Visualization Analysis & Design for Biology

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VanBUG: Vancouver Bioinformatics Users Group
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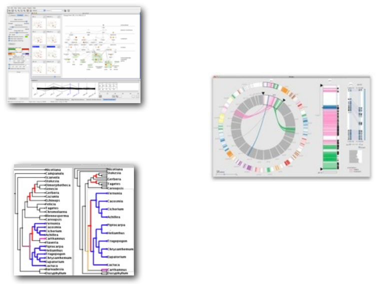
http://www.cs.ubc.ca/~tmm/talks.html#vanbug15 **@tamaramunzner**

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.

Why have a human in the loop?

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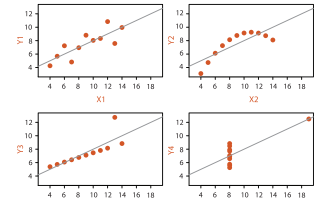
Visualization is suitable when there is a need to augment human capabilities rather than replace people with computational decision-making methods.

- 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

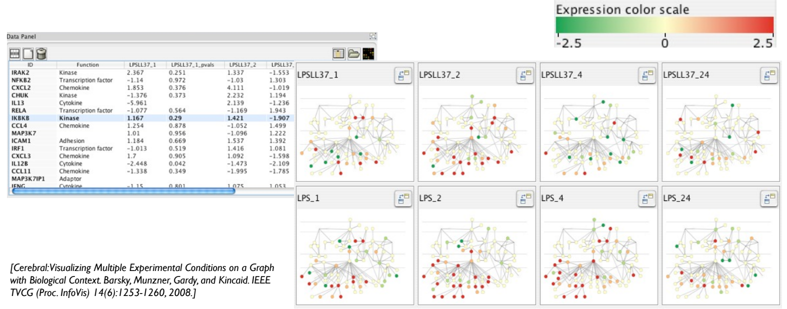
Identical statistics	
x mean	9
x variance	10
y mean	8
y variance	4
x/y correlation	1



Why use an external representation?

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

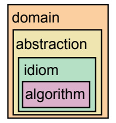
- external representation: replace cognition with perception



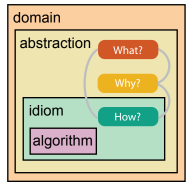
[Cerebral: Visualizing Multiple Experimental Conditions on a Graph with Biological Context. Barsky, Munzner, Gardy, and Kincaid. IEEE TVCG (Proc. InfoVis) 14(6):1253-1260, 2008.]

Analysis framework: Four levels, three questions

- *domain* situation
  - who are the target users?
- *abstraction*
  - translate from specifics of domain to vocabulary of vis
  - **what** is shown? **data abstraction**
    - often don't just draw what you're given: transform to new form
  - **why** is the user looking at it? **task abstraction**
- *idiom*
  - **how** is it shown?
    - **visual encoding idiom**: how to draw
    - **interaction idiom**: how to manipulate
- *algorithm*
  - efficient computation

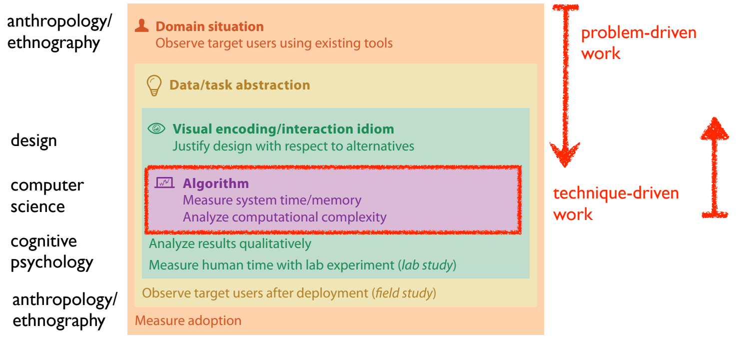


[A Nested Model of Visualization Design and Validation. Munzner. IEEE TVCG 15(6):921-928, 2009 (Proc. InfoVis 2009).]



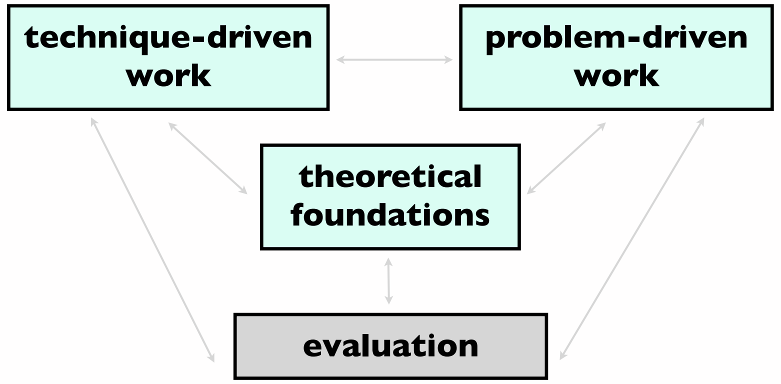
[A Multi-Level Typology of Abstract Visualization Tasks Brehmer and Munzner. IEEE TVCG 19(12):2376-2385, 2013 (Proc. InfoVis 2013).]

Validation methods from different fields for each level



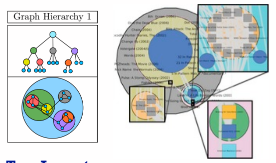
- mismatch: cannot show idiom good with system timings
- mismatch: cannot show abstraction good with lab study

Angles of attack



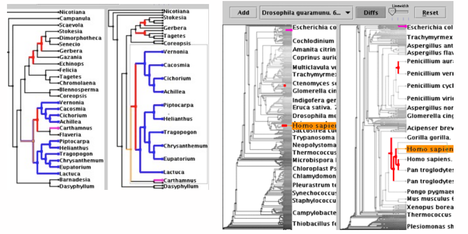
Technique-driven work: Networks

- 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/AWXAe8zxlt8



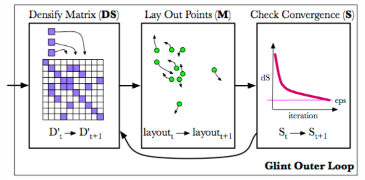
TreeJuxtaposer
PRISAD

http://youtu.be/fq8EIAOutvs
http://youtu.be/GdaPj8a9QEo

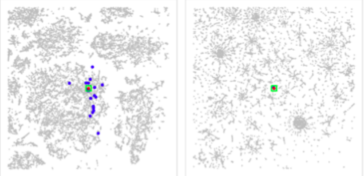
Technique-driven work: Dimensionality reduction

- 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



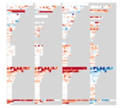
Glint

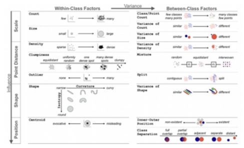


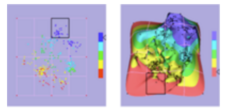
QSNE

Evaluation: Dimensionality Reduction

- guidance on scatterplot/DR choices
- taxonomy of cluster separation factors
- 2D points vs 3D landscapes

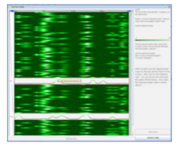


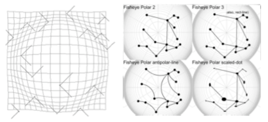




Evaluation: Focus+Context

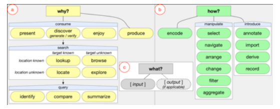
- overviews: separate vs. integrated views
- navigation: stretch and squish vs. pan/zoom navigation
- impact of distortion on visual search, visual memory

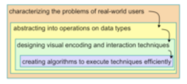


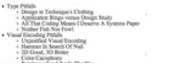


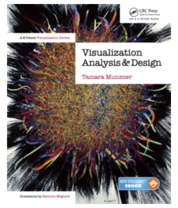
Theory/Models

- 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



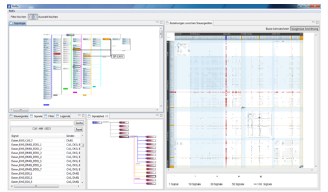






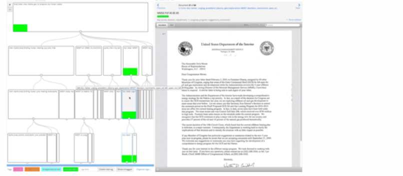
Problem-driven work: Many domains

http://youtu.be/ld0c3H0VSkw
LiveRAC: system management time-series



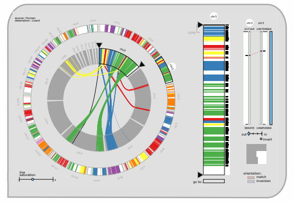
RelEx: in-car overlay networks http://youtu.be/89lsQXc6Ao4

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

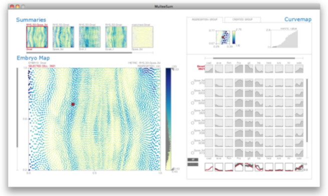


Overview: investigative journalism http://vimeo.com/71483614

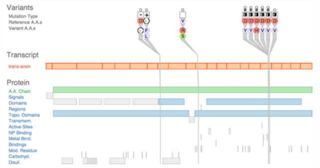
Problem-driven work: Genomics



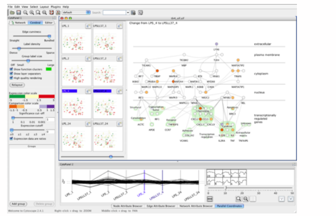
MizBee http://youtu.be/86p7brwuz2g



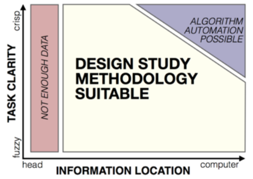
MulteeSum
Pathline



Variant View http://youtu.be/AHDnv_gMXxQ



Cerebral http://youtu.be/76HhG1FQngI



Design Study Methodology

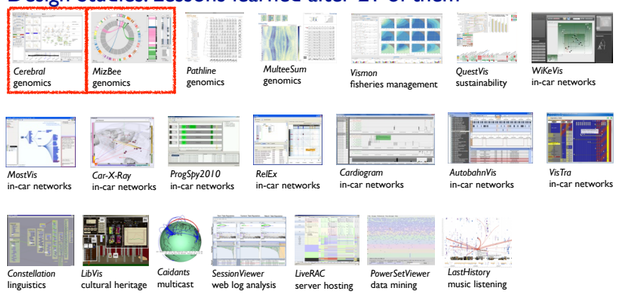
Reflections from the Trenches and from the Stacks

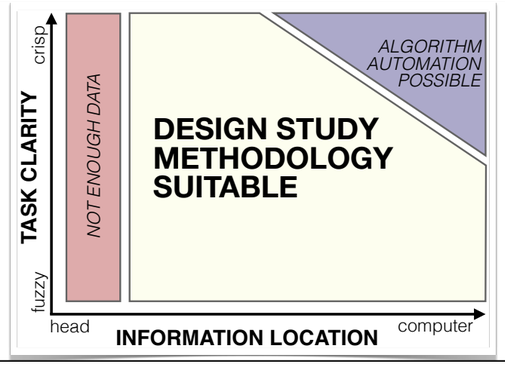
joint work with:
Michael Sedlmair, Miriah Meyer

http://www.cs.ubc.ca/labs/imager/tr/2012/dsm/

Design Study Methodology: Reflections from the Trenches and from the Stacks.
Sedlmair, Meyer, Munzner. IEEE Trans. Visualization and Computer Graphics 18(12): 2431-2440, 2012 (Proc. InfoVis 2012).

Design Studies: Lessons learned after 21 of them





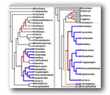
Problem-driven work and you

- enormous opportunity for bioinformatics
  - apply human-centered design methods beyond visualization!
  - task analysis: what do the target users really need?

Outline

- introduction
- Cerebral
- MizBee
- TreeJuxtaposer
- wrapup





Cerebral

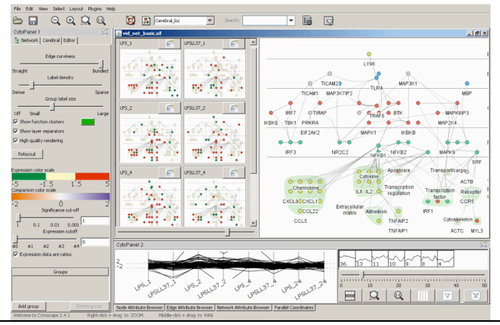
Visualizing Multiple Experimental Conditions on a Graph with Biological Context

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

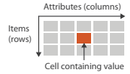


What: Data abstraction

- 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

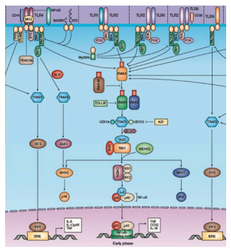
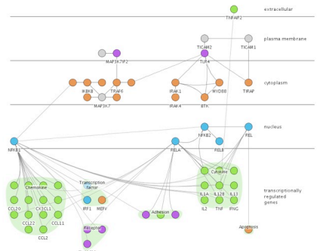
- arrange space for networks
  - custom node-link diagram layout
    - points for nodes
    - connection marks for links
  - vertical compartment according to subcellular location attribute
  - cluster according to functional grouping

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

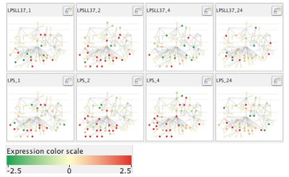



http://www.nature.com/nrifocus/tlr/nri1397.html

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

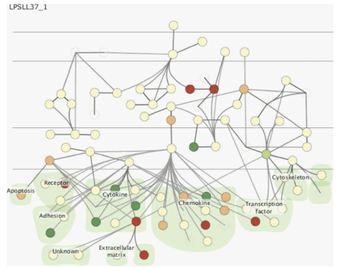
Facet
→ Juxtapose
→ Partition



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/

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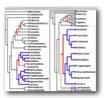
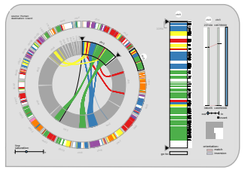


MizBee

A Multiscale Synteny Browser

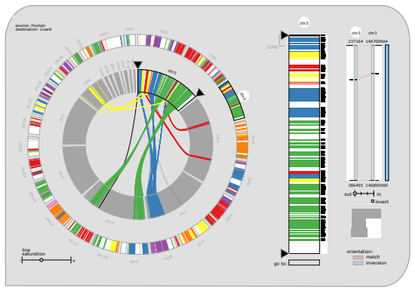
joint work with:
Miriah Meyer, Hanspeter Pfister

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

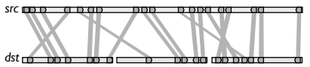
- relationship types: proximity, size, orientation, similarity
- data scales: genome, chromosome, block, feature
- topics: algorithm in/out, block reliability, high-level science

	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[55]

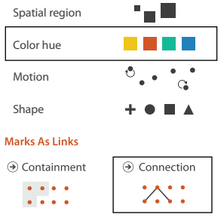
How: Idiom design choices

- encode match relationships between chromosome segments with both
  - color

  - connection marks



Identity Channels: Categorical Attributes



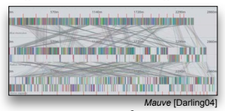
Marks As Links

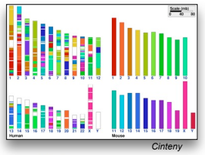
Containment

Connection

How: Arrange space

- design space of arrangements


Mauve [Darling04]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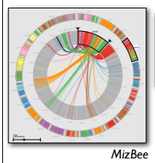
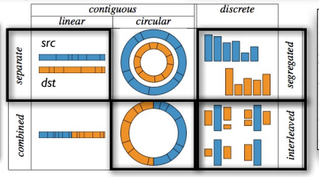
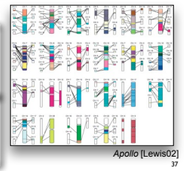

MizBee



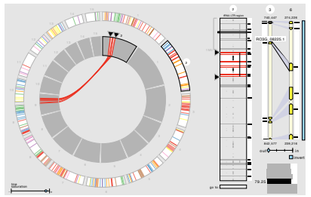

Apollo [Lewis02]

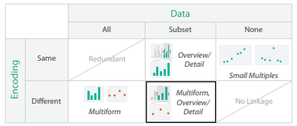
How: Idiom design choices

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

Facet

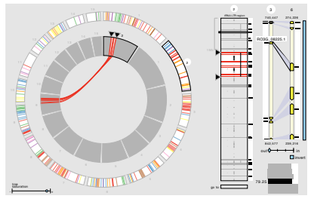
Juxtapose





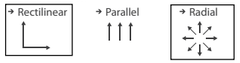
How: Idiom design choices

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

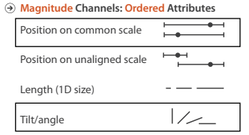


Arrange

Axis Orientation

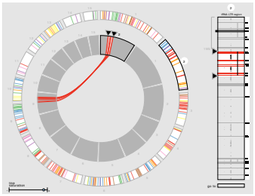


Magnitude Channels: Ordered Attributes



How: Idiom design choices

- filter

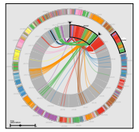


Reduce

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

Actions

Query

Identify

Compare

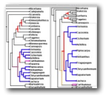
Summarise

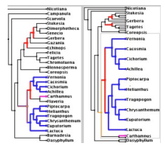
MizBee contributions

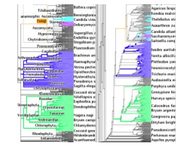
- first synteny browser with side-by-side linked views
  - across the range of scales
  - encoding all four conservation relationship types
    - proximity, size, orientation, similarity
- open source
  http://www.cs.utah.edu/~miriah/mizbee

Outline

- introduction
- Cerebral
- MizBee
- TreeJuxtaposer
- wrapup







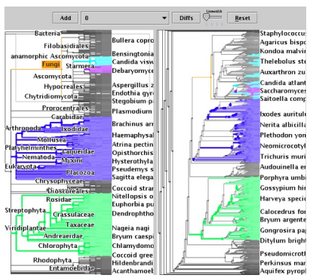
TreeJuxtaposer

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

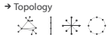
Dataset Types

Trees

Targets

Network Data

Topology



Paths

Actions

Query

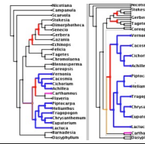
Identify

Compare

Summarise

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

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

Outline

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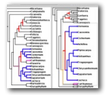
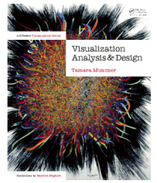
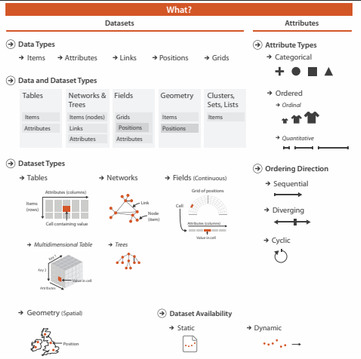


Visualization Analysis and Design

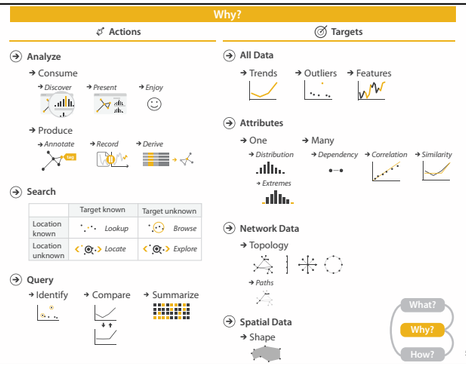
http://www.cs.ubc.ca/~tmm/vadbook/

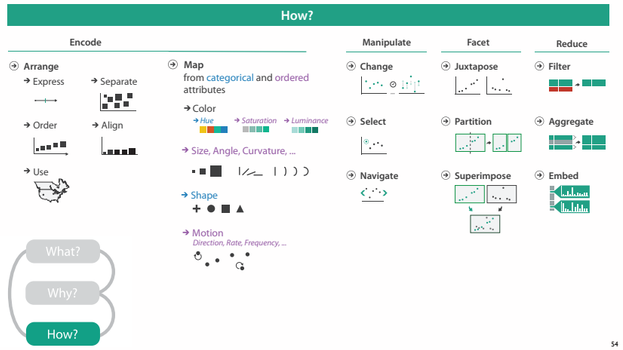


Visualization Analysis and Design
Munzner. AK Peters Visualization Series, CRC Press, 2014.



- {action, target} pairs
  - *discover distribution*
  - *compare trends*
  - *locate outliers*
  - *browse topology*





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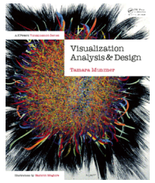
- acknowledgements
  - funding: Agilent, NSERC, NSF



@tamaramunzner