Ch 8/9: Spatial Data, Networks
Paper: Genealogical Graphs
Paper: ABySS-Explorer

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CPSC 547, Information Visualization
Week 5: 8 October 2019

www.cs.ubc.ca/~tmm/courses/547-19

News

- today
  - pitches first
    - idea: use Canvas thread to sort out groups
  - discussion/lecture second
    - tables/color (catch-up)
    - today's reading (get started)
- next time (Oct 15)
  - no exercises or guest lecture, catch up on discussions of reading
- week after that
  - **reminder no class Tue Oct 22!**
  - by Fri Oct 25:
    - presentation topics (there will be a Canvas thread)
    - final project teams (there will be a different Canvas thread than discussion one)

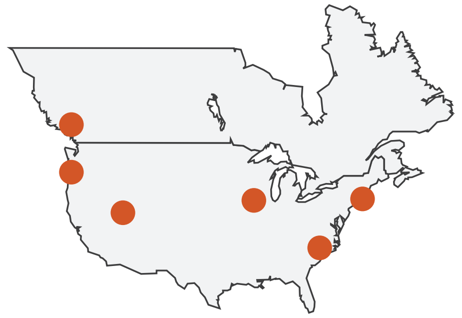
Pitches

Ch 8: Arrange Spatial Data

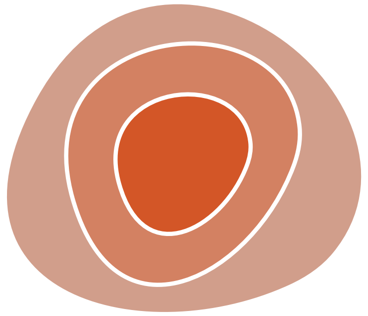
Arrange spatial data

➔ Use Given

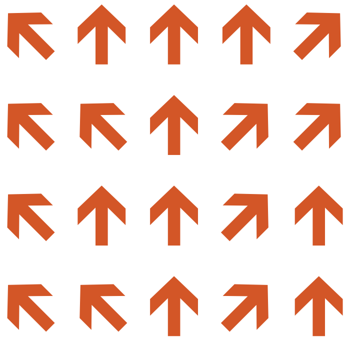
- ➔ Geometry
  - ➔ *Geographic*
  - ➔ *Other Derived*



- ➔ Spatial Fields
  - ➔ *Scalar Fields (one value per cell)*
    - ➔ *Isocontours*
    - ➔ *Direct Volume Rendering*

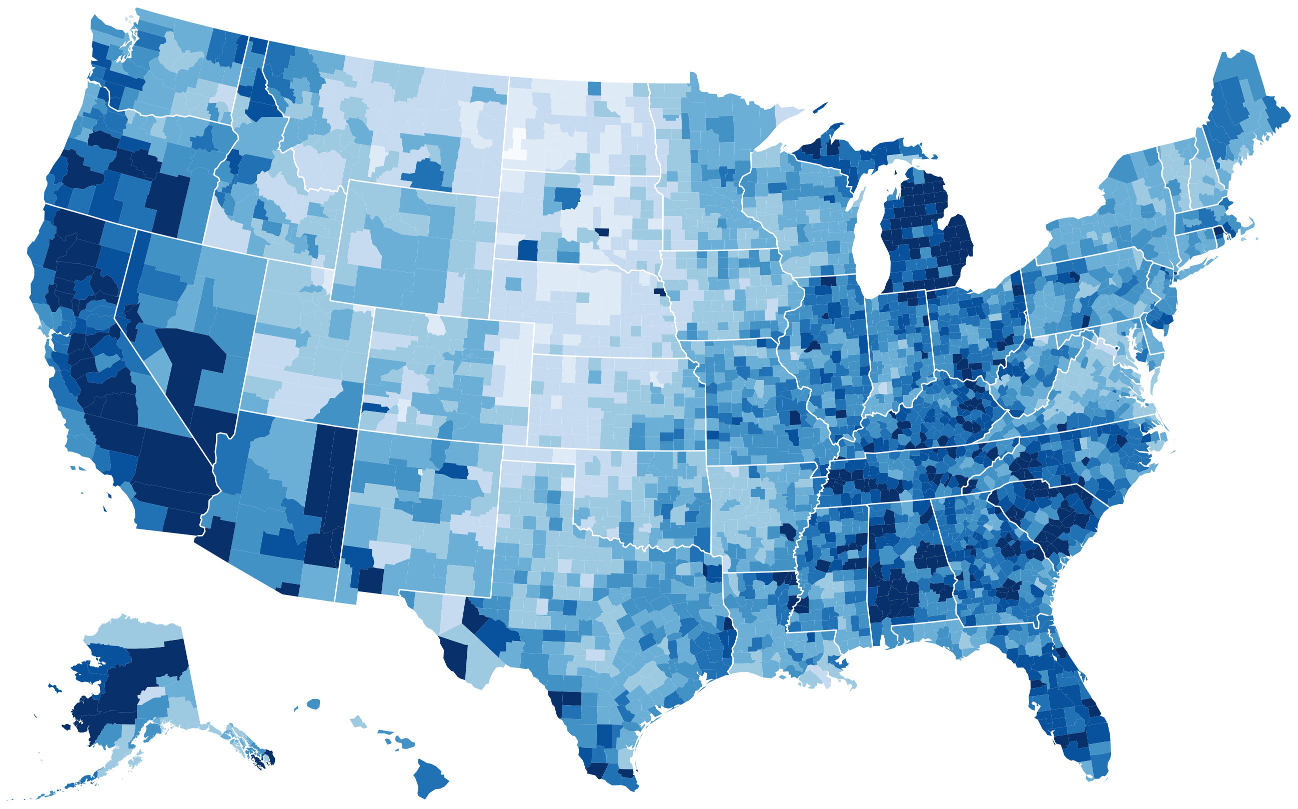


  - ➔ *Vector and Tensor Fields (many values per cell)*
    - ➔ *Flow Glyphs (local)*
    - ➔ *Geometric (sparse seeds)*
    - ➔ *Textures (dense seeds)*
    - ➔ *Features (globally derived)*



Idiom: **choropleth map**

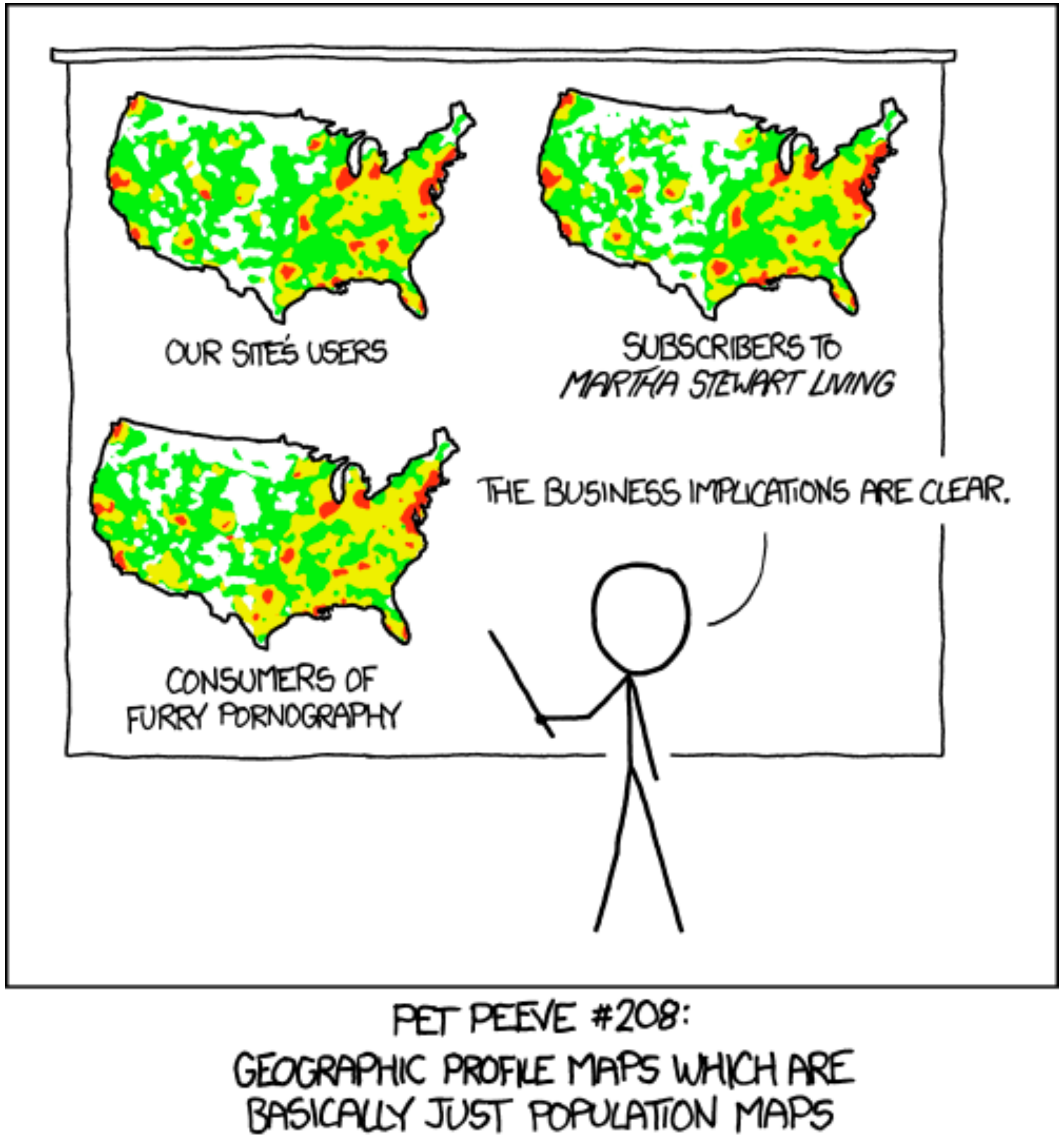
- ***use*** given spatial data
  - when central task is understanding spatial relationships
- data
  - geographic geometry
  - table with 1 quant attribute per region
- encoding
  - use given geometry for area mark boundaries
  - sequential segmented colormap *[more later]*
  - (geographic heat map)



http://bl.ocks.org/mbostock/4060606

Population maps trickiness

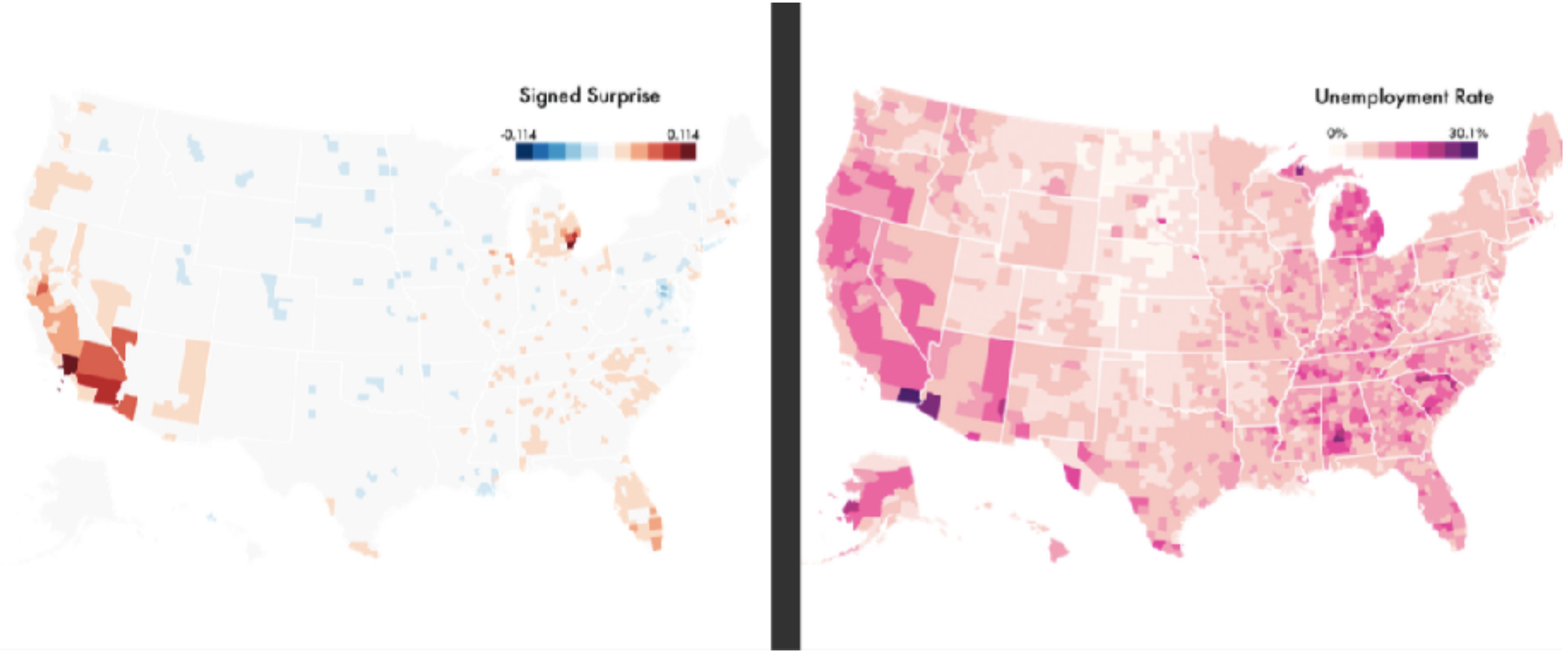
- beware!
- absolute vs relative again
  - population density vs per capita
- investigate with Ben Jones Tableau Public demo
  - http://public.tableau.com/profile/ben.jones#!/vizhome/PopVsFin/PopVsFin *Are Maps of Financial Variables just Population Maps?*
    - yes, unless you look at per capita (relative) numbers



[https://xkcd.com/1138]

Idiom: Bayesian surprise maps

- use models of expectations to highlight surprising values
- confounds (population) and variance (sparsity)

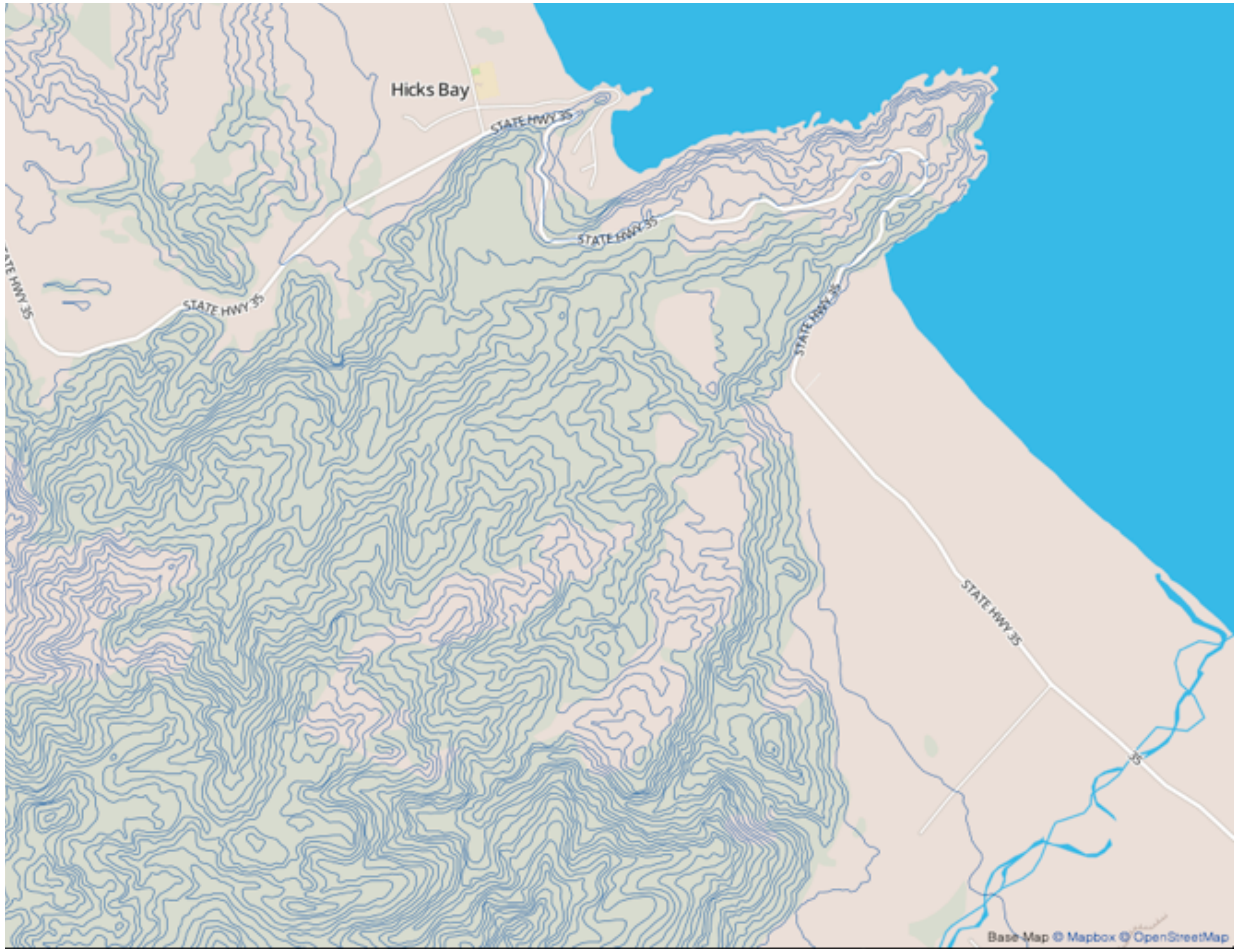


[Surprise! Bayesian Weighting for De-Biasing Thematic Maps. Correll and Heer. Proc InfoVis 2016]

https://medium.com/@uwdata/surprise-maps-showing-the-unexpected-e92b67398865 https://idl.cs.washington.edu/papers/surprise-maps/

Idiom: **topographic map**

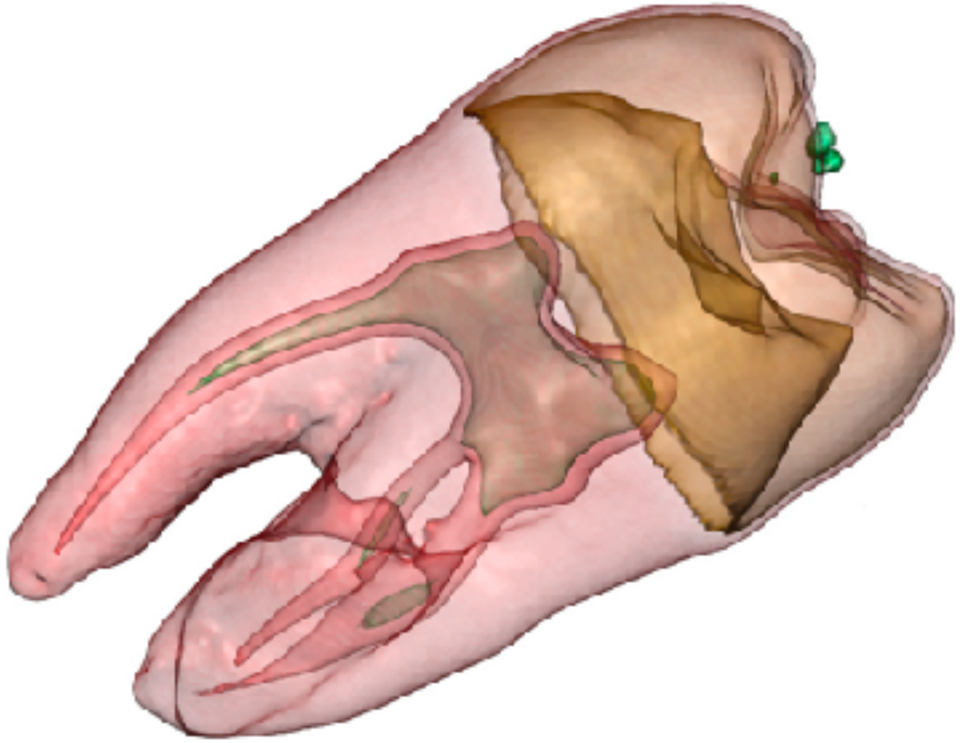
- data
  - –geographic geometry
  - –scalar spatial field
    - 1 quant attribute per grid cell
- derived data
  - –isoline geometry
    - isocontours computed for specific levels of scalar values



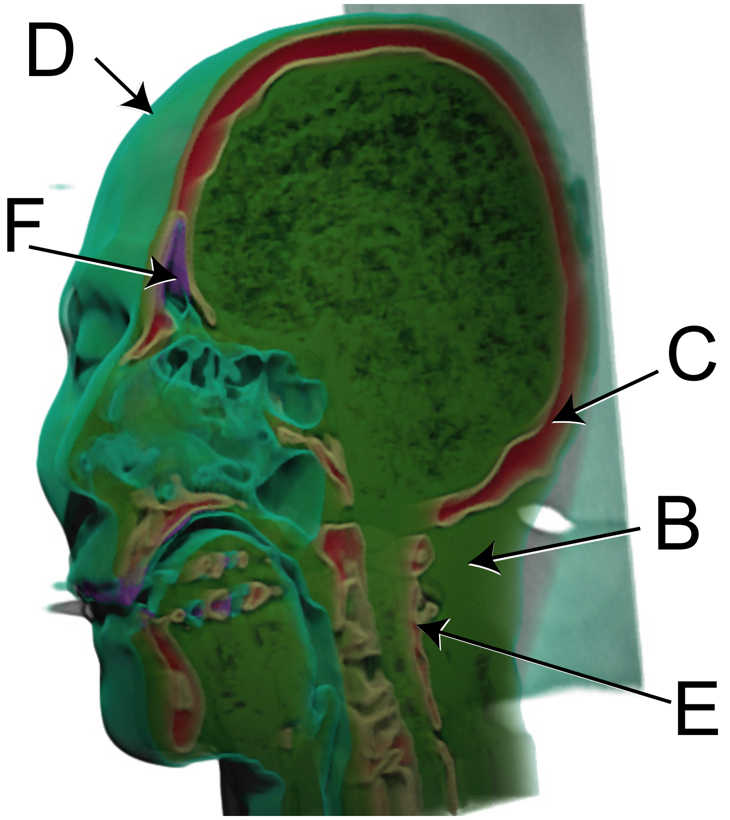
Land Information New Zealand Data Service

Idioms: **isosurfaces, direct volume rendering**

- data
  - scalar spatial field
    - 1 quant attribute per grid cell
- task
  - shape understanding, spatial relationships
- isosurface
  - derived data: isocontours computed for specific levels of scalar values
- direct volume rendering
  - transfer function maps scalar values to color, opacity



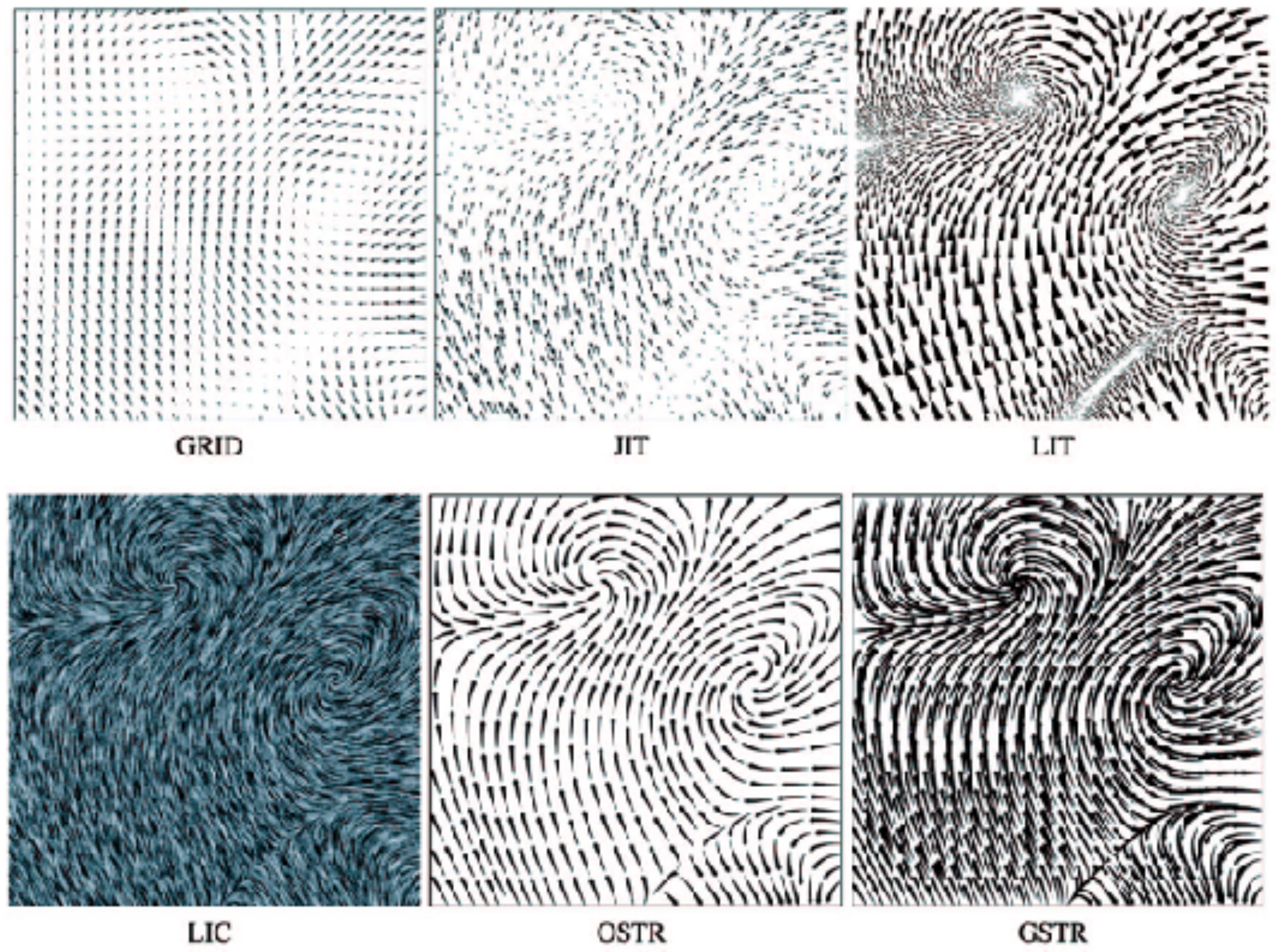
[Interactive Volume Rendering Techniques. Kniss. Master's thesis, University of Utah Computer Science, 2002.]



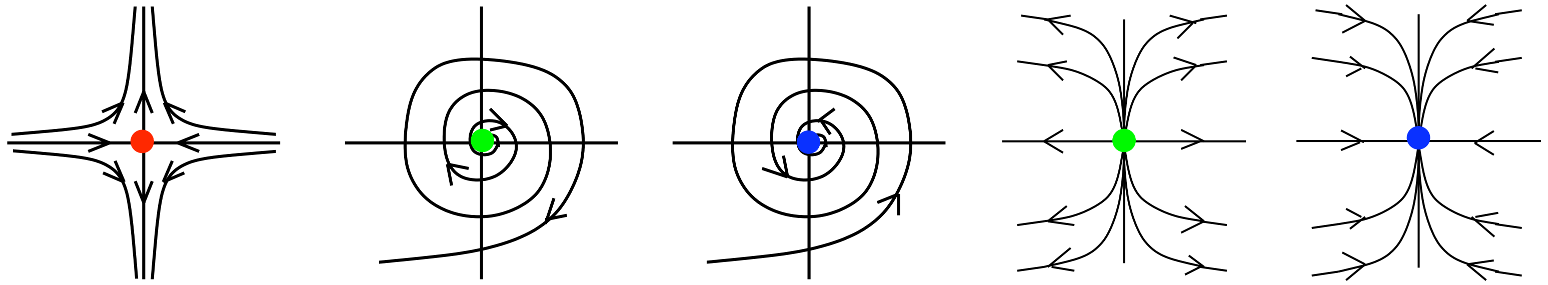
[Multidimensional Transfer Functions for Volume Rendering. Kniss, Kindlmann, and Hansen. In The Visualization Handbook, edited by Charles Hansen and Christopher Johnson, pp. 189–210. Elsevier, 2005.]

Vector and tensor fields

- data
  - many attribs per cell
- idiom families
  - flow glyphs
    - purely local
  - geometric flow
    - derived data from tracing particle trajectories
    - sparse set of seed points
  - texture flow
    - derived data, dense seeds
  - feature flow
    - global computation to detect features
      - encoded with one of methods above



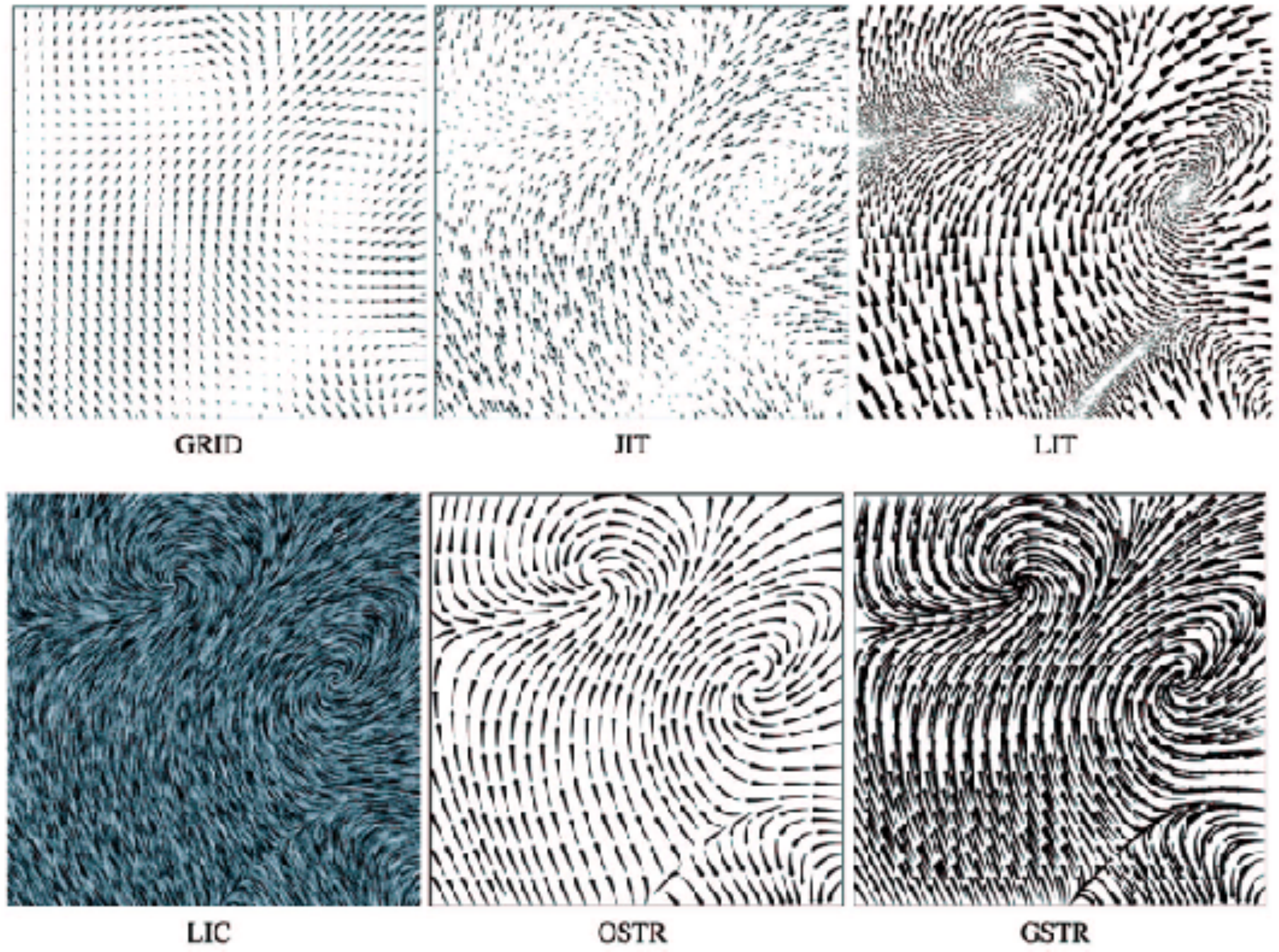
[Comparing 2D vector field visualization methods: A user study. Laidlaw et al. IEEE Trans. Visualization and Computer Graphics (TVCG) 11:1 (2005), 59–70.]



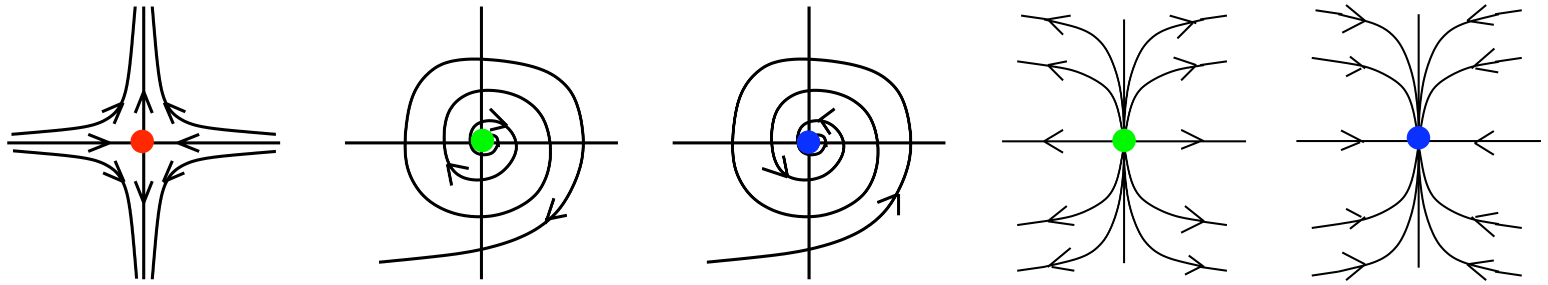
[Topology tracking for the visualization of time-dependent two-dimensional flows. Tricoche, Wischgoll, Scheuermann, and Hagen. Computers & Graphics 26:2 (2002), 249–257.]

Vector fields

- empirical study tasks
  - finding critical points, identifying their types
  - identifying what type of critical point is at a specific location
  - predicting where a particle starting at a specified point will end up (advection)



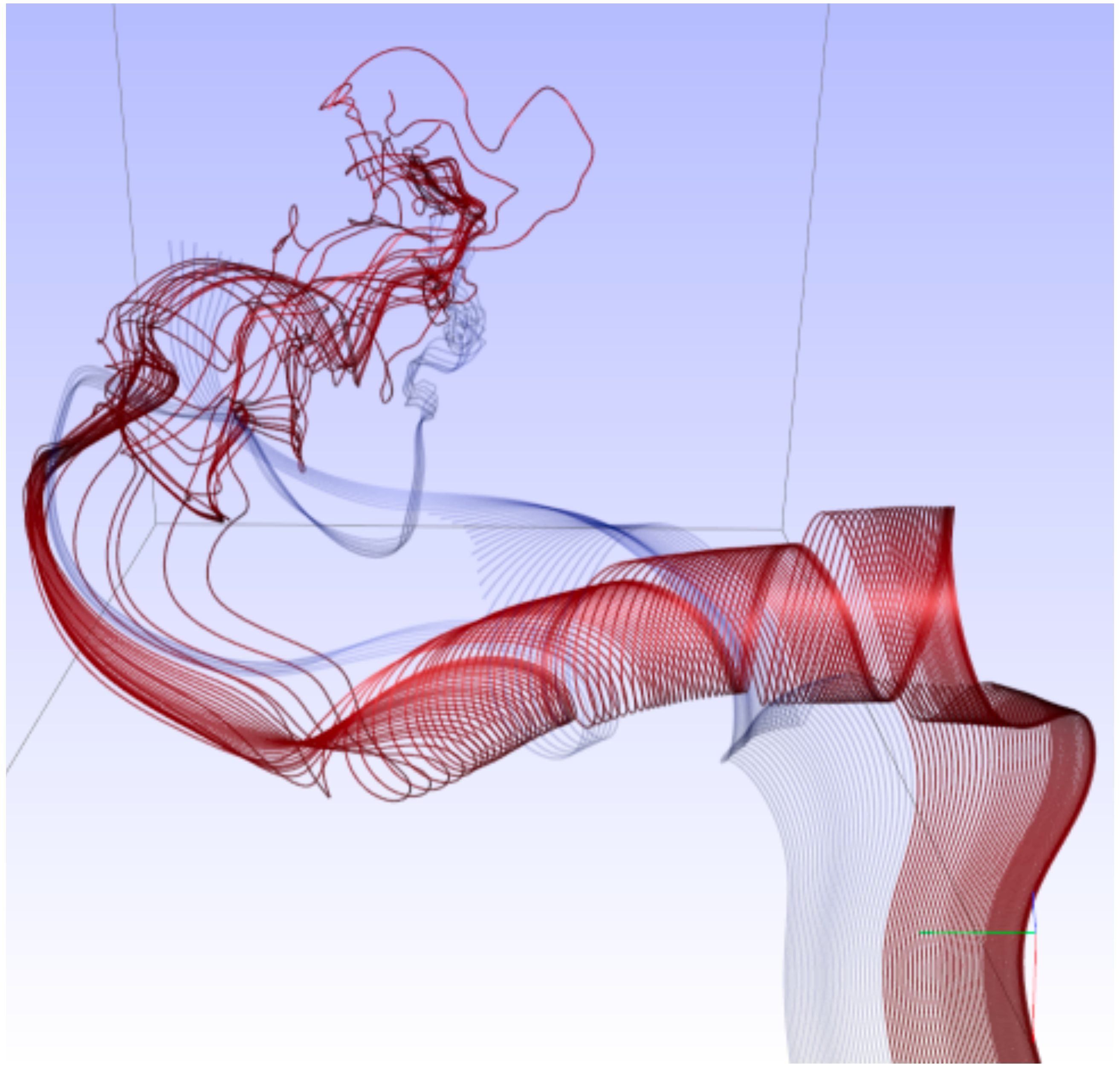
[Comparing 2D vector field visualization methods: A user study. Laidlaw et al. IEEE Trans. Visualization and Computer Graphics (TVCG) 11:1 (2005), 59–70.]



[Topology tracking for the visualization of time-dependent two-dimensional flows. Tricoche, Wischgoll, Scheuermann, and Hagen. Computers & Graphics 26:2 (2002), 249–257.]

Idiom: **similarity-clustered streamlines**

- data
  - 3D vector field
- derived data (from field)
  - streamlines: trajectory particle will follow
- derived data (per streamline)
  - curvature, torsion, tortuosity
  - signature: complex weighted combination
  - compute cluster hierarchy across all signatures
  - encode: color and opacity by cluster
- tasks
  - find features, query shape
- scalability
  - millions of samples, hundreds of streamlines



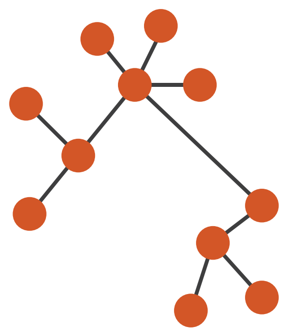
[Similarity Measures for Enhancing Interactive Streamline Seeding. McLoughlin,. Jones, Laramee, Malki, Masters, and. Hansen. IEEE Trans. Visualization and Computer Graphics 19:8 (2013), 1342–1353.]

Ch 9: Arrange Network Data

Arrange networks and trees

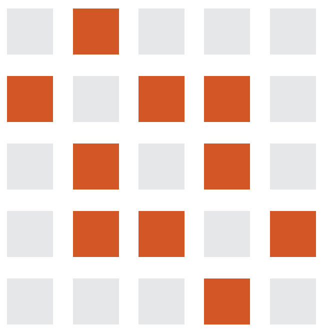
Node–Link Diagrams
Connection Marks

✔ NETWORKS ✔ TREES



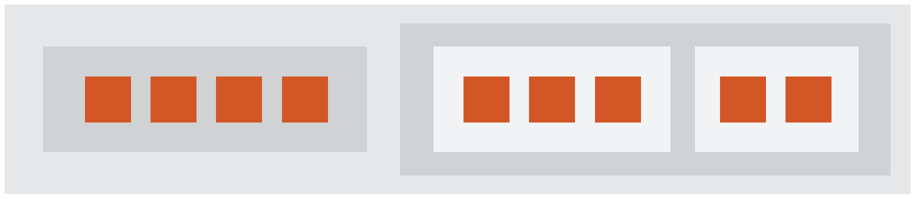
Adjacency Matrix
Derived Table

✔ NETWORKS ✔ TREES



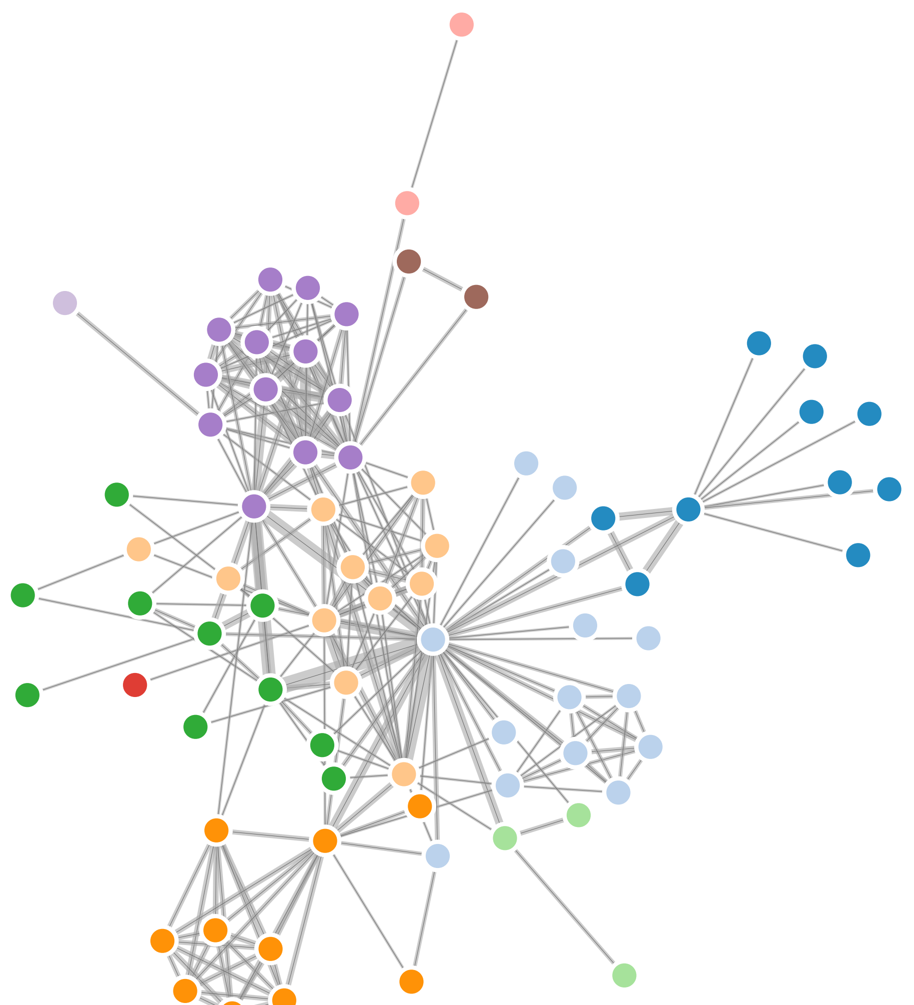
Enclosure
Containment Marks

✕ NETWORKS ✔ TREES



Idiom: **force-directed placement**

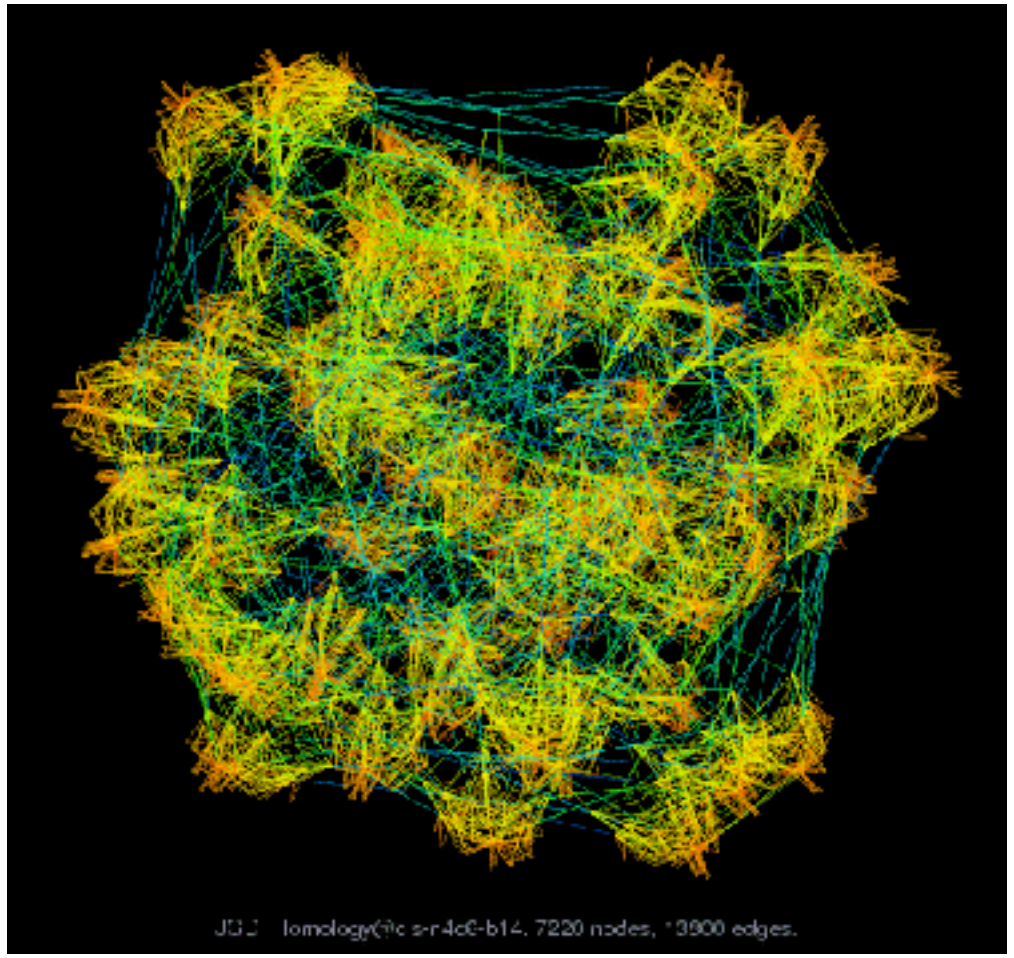
- visual encoding
  - link connection marks, node point marks
- considerations
  - spatial position: no meaning directly encoded
    - left free to minimize crossings
  - proximity semantics?
    - sometimes meaningful
    - sometimes arbitrary, artifact of layout algorithm
    - tension with length
      - long edges more visually salient than short
- tasks
  - explore topology; locate paths, clusters
- scalability
  - node/edge density E < 4N



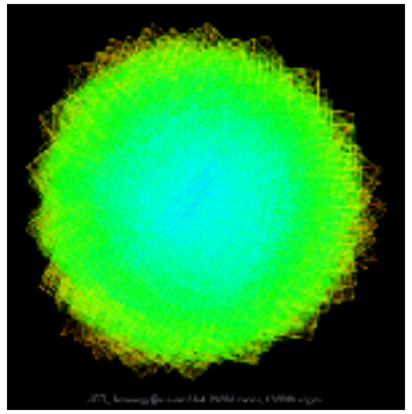
http://mbostock.github.com/d3/ex/force.html

Idiom: **sfdp** (multi-level force-directed placement)

- data
  - –original: network
  - –derived: cluster hierarchy atop it
- considerations
  - –better algorithm for same encoding technique
    - same: fundamental use of space
    - hierarchy used for algorithm speed/quality but not shown explicitly
    - (more on algorithm vs encoding in afternoon)
- scalability
  - –nodes, edges: 1K-10K
  - –hairball problem eventually hits



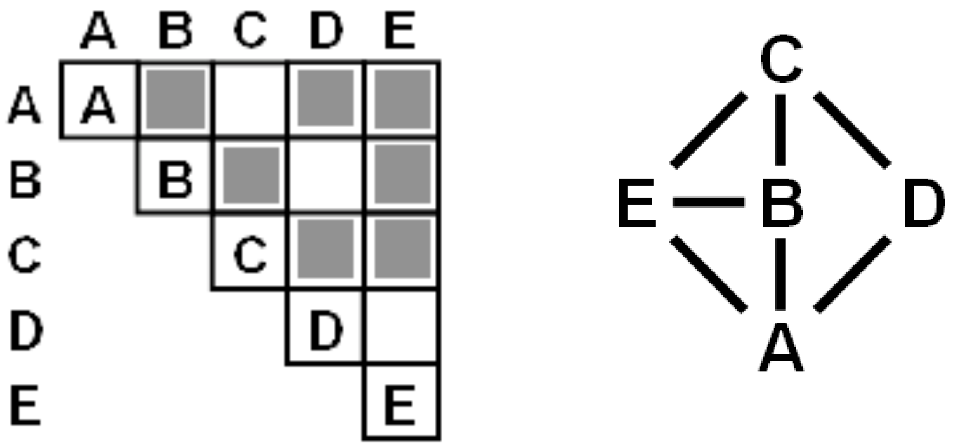
[Efficient and high quality force-directed graph drawing. Hu. The Mathematica Journal 10:37–71, 2005.]



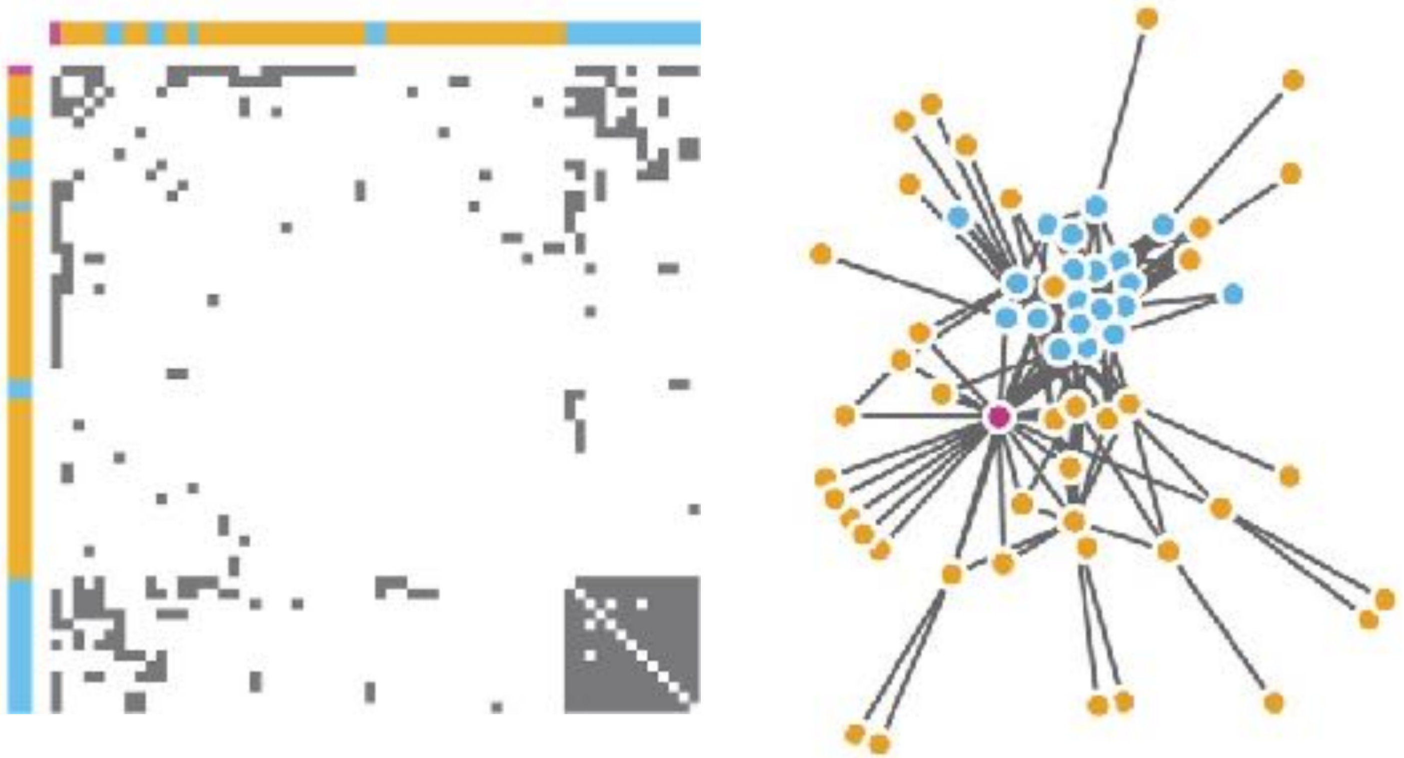
http://www.research.att.com/yifanhu/GALLERY/GRAPHS/index1.html

Idiom: **adjacency matrix view**

- data: network
  - transform into same data/encoding as heatmap
- derived data: table from network
  - 1 quant attrib
    - weighted edge between nodes
  - 2 categ attribs: node list x 2
- visual encoding
  - cell shows presence/absence of edge
- scalability
  - 1K nodes, 1M edges



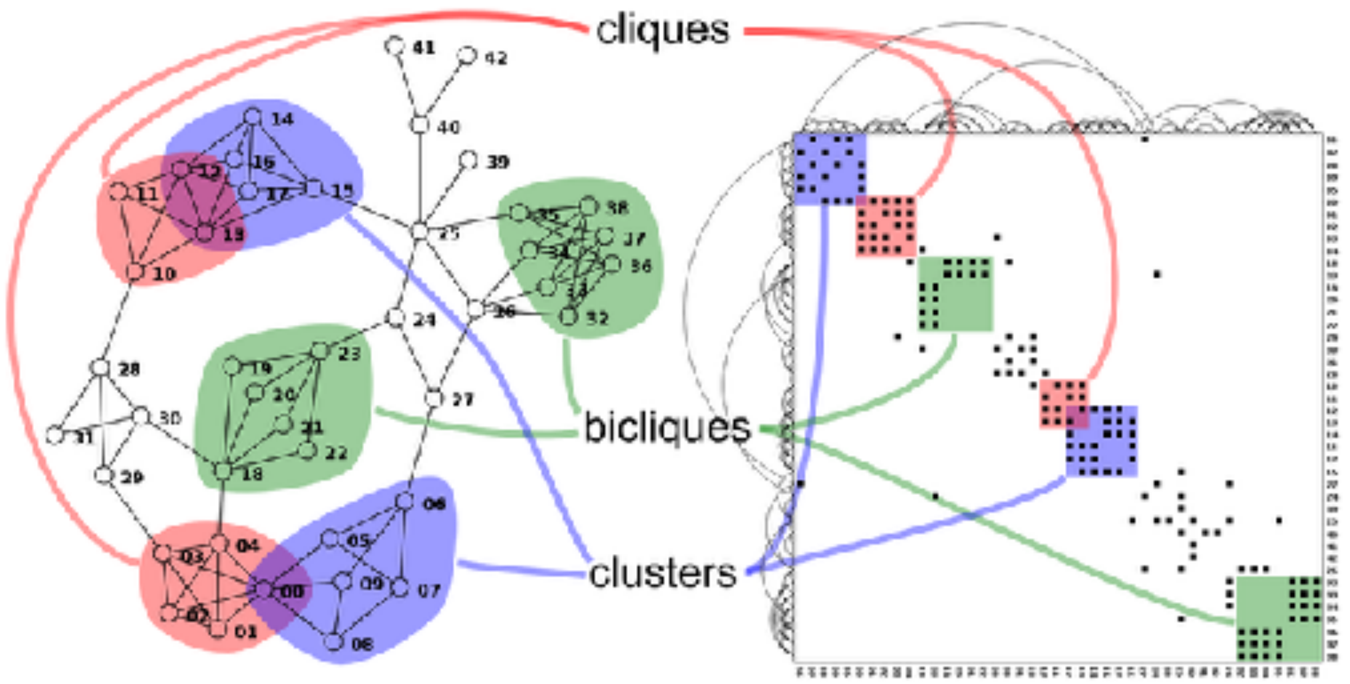
[NodeTrix: a Hybrid Visualization of Social Networks. Henry, Fekete, and McGuffin. IEEE TVCG (Proc. InfoVis) 13(6):1302-1309, 2007.]



[Points of view: Networks. Gehlenborg and Wong. Nature Methods 9:115.]

Connection vs. adjacency comparison

- adjacency matrix strengths
  - predictability, scalability, supports reordering
  - some topology tasks trainable
- node-link diagram strengths
  - topology understanding, path tracing
  - intuitive, no training needed
- empirical study
  - node-link best for small networks
  - matrix best for large networks
    - if tasks don't involve topological structure!

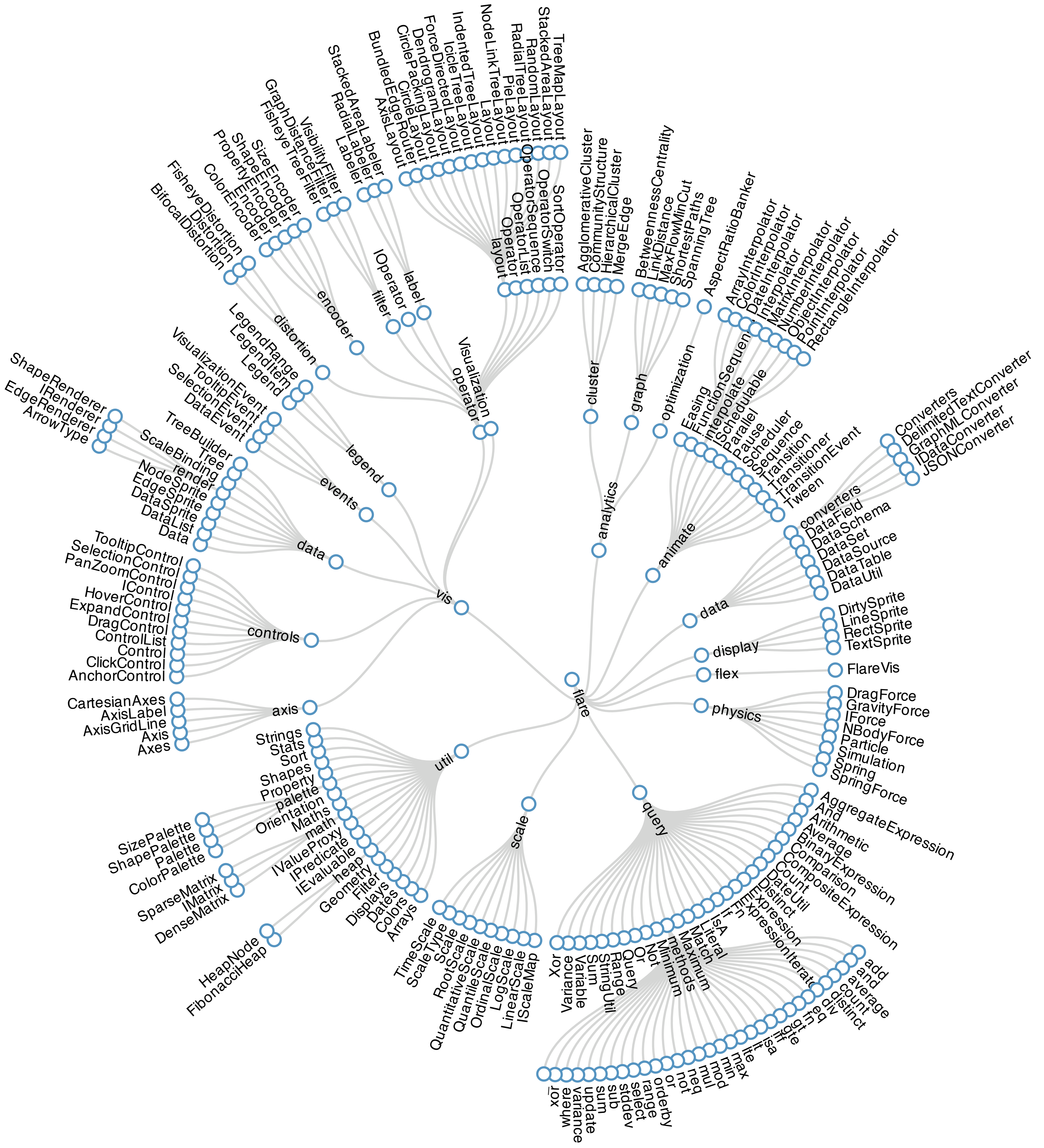


http://www.michaelmcguffin.com/courses/vis/patternsInAdjacencyMatrix.png

[On the readability of graphs using node-link and matrix-based representations: a controlled experiment and statistical analysis. Ghoniem, Fekete, and Castagliola. Information Visualization 4:2 (2005), 114–135.]

Idiom: **radial node-link tree**

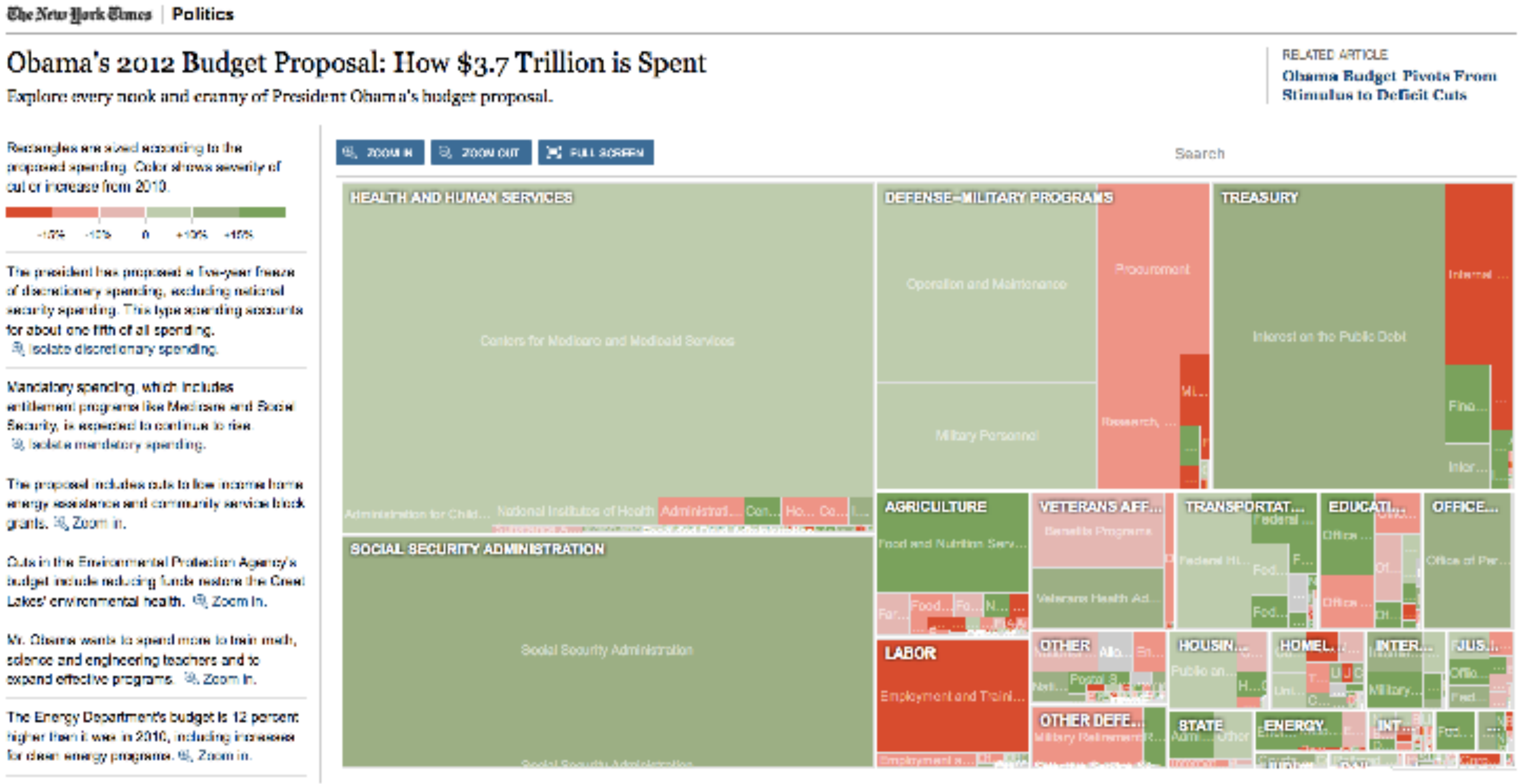
- data
  - tree
- encoding
  - link connection marks
  - point node marks
  - radial axis orientation
    - angular proximity: siblings
    - distance from center: depth in tree
- tasks
  - understanding topology, following paths
- scalability
  - 1K - 10K nodes



http://mbostock.github.com/d3/ex/tree.html

Idiom: **treemap**

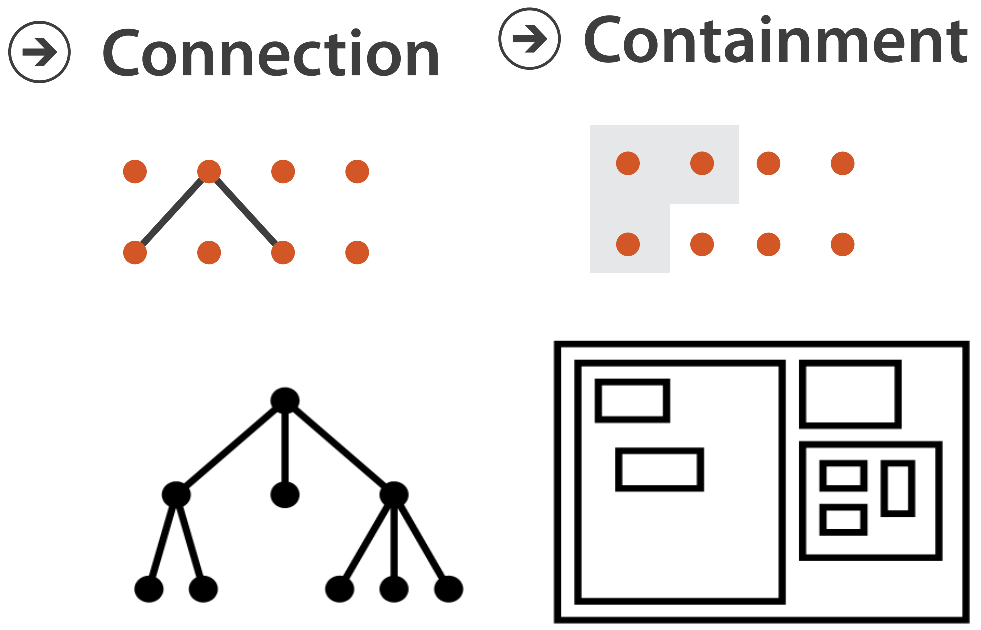
- data
  - tree
  - 1 quant attrib at leaf nodes
- encoding
  - area containment marks for hierarchical structure
  - rectilinear orientation
  - size encodes quant attrib
- tasks
  - query attribute at leaf nodes
- scalability
  - 1M leaf nodes

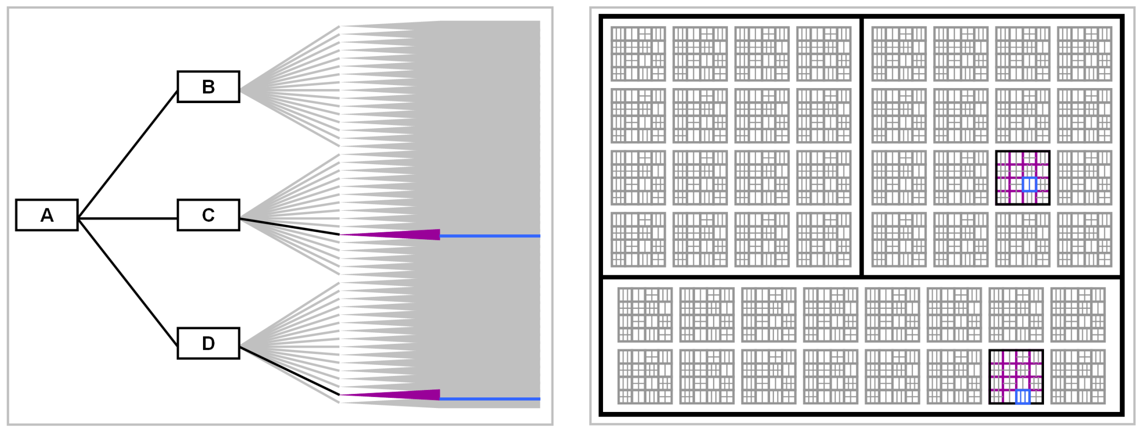


http://www.nytimes.com/packages/html/newsgraphics/2011/0119-budget/index.html

Link marks: Connection and containment

- marks as links (vs. nodes)
  - common case in network drawing
  - 1D case: connection
    - ex: all node-link diagrams
    - emphasizes topology, path tracing
    - networks and trees
  - 2D case: containment
    - ex: all treemap variants
    - emphasizes attribute values at leaves (size coding)
    - only trees



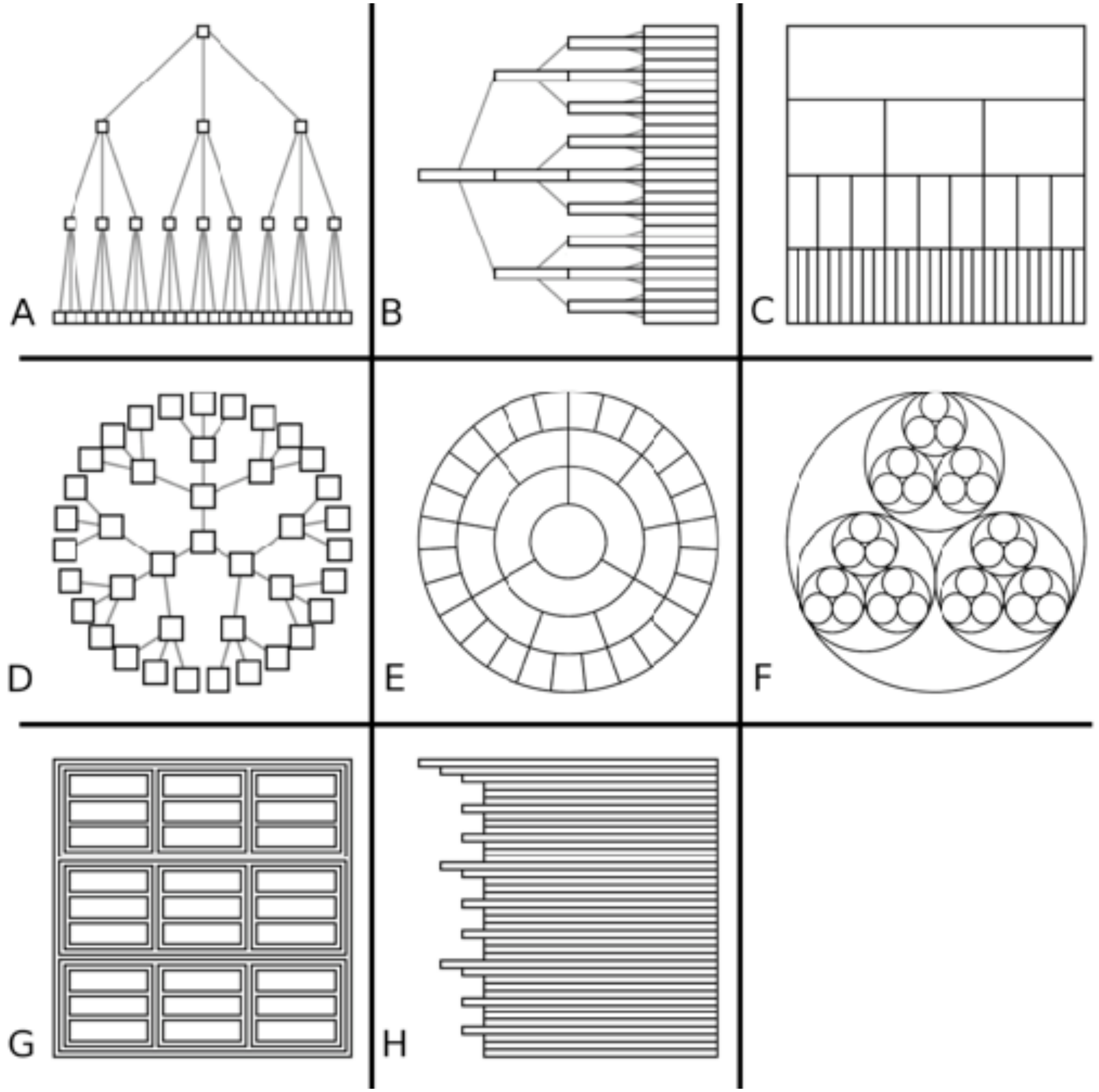


Node–Link Diagram **Treemap**

[Elastic Hierarchies: Combining Treemaps and Node-Link Diagrams. Dong, McGuffin, and Chignell. Proc. InfoVis 2005, p. 57-64.]

Tree drawing idioms comparison

- data shown
  - link relationships
  - tree depth
  - sibling order
- design choices
  - connection vs containment link marks
  - rectilinear vs radial layout
  - spatial position channels
- considerations
  - redundant? arbitrary?
  - information density?
    - avoid wasting space

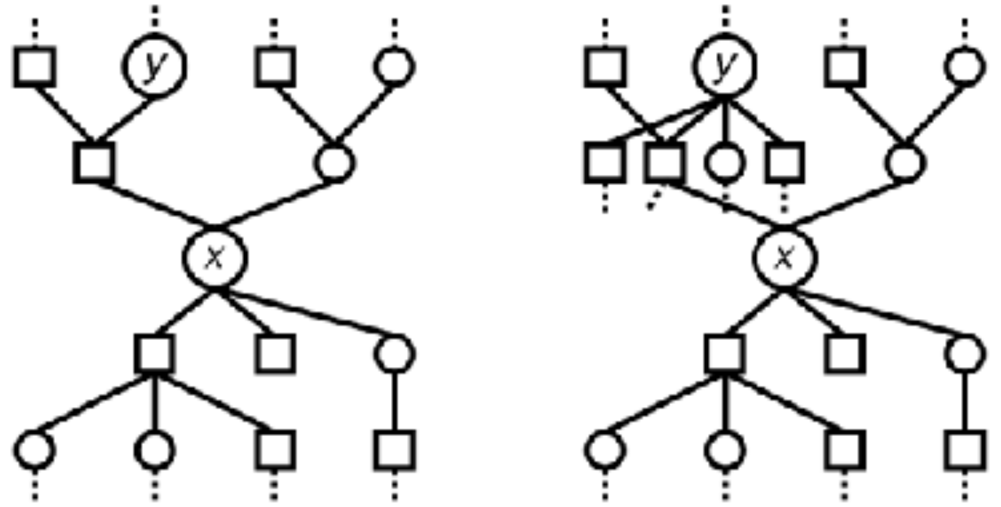


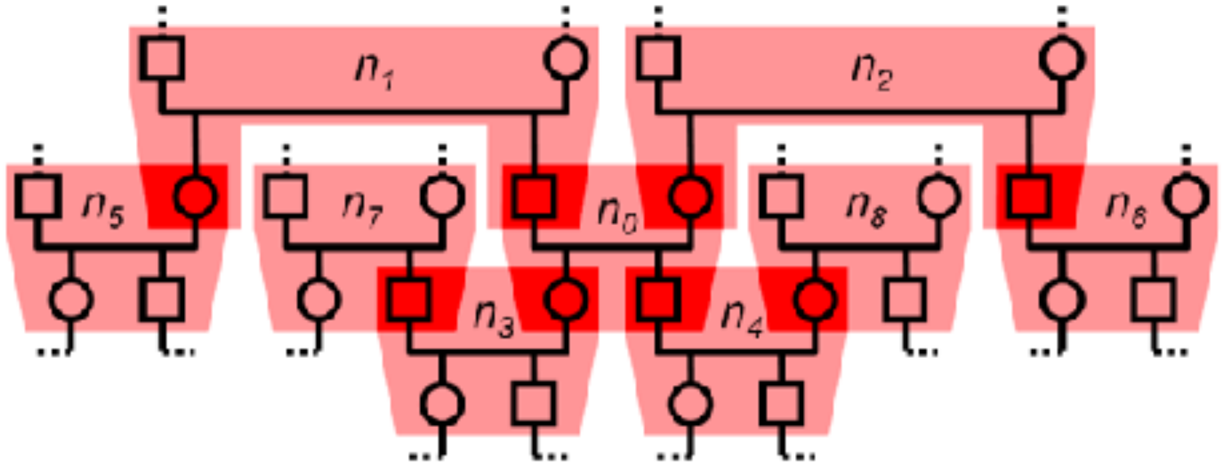
[Quantifying the Space-Efficiency of 2D Graphical Representations of Trees. McGuffin and Robert. Information Visualization 9:2 (2010), 115–140.]

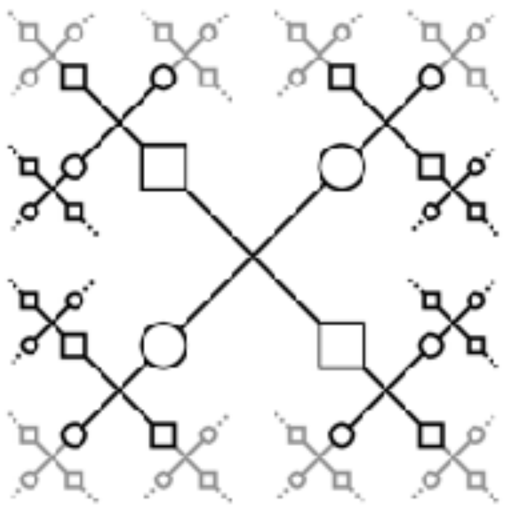
Paper: Genealogical Graphs

Genealogical graphs: Technique paper

- family tree is a misnomer
  - single person has tree of ancestors, tree of descendants
  - pedigree collapse inevitable
    - diamond in ancestor graph
- crowding problem
  - exponential
- fractal layout
  - poor info density
  - no spatial ordering for generations



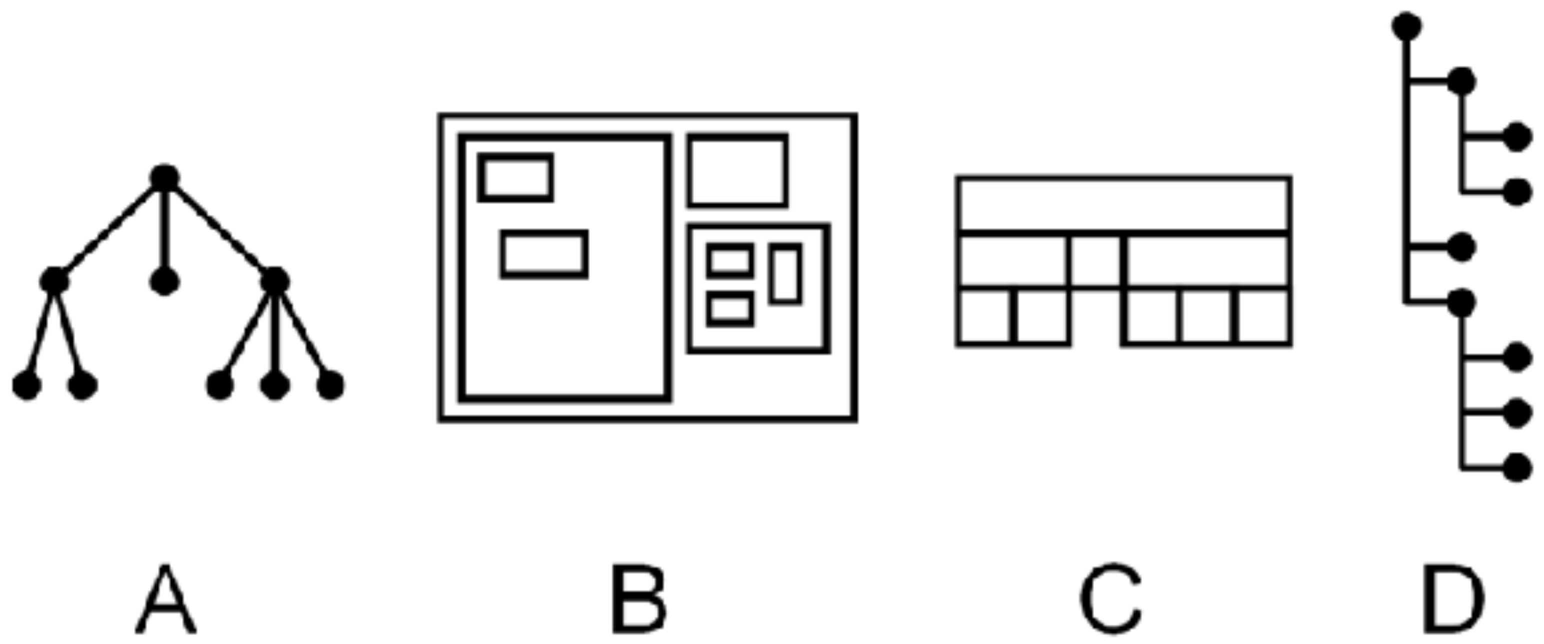




[Fig 2, 6, 7. Interactive Visualization of Genealogical Graphs. Michael J. McGuffin, Ravin Balakrishnan. Proc. InfoVis 2005, pp 17-24.]

Layouts

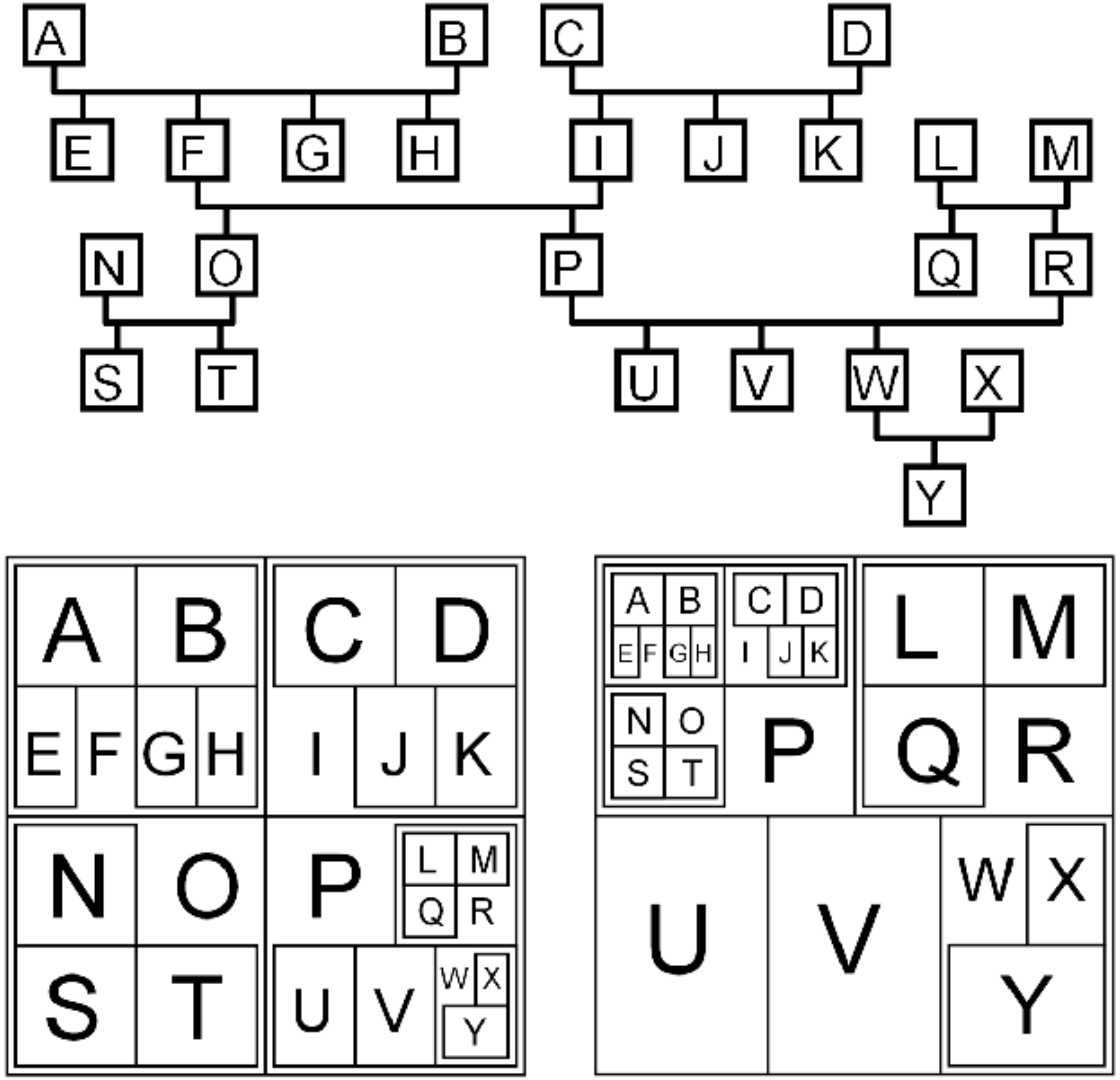
- rooted trees: standard layouts
  - –connection
  - –containment
  - –adjacent aligned position
  - –indented position



[Fig 8. Interactive Visualization of Genealogical Graphs. Michael J. McGuffin, Ravin Balakrishnan. Proc. InfoVis 2005, pp 17-24.]

Layouts

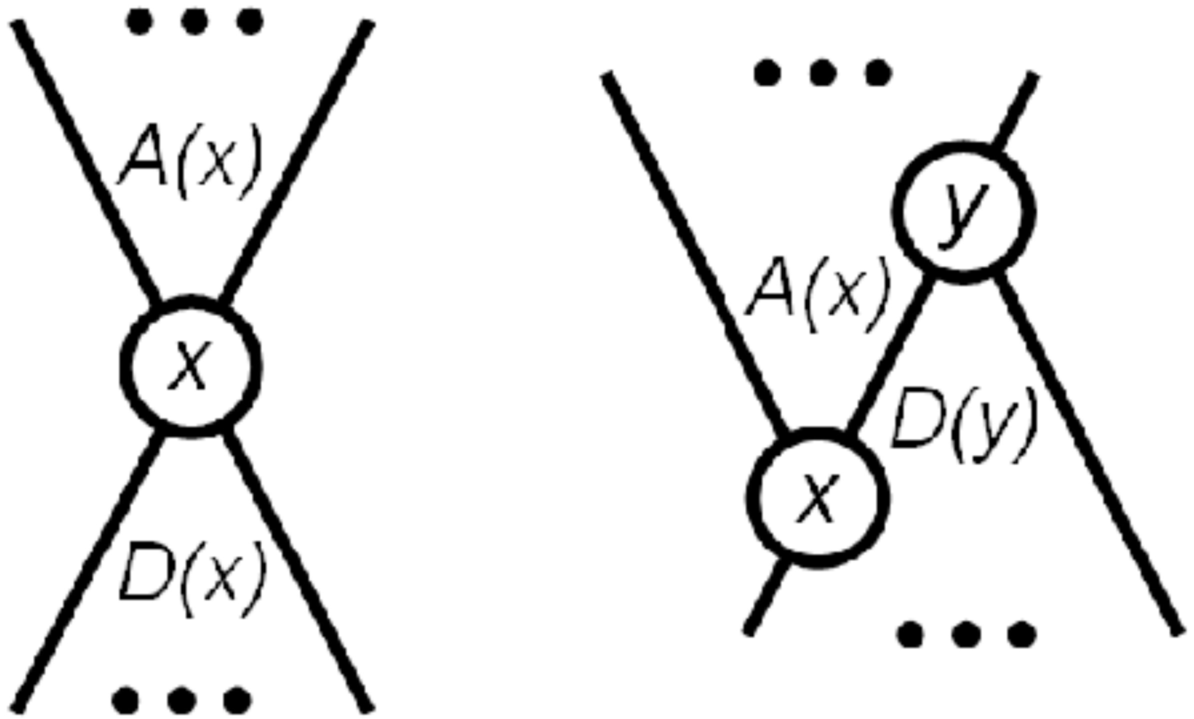
- free trees
  - no root
- adapting rooted methods
  - temporary root for given focus
  - containment (nested)

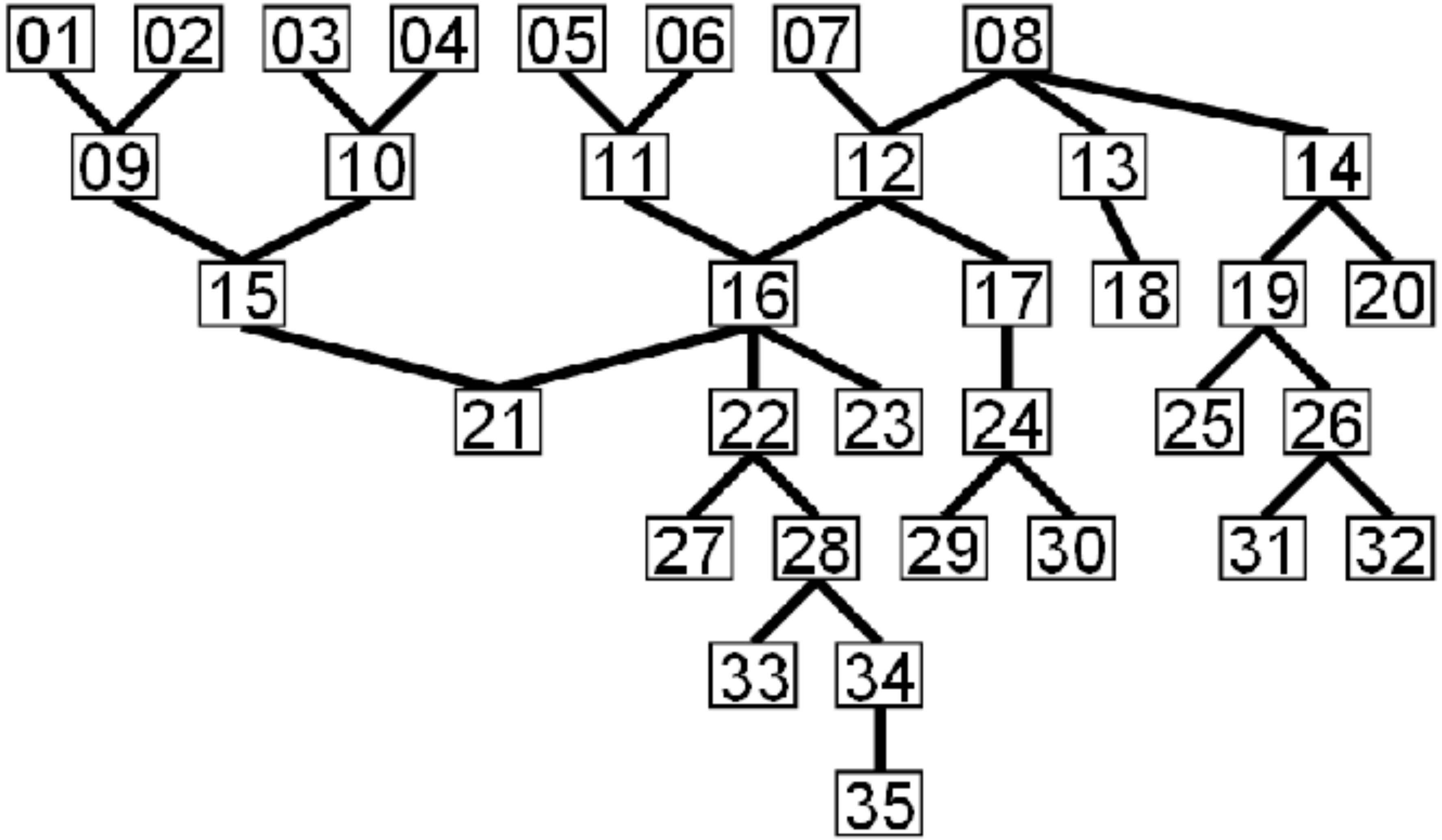


[Fig 9. Interactive Visualization of Genealogical Graphs. Michael J. McGuffin, Ravin Balakrishnan. Proc. InfoVis 2005, pp 17-24.]

Dual trees abstraction

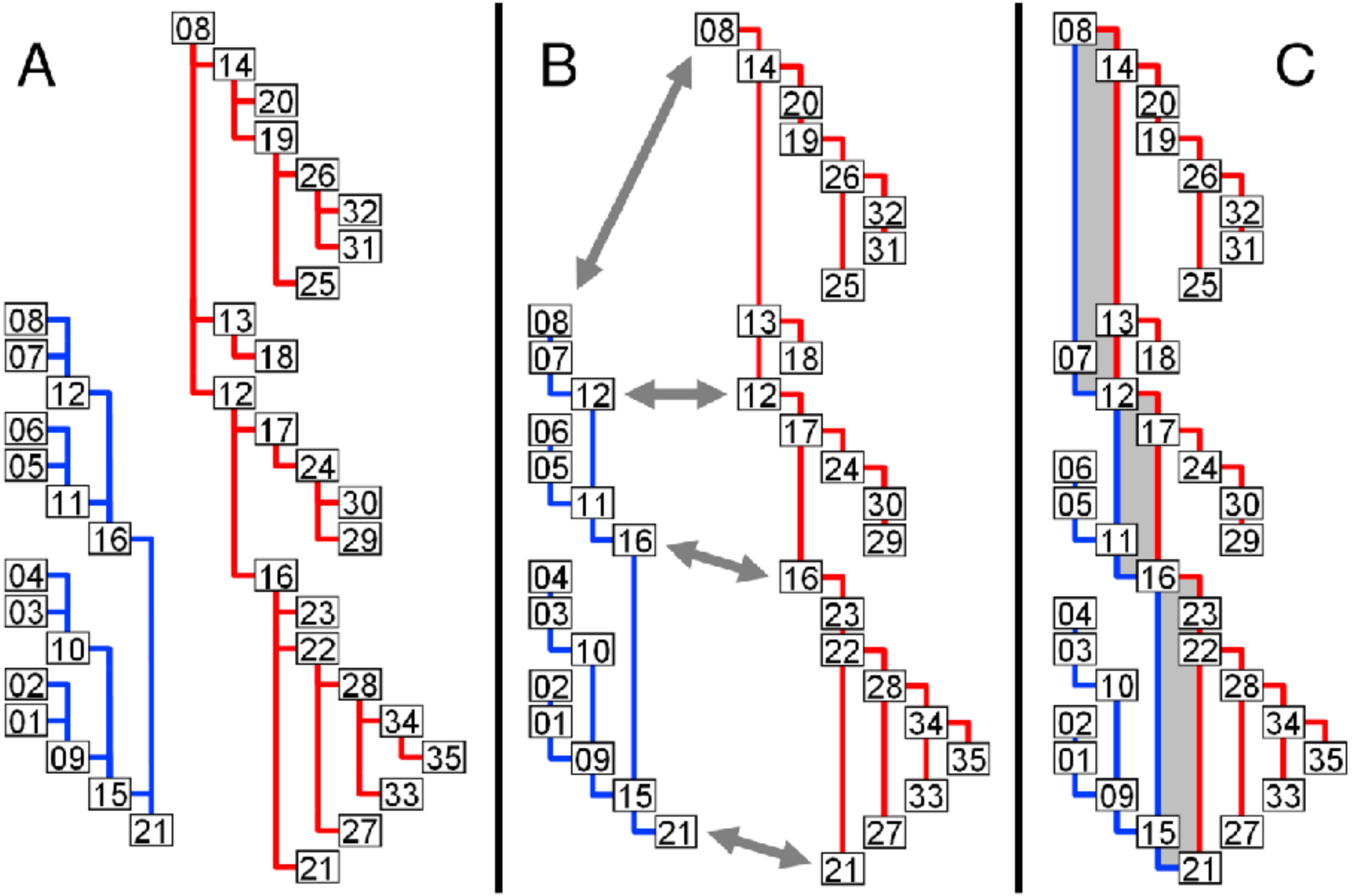
- explore canonical subsets and combinations, easy to interpret, scales well
- no crossings, nodes ordered by generation
- doubly rooted: x leftmost descend, y rightmost ancestor
  – offset roots from hourglass diagram





[Fig 10. Interactive Visualization of Genealogical Graphs. Michael J. McGuffin, Ravin Balakrishnan. Proc. InfoVis 2005, pp 17-24.]

Indented, flipped, combined

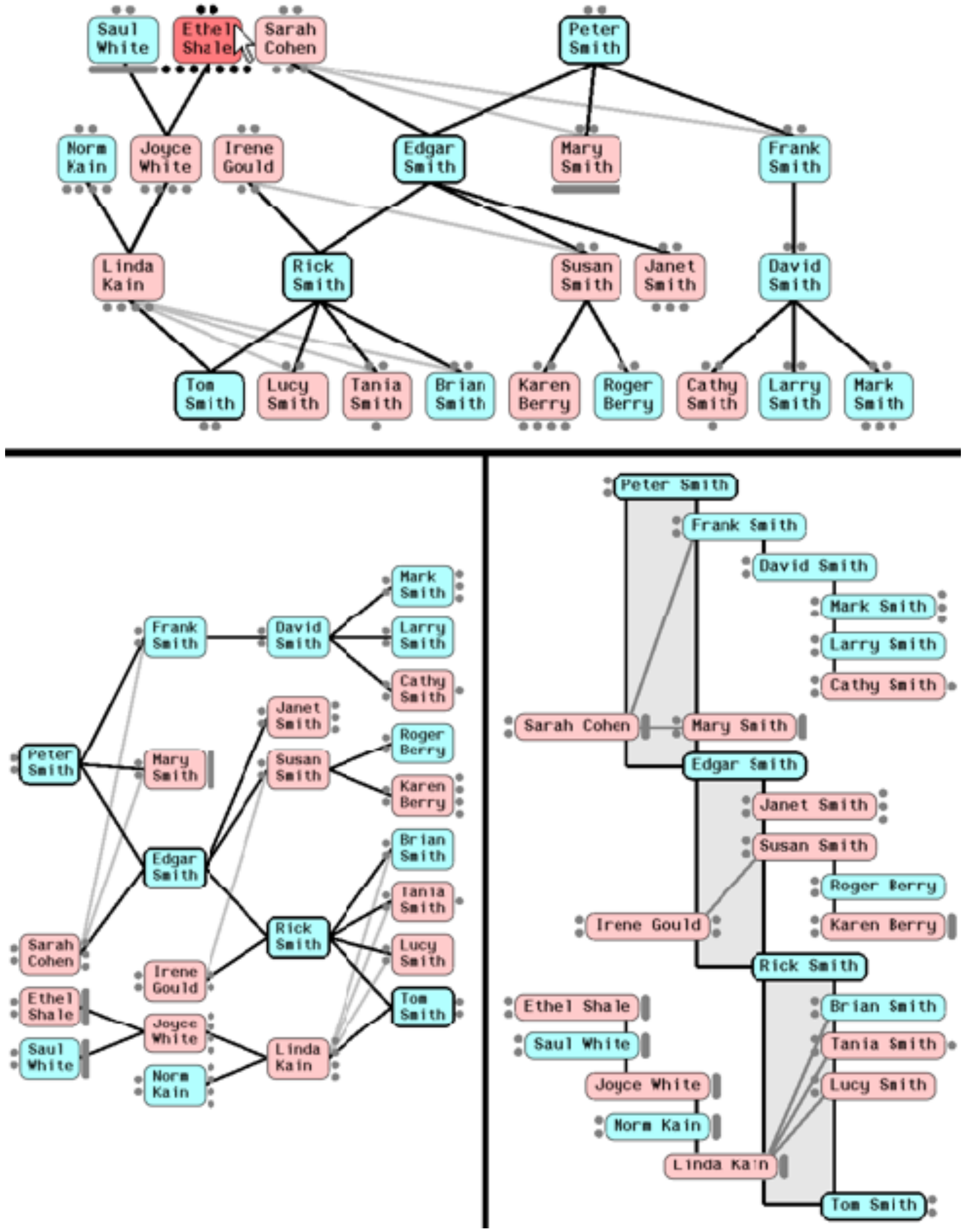


[Fig 11. Interactive Visualization of Genealogical Graphs. Michael J. McGuffin, Ravin Balakrishnan. Proc. InfoVis 2005, pp 17-24.]

Another example

- vertical connection
- horizontal connection
- indented

- upcoming chapters
  - –layering
  - –aggregation



[Fig 13. Interactive Visualization of Genealogical Graphs. Michael J. McGuffin, Ravin Balakrishnan. Proc. InfoVis 2005, pp 17-24.]

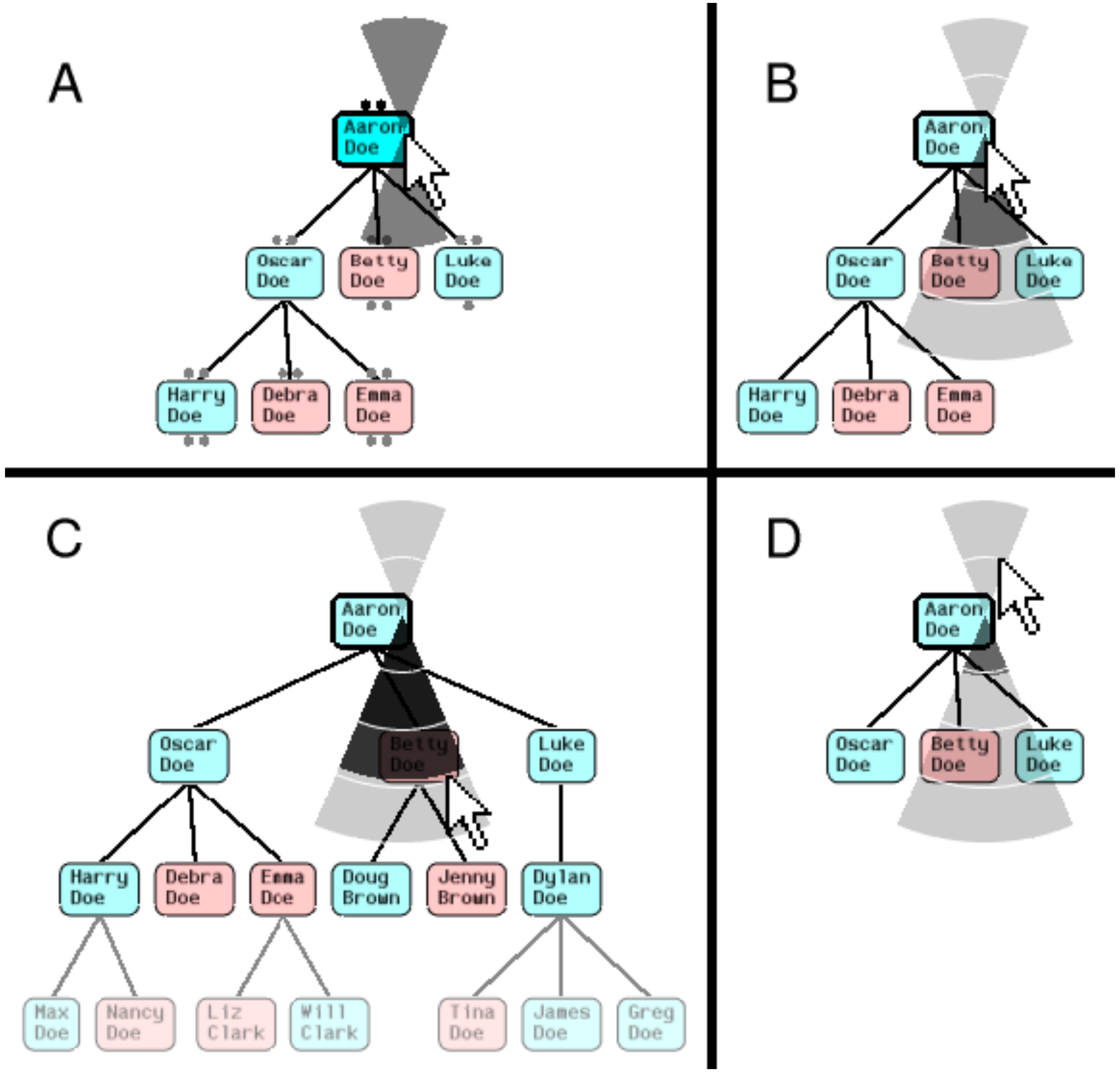
Interaction as fundamental to design

- navigation
  - topological navigation via collapse/expand on selection
    - parents, children
    - expand can trigger rotation
      - collapsing others
      - layout driven by navigation
  - geometric zoom/pan
  - constrained navigation: automatic camera framing
- animated transitions
  - 3 phases: fade out, move, fade in
- mouseover hover
  - preview dots: expand if collapsed

[Fig 14. Interactive Visualization of Genealogical Graphs. Michael J. McGuffin, Ravin Balakrishnan. Proc. InfoVis 2005, pp 17-24.]

Custom widget

- popup marking menu
  - flick up or down, ballistic
  - subtree drag-out widget



[Fig 14. Interactive Visualization of Genealogical Graphs. Michael J. McGuffin, Ravin Balakrishnan. Proc. InfoVis 2005, pp 17-24.]

Paper: ABySS-Explorer

ABySS-Explorer: Design study

- reconstructing genome with ABySS algorithm (Assembly By Short Sequences)
- domain task
  - go from short subsequences to ***contigs***, long contiguous sequences
  - extensive automatic support, but still human in the loop for visual inspection and manual editing
  - ambiguities, like repetitions longer than read length
- data, domain:abstract
  - millions of reads of 25-100 nucleotides (nt): strings
  - read coverage, proxy for quality: quant attrib
  - read pairing distances, proxy for size distribution: quant

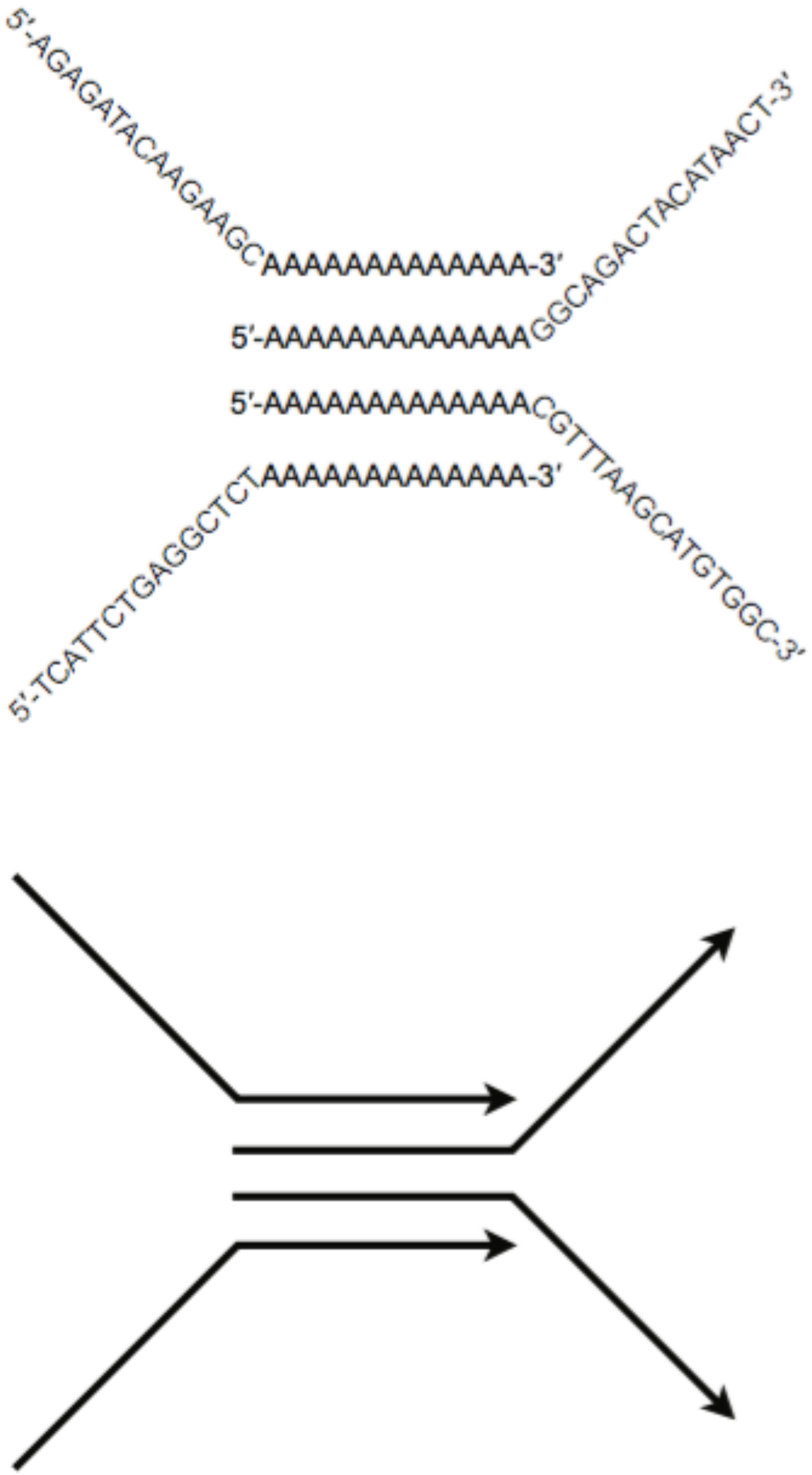


Fig 2. ABySS-Explorer: visualizing genome sequence assemblies. Nielsen, Jackman, Birol, Jones. TVCG 15(6):881-8, 2009 (Proc. InfoVis 2009).

Contigs: abstraction as derived network data

- derived data: de Bruijn graph/network
  - directed network, compact representation of sequence overlaps
  - node: contig
  - edge: overlap of k − 1 nt between two contigs
  - good for computing, bad for reasoning about sequence space
- derived data: dual de Bruijn graph
  - node: points of contig overlap
  - edge: contig
  - better match for arrow diagrams used in hand drawn sketches
- base layout: force-directed

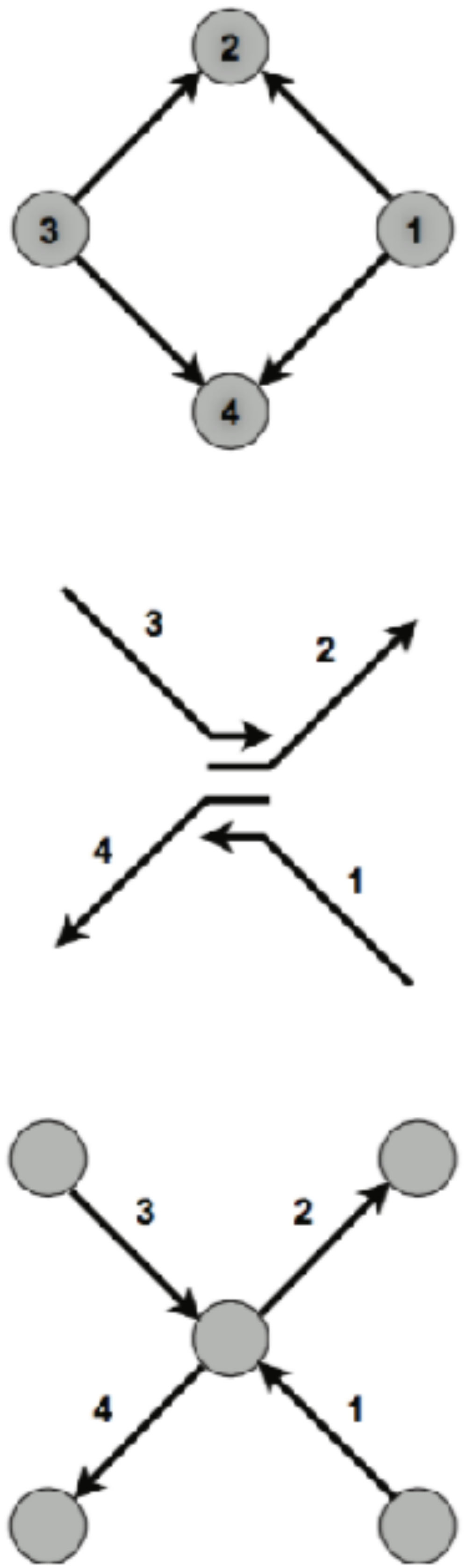


Fig 3. ABySS-Explorer: visualizing genome sequence assemblies. Nielsen, Jackman, Birol, Jones. TVCG 15(6):881-8, 2009 (Proc. InfoVis 2009).

DNA as double stranded: idiom for encoding & interaction

- rejected option: 2 nodes per contig
  - excess clutter if one for each direction
  - choice at data abstraction level
- encoding & interaction idiom: *polar* node
  - encoding: upper vs lower attachment point
    - redundant with arc direction
      - large-scale visibility, without need to zoom
    - arbitrary but consistent
  - interaction: click to reverse direction
    - switches polarity of vertex connections
    - changes sign of label

Fig 4. ABySS-Explorer: visualizing genome sequence assemblies. Nielsen, Jackman, Birol, Jones. TVCG 15(6):881-8, 2009 (Proc. InfoVis 2009).

Contig length: encoding

- rejected option: scale edge lengths by sequence lengths
  - short contigs are important sources of ambiguity, would be hard to distinguish
  - task guidance: only low-res judgements needed, relatively long or short
- encoding idiom: wave pattern
  - oscillation shows fixed number, shapes distinguishable
  - min amplitude at connections so edges visible
  - orientation with max amplitude asymmetric wrt start
    - rejected initial option: max in middle
    - rejected options:
      - color (keep for other attribute)
      - half-lines
      - curvature (used for polar nodes)
    - aligned with empirical guidance for tapered edges

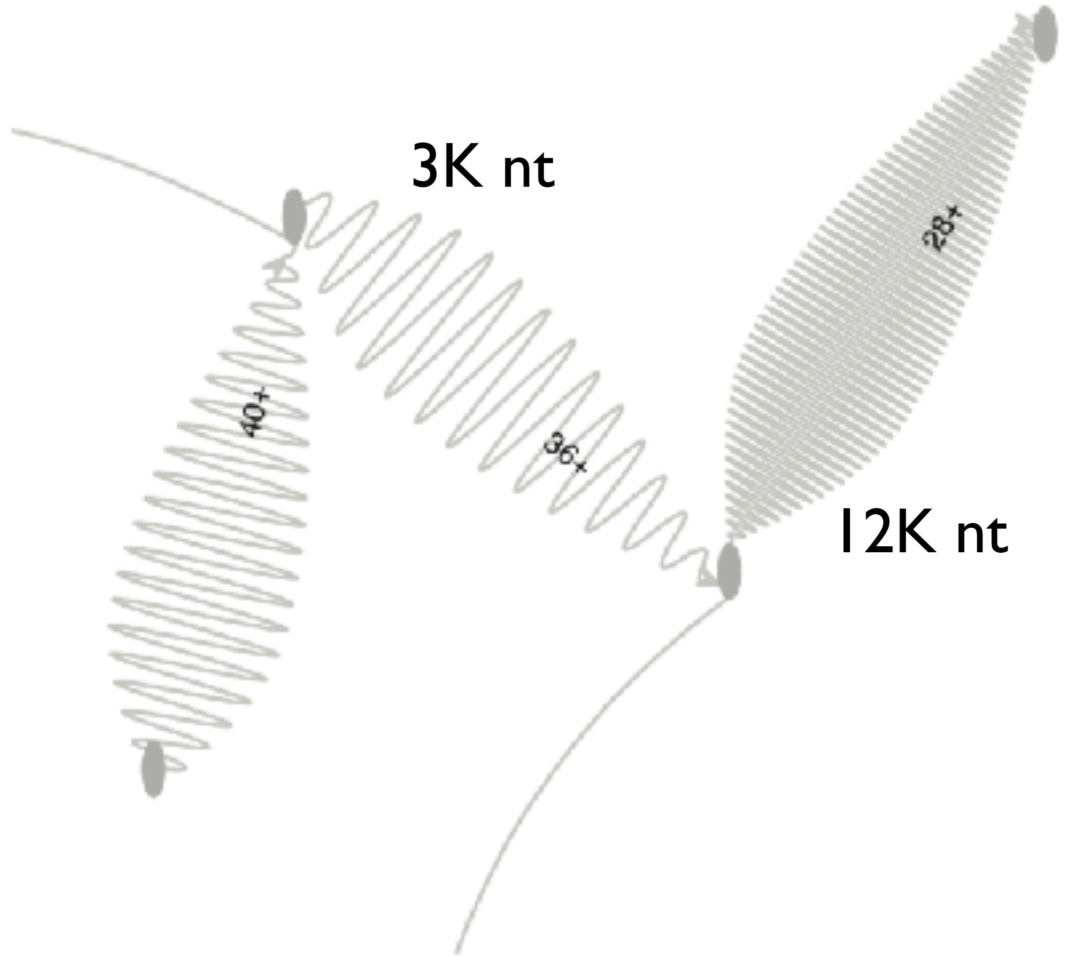


Fig 5. ABySS-Explorer: visualizing genome sequence assemblies. Nielsen, Jackman, Birol, Jones. TVCG 15(6):881-8, 2009 (Proc. InfoVis 2009).

Contig coverage: encoding

- rejected options: luminance/lightness
  - not distinguishable given denseness variation from wave shapes
  - also problematic with desire for separable color/hue encoding
- chosen: line thickness
  - not distinguishable for extremely long contigs
  - can address by adjusting oscillation frequency to suitable size

Read pairs: encoding

- data:
  - distance estimate
  - orientation
- encoding:
  - dashed line (shape channel for line mark)
    - implying inferred vs observed sequences
  - color for both dashed line and contig leaf
  - [same length as for contigs]
  - rejected initial option: line color alone
    - too ambiguous
  - interaction to fully resolve remaining ambiguity
  - or color by unambiguous paths in grey

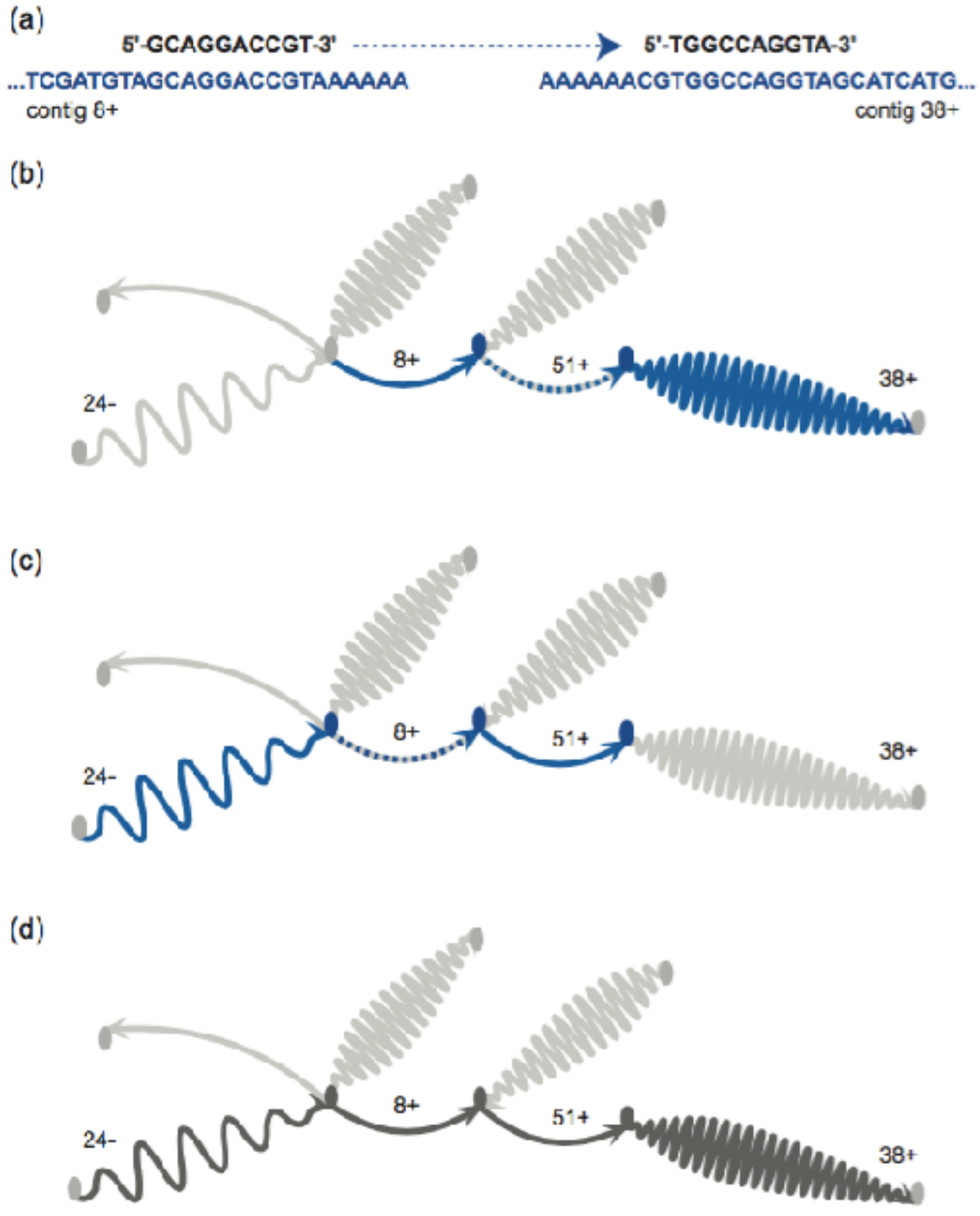
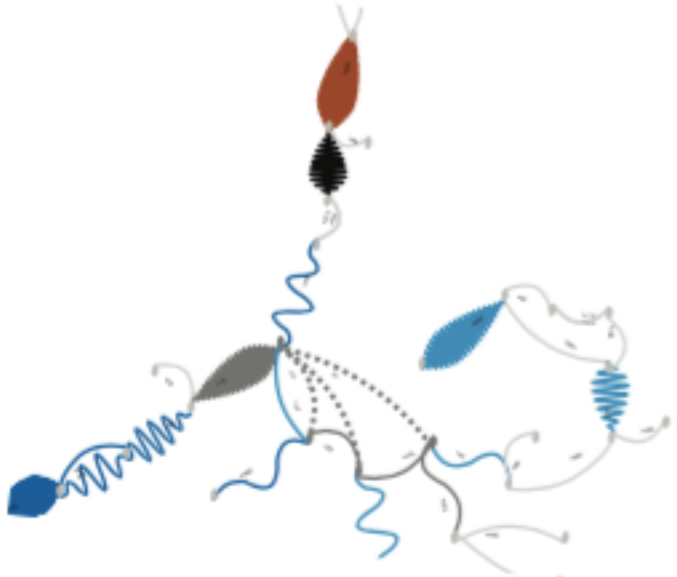


Fig 6. ABySS-Explorer: visualizing genome sequence assemblies. Nielsen, Jackman, Birol, Jones. TVCG 15(6):881-8, 2009 (Proc. InfoVis 2009).

Displaying meta-data

- reserve color for additional attributes
- ex: color to compare reference human to lymphoma genome
  - inconsistencies visible as interconnections between different colors
  - inversion breakpoint visible
  - interaction to check if error in metadata from experiments vs assembly
    - read pair info supports metadata
      - speedup claim vs prev work



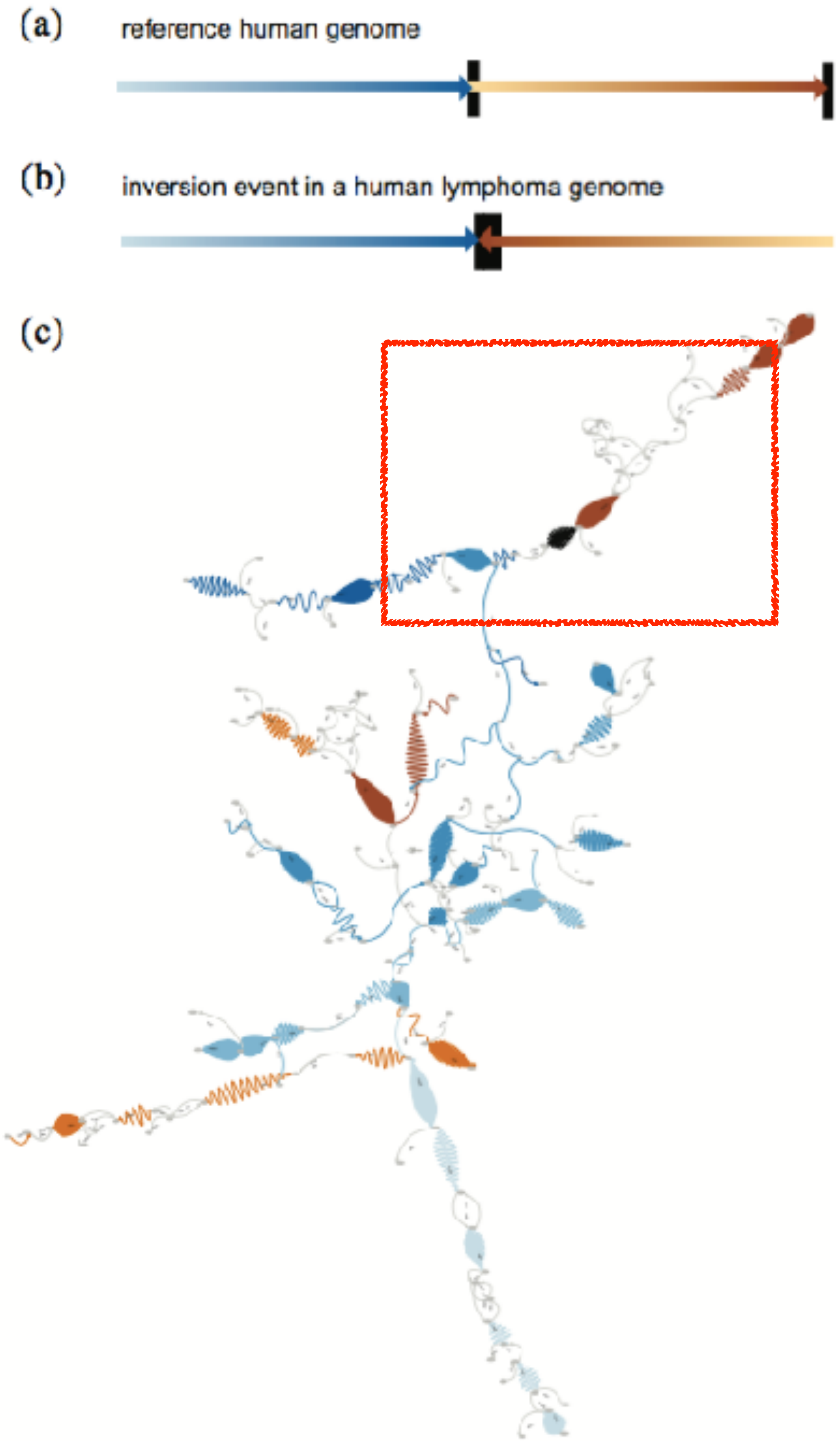


Fig 10. ABySS-Explorer: visualizing genome sequence assemblies. Nielsen, Jackman, Birol, Jones. TVCG 15(6):881-8, 2009 (Proc. InfoVis 2009).

Assembly examples

- ideal: single large contig
  - overview/gist: many small contigs remain
- interaction to resolve
  - integrate paired read highlighting on top of contig paths structure

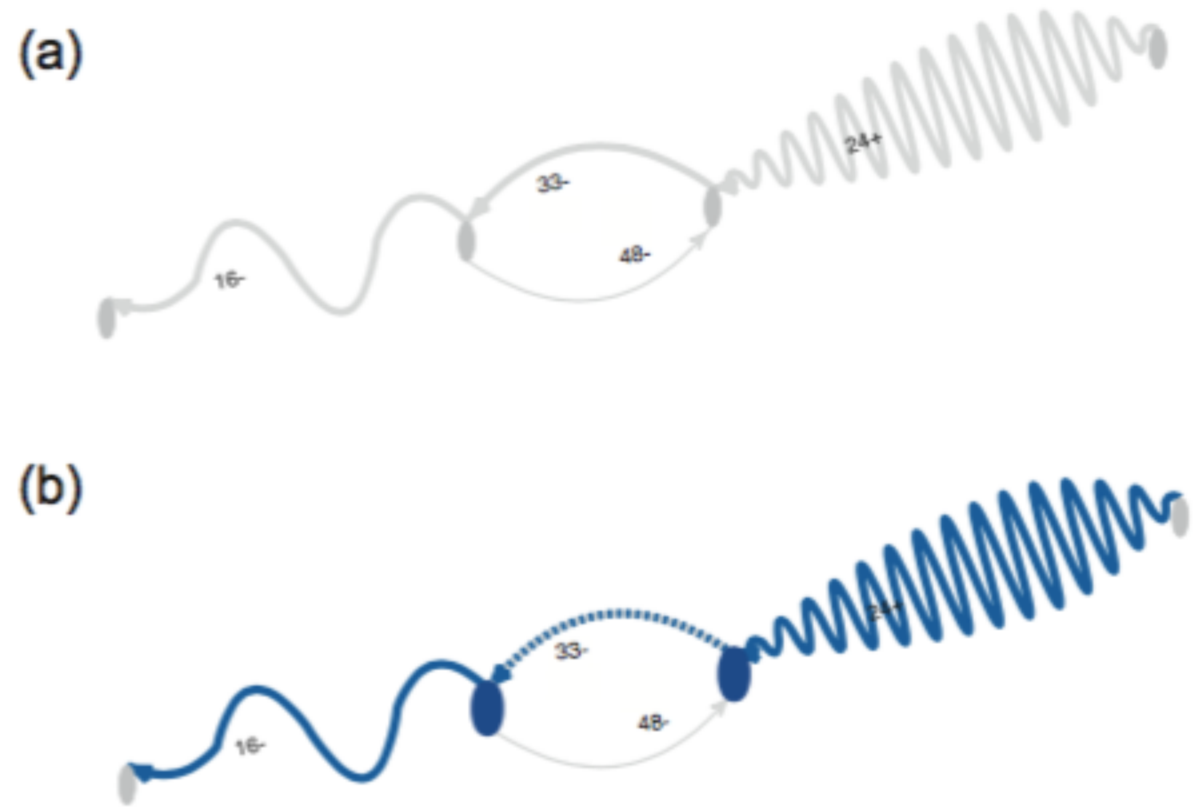


Fig 7/9. ABySS-Explorer: visualizing genome sequence assemblies. Nielsen, Jackman, Birol, Jones. TVCG 15(6):881-8, 2009 (Proc. InfoVis 2009).

Reading for next time

- VAD Chapter 11. Manipulate View
- VAD Chapter 12. Facet into Multiple Views
- paper:
  Visualization of Parameter Space for Image Analysis.
  Pretorius, Ruddle, Bray, Carpenter. TVCG 12(17):2402-2411 2011 (Proc. InfoVis 2011).
  - [type: design study]