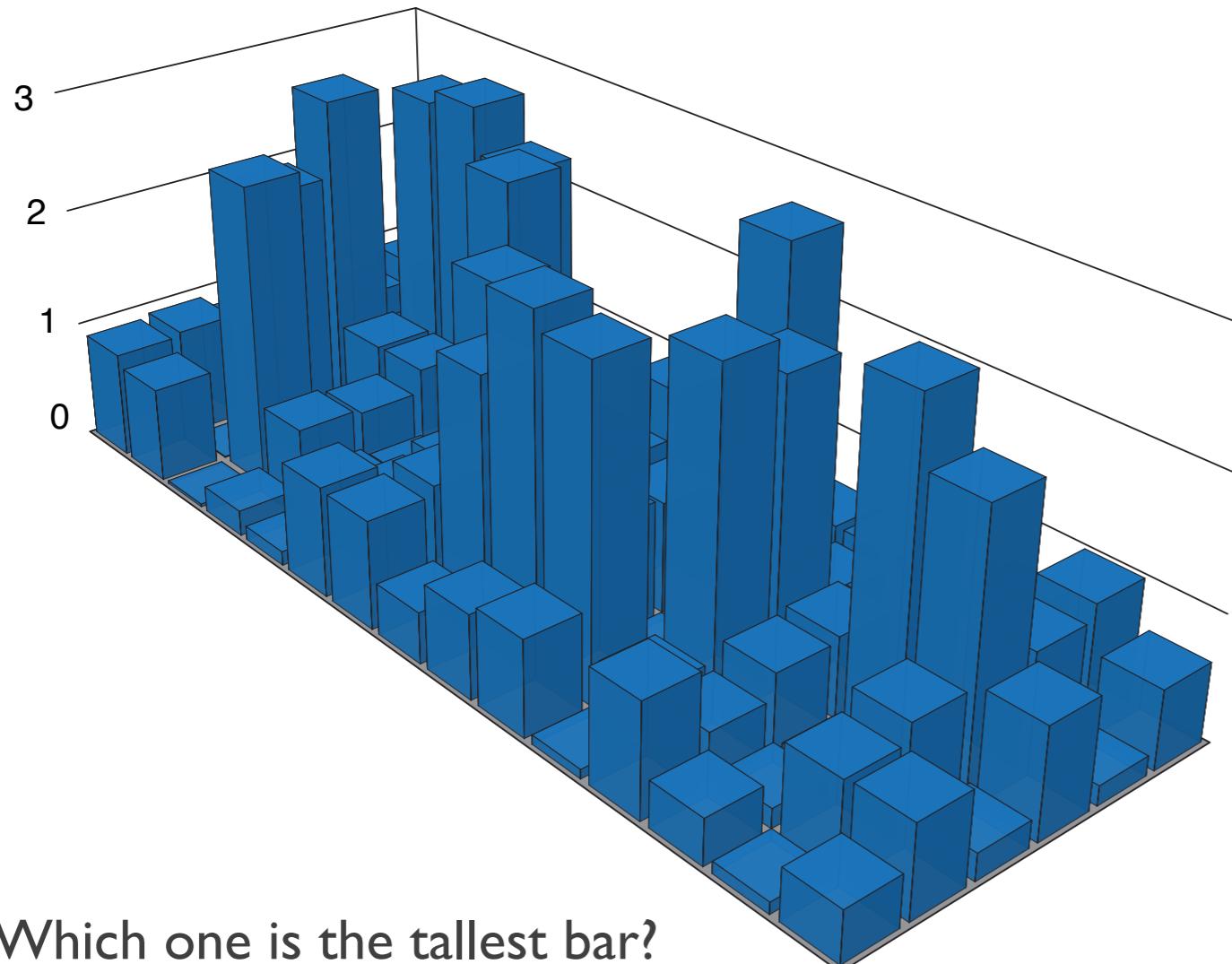


3D Pitfall: Occlusion and Perspective

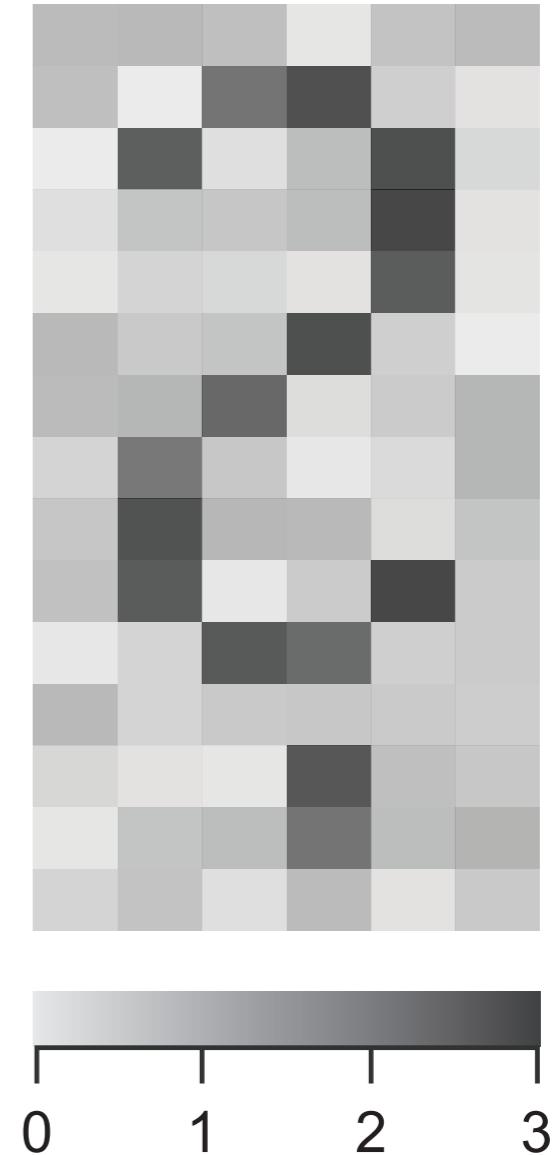


Which one is the tallest bar?
What is the pattern in the data?

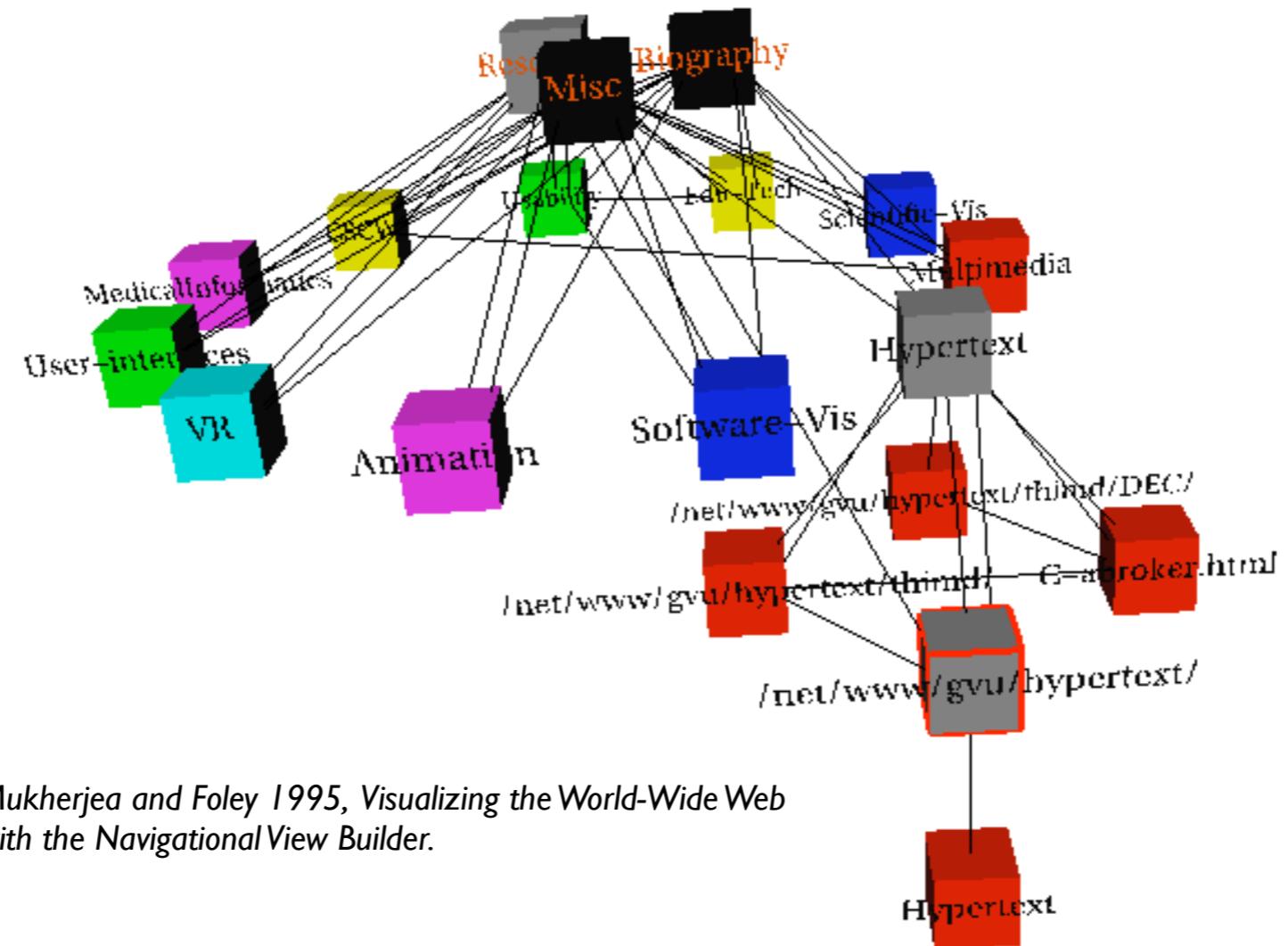
3D Pitfall: Occlusion and Perspective



Which one is the tallest bar?
What is the pattern in the data?



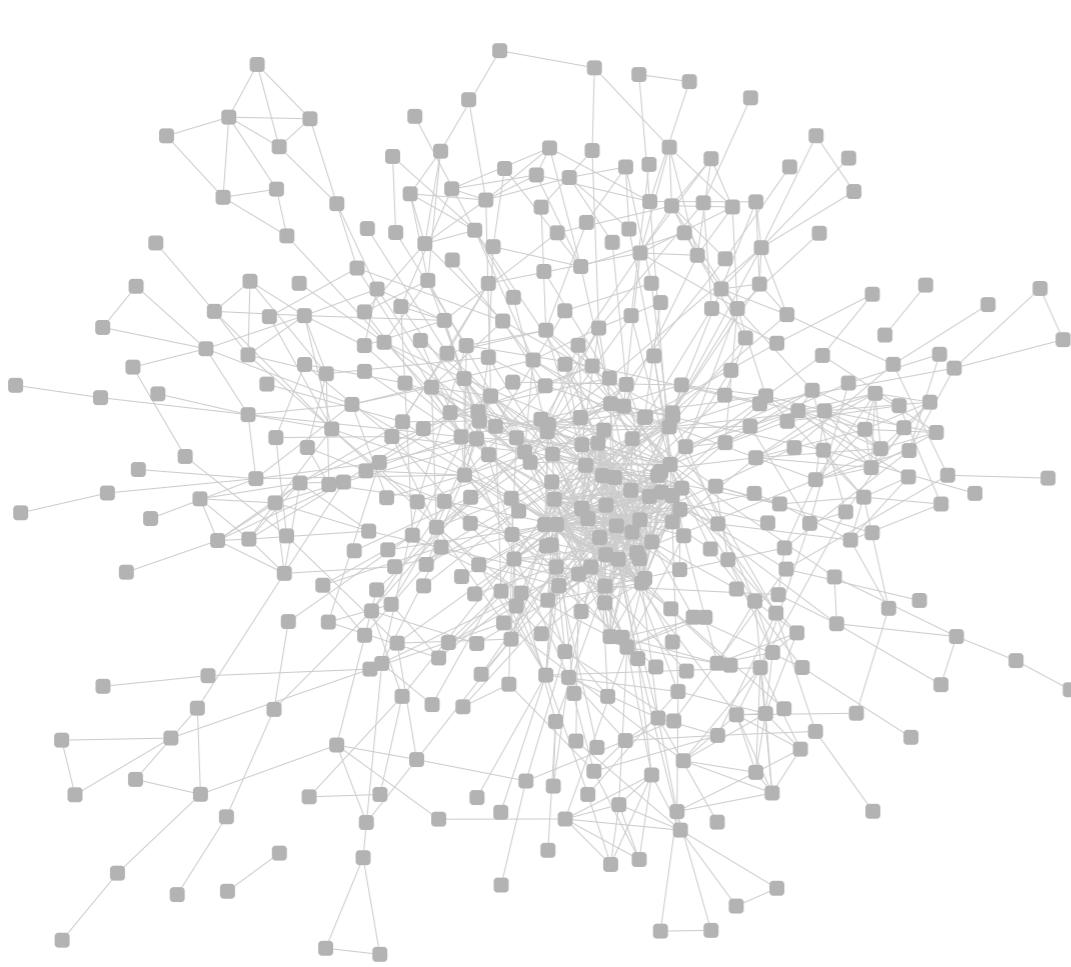
3D Pitfall: Text Legibility



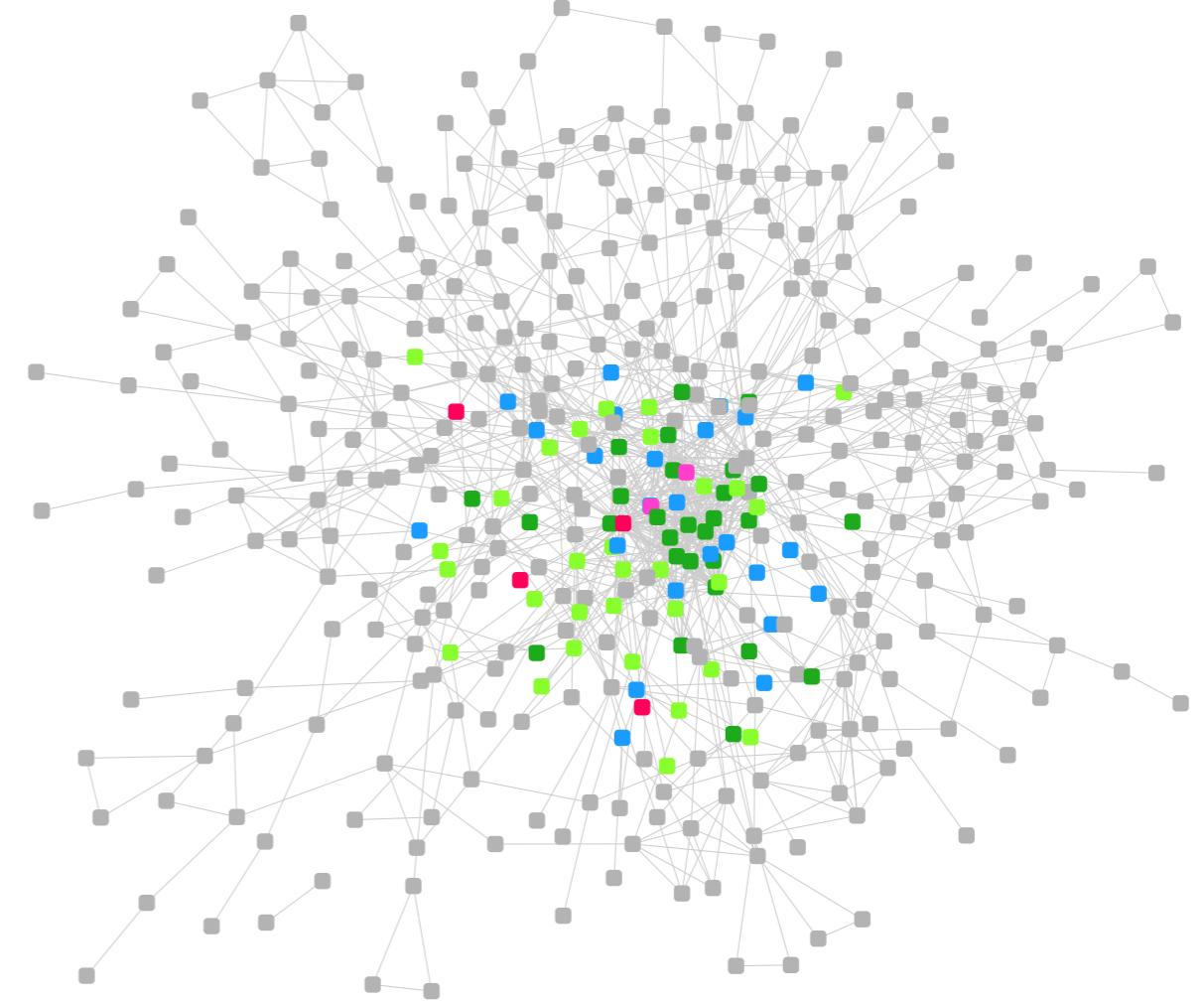
*Mukherjea and Foley 1995, Visualizing the World-Wide Web
with the Navigational View Builder.*

Interactions: Manual Layout

Step 1

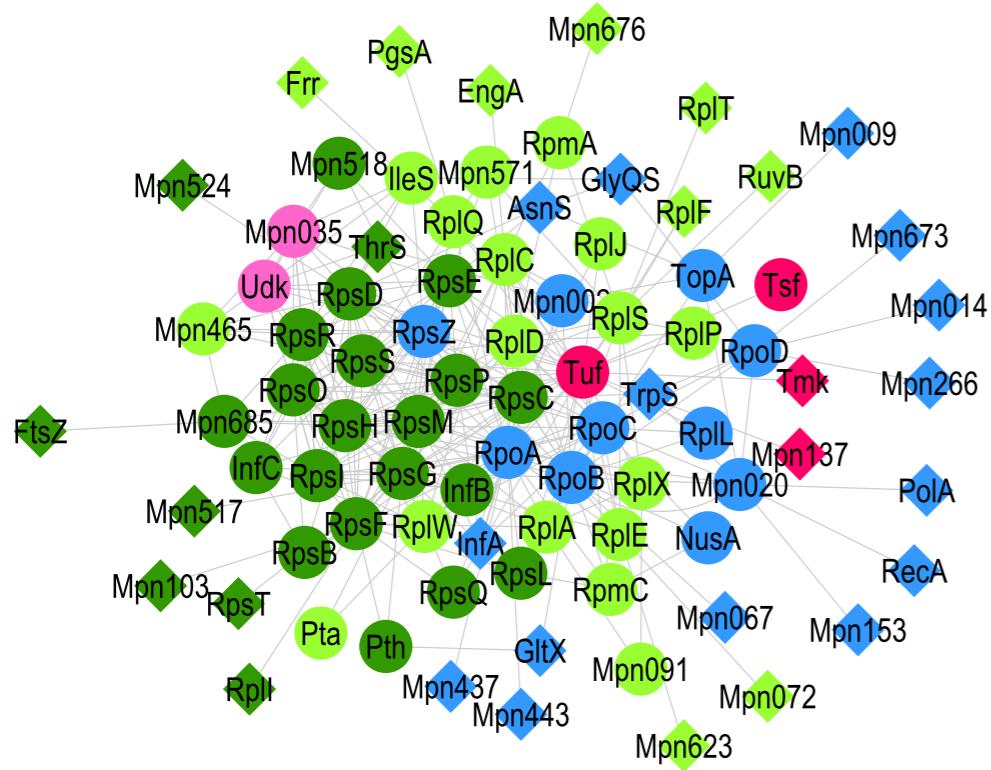


Step 2

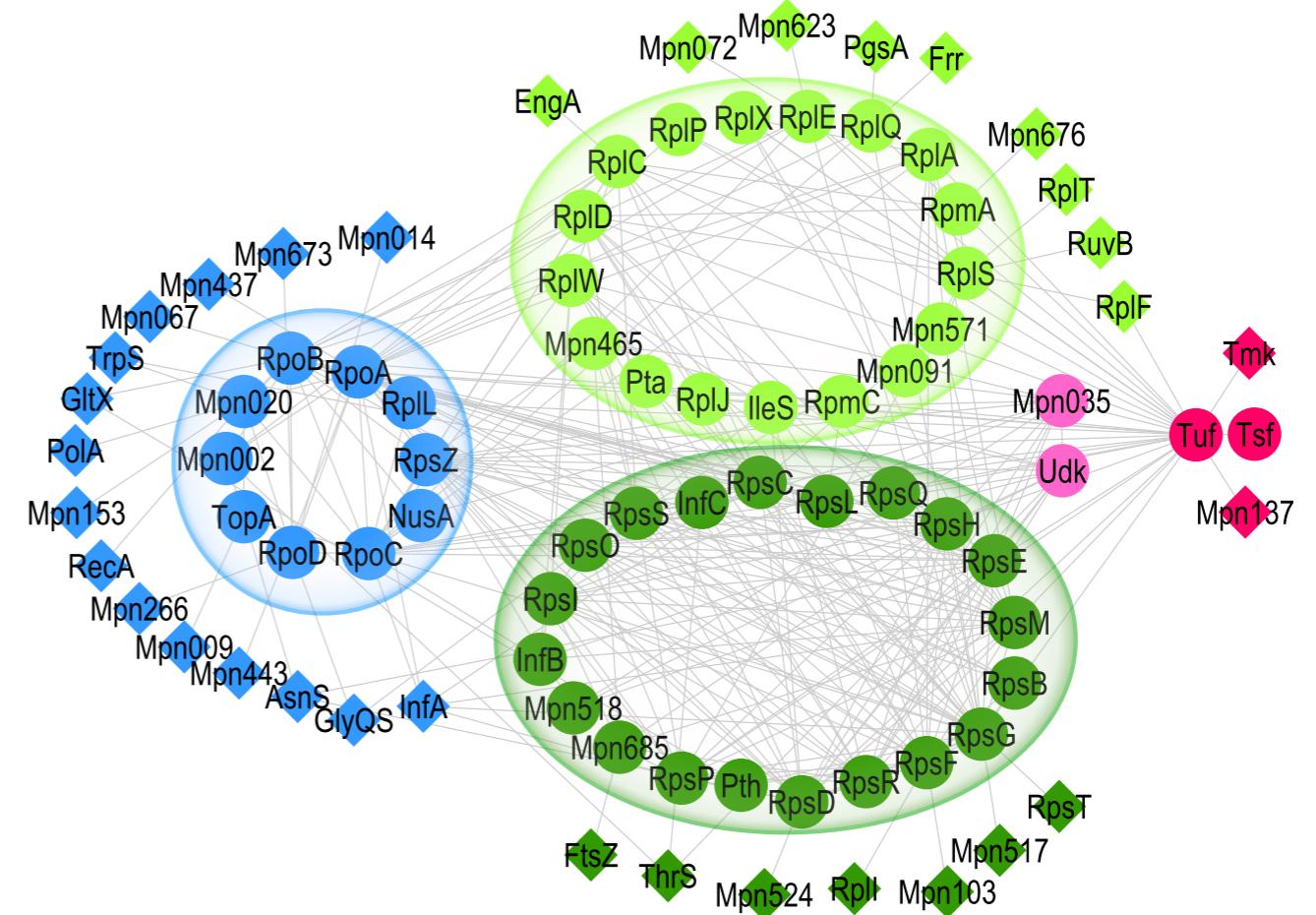


Interactions: Manual Layout

Step 3

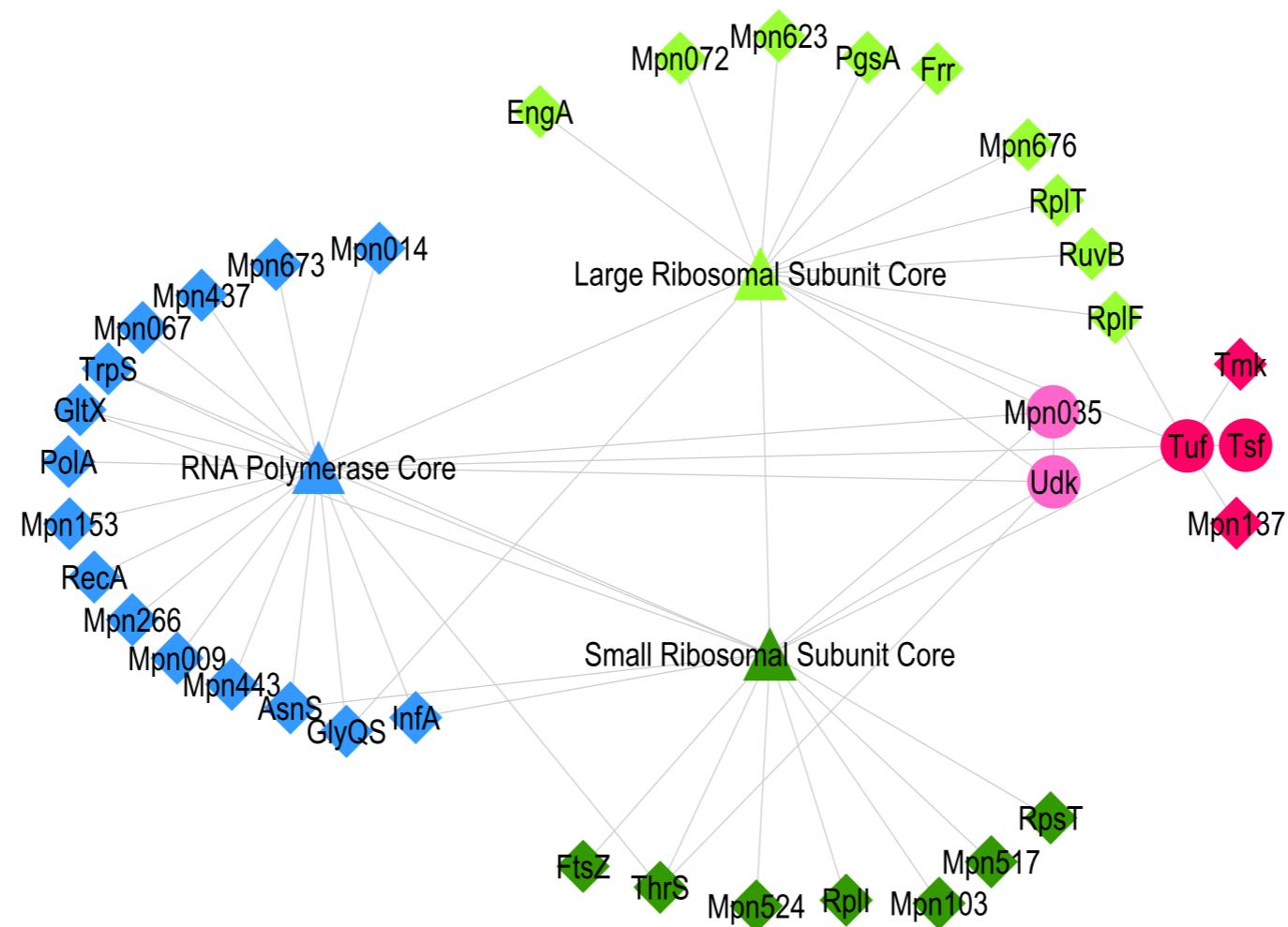


Step 4

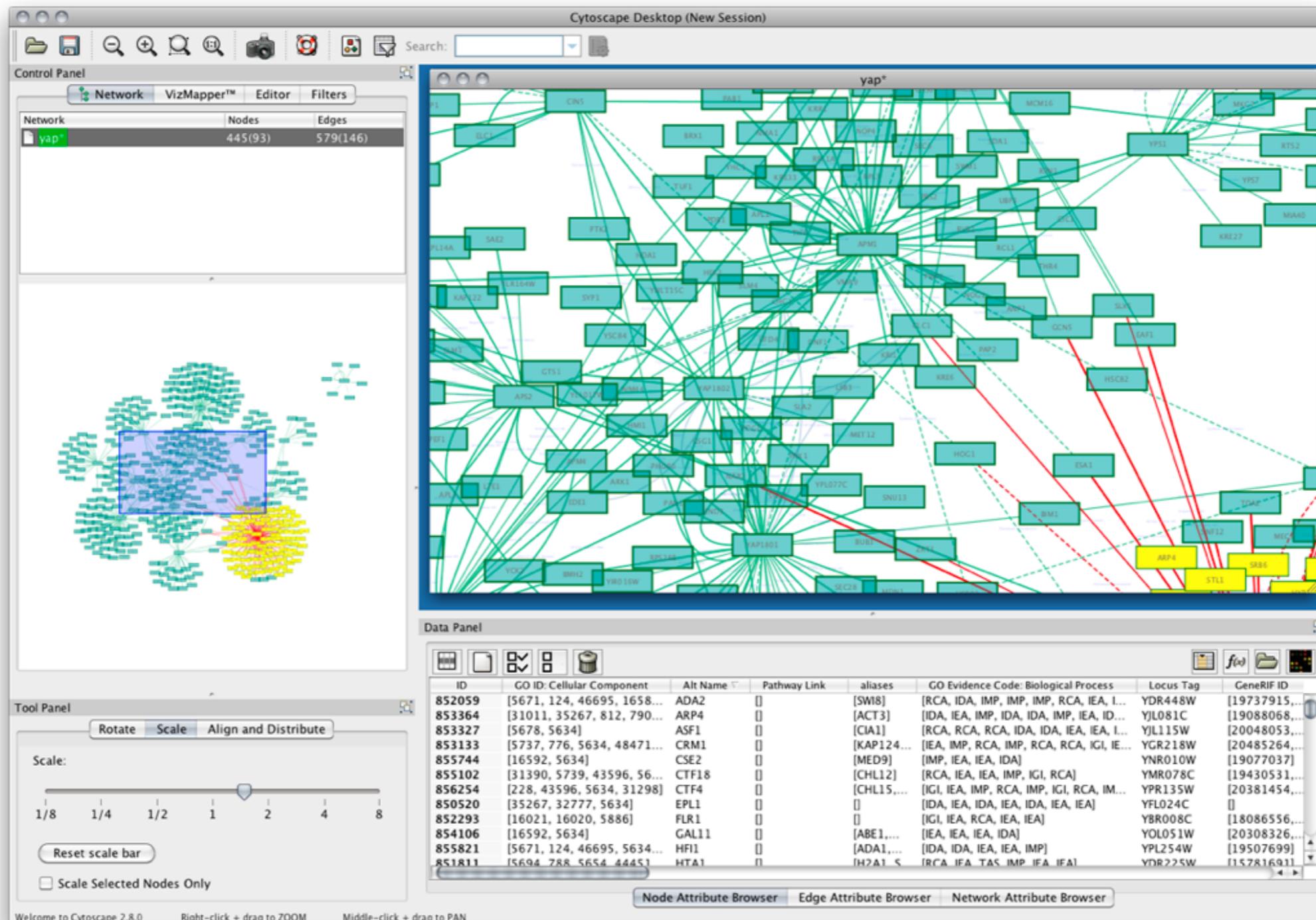


Interactions: Manual Layout

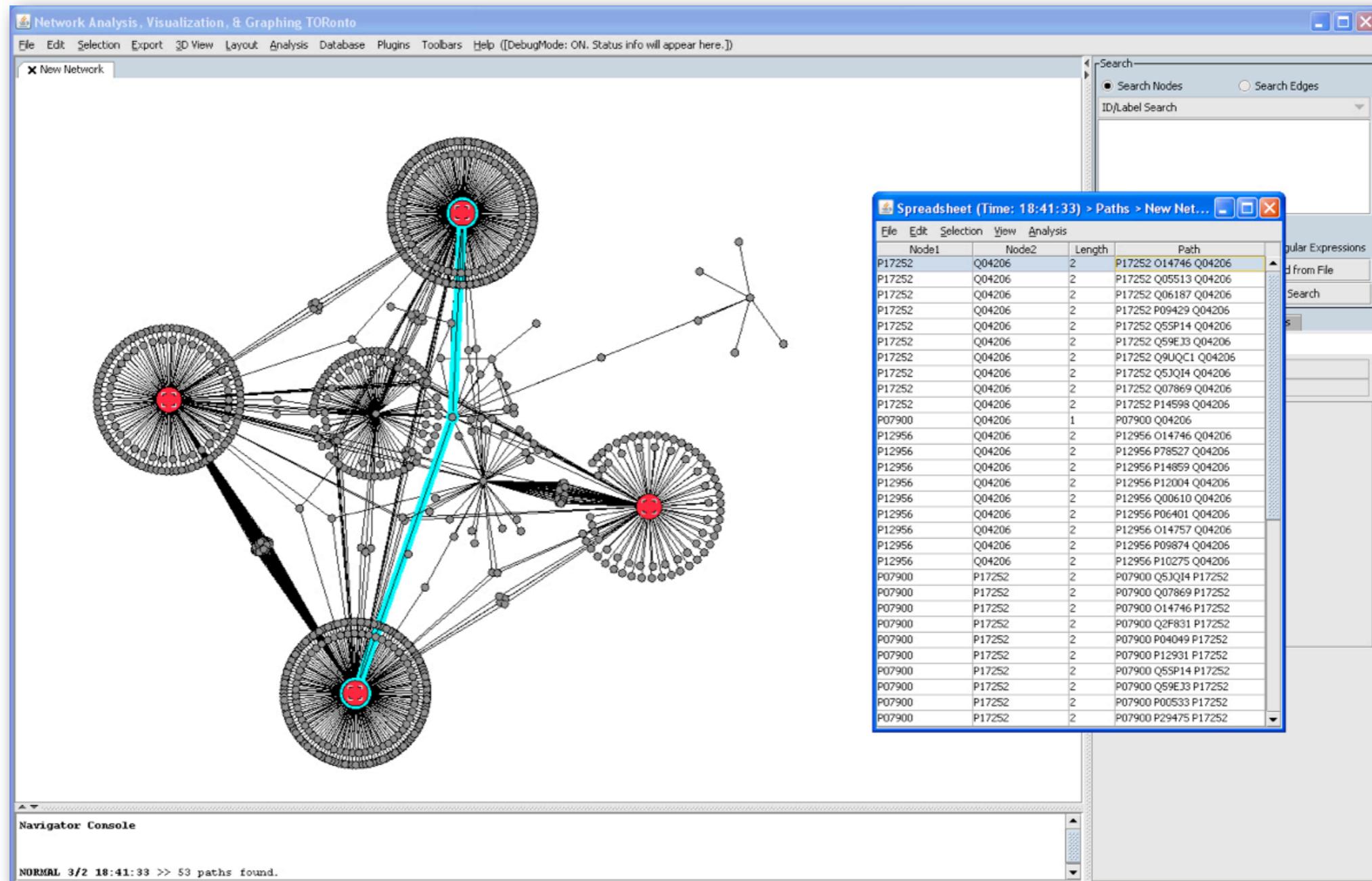
Step 5



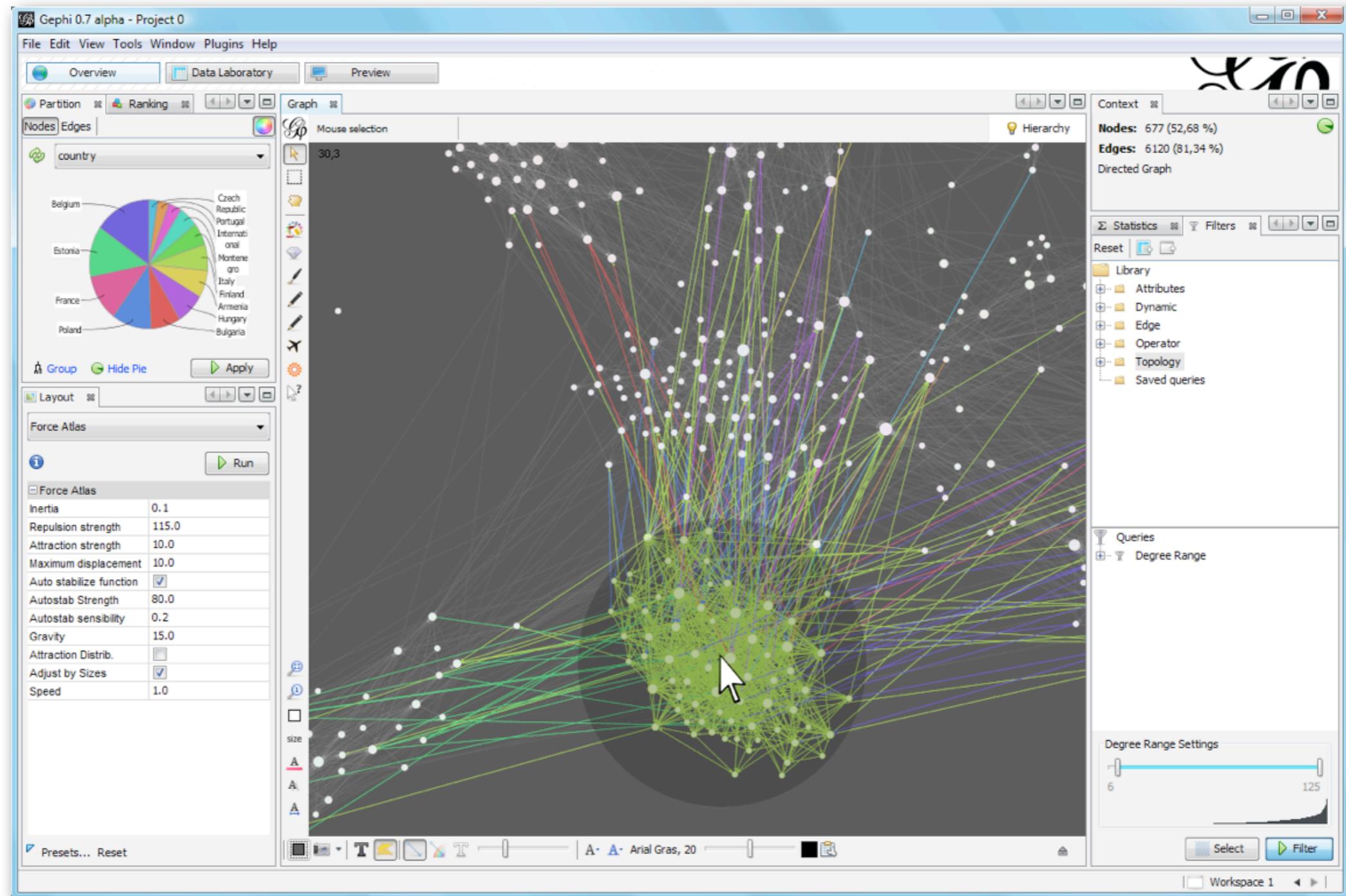
Cytoscape



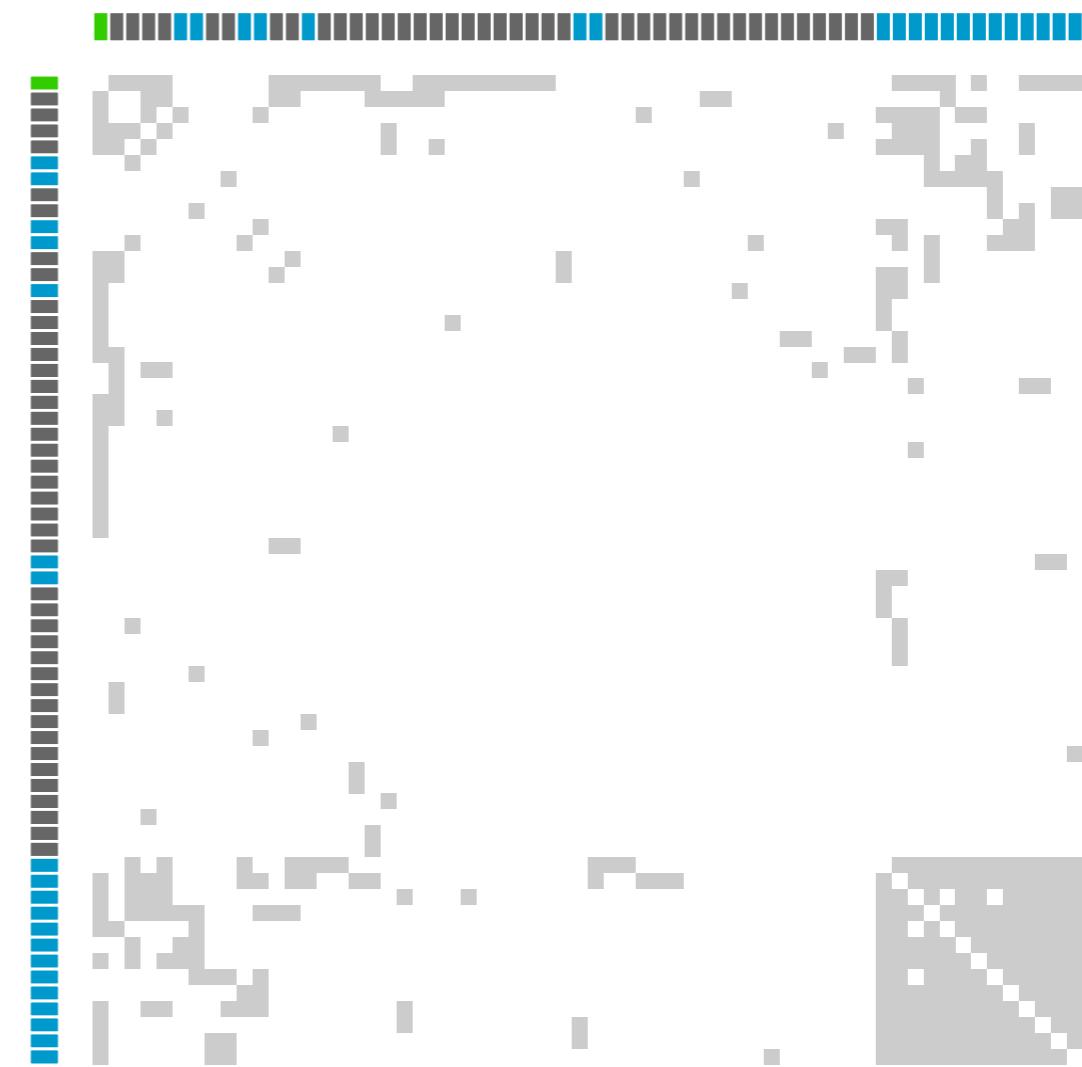
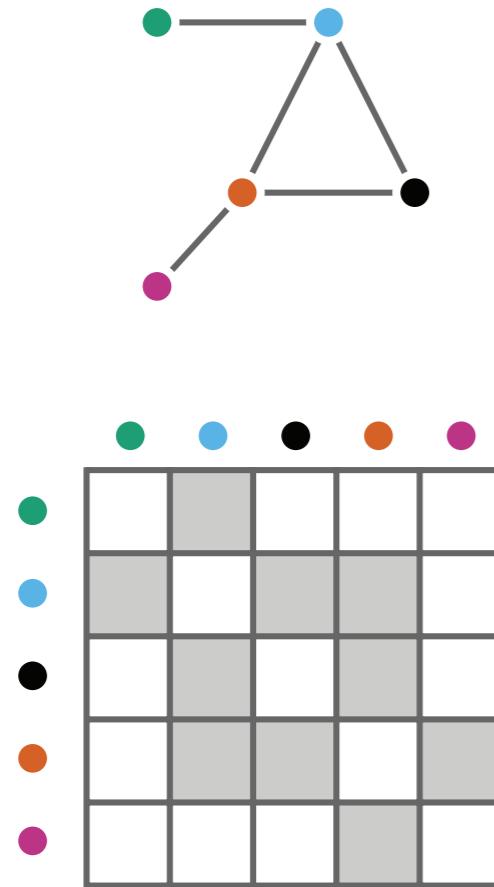
NAViGaTOR



Gephi



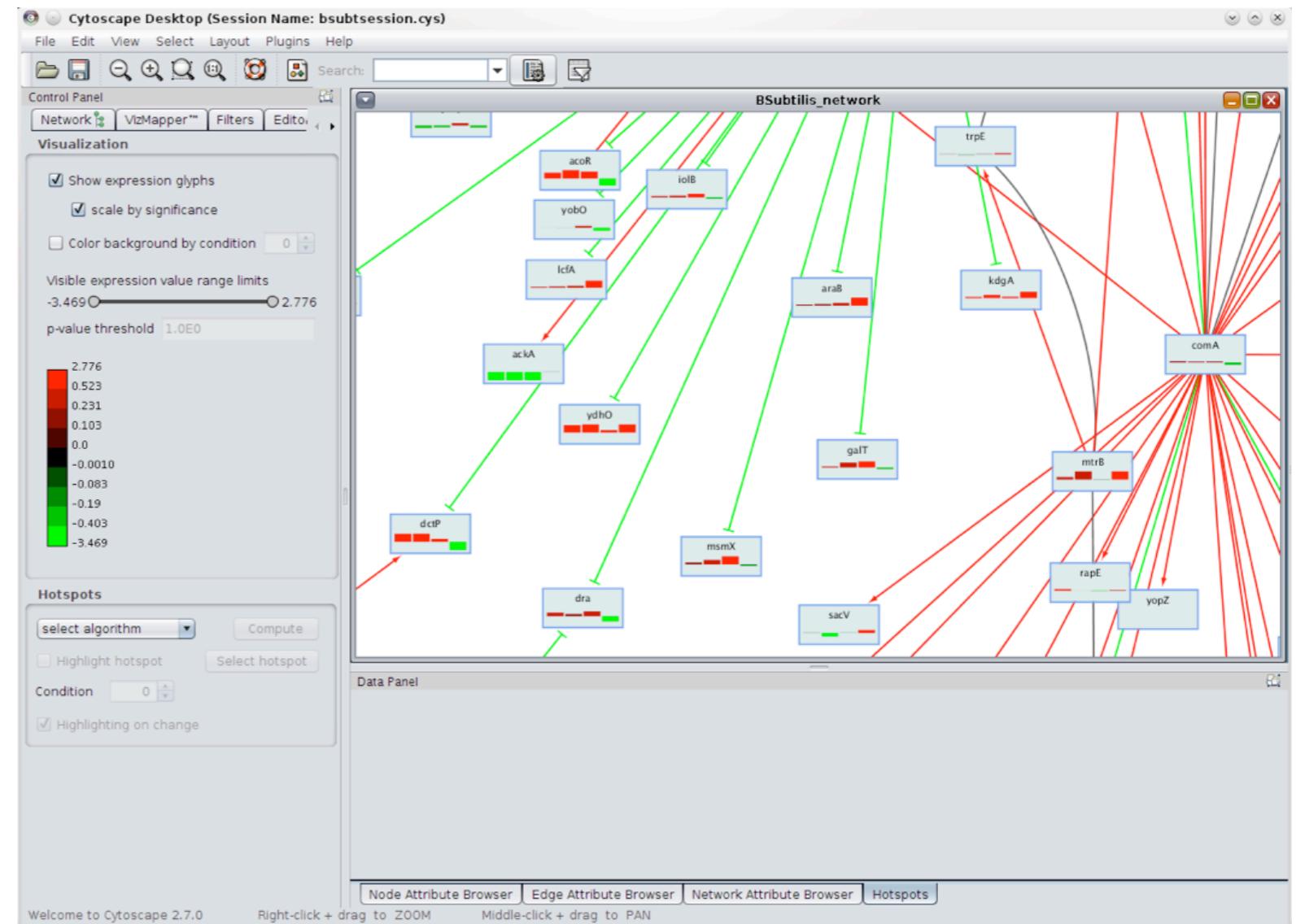
Interactions: Adjacency Matrices



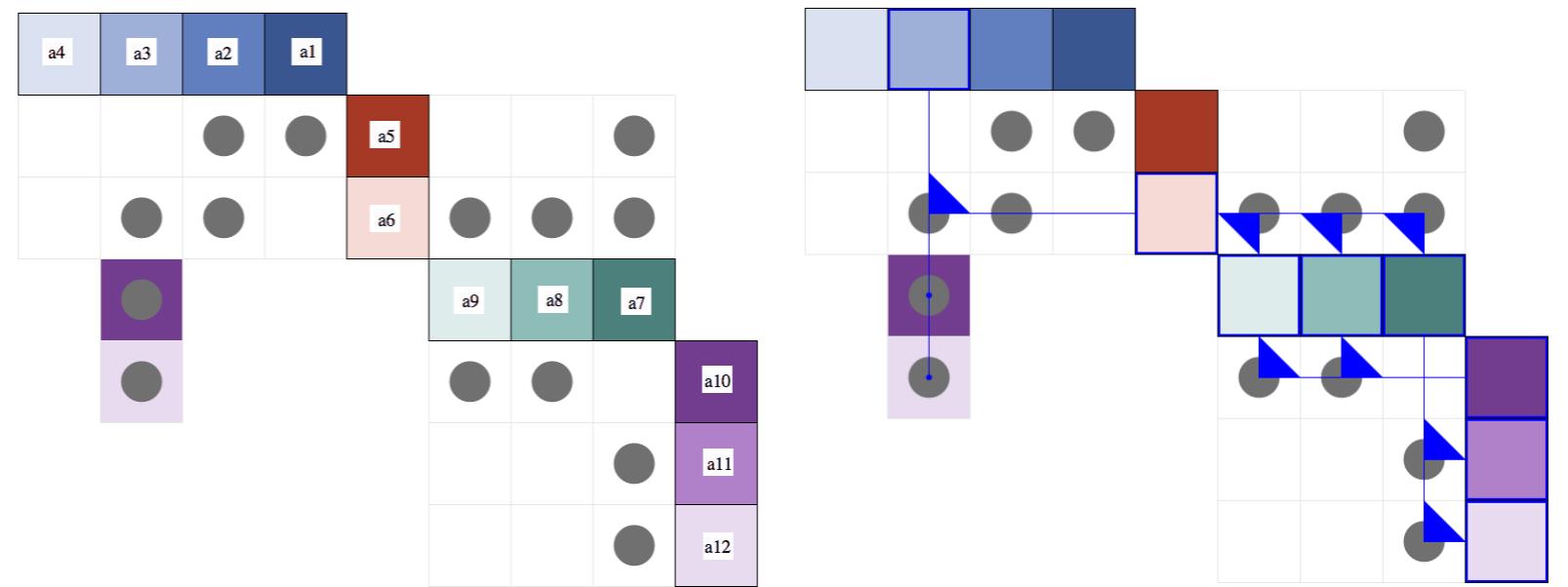
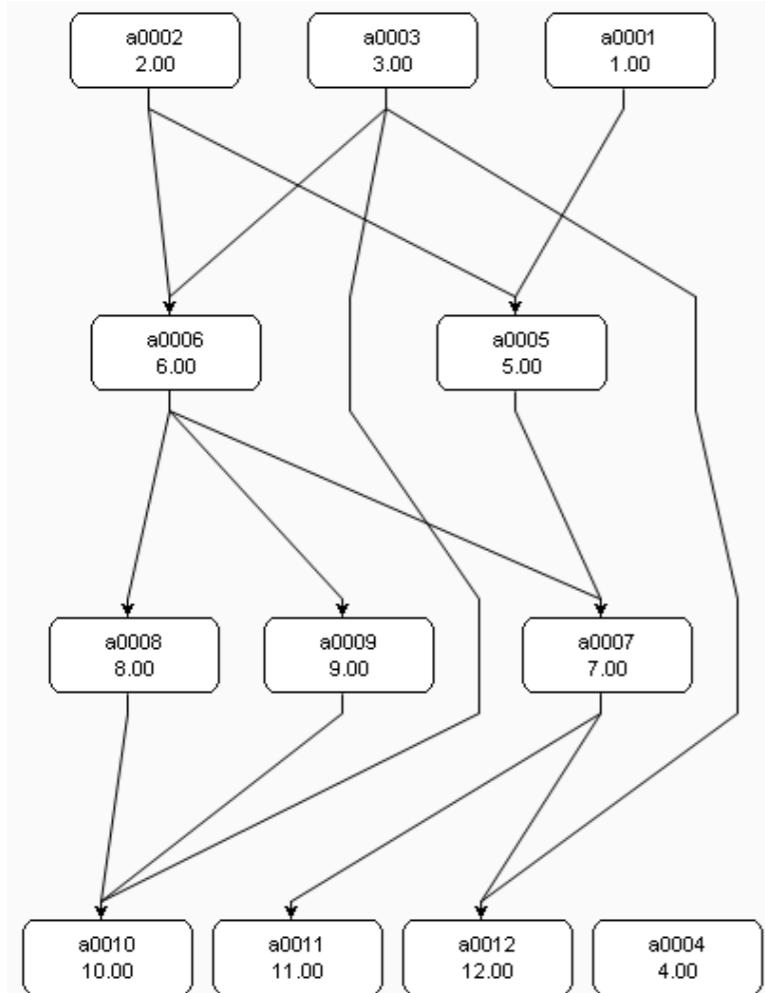
Interactions: Gene Regulatory Networks

SpotXplore

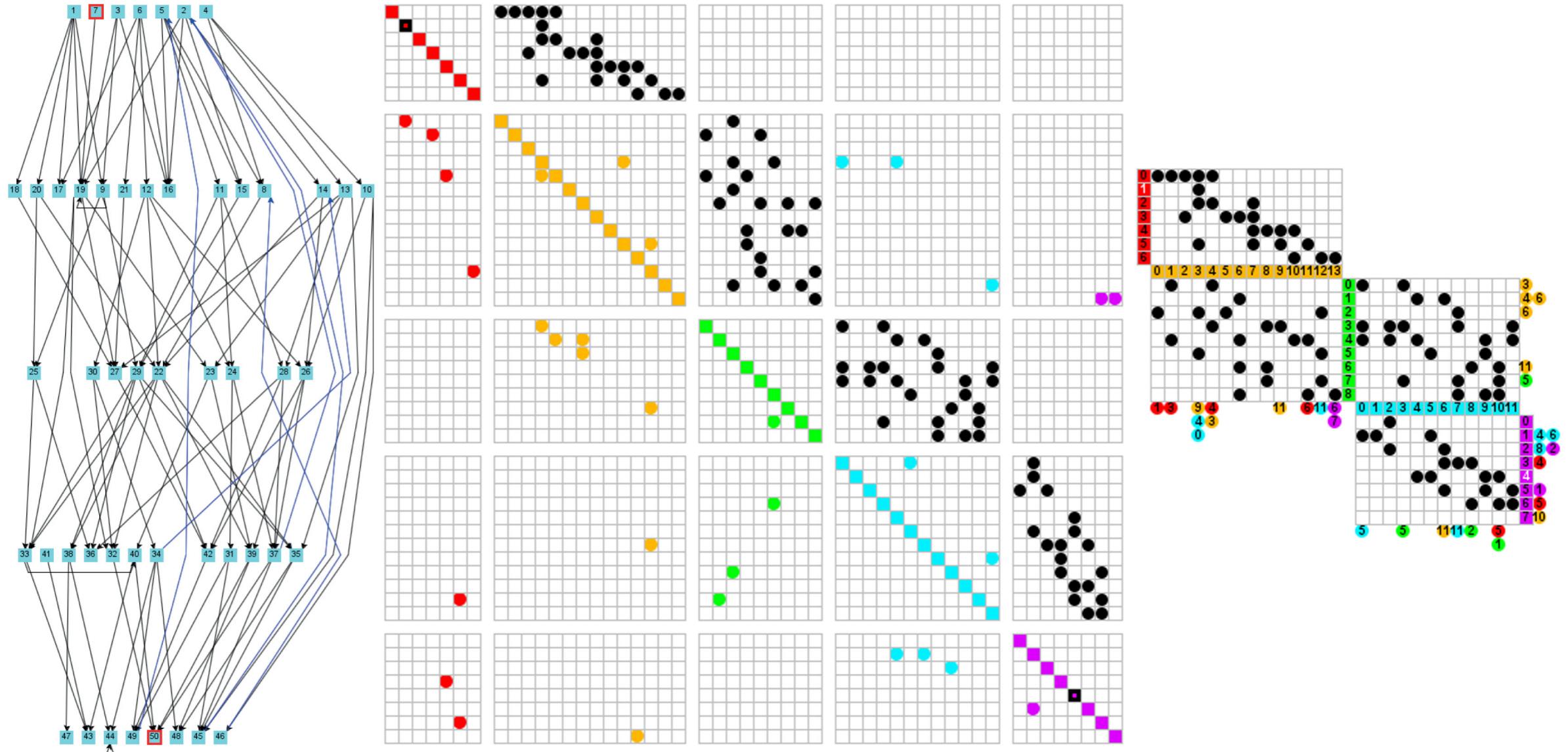
- maps expression profiles onto regulatory network
- statistics can be visualized
- interaction
- highlight subnetworks
- Cytoscape plugin



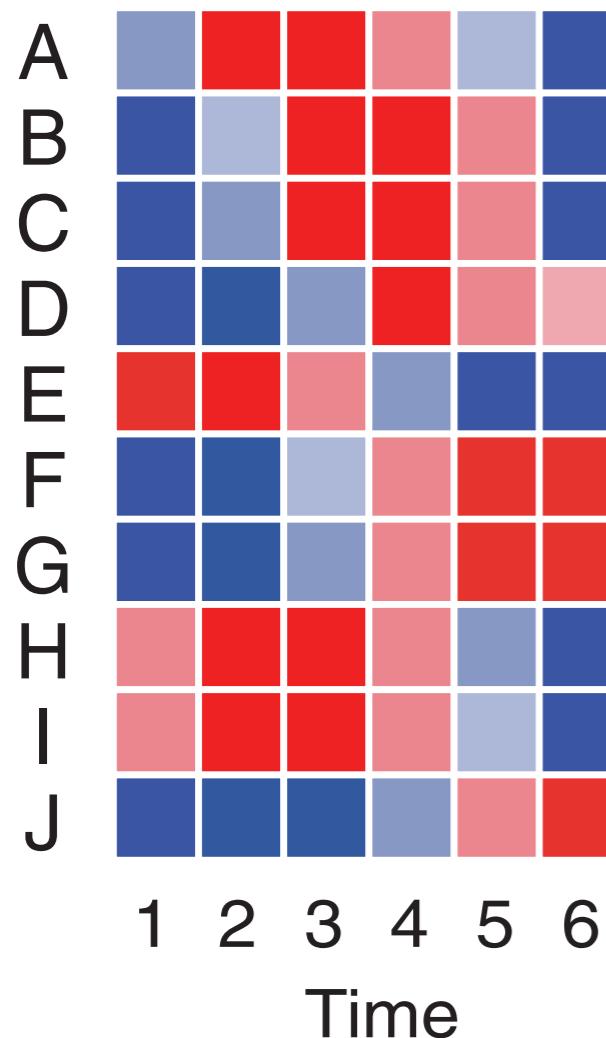
Interactions: Quilts



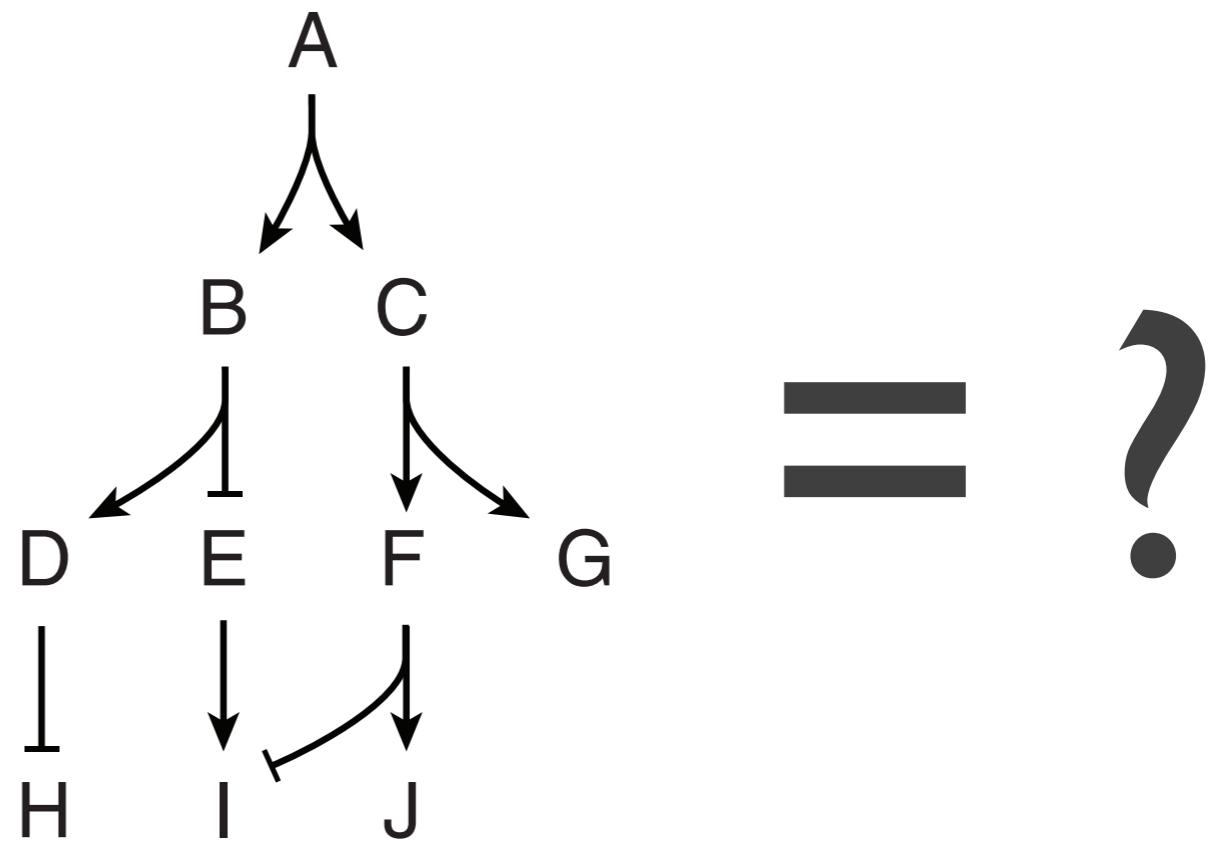
Interactions: Quilts



Interactions: And Multivariate Data?

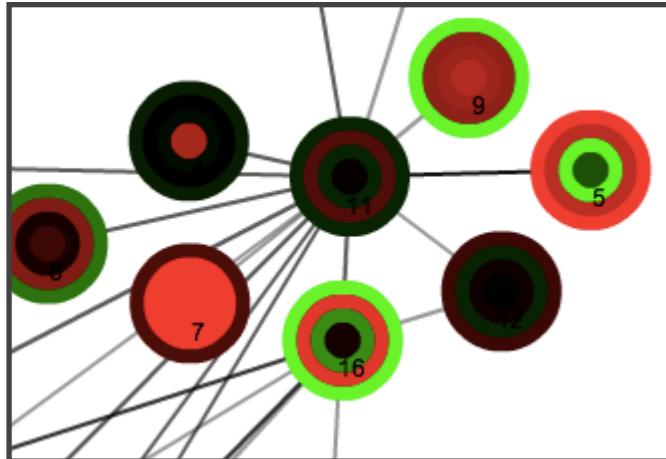


+

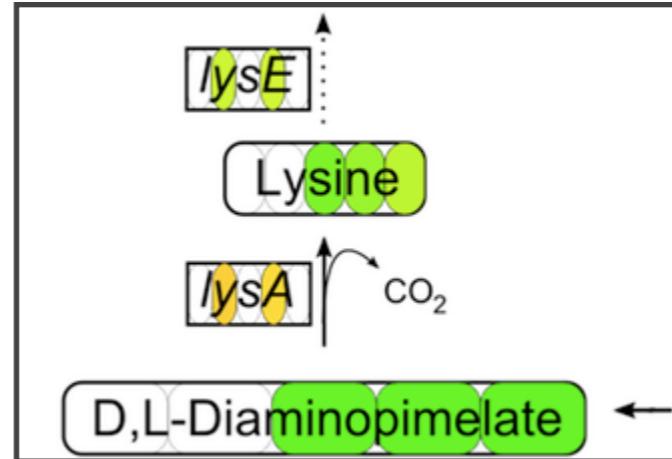


= ?

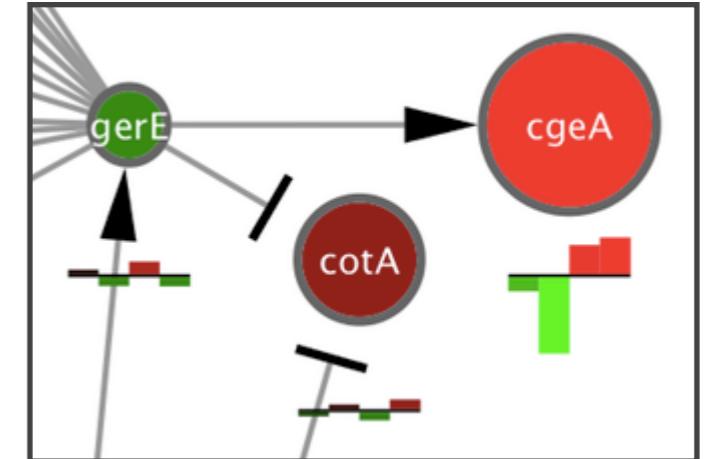
Interactions: And Multivariate Data!



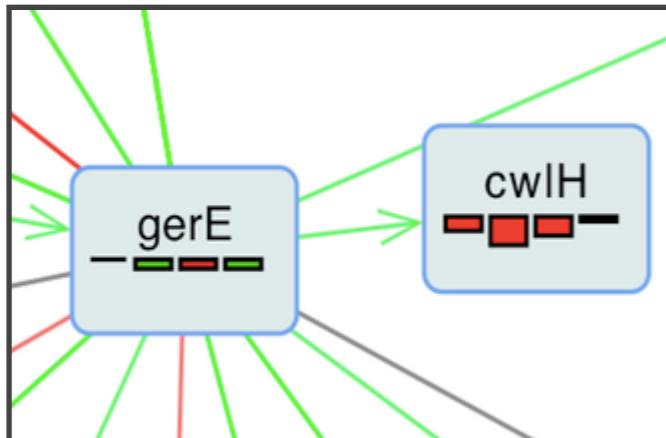
Lichen



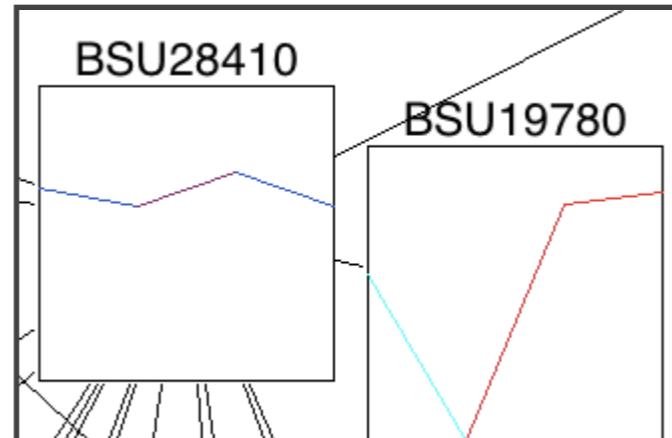
Prometra



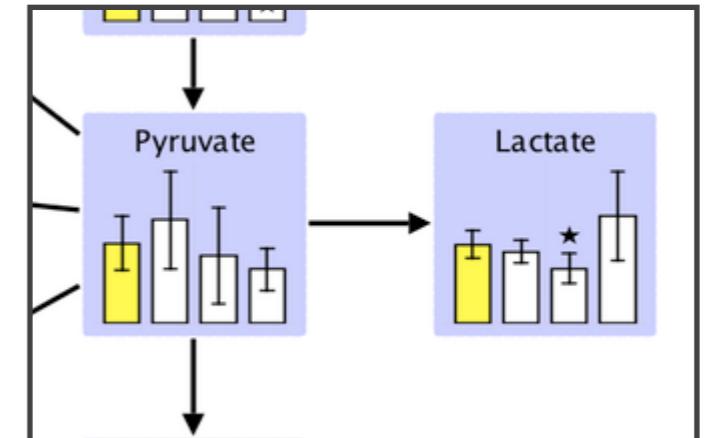
VistaClara (Cytoscape)



GENeVis



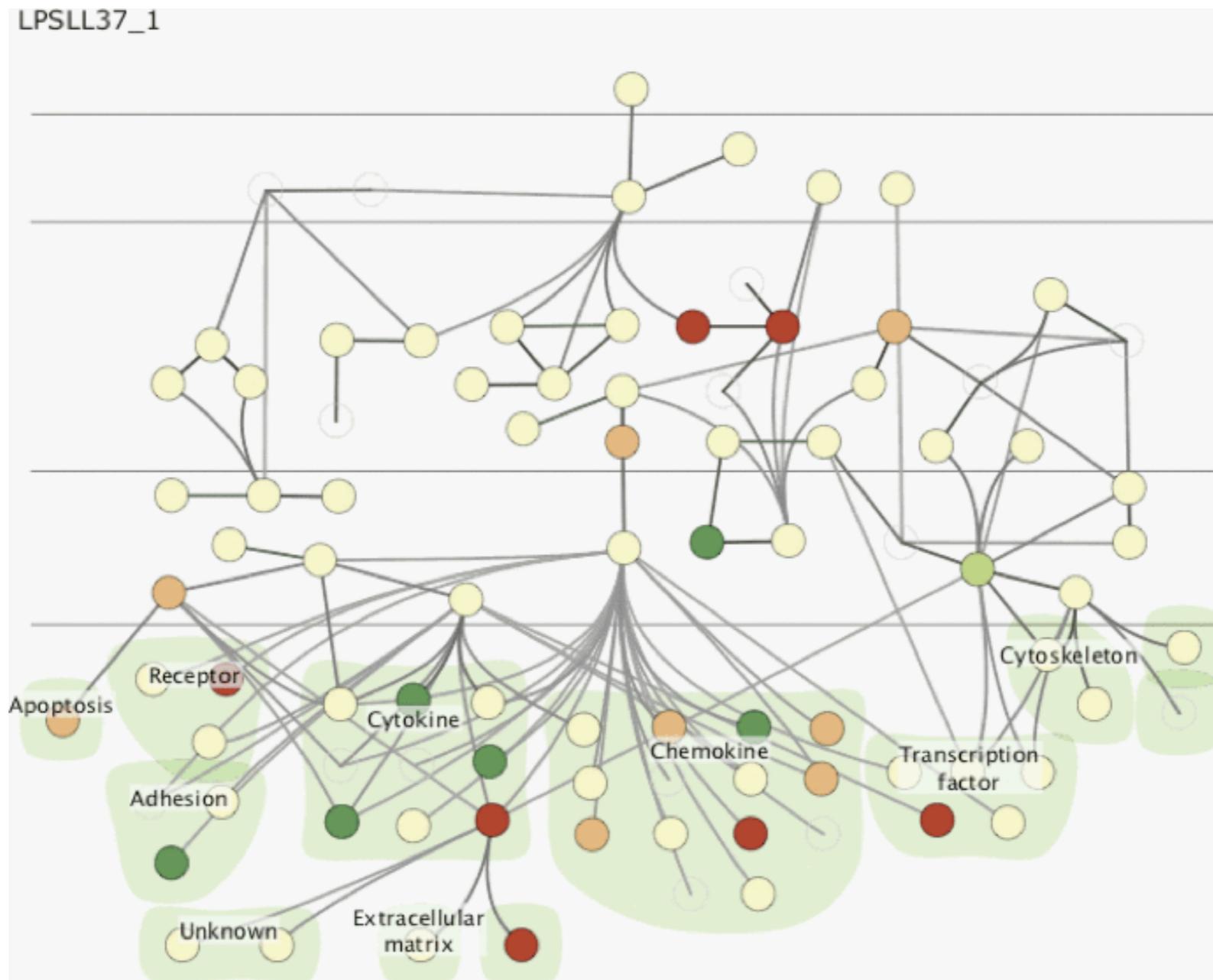
VisANT



VANTED

Animation Pitfall: Across Multiple States

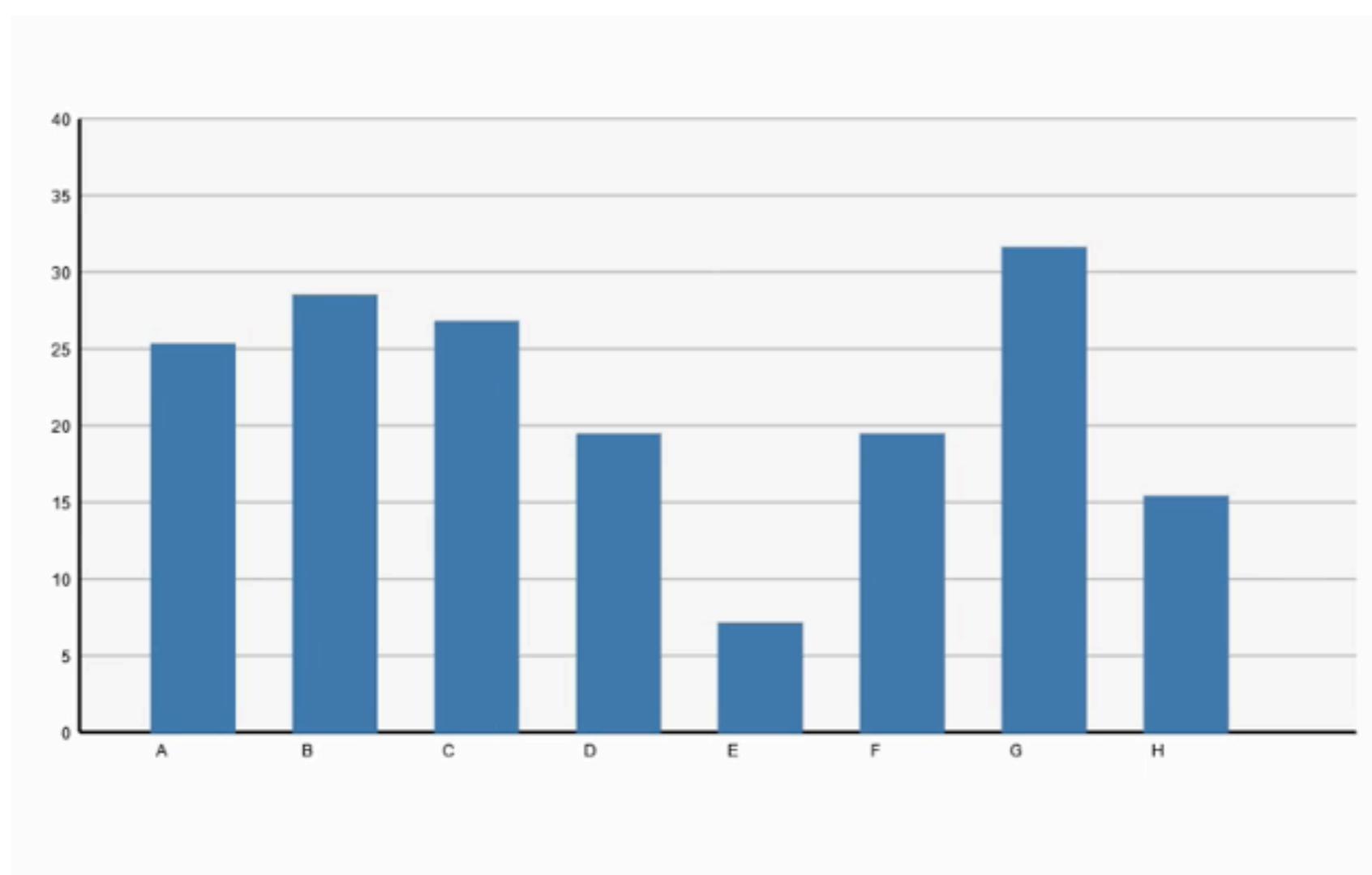
Global comparisons are difficult



Animation

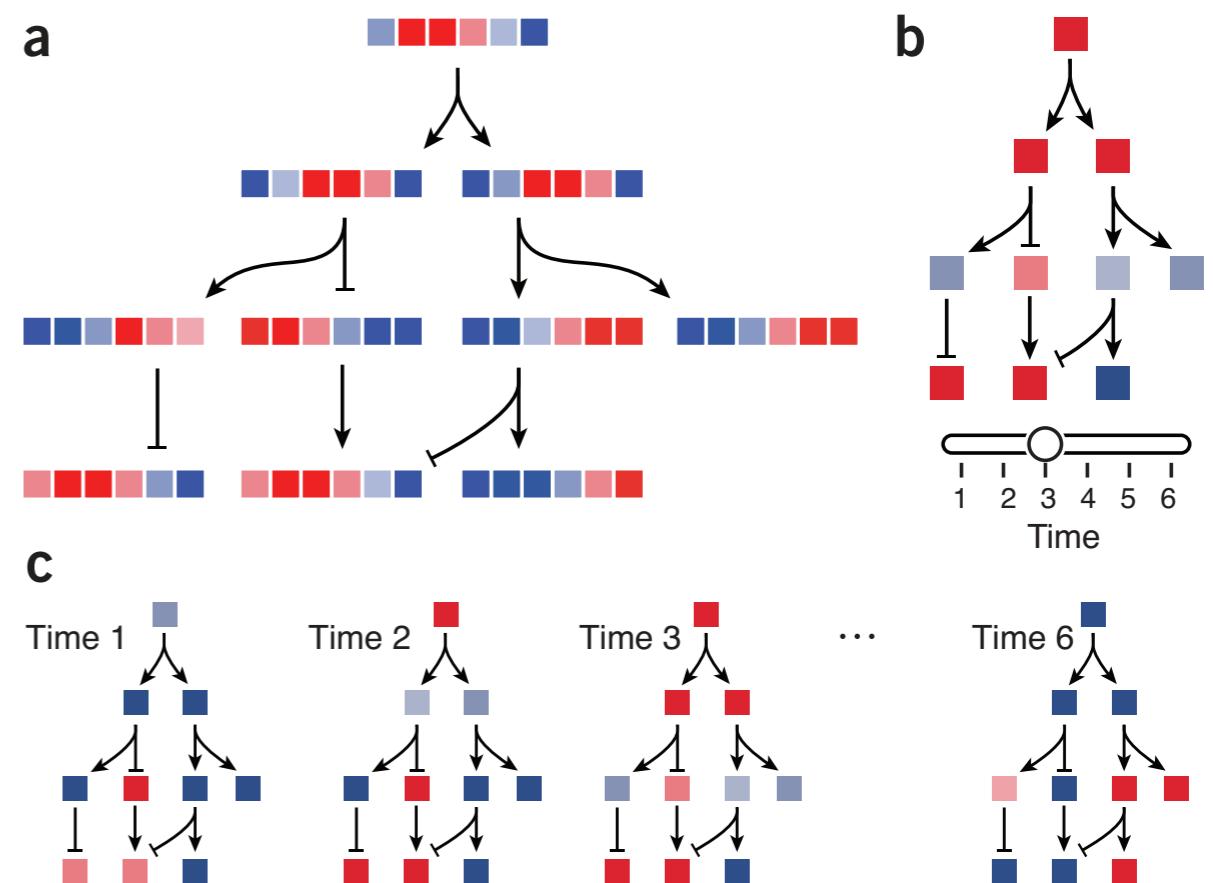
- external versus internal memory
 - easy to compare by moving eyes between views
 - hard to compare view to memory of what you saw
- when to use animation?
 - **good:** chronological storytelling
 - **good:** transition between states
 - **poor:** multiple states with multiple changes

Animation



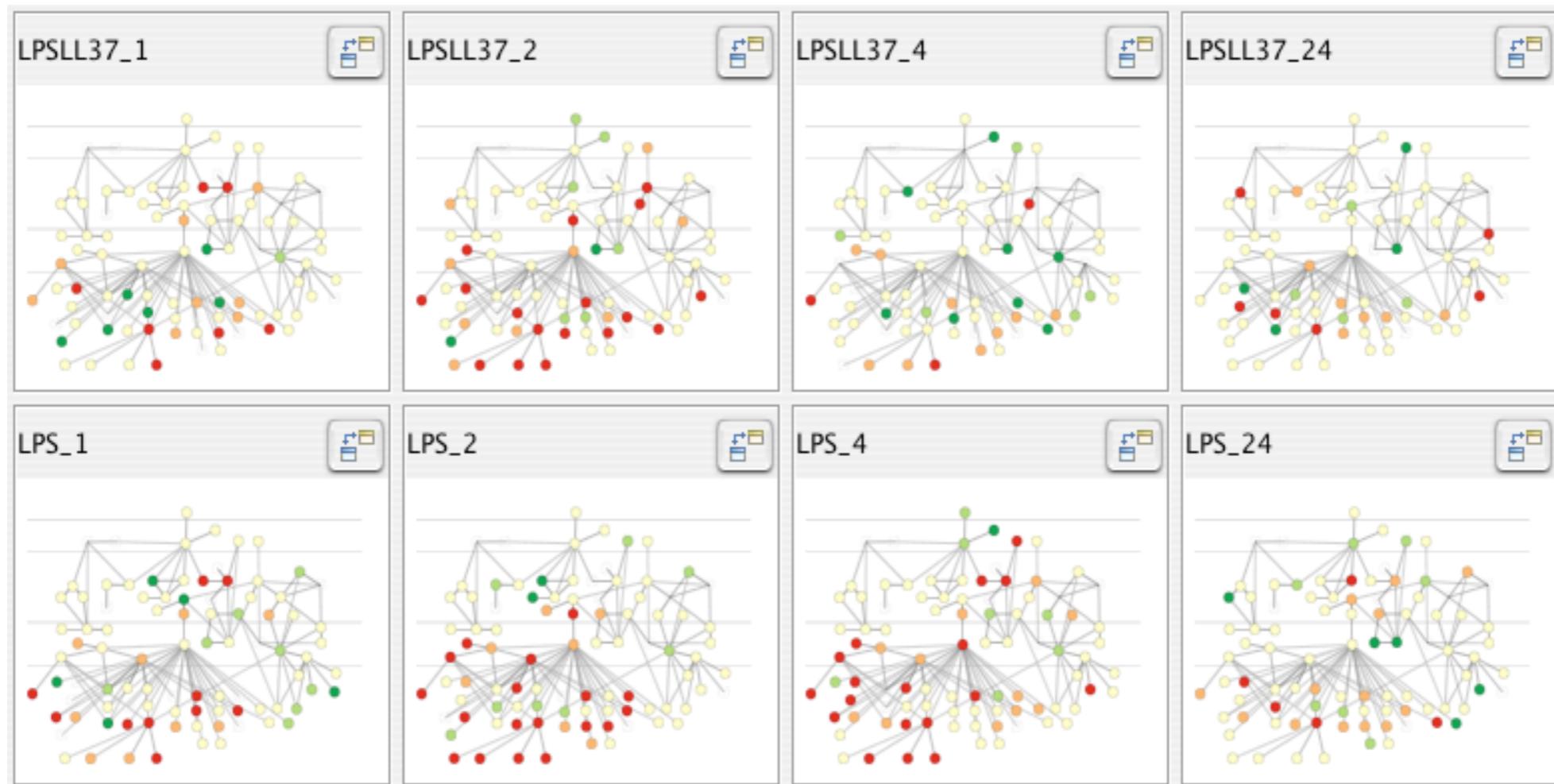
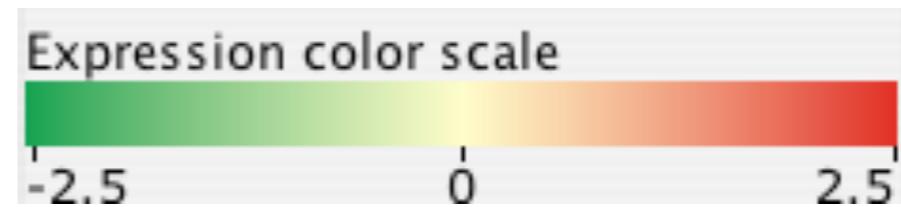
Interactions: And Multivariate Data!?

- (a) **Complex glyphs** = multiple values per node?
- (b) **Animation** = one value per node, one network shown at a time?
- (c) **Small multiples** = one value per node, all networks shown simultaneously?



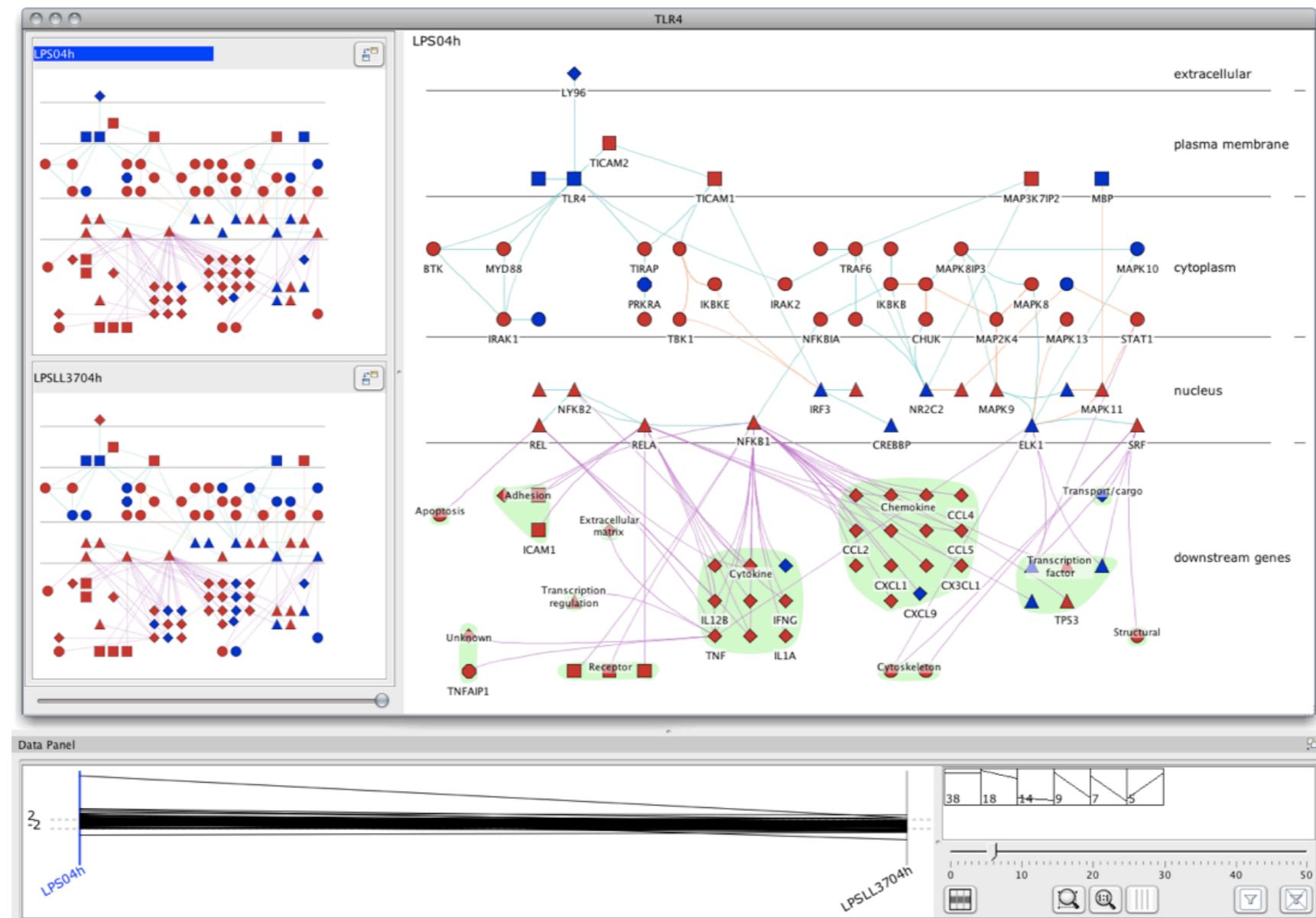
Small Multiples

Small Multiples: one view per state
- show time with space



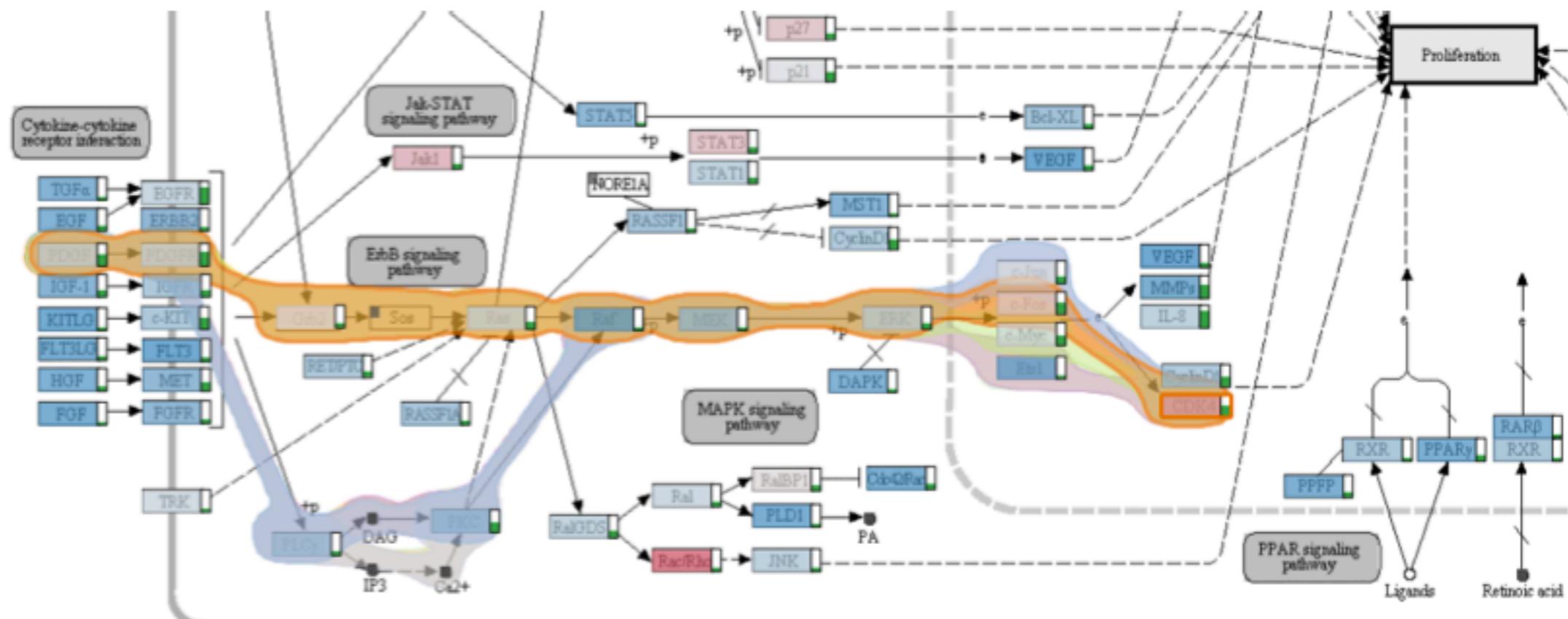
Barsky, Munzner, Gardy, Kincaid 2008, Cerebral:Visualizing Multiple Experimental Conditions on a Graph with Biological Context.

Interactions: And Multivariate Data!

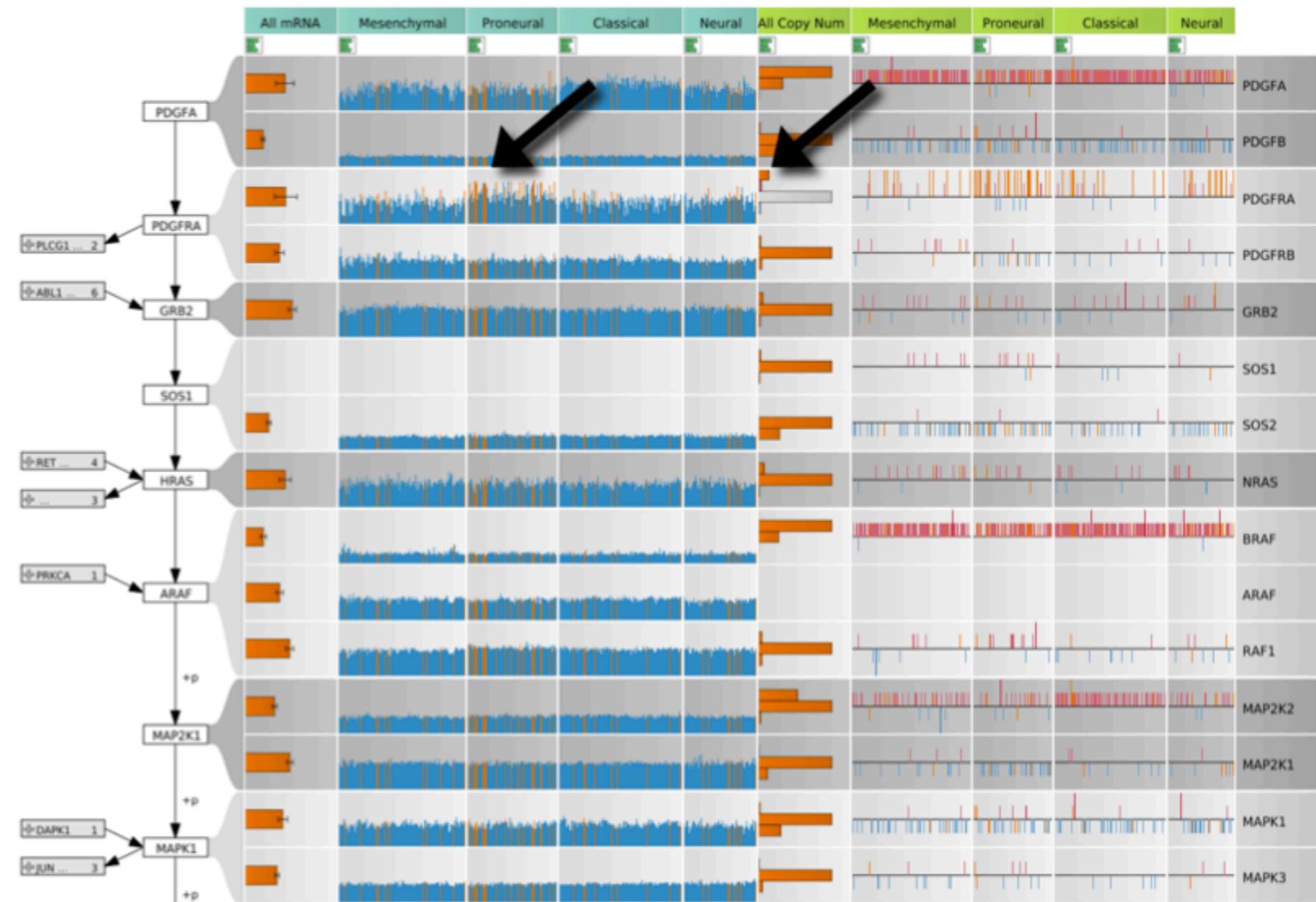


Cerebral (Cytoscape plugin)

Interactions: And Multivariate Data!



Interactions: And Multivariate Data!



Take Home Message

**Biological data visualization
is science, not art.**

Slide Acknowledgements

Miriah Meyer (University of Utah, USA)

Kay Nieselt (University of Tübingen, Germany)

Tamara Munzner (University of British Columbia, Canada)

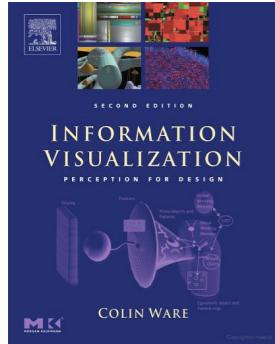
Jessie Kennedy (Edinburgh Napier University)

Resources

Scientific and Information Visualization

- Scientific Visualization (“scivis”) and Information Visualization (“infovis”) are very ill-defined terms
- Scientific Visualization is often used to describe visualization of data that is intrinsically spatial (such as medical imaging data, fluid flows or protein structures)
- Information Visualization is typically used to describe visualization of abstract data (such as gene expression data or interaction networks)
- there is plenty of overlap and the separation is quite arbitrary
- both Scientific and Information Visualization are used to visualize scientific data

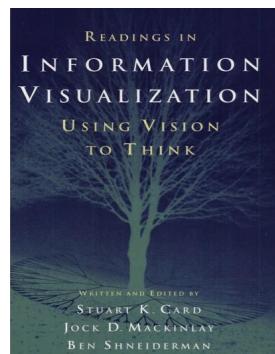
Recommended Books



Information Visualization - Perception for Design

Colin Ware, Morgan Kaufmann, 2004

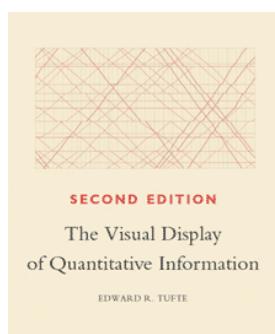
An introduction to information visualization with a strong focus on visual information processing and perception.



Information Visualization - Using Vision to Think

Stuart K Card, Jock D Mackinlay, Ben Shneiderman, Morgan Kaufmann, 1999

Primarily a collection of classic papers in information visualization with introductory chapters.

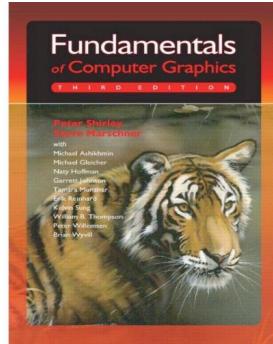


The Visual Display of Quantitative Information (2nd Edition)

Edward R Tufte, Graphics Press, 2001

One of the must-read books by Edward Tufte. This one is the most relevant one for anybody working with data.

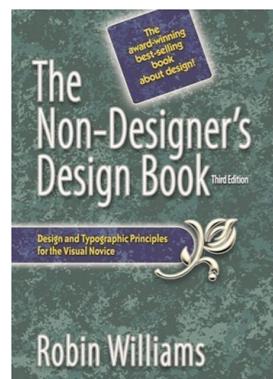
Recommended Books



Fundamentals of Computer Graphics (3rd Edition)

Peter Shirley, Steve Marschner, AK Peters Publishers, 2009

In particular: "Chapter 27 - Visualization", also as free PDF from Tamara Munzner's website.



The Non-Designer's Design Book (3rd Edition)

Robin Williams, Peachpit Press, 2008

A basic introduction to common design strategies.

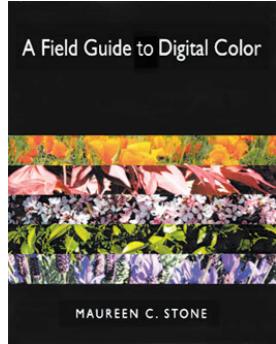


Visual Strategies

Felice C Frankel & Angela H DePace, Yale University Press, 2012

Many useful examples on how to improve figures. All about communication and presentation.

Recommended Resources on Color



A Field Guide to Digital Color
Maureen C Stone, AK Peters Publishers, 2003



ColorBrewer 2.0
Cynthia Brewer, Mark Harrower, <http://www.colorbrewer2.org>

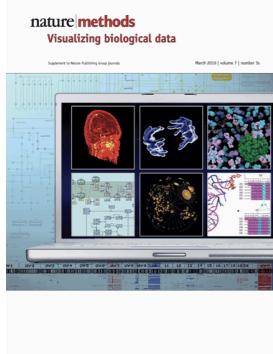


VisCheck
<http://www.vischeck.com>



Color Oracle
<http://colororacle.cartography.ch>

Recommended Journals

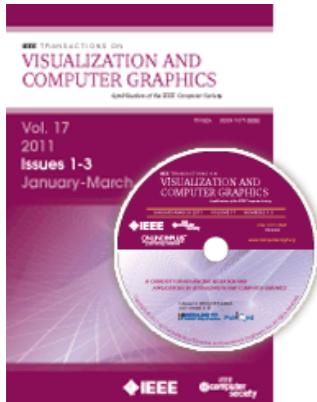


Nature Methods Special Issue on Visualizing Biological Data

<http://www.nature.com/nmeth/journal/v7/n3s>

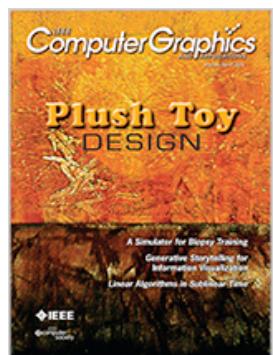
Nature Methods Points of View Column by Bang Wong et al.

<http://bang.clearscience.info/?p=546>



IEEE Transactions on Visualization and Computer Graphics

<http://www.computer.org/portal/web/tvcg>



IEEE Computer Graphics and Applications

<http://www.computer.org/portal/web/cga/home>

Recommended Meetings



IEEE Symposium on Biological Data Visualization - BioVis

www.biovis.net



Workshop on Visualizing Biological Data - VIZBI

www.vizbi.org



IEEE VisWeek with InfoVis, Vis and VAST Conferences

www.visweek.org

Tools for Interaction Network Visualization

Name	Cost	Availability	Description	URL
Stand-alone				
Arena 3D	Free	Win Mac Linux	Visualization of biological multi-layer networks in 3D	http://www.arena3d.org
BiNA	Free	Win Mac Linux	Exploration and interactive visualization of pathways	http://www.bnplusplus.org/bina
BioLayout Express 3D	Free	Win Mac Linux	Generation and cluster analysis of networks with 2D/3D visualization	http://www.biologayout.org
BiologicalNetworks 2	Free	Win Mac Linux	Analysis suite; visualizes networks and heat map; maps abundance data	http://www.biologicalnetworks.org
Cytoscape	Free	Win Mac Linux	Network analysis; extensive list of plug-ins for advanced visualization	http://www.cytoscape.org
GENeVis	Free	Win Mac Linux	Network and pathway visualization; abundance data	http://tinyurl.com/genevis
Medusa	Free	Win Mac Linux	Basic network visualization tool	http://coot.embl.de/medusa
NBrowse	Free	Win Mac Linux	Network visualization software for heterogeneous interaction data	http://www.gnetbrowse.org
NAViGaTOR	Free	Win Mac Linux	Visualization of large protein-protein interaction data sets; abundance data	http://tinyurl.com/navigatorI
Ondex	Free	Win Mac Linux	Integrative workbench; large network visualizations; abundance data	http://www.ondex.org
Osprey	Free	Win Mac Linux	Tool for visualization of interaction networks	http://tinyurl.com/ospreyI
Pajek	Free	Win	Generic network visualization and analysis tool	http://pajek.imfm.si
ProViz	Free	Win Mac Linux	Software for visualization and exploration of interaction networks	http://tinyurl.com/proviz
SpectralNET	Free	Win	Network visualizations; scatter plots for dimensionality reduction methods	http://tinyurl.com/spectralnet
Tulip	Free	Win Mac Linux	Generic visualization and analysis tool; extremely large networks; 3D support	http://tulip.labri.fr/TulipDrupal
VANTED	Free	Win Mac Linux	Combined visualization of abundance data and pathways	http://tinyurl.com/vanted
yEd	Free	Win Mac Linux	Generic network visualization software; offers many layout algorithms.	http://tinyurl.com/yEdGraph
Cytoscape Plug-ins				
BiNoM	Free	Win Mac Linux	Extensive support for common systems biology network formats	http://tinyurl.com/binomI
BioModules	Free	Win Mac Linux	Detects modules in networks; maps abundance data onto nodes and modules	http://tinyurl.com/biomodules
Cerebral	Free	Win Mac Linux	Biologically motivated layout algorithm; maps abundance data; clustering	http://tinyurl.com/cerebrall
MCODE	Free	Win Mac Linux	Network clustering algorithm; support for manual cluster refinement	http://preview.tinyurl.com/MCODEI23
VistaClara	Free	Win Mac Linux	Mapping of abundance data to nodes and “heat strips”; provides heat map	http://www.cytoscape.org/plugins
Web-based				
Graphle	Free		Distributed client/server network exploration and visualization tool	http://tinyurl.com/graphle
Lichen	Free		Library for web-based visualization of network and abundance matrix data	http://tinyurl.com/LichenI
MAGGIE Data Viewer	Free		Visualization of networks; abundance data in heat maps and profile plots	http://maggie.systemsbiology.net
STITCH 2	Free		Construction and visualization of networks from a wide range of sources	http://stitch.embl.de
VisANT	Free	Win Mac Linux	Analysis, mining and visualization of pathways and integrated omics data	http://visant.bu.edu

Tools for Pathway Visualization

Name	Cost	Availability	Description	URL
Stand-alone				
BioTapestry	Free	Win Mac Linux	Visualization of genetic regulatory networks, also with experimental data.	http://www.biotastry.org
Caleydo	Free	Win Linux	Interactive framework for pathway and expression data; 3D “bucket” view	http://www.caleydo.org
CellDesigner	Free	Win Mac Linux	Drawing and simulation of pathways and models, supports SBGN	http://www.celldesigner.org
Edinburgh Pathway Editor	Free	Win Mac Linux	Construction and visualization of pathway diagrams, supports SBGN	http://tinyurl.com/EdinburghPE
GenMAPP 2	Free	Win	Pathway visualization and construction; abundance data	http://www.genmapp.org
IngenuityPathways	\$	Win Mac Linux	Full analysis suite; network and pathway visualizations; abundance data.	http://tinyurl.com/IngenuityPath
JDesigner	Free	Win	Drawing and simulation of pathways and models	http://tinyurl.com/jdesigner
KaPPA View	Free	Win	Analysis and visualization of plant pathways and mapped abundance data	http://tinyurl.com/kappa-view
KEGG Atlas	Free	Win Mac Linux	Visualization of abundance data on interactive KEGG pathways	http://www.genome.jp/kegg
MetaCore	\$	Win Mac Linux	Pathway, network and omics data analysis and visualization suite	http://www.genego.com
PathVisio	Free	Win Mac Linux	Visualization and editing pathways, supports mapping of omics data	http://www.pathvisio.org
VitaPad	Free	Win Mac Linux	Editing of pathway diagrams, integration of abundance data	http://tinyurl.com/vitapad
Web-based				
ArrayXPath	Free		Mapping of abundance data to pathway visualizations	http://tinyurl.com/ArrayXPath
GEPA	Free		Analysis suite; visualization of transcriptomics data on pathways maps	http://tinyurl.com/GEPATI
iPath	Free		Visualization and exploration of combined KEGG pathways	http://pathways.embl.de
MapMan	Free		Application that visualizes abundance data on metabolic pathways	http://tinyurl.com/MapManApp
Omics Viewer	Free		Tool that maps abundance data to BioCyc pathway diagrams	http://www.biocyc.org
Pathway Explorer	Free		Visualization of abundance data on pathways	http://tinyurl.com/pathwayexp
PATIKA	Free		Extensive pathway visualization tool; good support for signaling pathways	http://www.patika.org
Payaologue	Free		Collaborative pathway annotation and visualization tool	http://celldesigner.org/payao
ProMeTra	Free		Maps abundance matrices of multiple omics data types on pathways	http://tinyurl.com/ProMeTra
Reactome SkyPainter	Free		Visualization of overrepresented pathways and reactions from gene lists	http://reactome.org
WikiPathways	Free		Wiki-based, community-driven pathway curation and visualization tool	http://www.wikipathways.org

Tools for Visualization of Multivariate Data

Name	Cost	OS	Description	URL
Stand-alone				
BicOverlapper	Free	Win Mac Linux	Visualization of biclusters combined with profile plots and heat maps	http://vis.usal.es/bicoverlapper/
BiGGEsTS	Free	Win Mac Linux	Heat map-based bicluster visualization	http://tinyurl.com/BiGGEsTS
Brain Explorer	Free	Win Mac	Visualization of 3D transcription data in the central nervous system	http://tinyurl.com/brainExplorer
Caryoscope	Free	Win Mac Linux	Abundance data mapped to chromosomal location	http://tinyurl.com/caryoscope
Data Matrix Viewer	Free	Win Mac Linux	Simple profile plot visualization; supports Gaggle	http://gaggle.systemsbiology.net
EXPANDER	Free	Win Linux	Heat maps, scatter plots and profile plots of cluster averages	http://acgt.cs.tau.ac.il/expander
GENESIS	Free	Win Mac Linux	Analysis suite; offers several interactive visualizations	http://genome.tugraz.at
GeneSpring GX	\$	Win Mac Linux	Analysis suite; interactive and linked visualizations; also networks	http://tinyurl.com/genespring
GeneVAnD	Free	Win Mac Linux	Linked heat maps, dendograms and 2D/3D scatter plots	http://tinyurl.com/GeneVAnD
geWorkbench	Free	Win Mac Linux	Modular suite; heat maps, dendograms, profile and scatter plots	http://tinyurl.com/geWorkbench
Hierarchical Clustering Explorer	Free	Win	Linked heat map, profile and scatter plots; systematic exploration	http://tinyurl.com/HCExplorer
Java TreeView	Free	Win Mac Linux	Linked heat maps, karyoscopes, sequence alignments, scatter plots	http://jtreeview.sourceforge.net
Mayday	Free	Win Mac Linux	Modular suite; many linked visualizations; enhanced heat map 113	http://tinyurl.com/maydaywp
MultiExperiment Viewer	Free	Win Mac Linux	Analysis suite; heat maps, dendograms, profile and scatter plots	http://www.tm4.org
PointCloudXplore	Free	Win Mac Linux	Visualization of 3D transcription data in Drosophila embryos	http://tinyurl.com/PointCloudXplore
Spotfire Functional Genomics	\$	Win	Analysis suite; many linked visualizations and exploration tools	http://spotfire.tibco.com
TimeSearcher	Free	Win	Exploration and analysis of time series; advanced profile plots	http://tinyurl.com/timesearcher
R/BioConductor				http://www.bioconductor.org
Geneplotter	Free	Win Mac Linux	Karyoscope-style plots and other visualizations	
Web-based				
ExpressionProfiler	Free		Transcriptomics data analysis suite with basic visualizations	http://tinyurl.com/exprespro
GenePattern	Free		Modular analysis platform; several visualization modules available	http://tinyurl.com/GenePatt