Visualization Analysis & Design for Genomics

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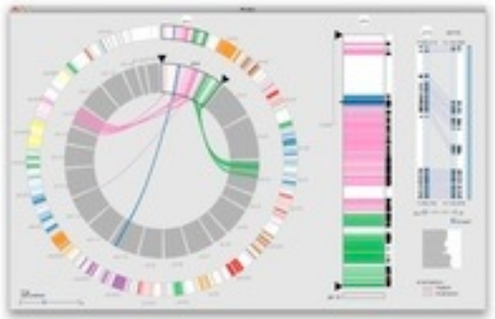
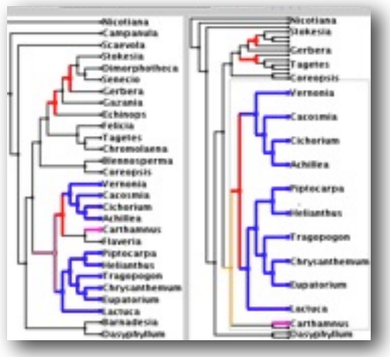
http://www.cs.ubc.ca/~tmm/talks.html#daley15 **@tamaramunzner**

Outline

- introduction
- Cerebral
- MizBee
- TreeJuxtaposer
- wrapup





Why have a human in the loop?

Computer-based visualization systems provide visual representations of datasets designed to help people carry out tasks more effectively.

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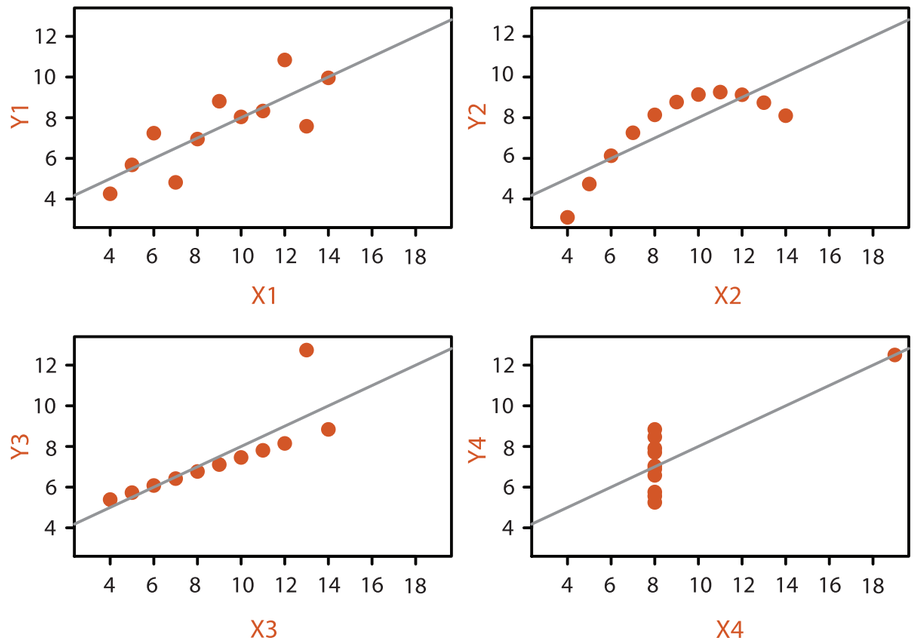
Visualization is suitable when there is a need to augment human capabilities rather than replace people with computational decision-making methods.

- many analysis problems ill-specified, not clear what questions to ask in advance
  - don't need vis when fully automatic solution exists and is trusted

Anscombe's Quartet

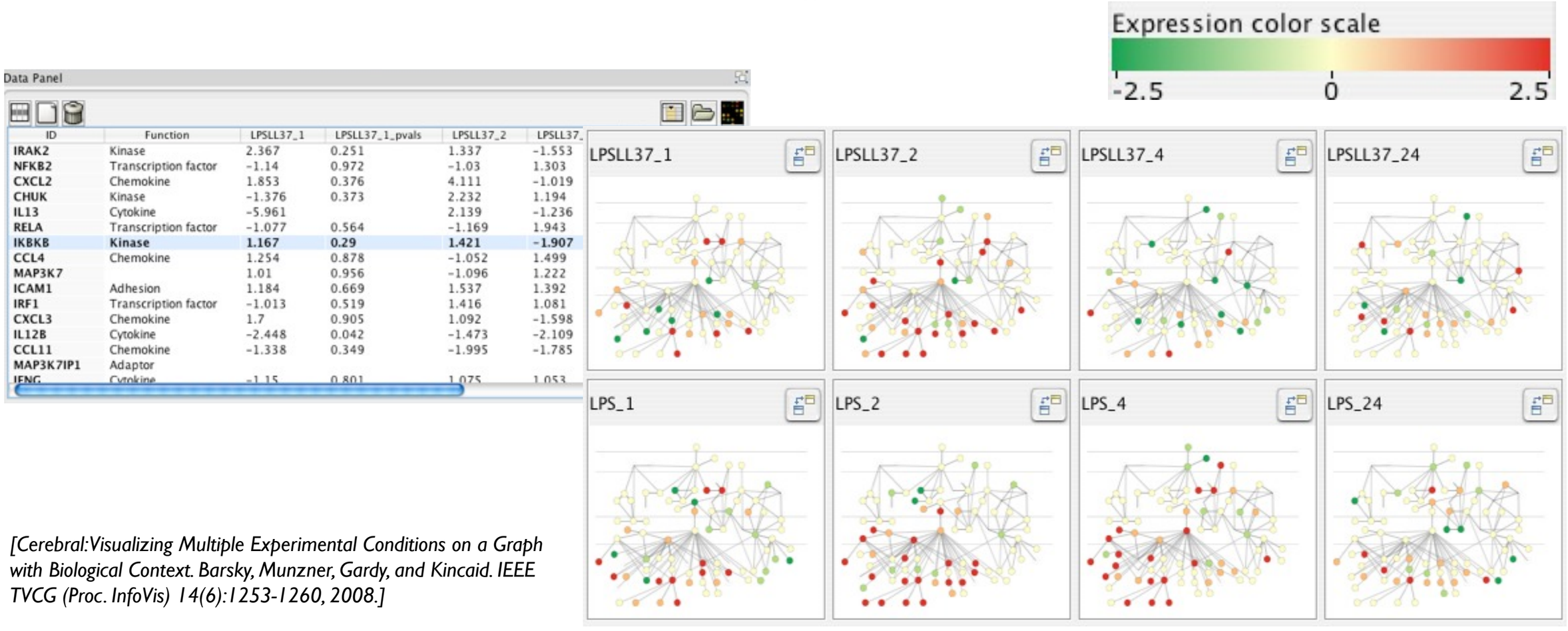
Identical statistics	
x mean	9
x variance	10
y mean	8
y variance	4
x/y correlation	1



Why use an external representation?

Computer-based visualization systems provide visual representations of datasets designed to help people carry out tasks more effectively.

- external representation: replace cognition with perception

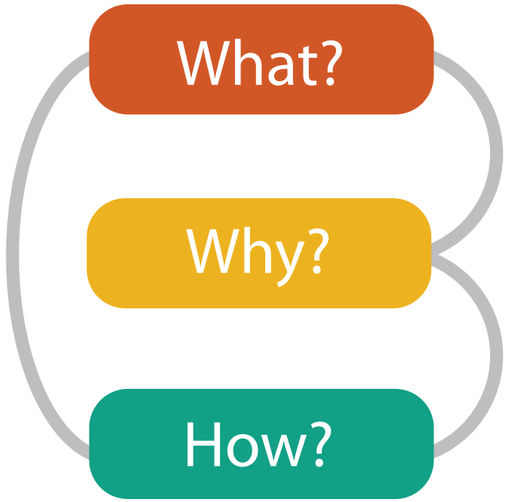


[Cerebral:Visualizing Multiple Experimental Conditions on a Graph with Biological Context. Barsky, Munzner, Gardy, and Kincaid. IEEE TVCG (Proc. InfoVis) 14(6):1253-1260, 2008.]

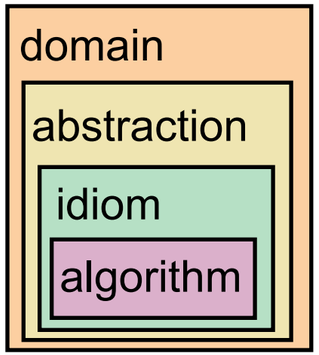
How to analyze vis design?

Vis usage can be analyzed in terms of what data is shown, why the user needs it, and how the idiom is designed.

- abstractions
  - translate from specifics of domain to vocabulary of vis
    - *data abstraction*: **what** to show
      - might not draw what you're given: transform data into form useful for task
    - *task abstraction*: **why** they're looking at it
- idioms
  - *visual encoding idiom*: **how** to draw
  - *interaction idiom*: **how** to manipulate
- analysis framework: scaffold to think systematically about design space
  - huge, and most possibilities ineffective for particular task/data combination



How to validate design?



anthropology/ ethnography

design

computer science

cognitive psychology

anthropology/ ethnography

Domain situation
Observe target users using existing tools

Data/task abstraction

Visual encoding/interaction idiom
Justify design with respect to alternatives

Algorithm
Measure system time/memory
Analyze computational complexity

Analyze results qualitatively

Measure human time with lab experiment (*lab study*)

Observe target users after deployment (*field study*)

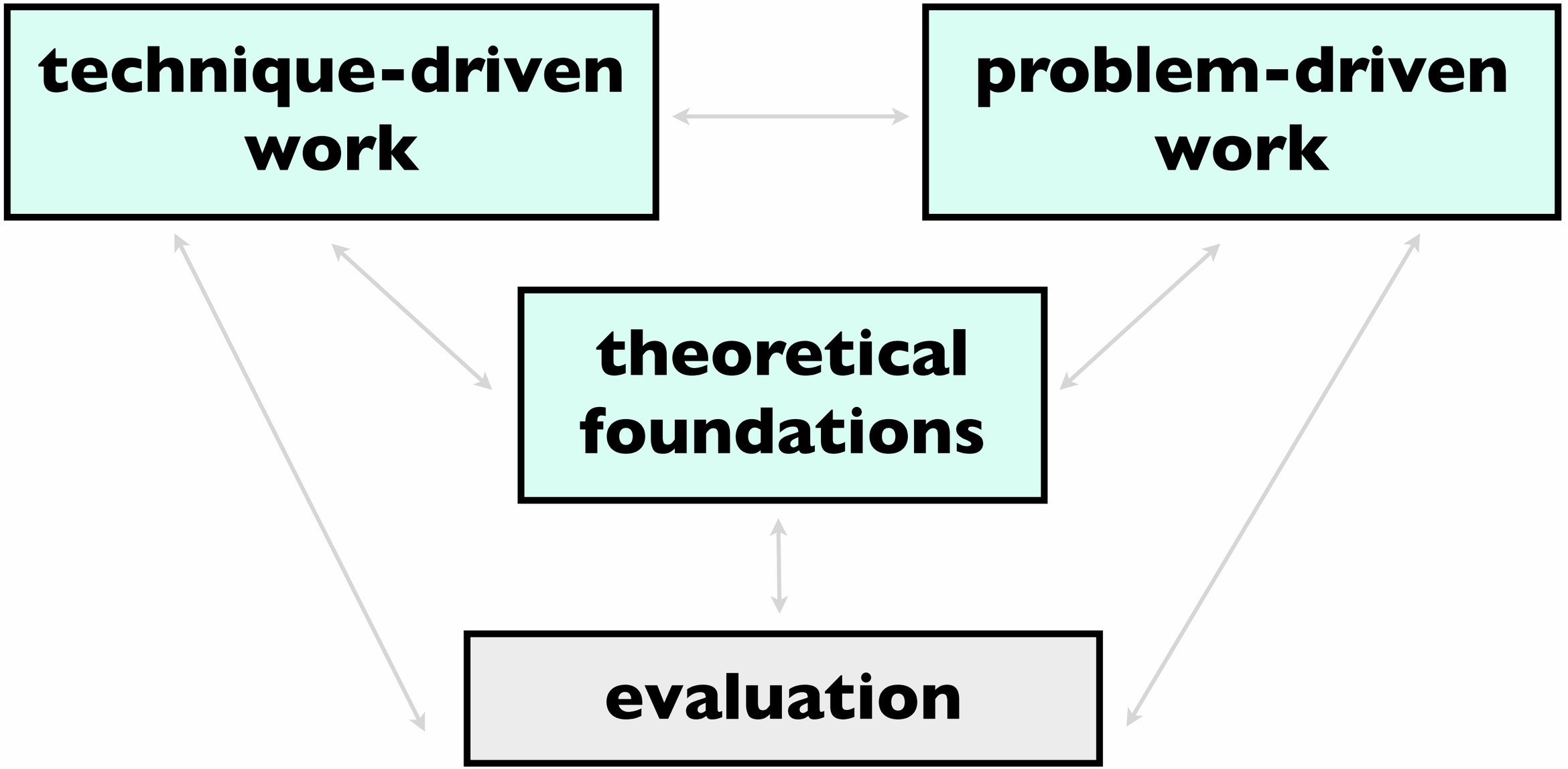
Measure adoption

problem-driven work

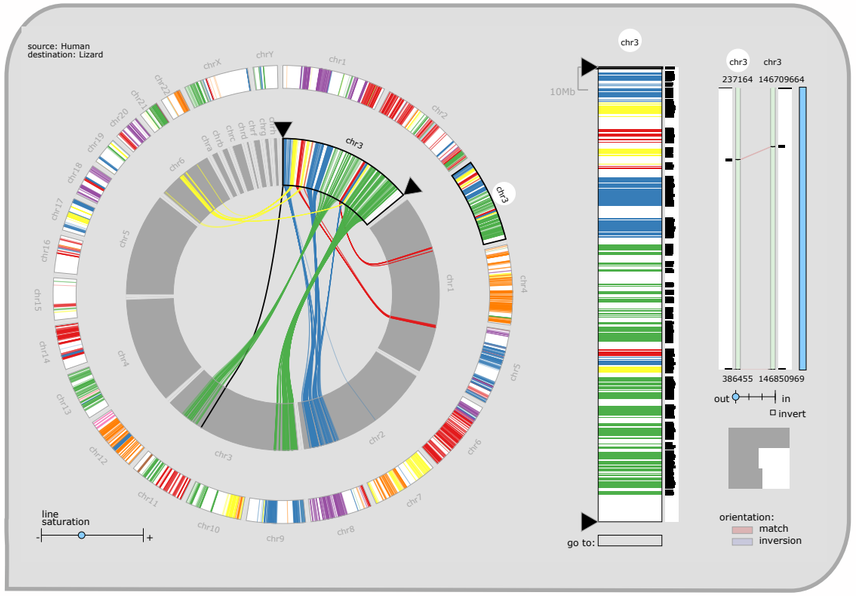
technique-driven work

[A Nested Model of Visualization Design and Validation.
Munzner. IEEE TVCG 15(6):921-928, 2009 (Proc. InfoVis 2009).]

Angles of attack

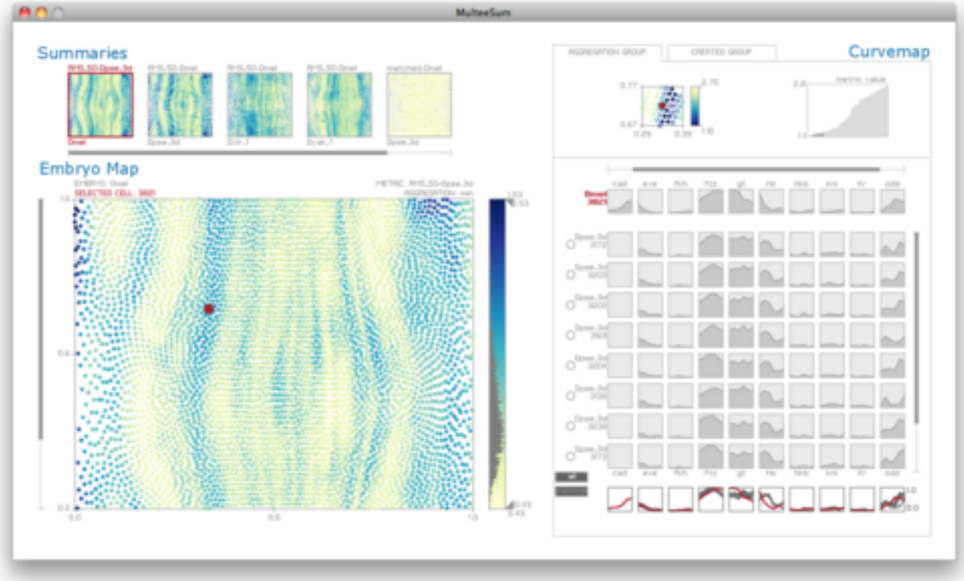


Problem-driven work: Genomics

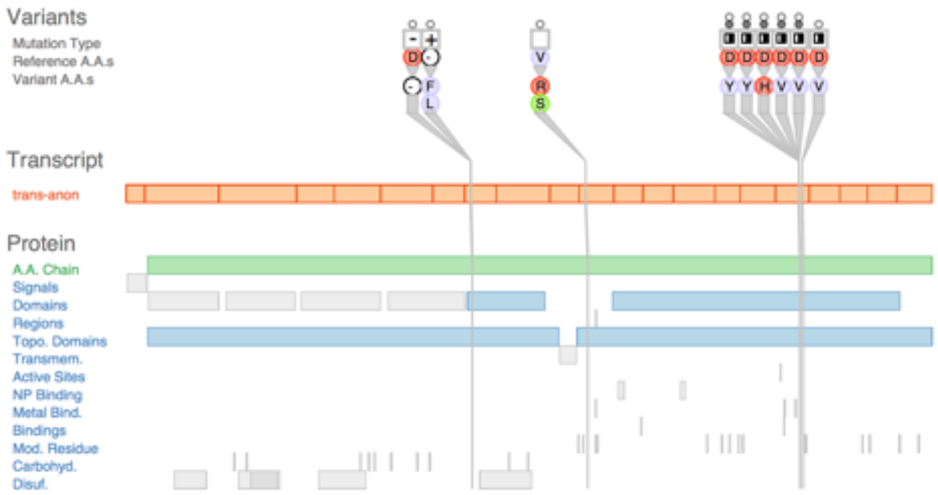


MizBee

http://youtu.be/86p7brwuz2g

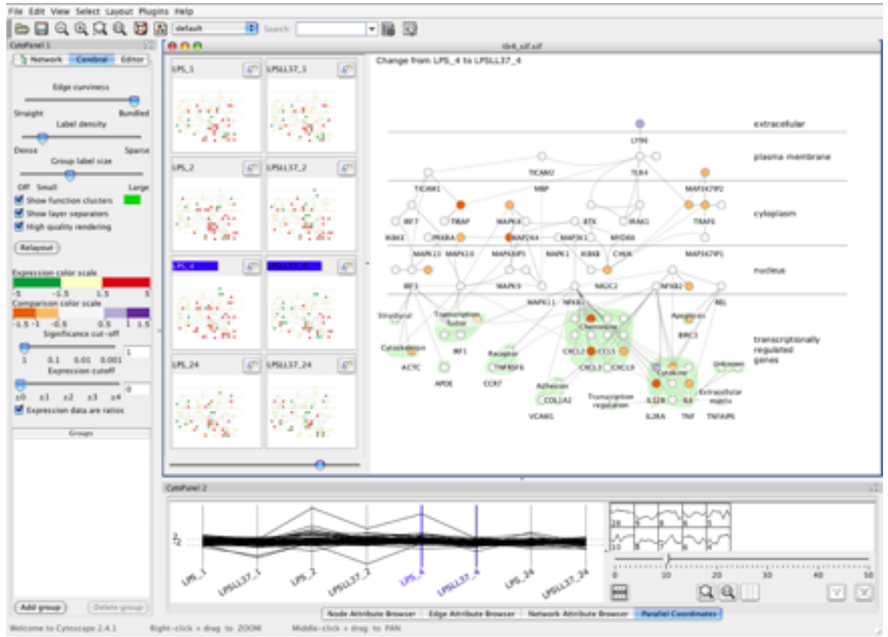


MulteeSum Pathline



Variant View

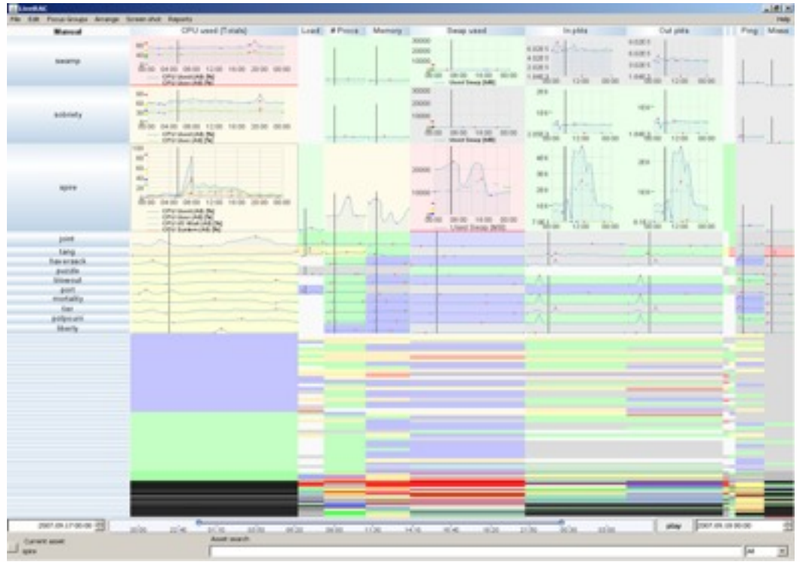
http://youtu.be/AHDnv_qMXxQ



Cerebral

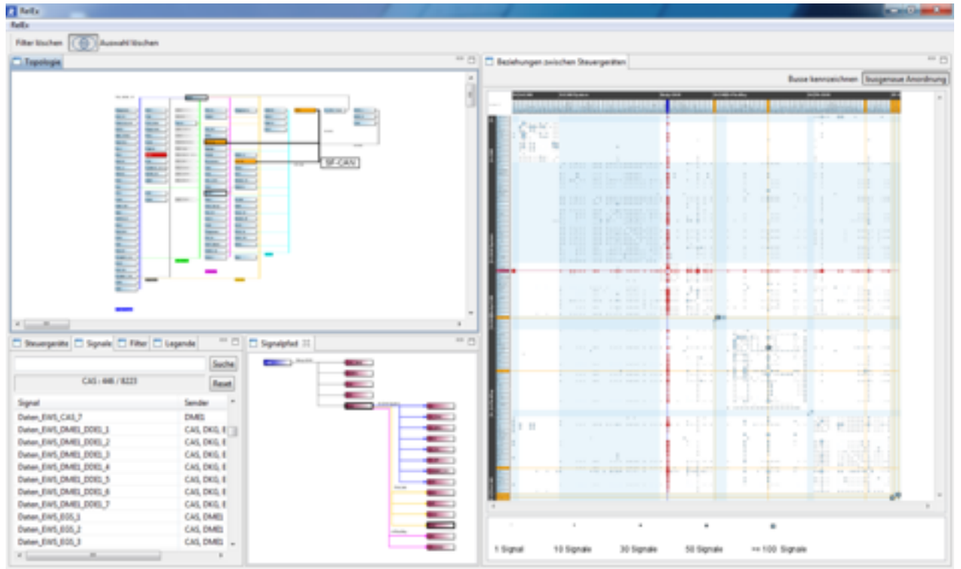
http://youtu.be/76HhG1FQngI

Problem-driven work: Many other domains

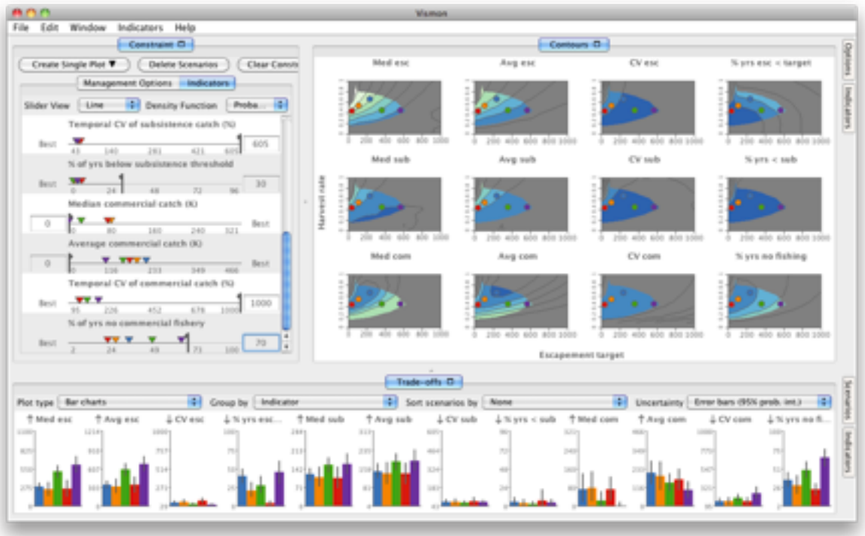


http://youtu.be/ld0c3H0VSkw

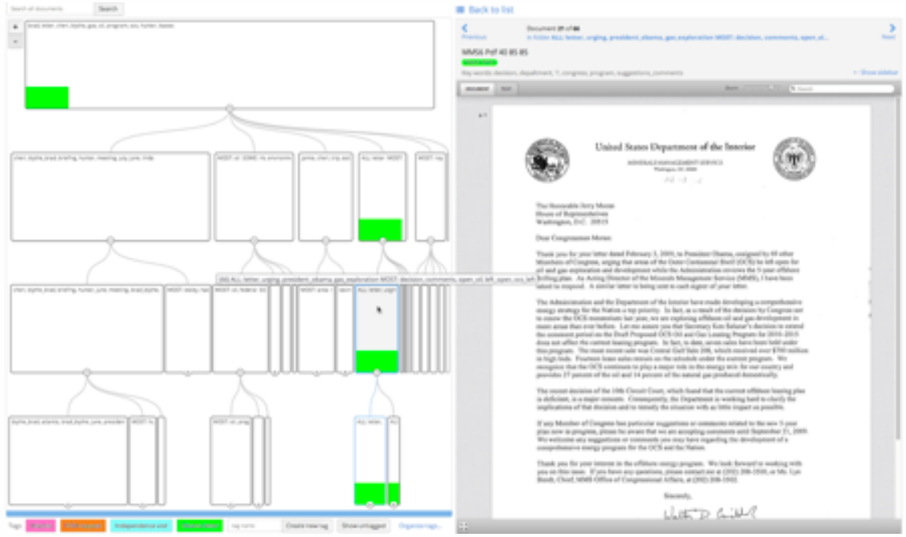
LiveRAC: system management time-series



RelEx: in-car overlay networks http://youtu.be/89lsQXc6Ao4



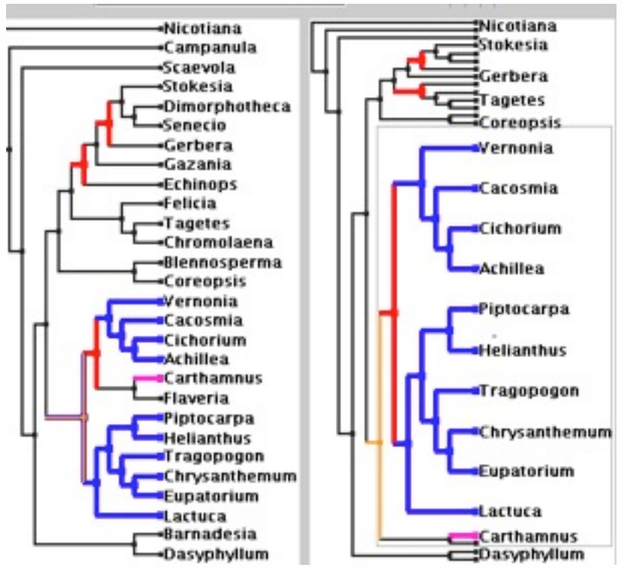
Vismon: fisheries management http://youtu.be/h0kHoS4VYmk

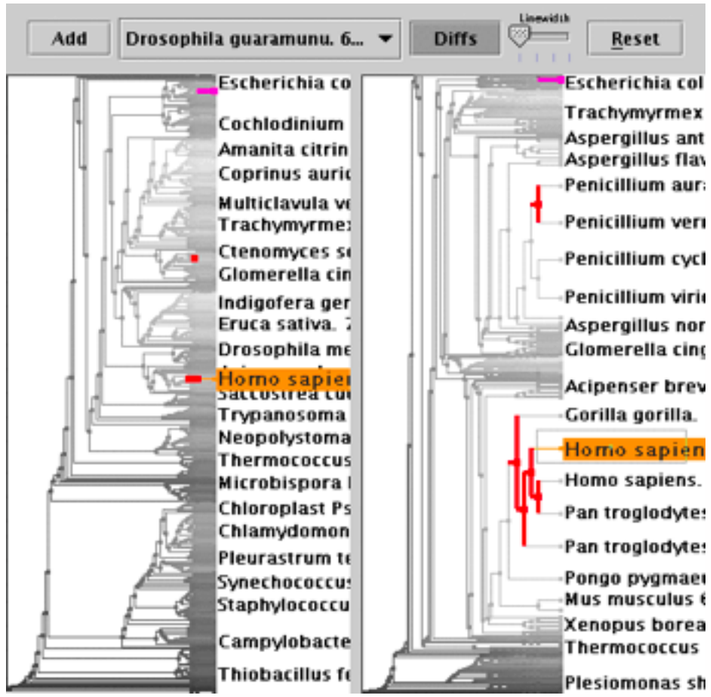


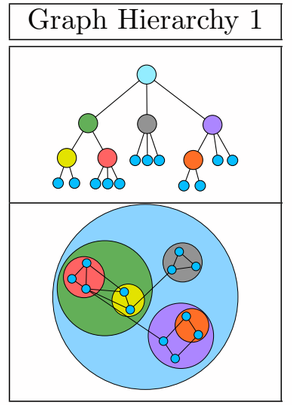
Overview: investigative journalism http://vimeo.com/71483614

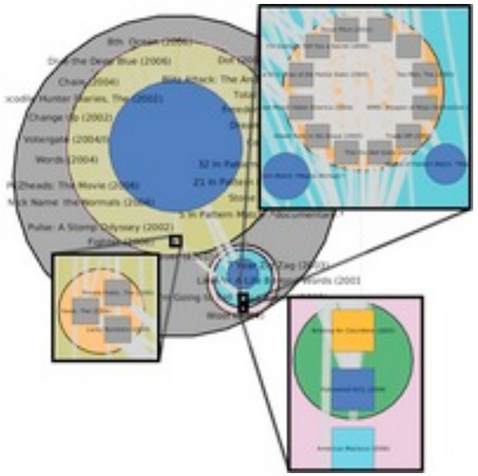
Technique-driven work: Networks

- scaling up networks
  - multilevel networks, 10K-100K nodes
    - topologically aware decomposition, layout, browsing
  - trees, millions of nodes
    - guaranteed visibility of semantically meaningful marks









TopoLayout
Smashing Peacocks Further
Grouse
GrouseFlocks
TugGraph

http://youtu.be/t1Xbt6XOWp8

http://youtu.be/AWXAe8zvkt8

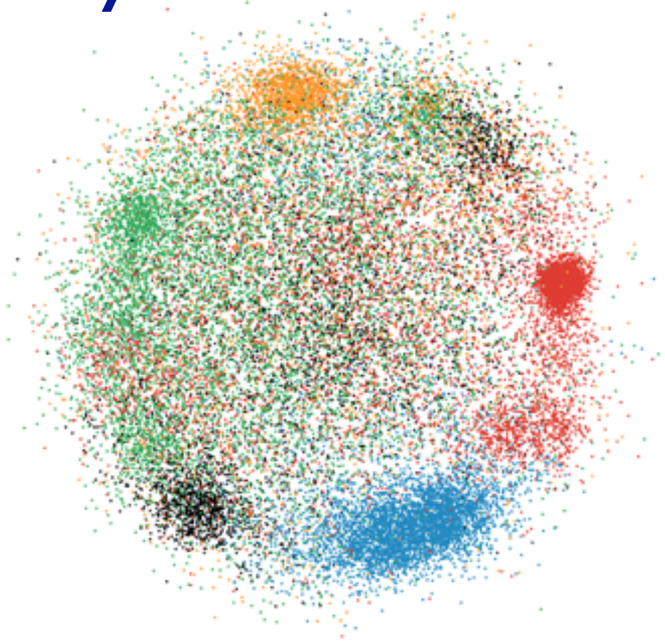
TreeJuxtaposer
PRISAD

http://youtu.be/fq8EIAOutvs

http://youtu.be/GdaPj8a9QEo

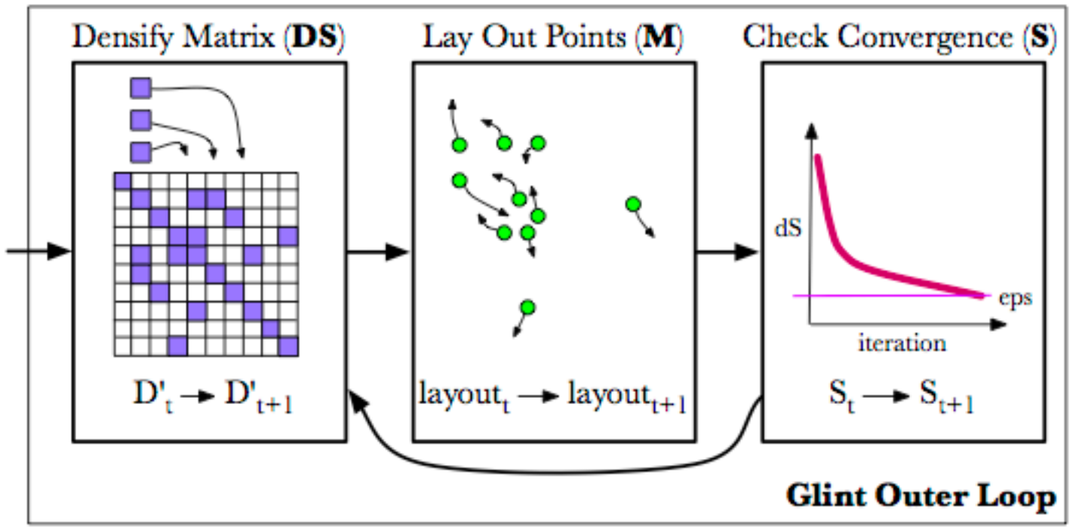
Technique-driven work: Dimensionality reduction

- close overlap with machine learning
  - Glimmer: MDS on the GPU
  - Glint: DR for costly distances
  - QSNE: sparse documents
    - high quality for millions of items

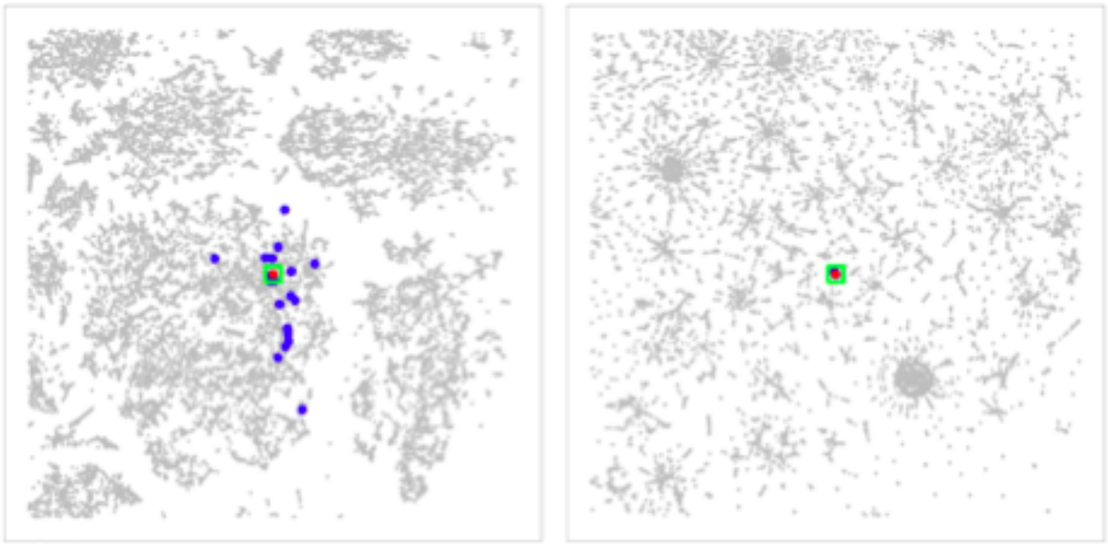


Glimmer

http://youtu.be/PLaBAPM6qLI



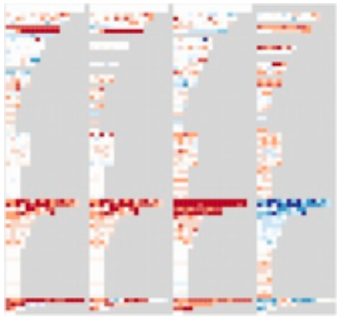
Glint



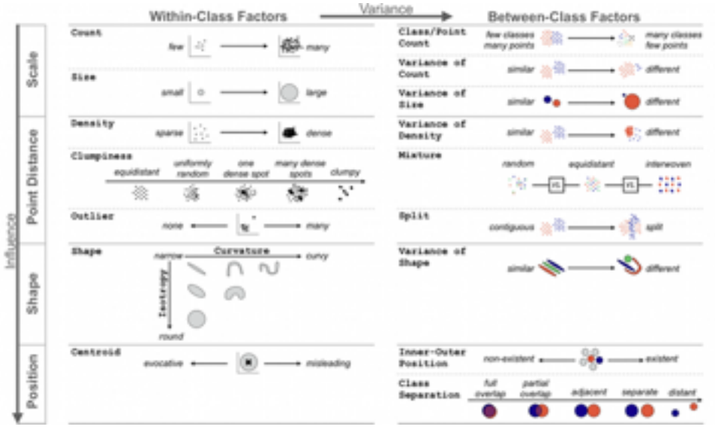
QSNE

Evaluation: Dimensionality Reduction

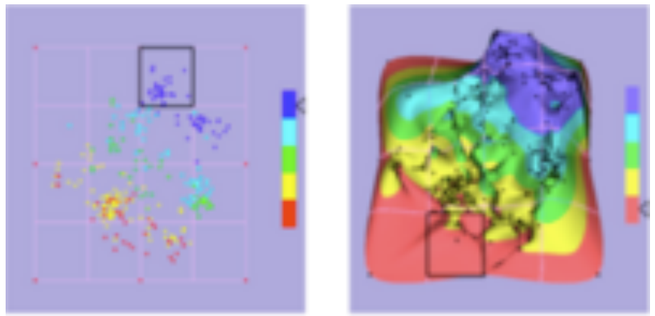
- guidance on scatterplot/DR choices



- taxonomy of cluster separation factors

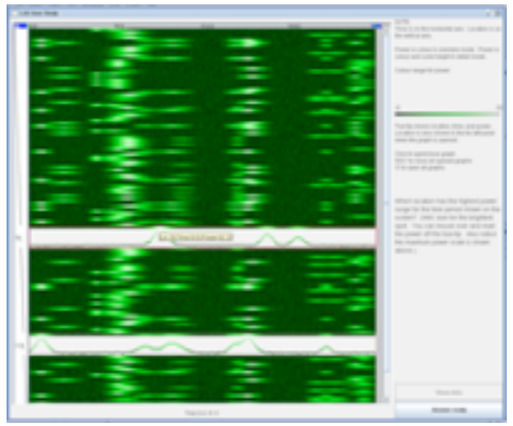


- 2D points vs 3D landscapes



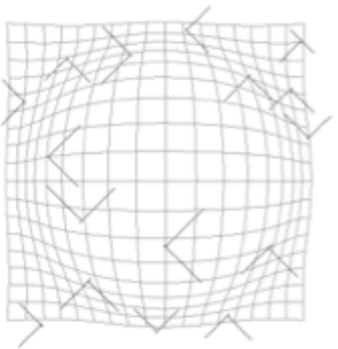
Evaluation: Focus+Context

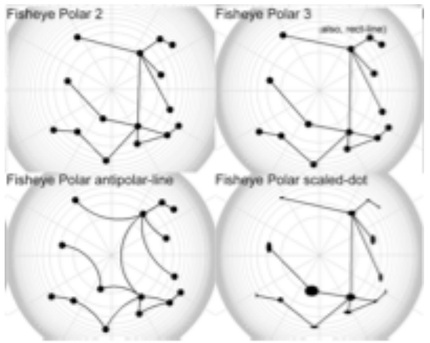
- overviews: separate vs. integrated views



- navigation: stretch and squish vs. pan/ zoom navigation

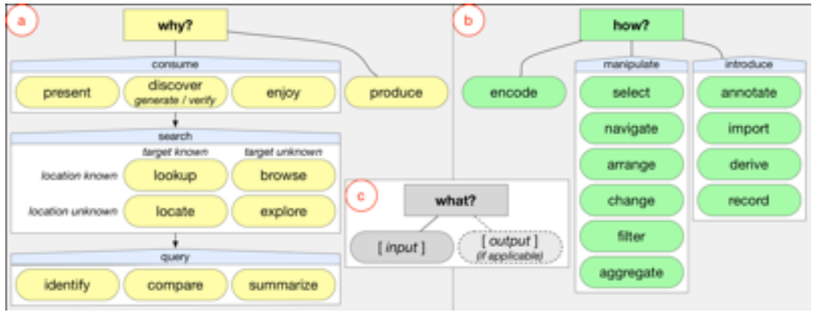
- impact of distortion on visual search, visual memory

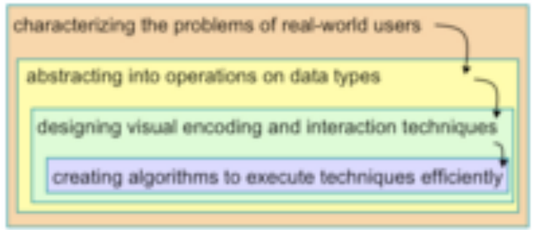


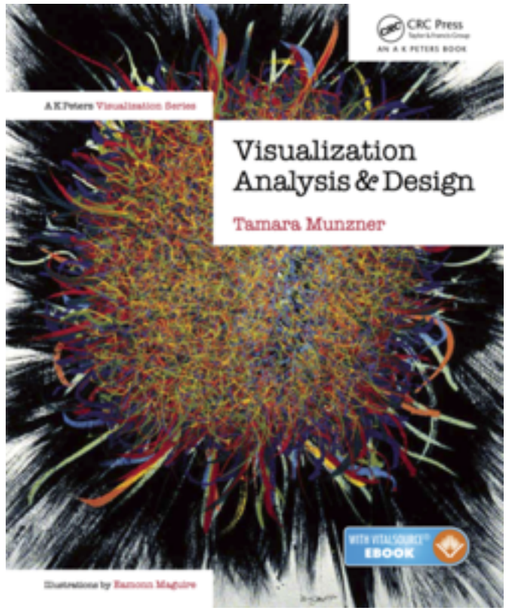


Theory/Models

- multi-level typology of abstract visualization tasks
- design study methodology
- nested model for vis design and validation
- papers process and pitfalls
- book: Visualization Analysis and Design







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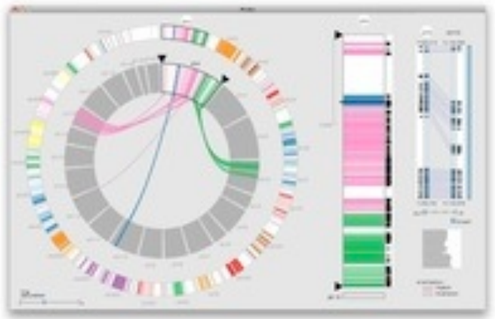
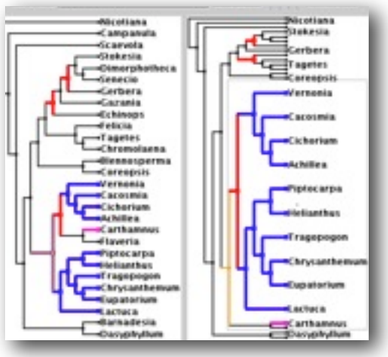
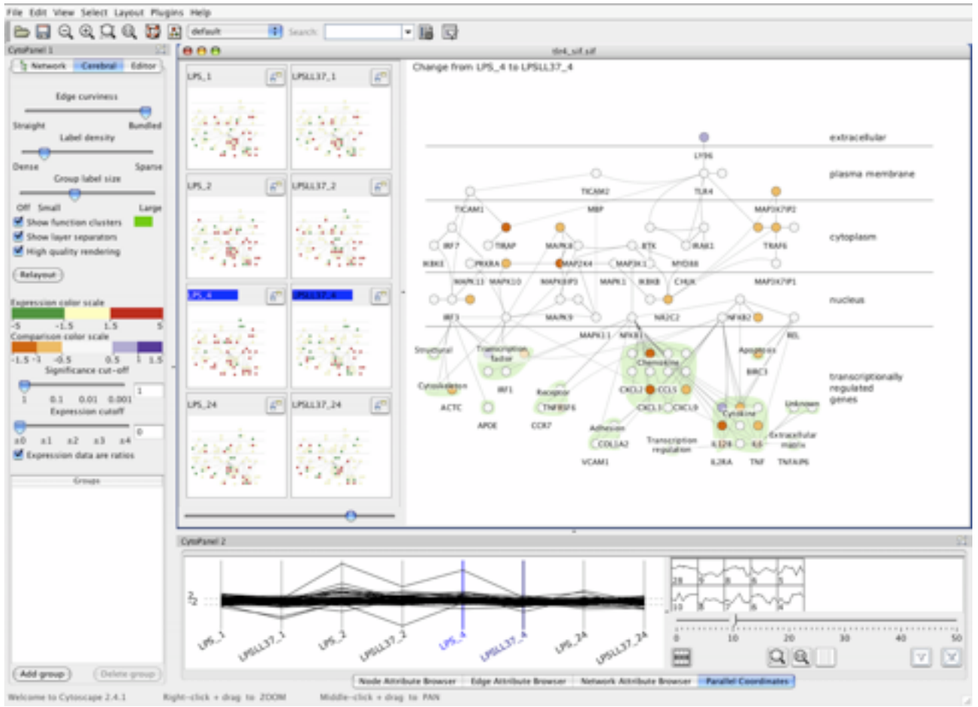






Cerebral

Visualizing Multiple Experimental Conditions on a Graph with Biological Context

joint work with:

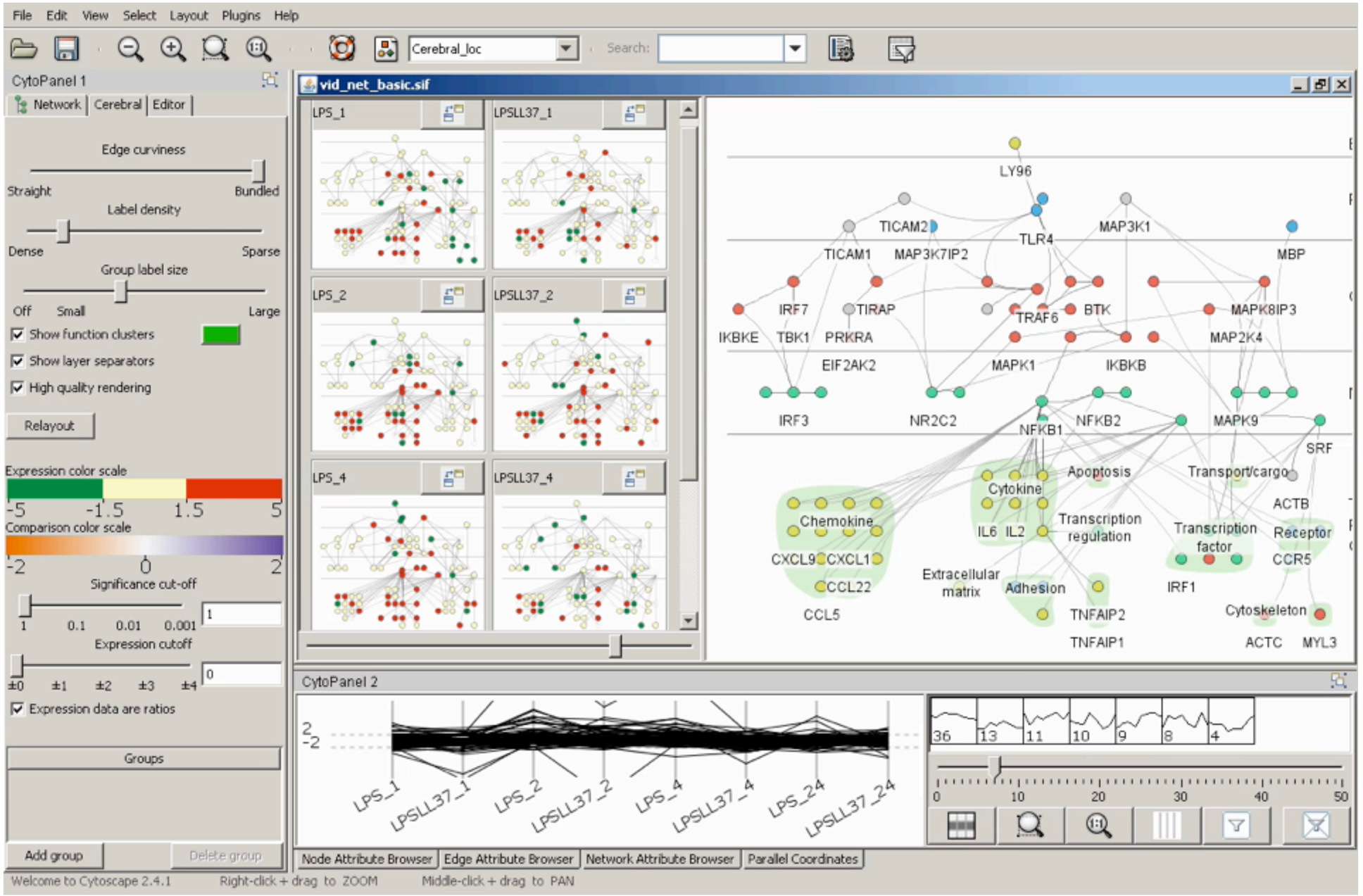
Aaron Barsky, Jennifer Gardy, Robert Kincaid

http://www.pathogenomics.ca/cerebral/

Cerebral: Visualizing Multiple Experimental Conditions on a Graph with Biological Context.

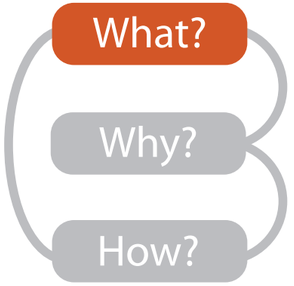
Barsky, Munzner, Gardy, Kincaid. IEEE Trans. Visualization and Computer Graphics 14(6):1253-1260 2008. (Proc. InfoVis 2008).

Cerebral video

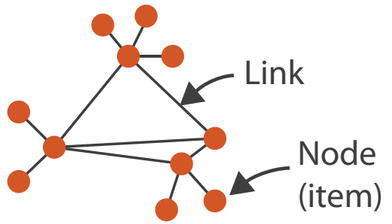


What: Data abstraction

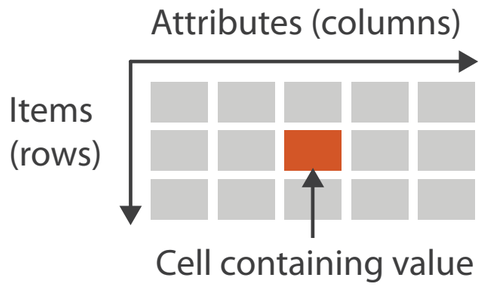
- dataset types
  - network
    - nodes: genes
    - links: known interactions between genes
  - table
    - quantitative attributes
      - gene expression levels for nodes across different experimental conditions
    - categorical attributes
      - subcellular location of interaction
      - functional groups



➔ Networks



➔ Tables



➔ **Attribute Types**

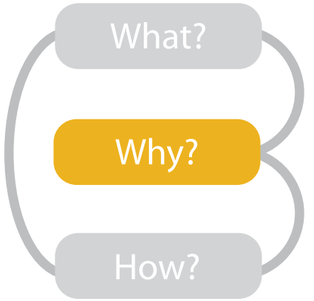
➔ Categorical

➔ Ordered

➔ *Ordinal*

➔ *Quantitative*

Why: Task abstraction

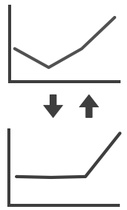


- task: interpret microarray experiment results with respect to gene network
  - goal: accelerate existing discovery workflow
  - compare distributions between attributes
    - experimental conditions
  - interpret attributes in context of current network topological structure

→ *Discover*

Actions

→ Compare

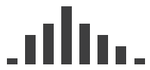


Targets

Attributes

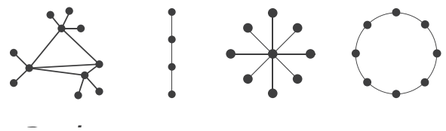
→ One

→ *Distribution*



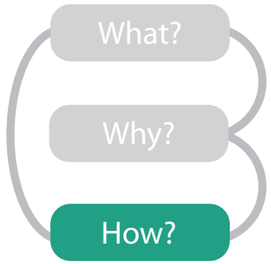
Network Data

→ Topology



How: Idiom design decisions

- arrange space for networks
  - custom node-link diagram layout
    - points for nodes
    - connection marks for links
  - vertical compartment according to subcellular location attribute
  - cluster according to functional grouping

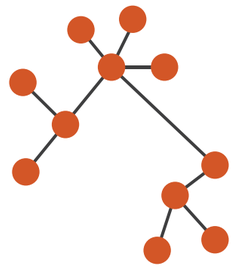


Arrange Networks And Trees

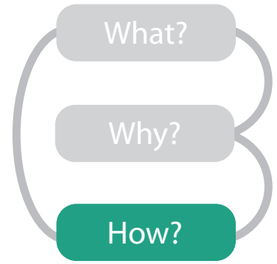
Node-link Diagrams

Connections and Marks

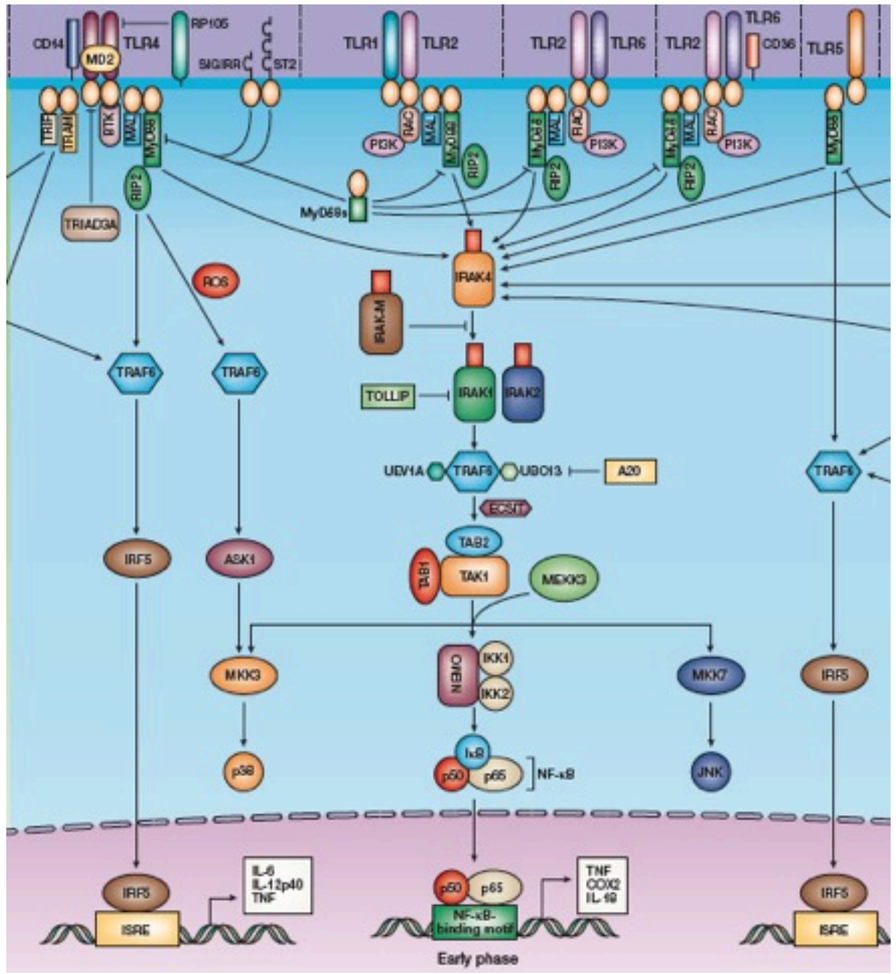
✔ NETWORKS ✔ TREES

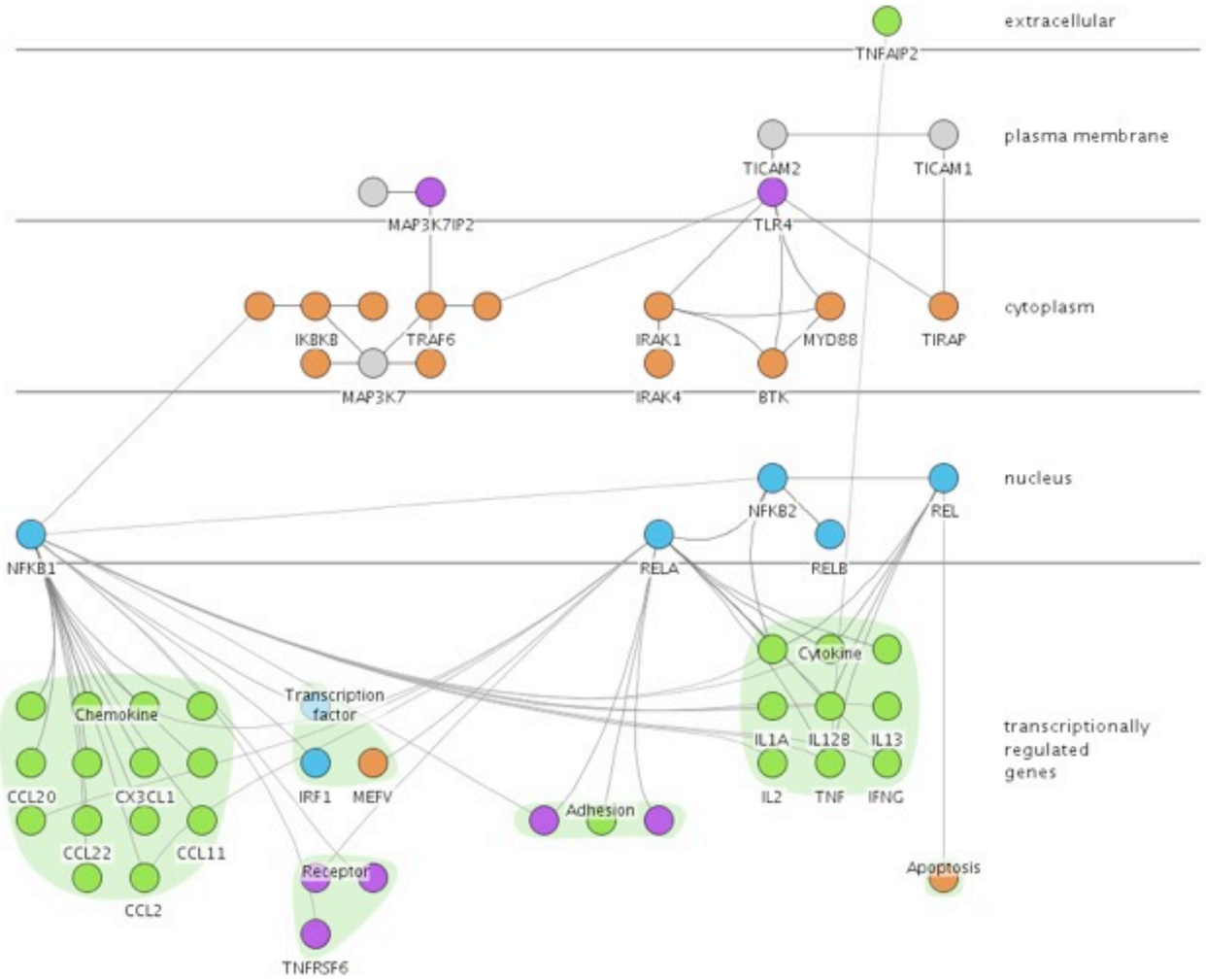


How: Arrange space



- automatic layout similar to hand-drawn diagrams
  - vertical compartment according to subcellular location attribute

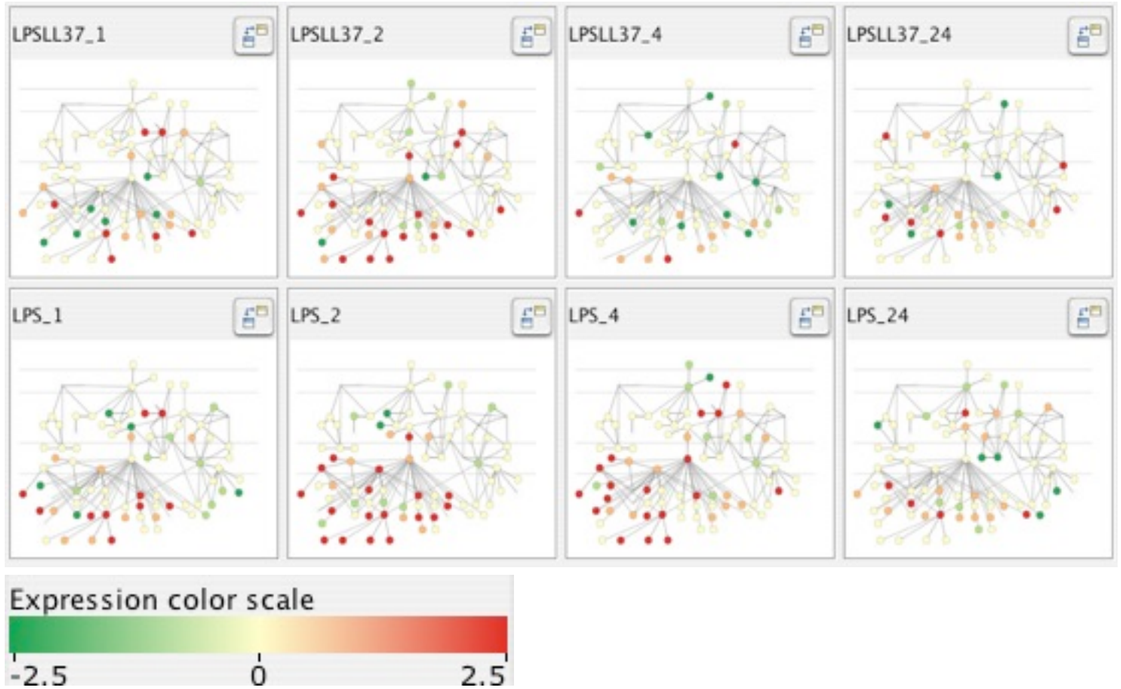




http://www.nature.com/nri/focus/tlr/nri1397.html

How: Idiom design decisions

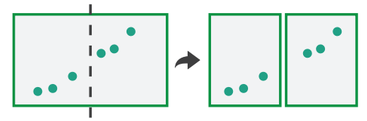
- facet: partition data into multiple views
  - juxtapose views side by side
    - same encoding, different data: *small multiples*
    - nodes in each view colored by expression levels for experimental condition

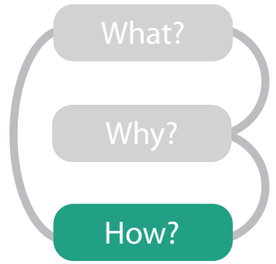


Facet

Juxtapose

Partition





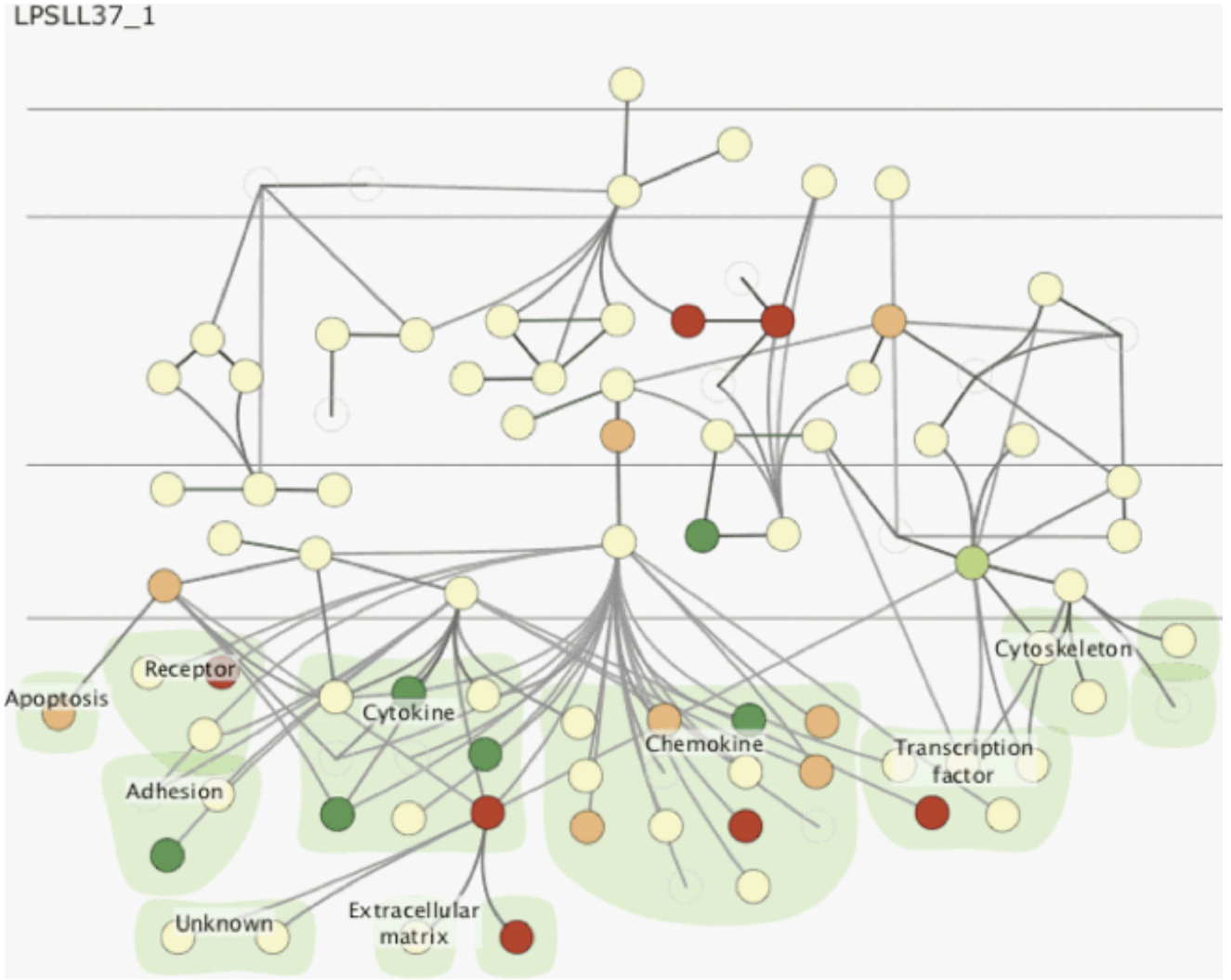
		Data		
		All	Subset	None
Encoding	Same	Redundant	*Overview/ Detail*	*Small Multiples*
	Different	*Multiform*	*Multiform, Overview/ Detail*	No Linkage

How: Juxtapose vs. animate

Manipulate

Change

- comparison difficult across many frames with with many changes everywhere
- rule of thumb: eyes beat memory
  - principle: external cognition vs. internal memory
    - easy to compare by moving eyes between side-by-side views
    - harder to compare memory of what you saw to visible view



Cerebral contributions

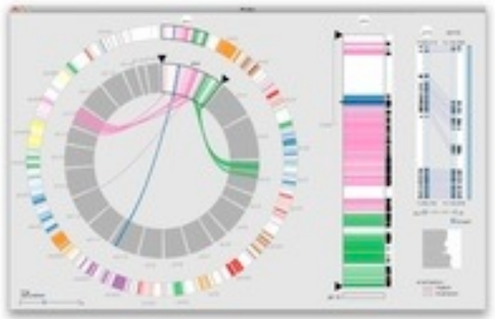
- multiple juxtaposed views support interactive comparison between gene expression level experimental data and network context
- automatic network layout algorithm in spirit of hand drawn diagrams
  - localization and functional group attributes affect spatial position

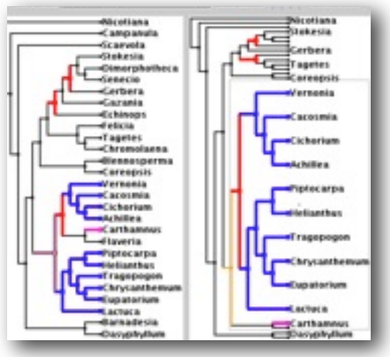
- open source
  - Cytoscape plugin
  - InnateDB database integration

http://www.pathogenomics.ca/cerebral/

Outline

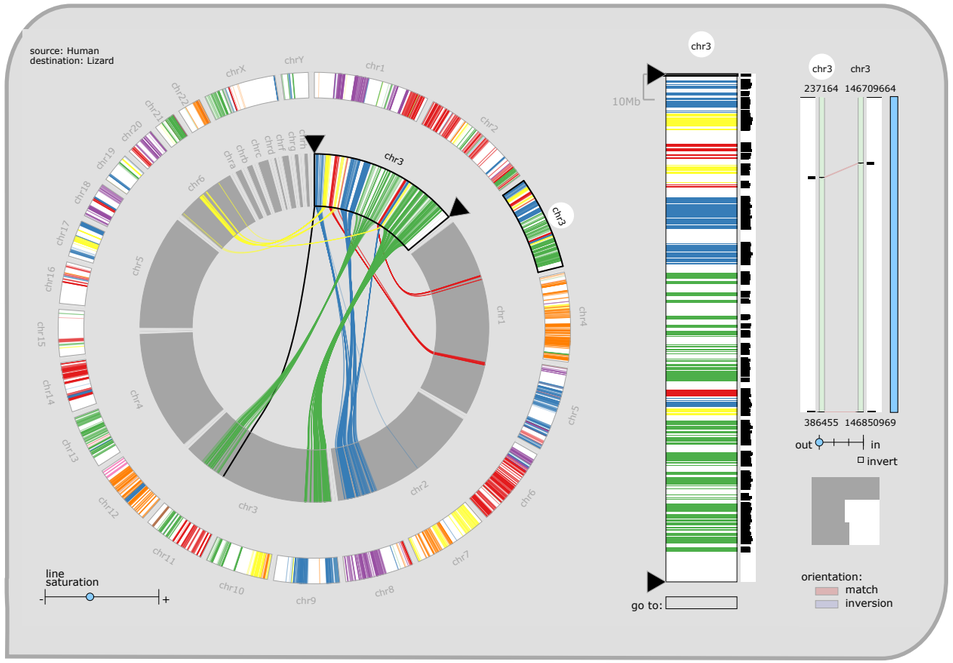
- introduction
- Cerebral
- MizBee
- TreeJuxtaposer
- wrapup





MizBee

A Multiscale Synteny Browser



joint work with:

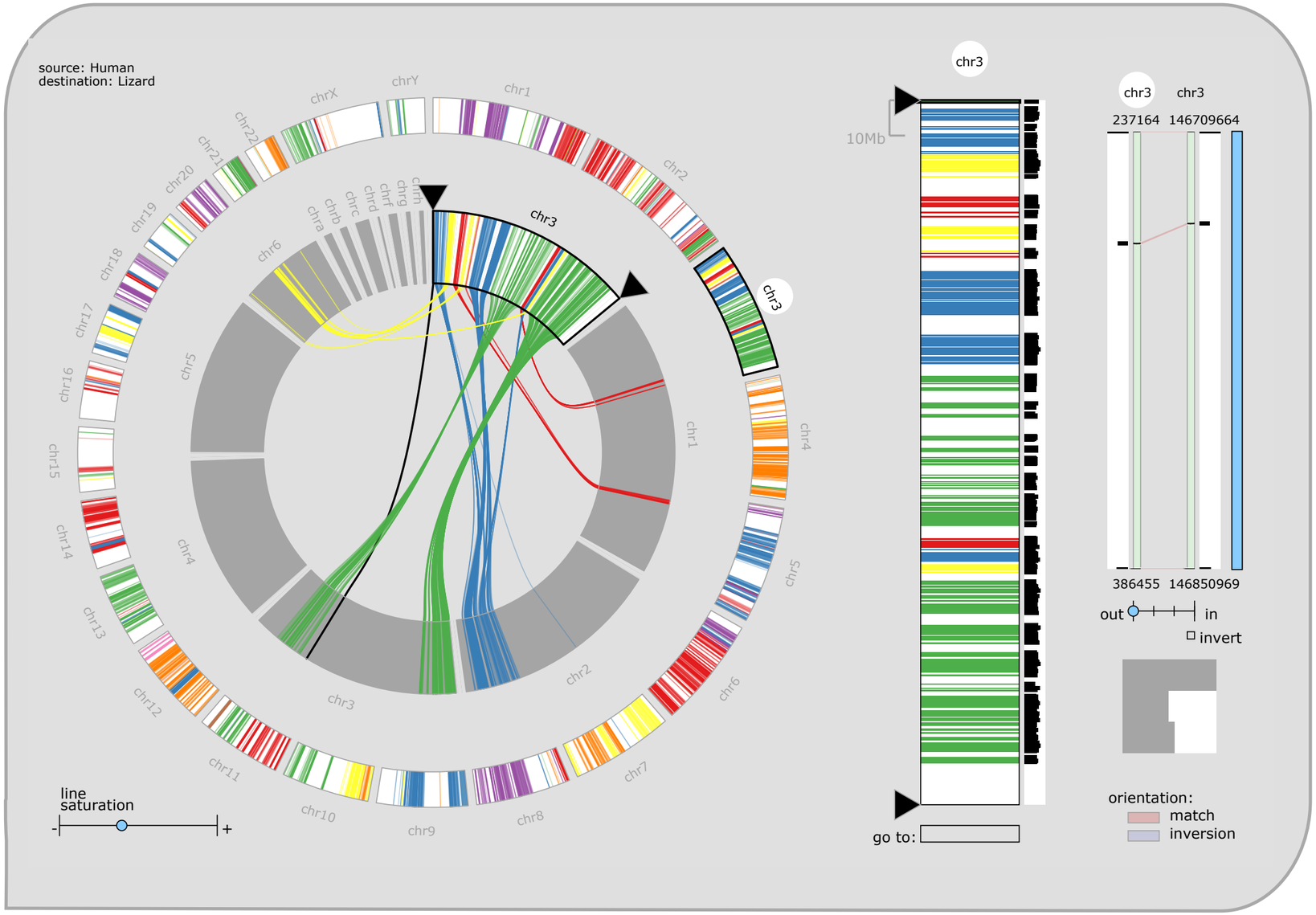
Miriah Meyer, Hanspeter Pfister

http://www.cs.utah.edu/~miriah/mizbee

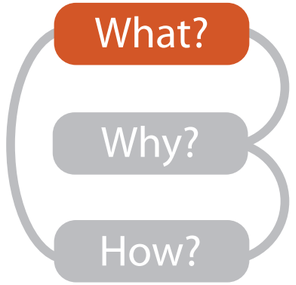
MizBee: A Multiscale Synteny Browser.

Meyer, Munzner, Pfister. IEEE Trans. Visualization and Computer Graphics 15(6):897-904, 2009 (Proc. InfoVis 2009).

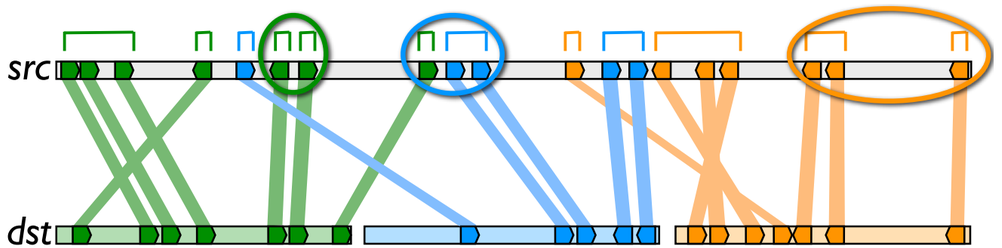
MizBee video



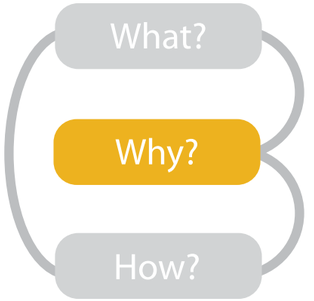
What: Data abstraction



- data: multiscale lists
  - features: hundreds of thousands
    - ordered attribute: position in chromosome sequence coordinates
    - categorical attributes: orientation, chromosome of matching feature
    - quantitative attributes: length, similarity score
  - syntenic blocks: thousands
    - contiguous sets of features on same chromosome
    - combine thresholded features if
      - destination chromosome and orientation match
      - close together
  - chromosomes: dozens
  - genomes: two



Why: Tasks in domain language



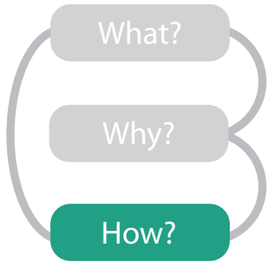
- analyze conservation (similarity) relationships between genomic features
  - high-level biology questions
    - evolution
      - how long ago did two species share common ancestor?
    - function
      - which segment of the genome is responsible for specific function in the cell?
    - ...
  - low-level data-centric questions
    - algorithm refinement
      - are paired features within a block contiguous?
      - which chromosomes share conserved blocks?
      - are similarity scores alike within block?
      - ...

Why: Tasks abstraction

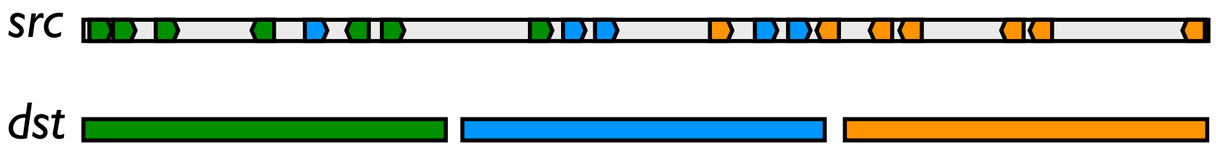
- relationship types: proximity, size, orientation, similarity
- data scales: genome, chromosome, block, feature
- topics: algorithm in/out, block reliability, high-level science

	relationship					scale			
	genome	chromosome	block	feature	proximity / location	size	orientation	similarity
Which chromosomes share conserved blocks?	x				x			
For one chromosome, how many other chromosomes does it share blocks with?	x	x			x			
What is the density of coverage and where are the gaps on: chromosomes? blocks?	x	x	x		x			
Where are the blocks: on chromosomes? around a specific location on a chromosome?	x	x			x			
What are the sizes and locations of other genomic features near a block?		x			x	x		
How large are the blocks?		x				x		
Do neighboring blocks go to the same: chromosomes? relative location on a chromosome?	x	x			x			
Are the orientations matched or inverted for: block pairs? feature pairs?		x	x				x	
Do the orientations match for pairs of: neighboring blocks? features within a block?		x	x				x	
Are similarity scores alike: with respect to neighboring blocks? within a block?		x	x					x
Are the paired features within a block contiguous?			x		x			
How large is a feature relative to other genes within a block?			x			x		
What are the sizes, locations, and names of features within a block?			x		x	x		
What are the differences between individual nucleotides of feature pairs?				x				x

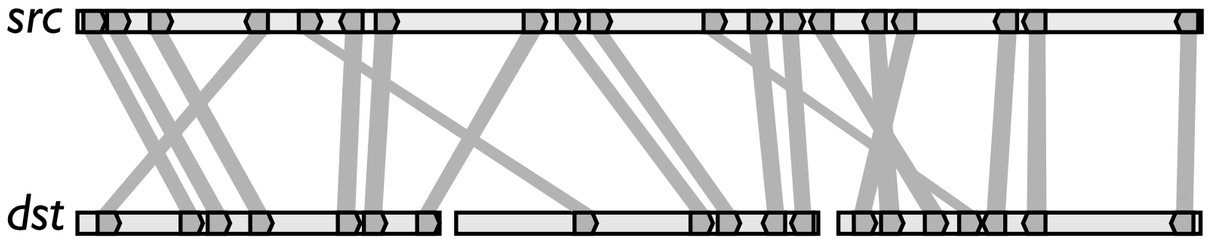
How: Idiom design choices



- encode match relationships between chromosome segments with both
  - color



  - connection marks



Identity Channels: Categorical Attributes

Spatial region

Color hue

Motion

Shape

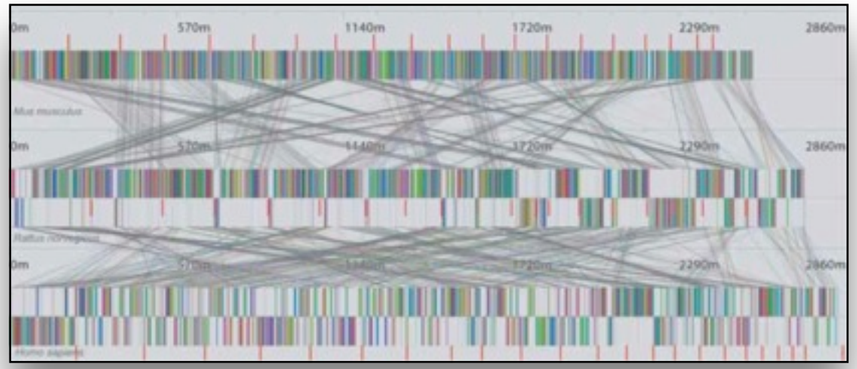
Marks As Links

Containment

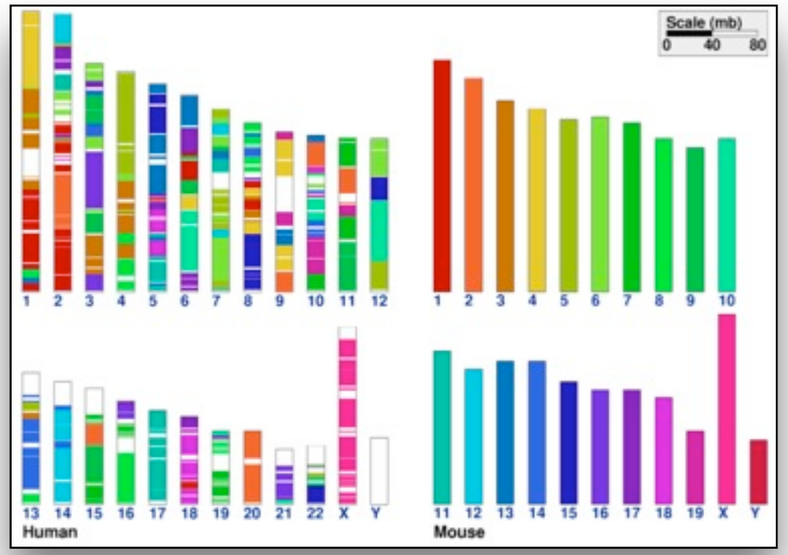
Connection

How: Arrange space

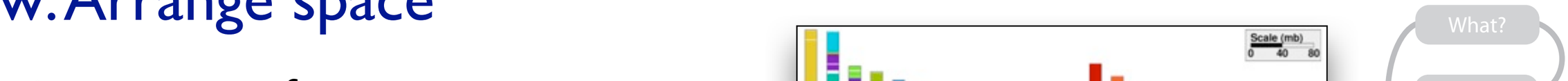
- design space of arrangements

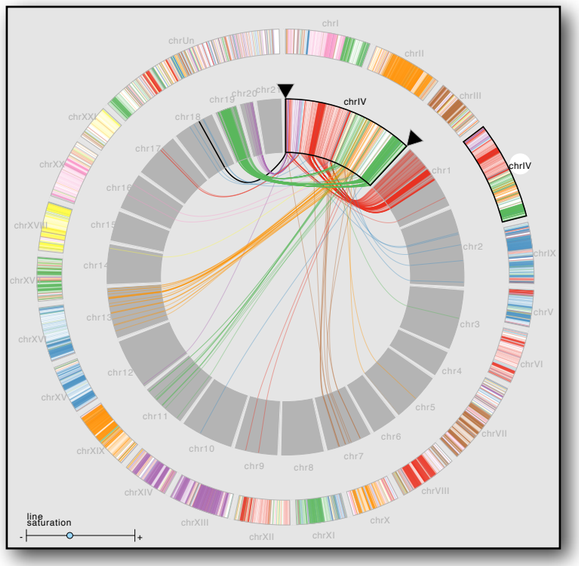


Mauve [Darling04]

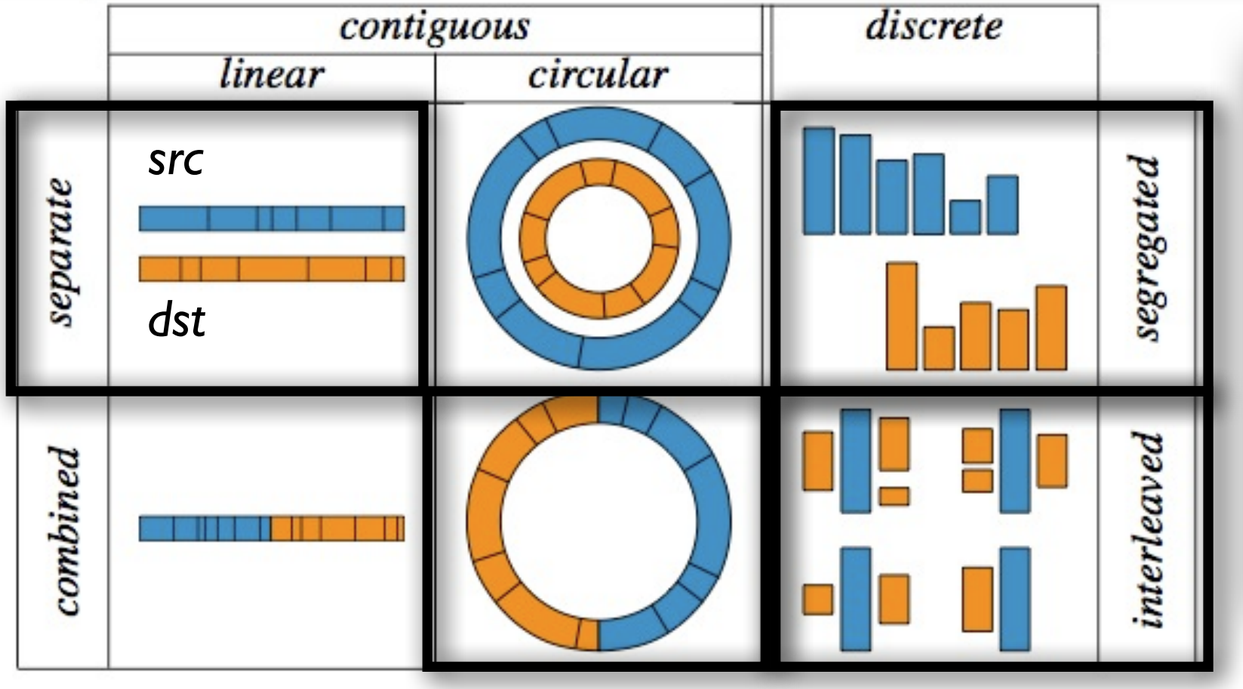


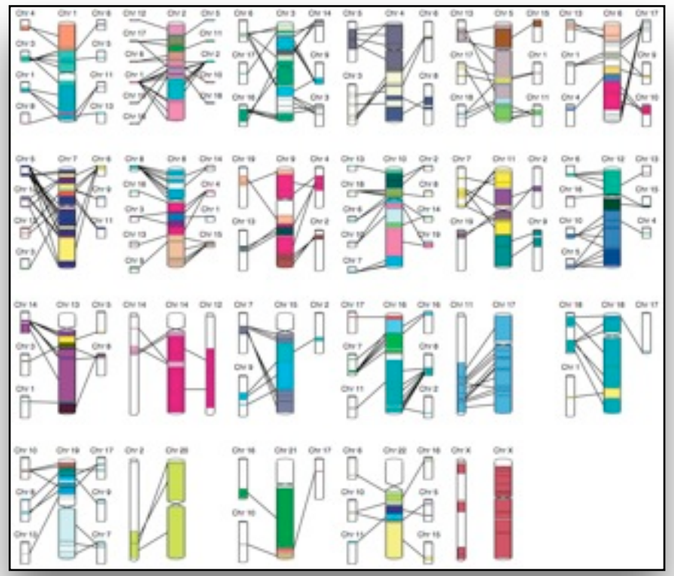
Cinteny





MizBee

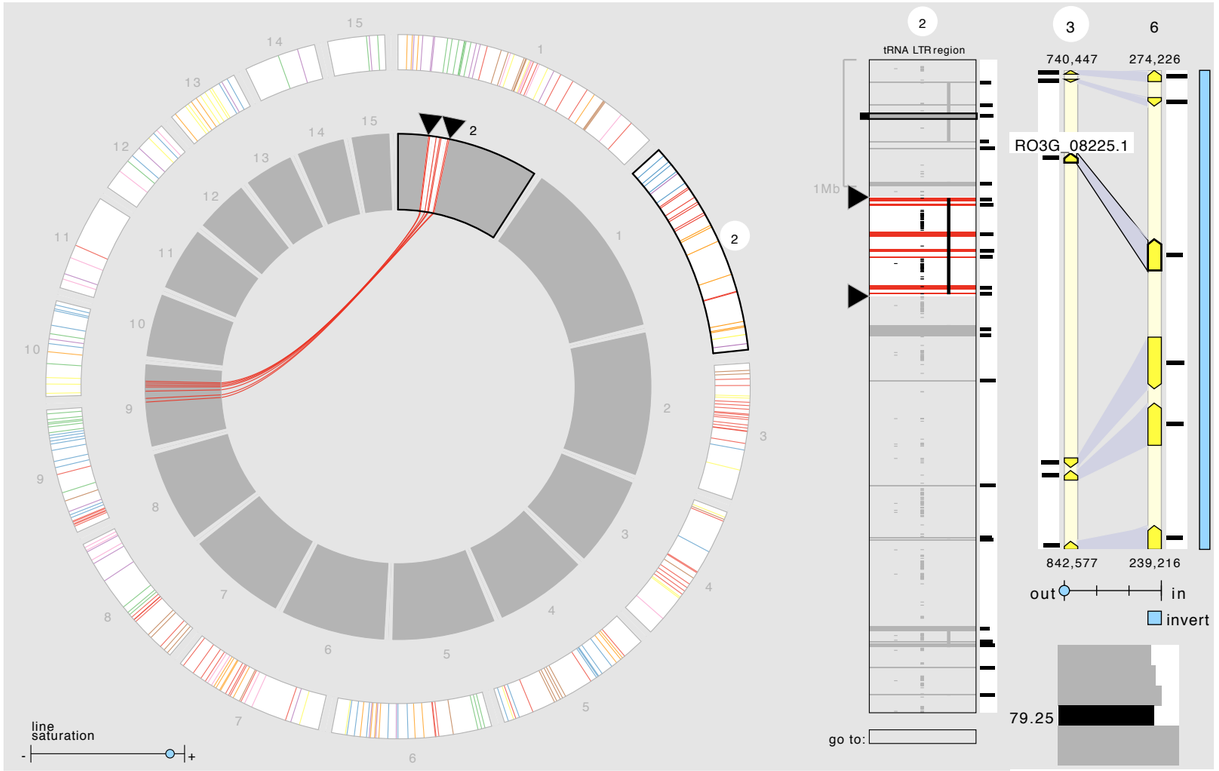




Apollo [Lewis02]

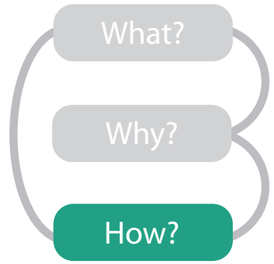
How: Idiom design choices

- juxtapose linked views
  - *multiform overview-detail*
    - three views: genome, chromosome, block
    - different visual encoding in each



Facet

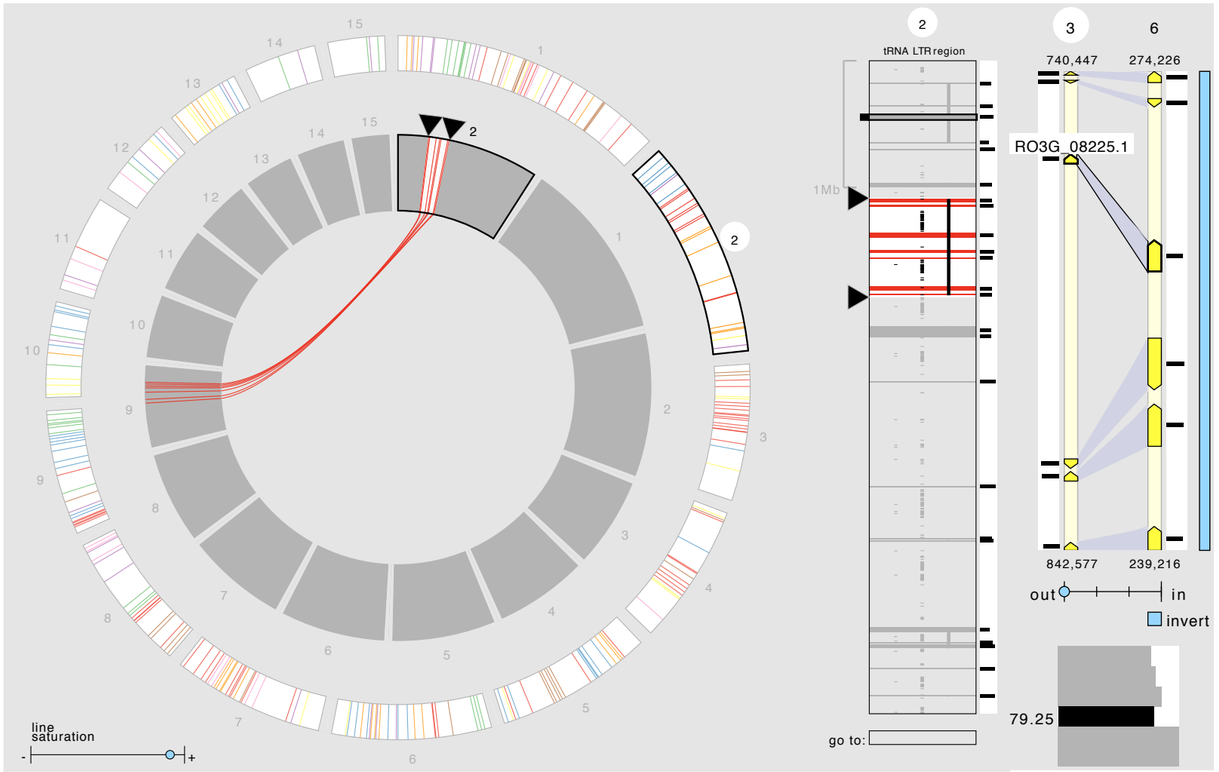
Juxtapose

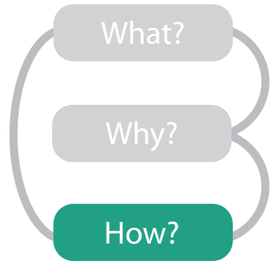


		Data		
		All	Subset	None
Encoding	Same	Redundant	*Overview/ Detail*	*Small Multiples*
	Different	*Multiform*	*Multiform, Overview/ Detail*	No Linkage

How: Idiom design choices

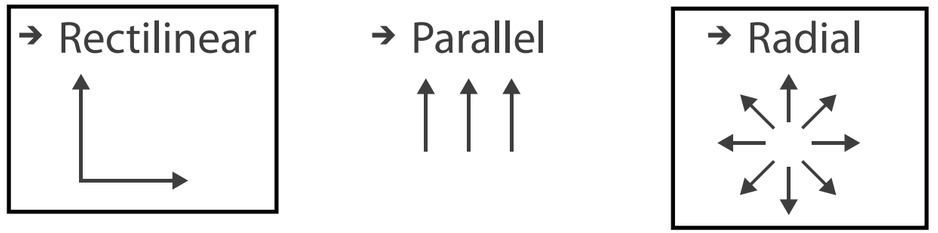
- axis orientation
  - radial: genome
  - rectilinear: chromosome, block
    - aligned position more accurate than angle



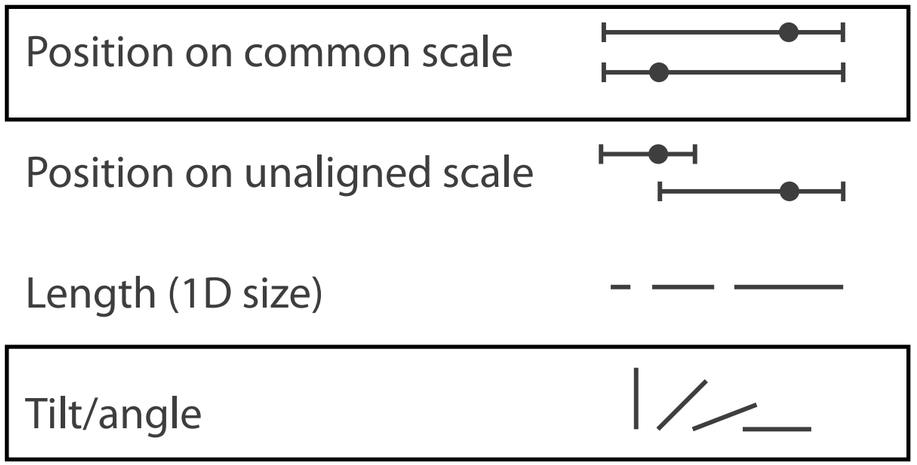


Arrange

Axis Orientation

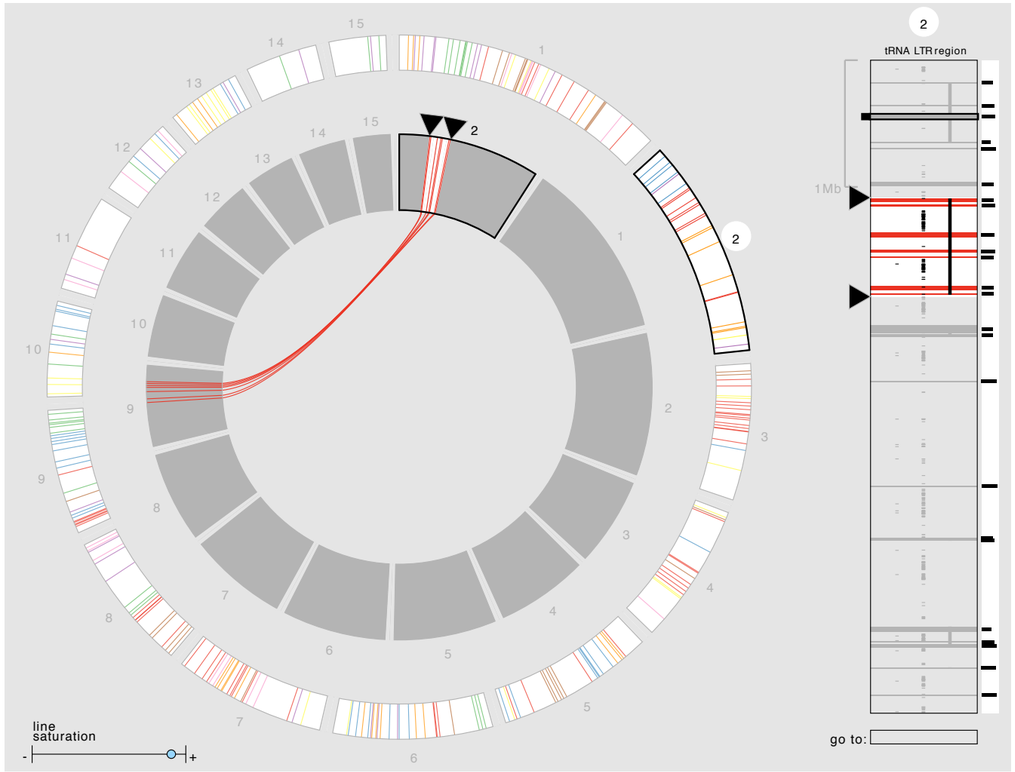


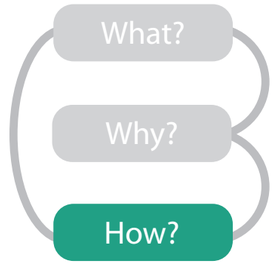
Magnitude Channels: Ordered Attributes



How: Idiom design choices

- filter



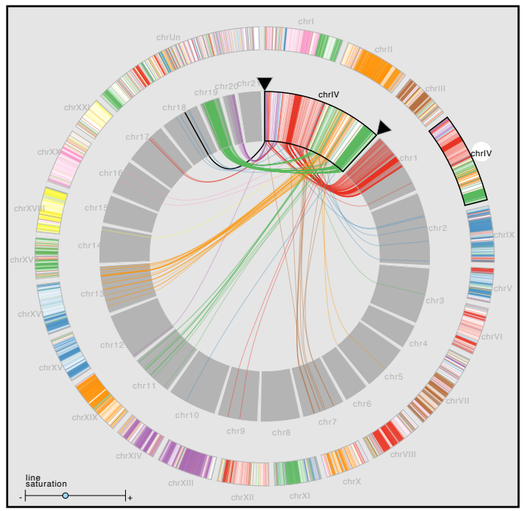


Reduce

Filter

How: Idiom design choices

- outer ring: summarize relationships with color
  - select one chromosome from set of source chromosomes
- inner ring:
  - destination chromosomes around copy of selected source chromosome
  - show relationship details with connection marks as well as color



Manipulate

Select

What?

Why?

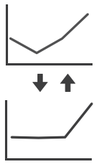
How?

Actions

Query

→ Identify

→ Compare



→ Summarise

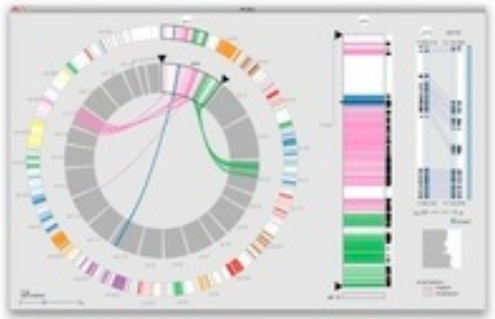
MizBee contributions

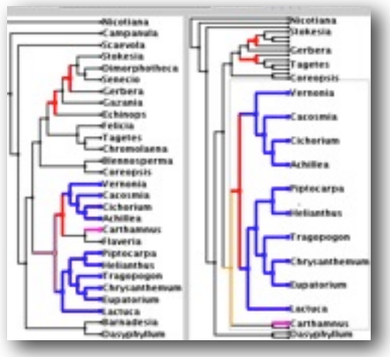
- first synteny browser with side-by-side linked views
  - across the range of scales
  - encoding all four conservation relationship types
    - proximity, size, orientation, similarity

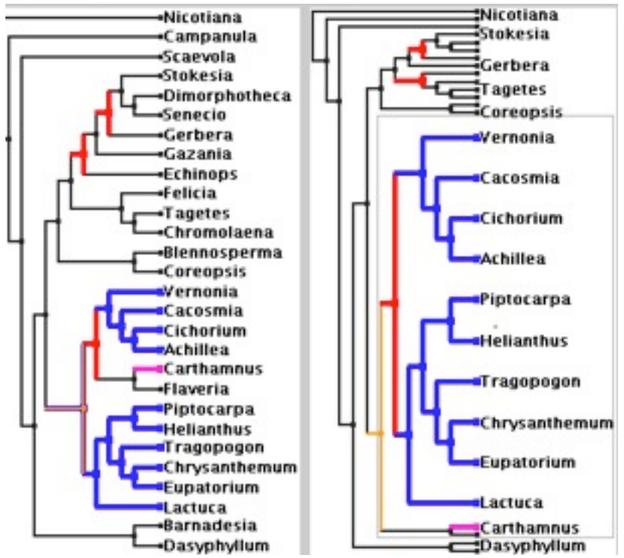
- open source
  http://www.cs.utah.edu/~miriah/mizbee

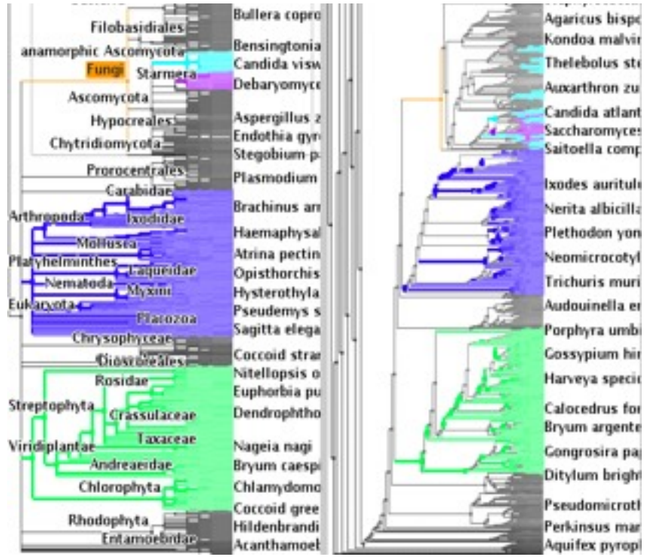
Outline

- introduction
- Cerebral
- MizBee
- TreeJuxtaposer
- wrapup









TreeJuxtaposer

Scalable Tree Comparison using Focus+Context with Guaranteed Visibility

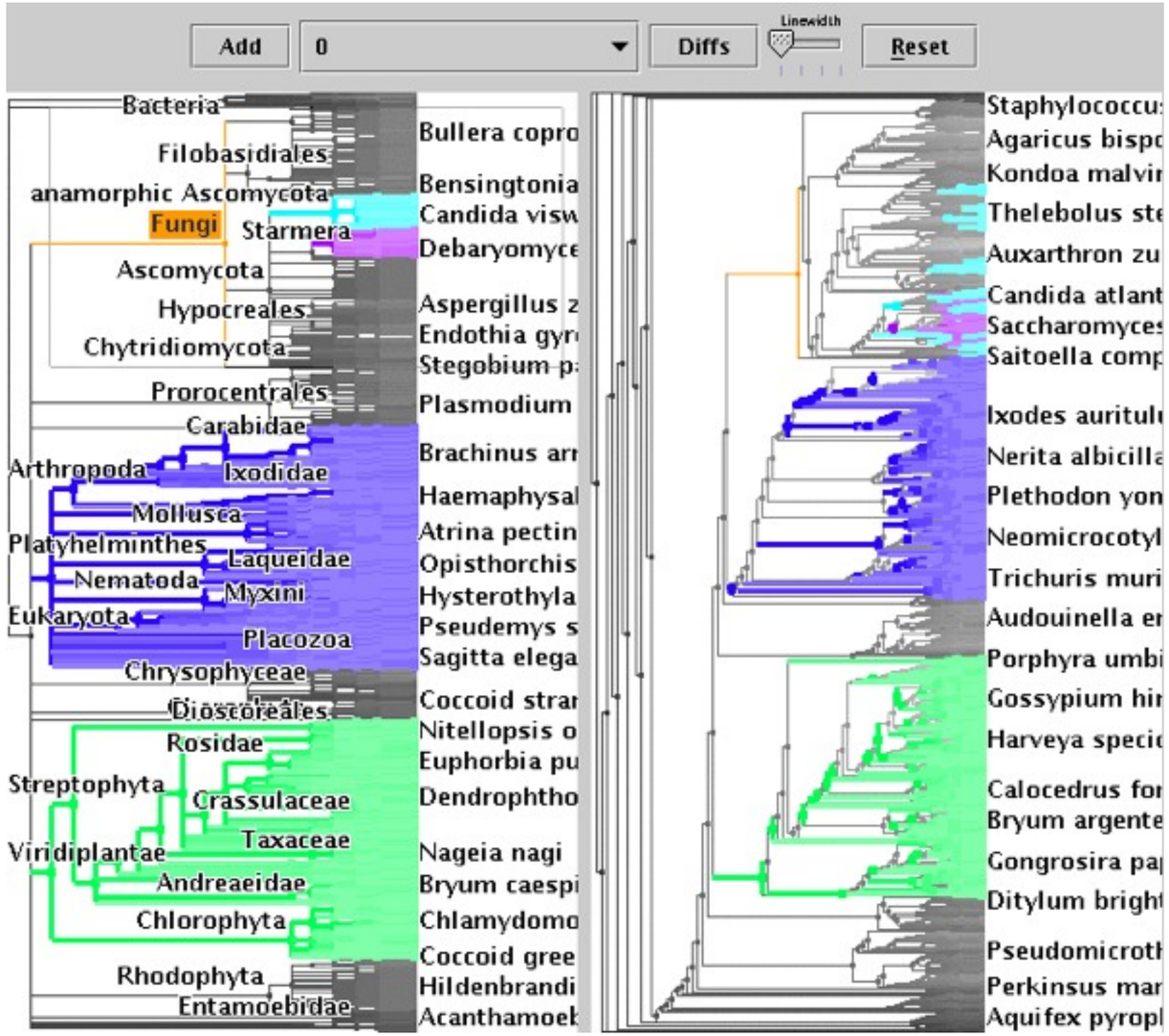
joint work with:

François Guimbretière, Serdar Tasiran, Li Zhang, Yunhong Zhou

http://www.cs.ubc.ca/labs/imager/tr/2003/tj/

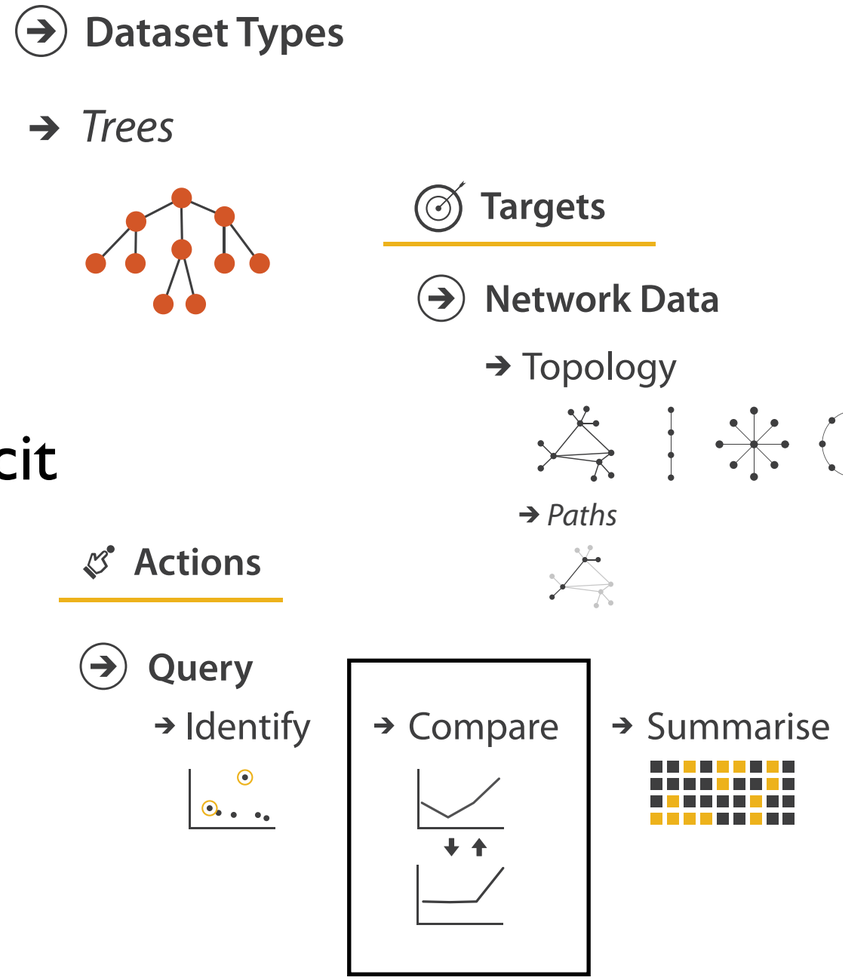
TreeJuxtaposer: Scalable Tree Comparison using Focus+Context with Guaranteed Visibility.
Munzner, Guimbretière, Tasiran, Zhang, Zhou. ACM SIGGRAPH 2003.

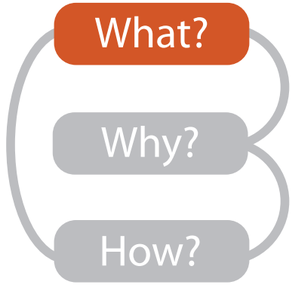
TreeJuxtaposer video

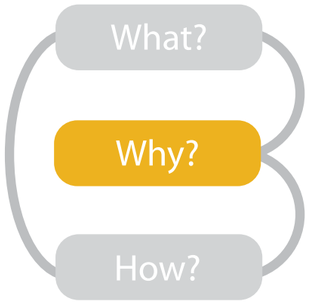


What and why: Data and task abstraction

- data: trees
  - phylogenetic tree reconstruction
    - siblings unordered, interior nodes inferred
- task: compare topological structure
  - larger query scopes require more explicit tool support
    - compare several is more difficult than identify/inspect one
      - even trickier: summarize all
- derived data: structural differences
  - best corresponding node in other tree



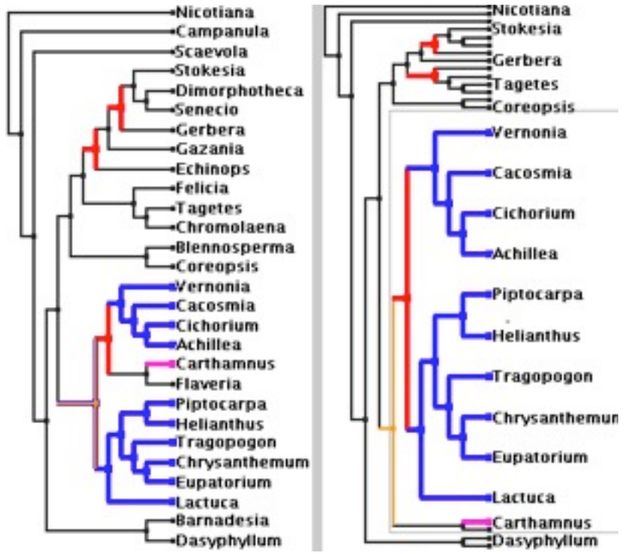




Derive

How: Idiom design decisions

- juxtapose linked views
  - show two tree layouts side by side
  - linked navigation
- encode with color: linked highlighting
  - structural differences
  - corresponding subtree (click select)
  - best corresponding node (hover select)

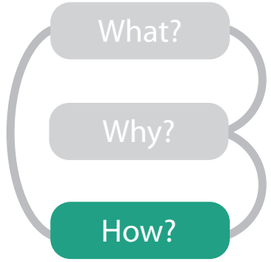


Facet

Juxtapose

Manipulate

Select



Facet

Juxtapose and Coordinate Views

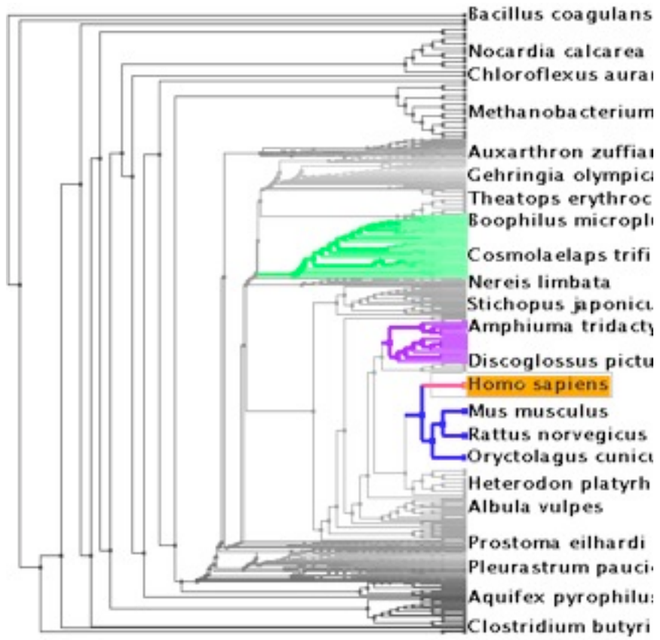
- Share Encoding: Same/Different
  - *Linked Highlighting*

- Share Data: All/Subset/None

- Share Navigation

How: Idiom design decisions

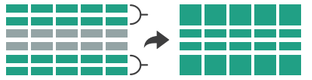
- embed focus+context in single view
  - reduce with complex combination of filtering and aggregation
- distort geometry
  - metaphor: stretch and squish navigation
  - shape: rectilinear
  - foci: multiple
  - impact: global



Reduce

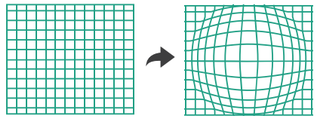
- Filter

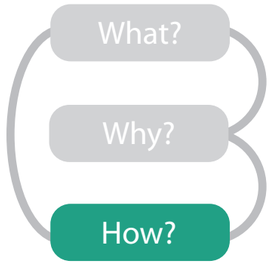
- Aggregate



- Embed

→ Distort Geometry



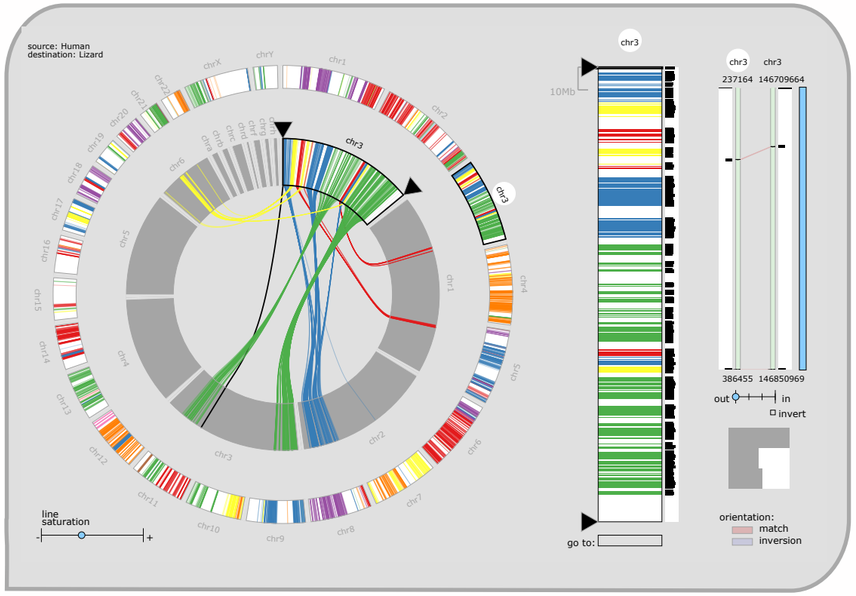


TreeJuxtaposer contributions

- first interactive tree comparison system
  - derive structural difference data to support comparison task
    - subquadratic algorithm: best corresponding node
  - juxtapose views with cross-dataset linked highlighting
- embed focus+context information in single view with stretch and squish navigation
  - sublinear algorithm: guaranteed visibility of structure marks even when squished

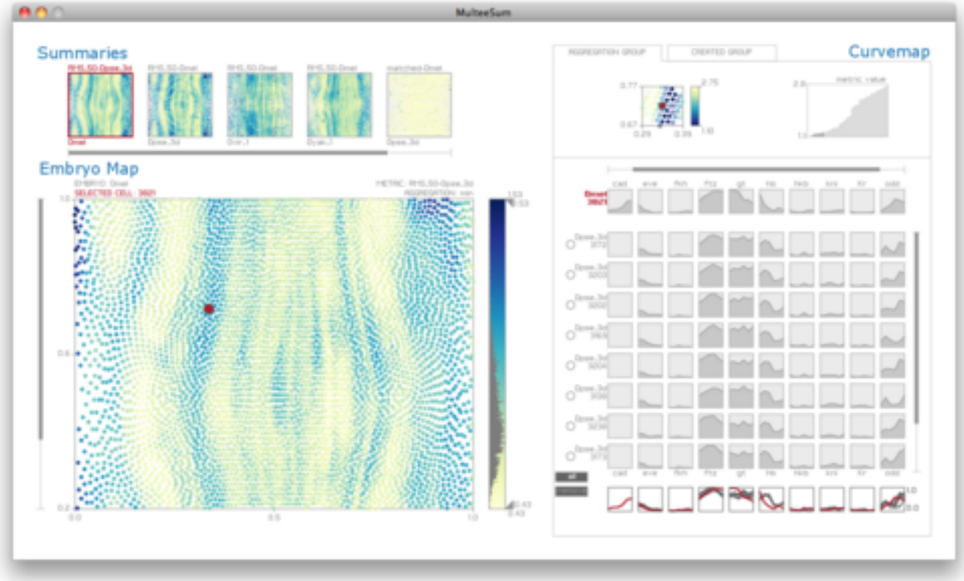
- open source
  http://olduvai.sf.net/tj

Problem-driven work: Genomics

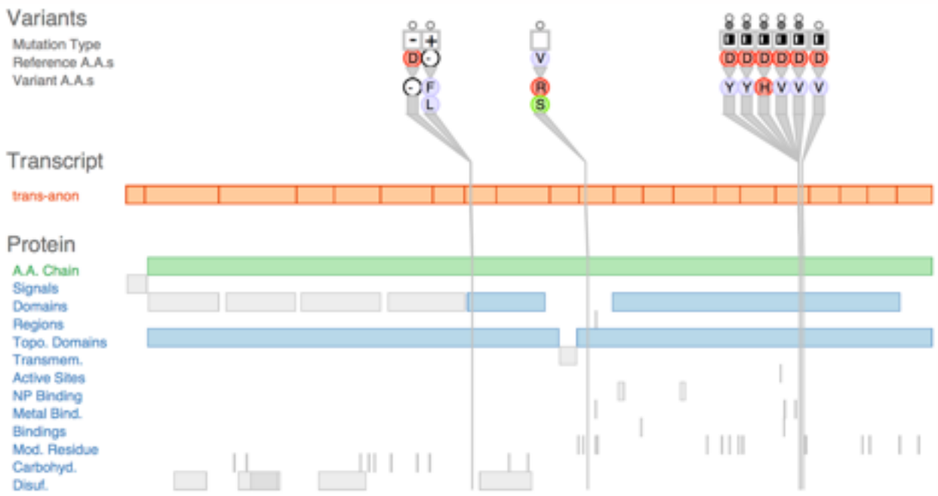


MizBee

http://youtu.be/86p7brwuz2g

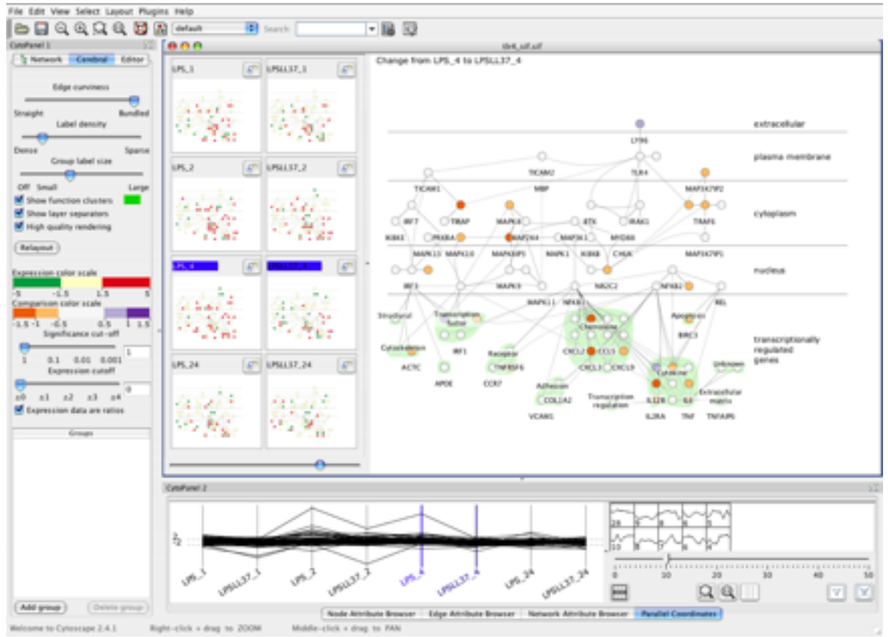


MulteeSum
Pathline



Variant View

http://youtu.be/AHDnv_qMXxQ

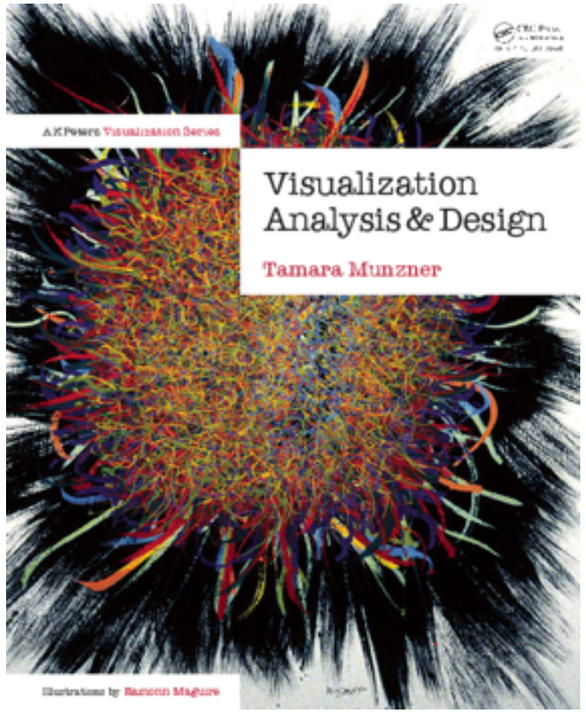


Cerebral

http://youtu.be/76HhG1FQngI

More Information

- this talk
  http://www.cs.ubc.ca/~tmm/talks.html#daley15
- papers, videos, software, talks, courses
  http://www.cs.ubc.ca/group/infovis
  http://www.cs.ubc.ca/~tmm
- book
  http://www.cs.ubc.ca/~tmm/vadbook



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