

cs6964 | February 28 2012

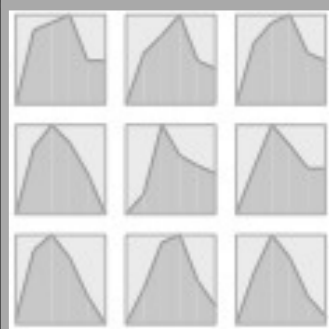
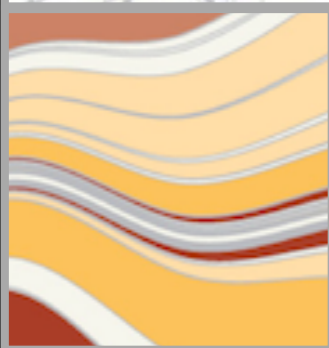
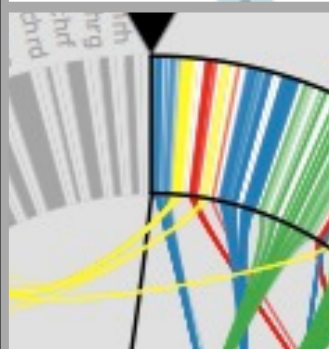
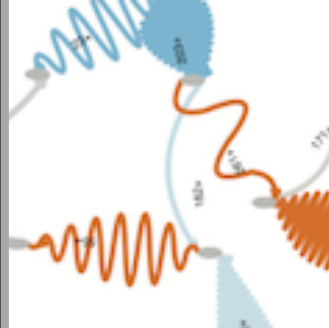
# TREES & GRAPHS

Miriah Meyer  
*University of Utah*

*slide acknowledgements:*

Hanspeter Pfister, Harvard University

Jeff Heer, Stanford University



administrivia

**feb 14-23** : proposal meetings

**march 7** : presentation topics due

**march 9** : proposals due

**march 27-april 3** : project updates

**april 5-24** : paper presentations

**may 1** : final project presentations

**may 3** : process books due

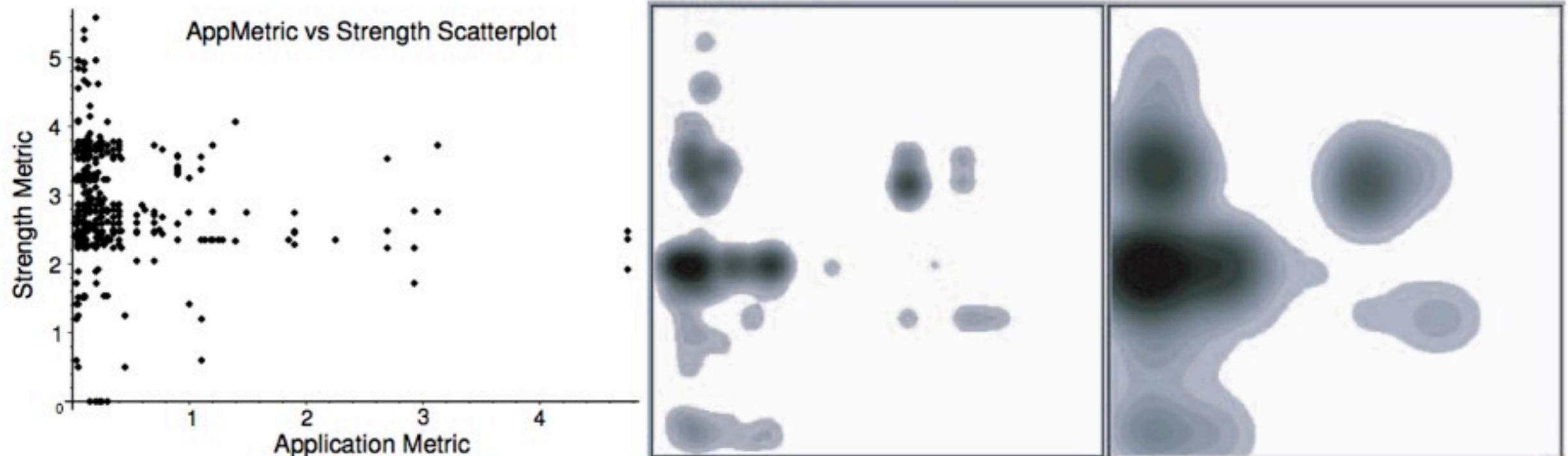
LAST TIME

# MULTISCALE SCATTERPLOTS

- **blur shows structure at multiple scales**

- convolve with Gaussian
- slider to control scale parameter interactively

- **easily selectable regions in quantized image**



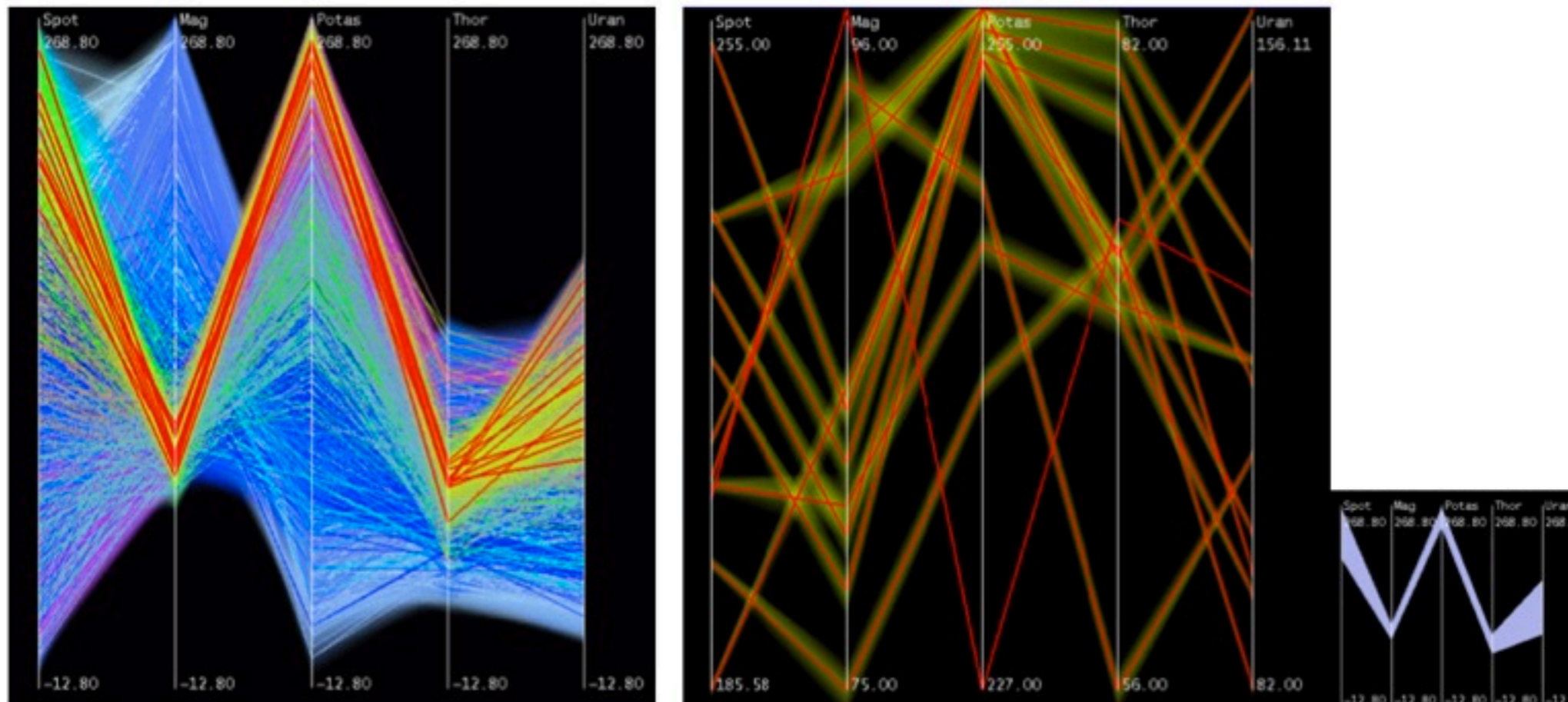
# HIERARCHICAL PARALLEL COORDINATES

- **technique-driven paper**

- no problem characterization

- **goal: scale up parallel coordinates to large datasets**

- challenge: overplotting/occlusion



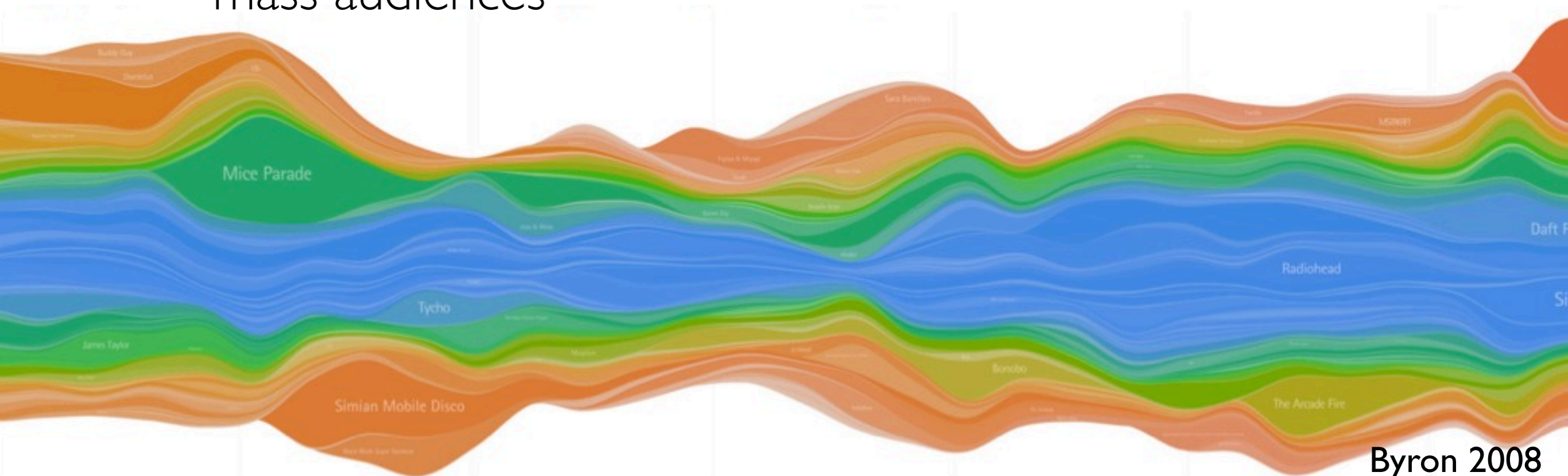
# STREAMGRAPH

## -**problem-driven paper**

- development of new technique to solve a specific problem

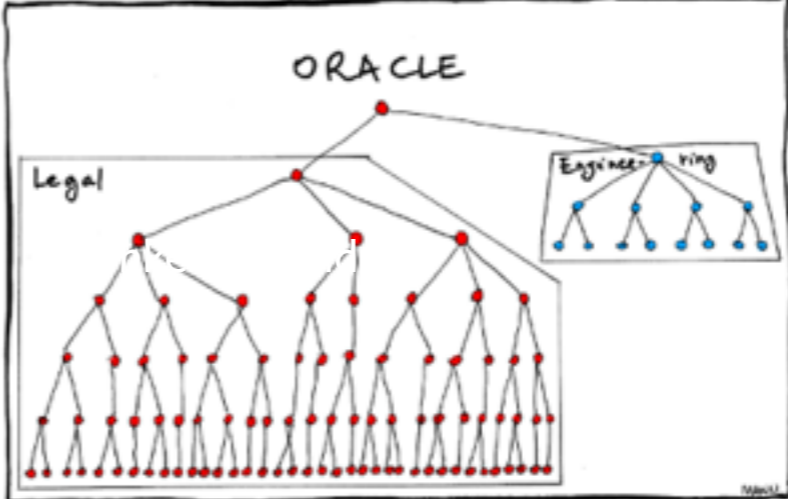
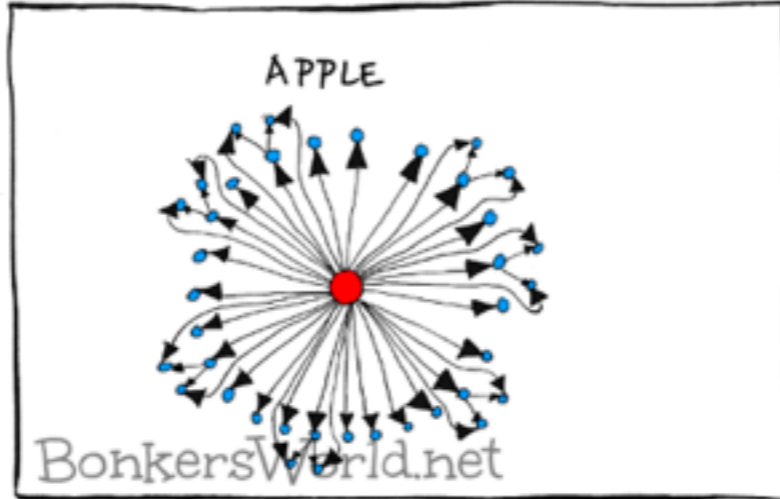
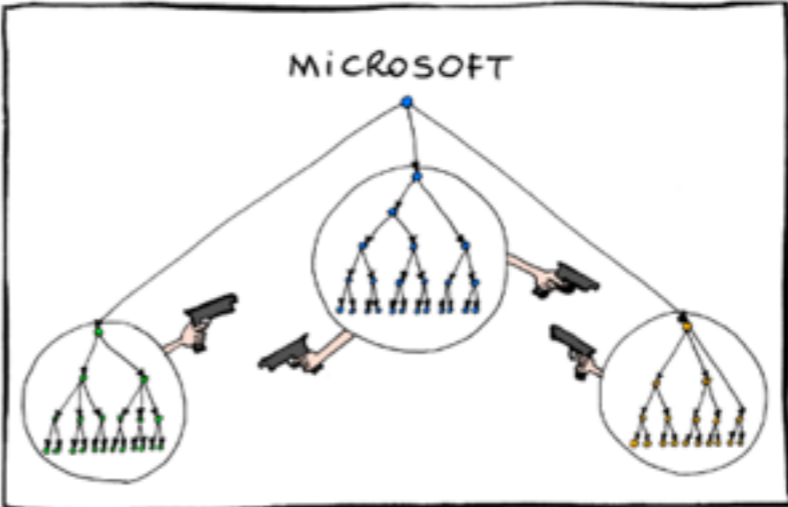
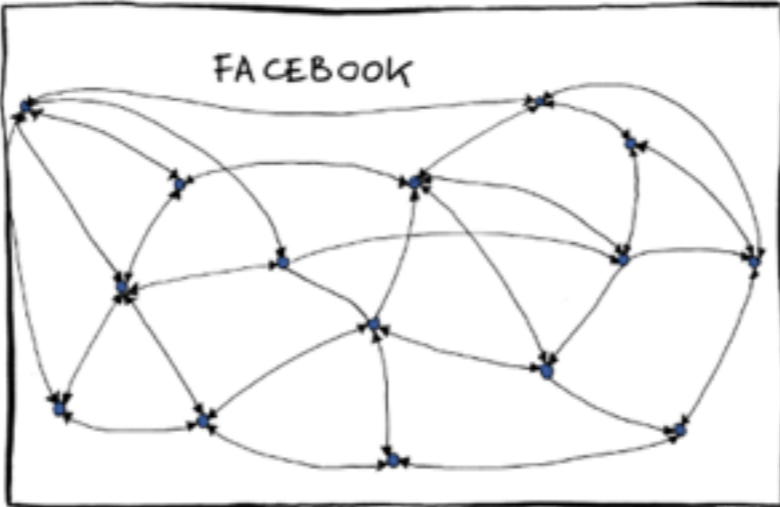
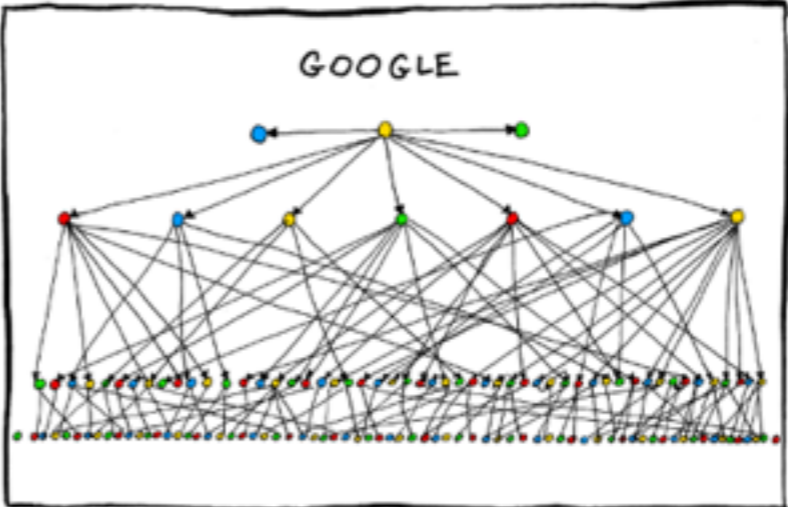
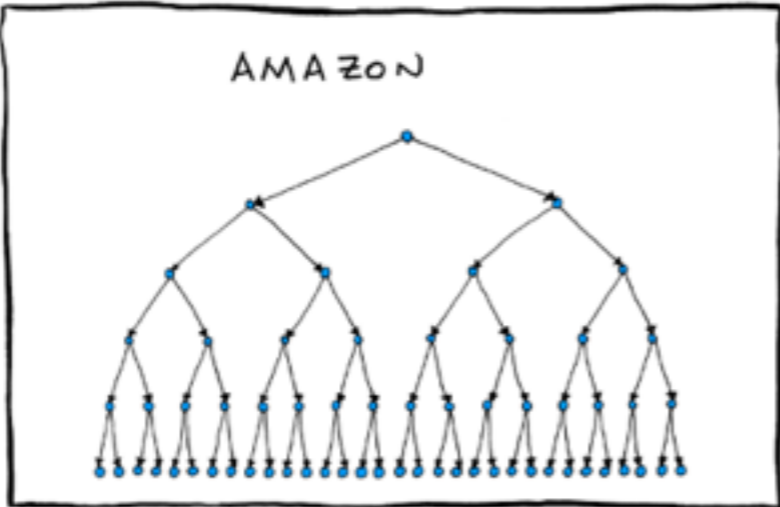
## -**challenge**

- convey a large amount of data in a way that engages mass audiences



# TREES & GRAPHS







**facebook**

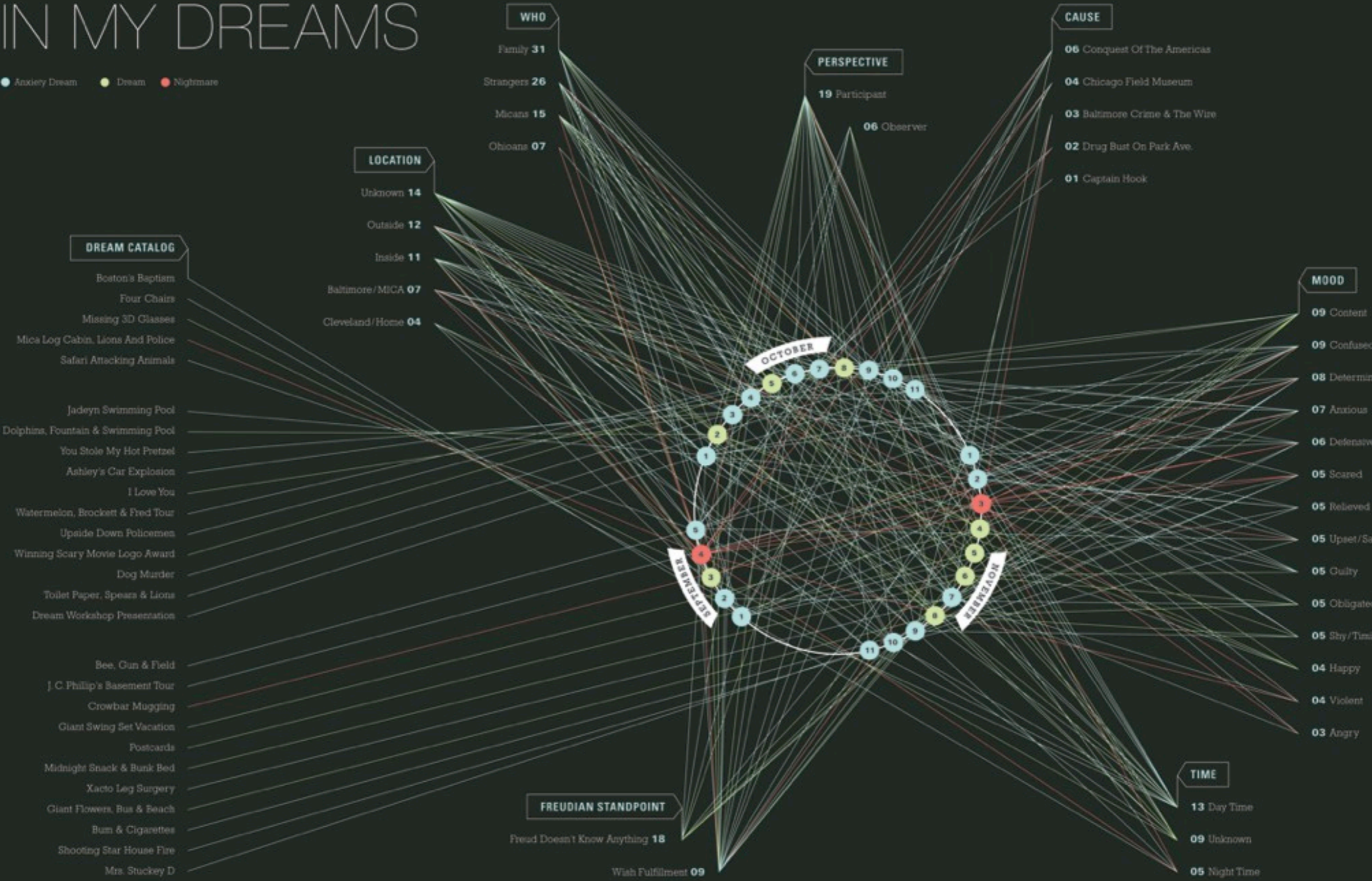


December 2010

Paul Butler

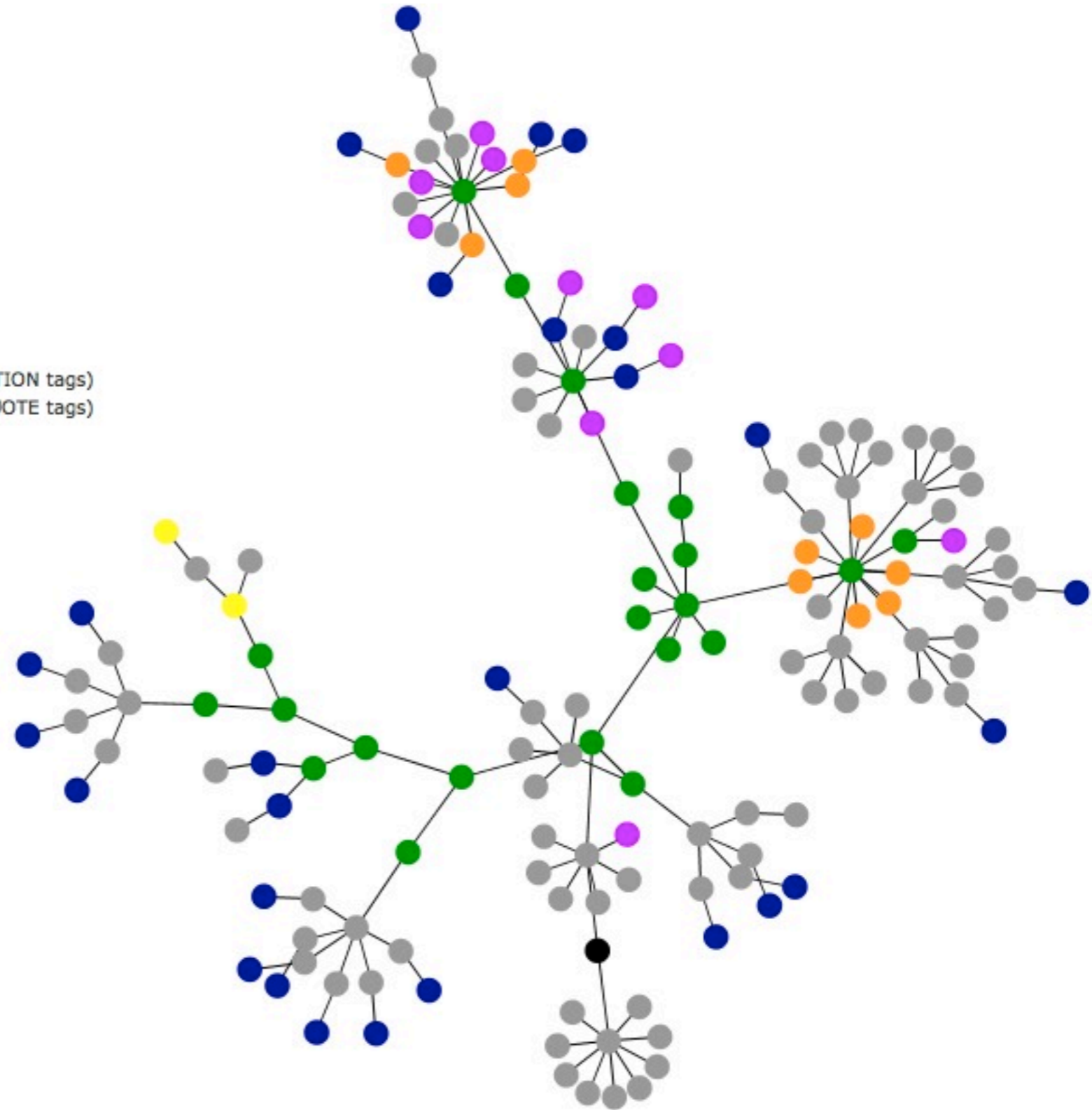
# IN MY DREAMS

● Anxiety Dream ● Dream ● Nightmare

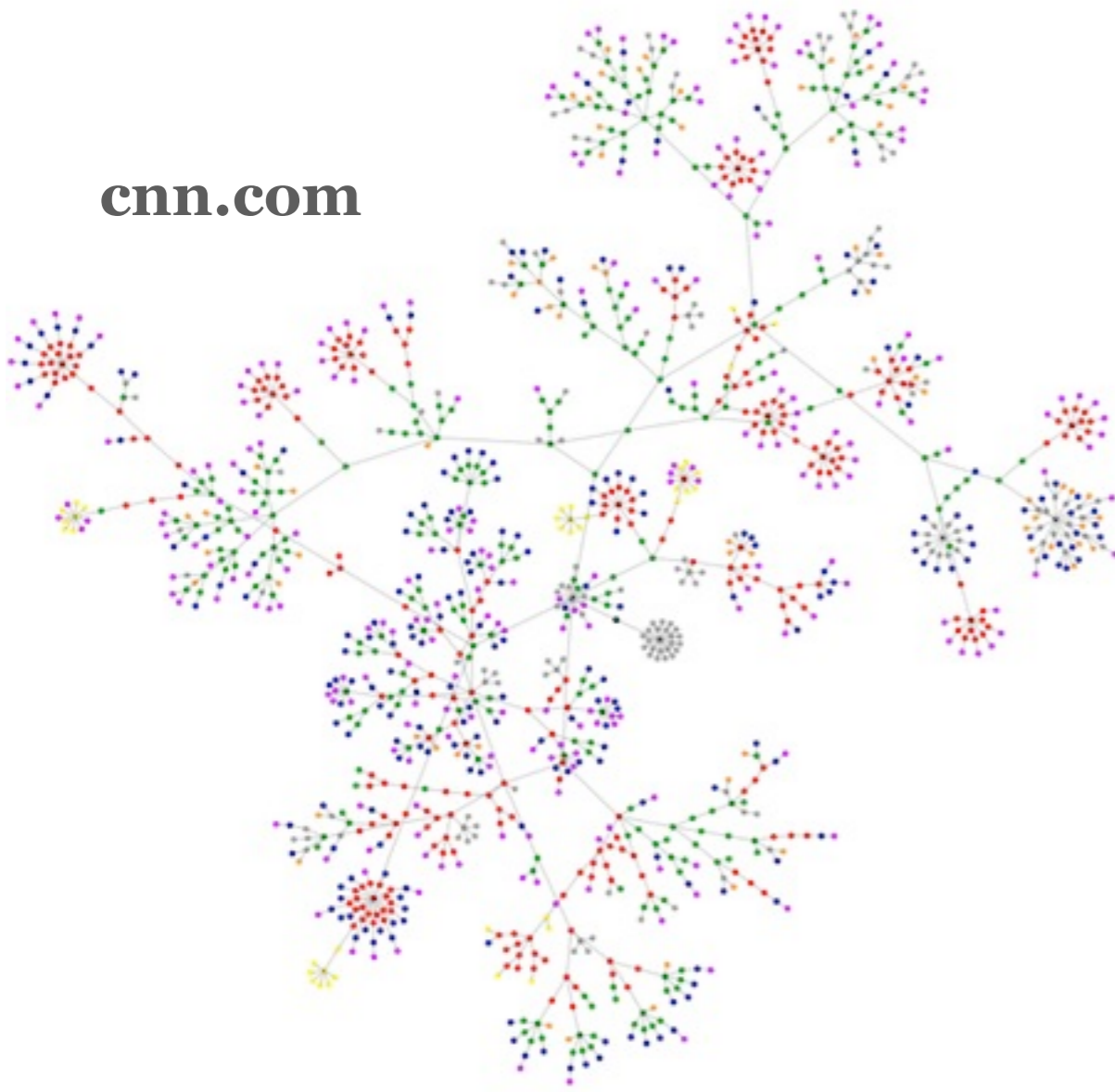


# www.cs.utah.edu

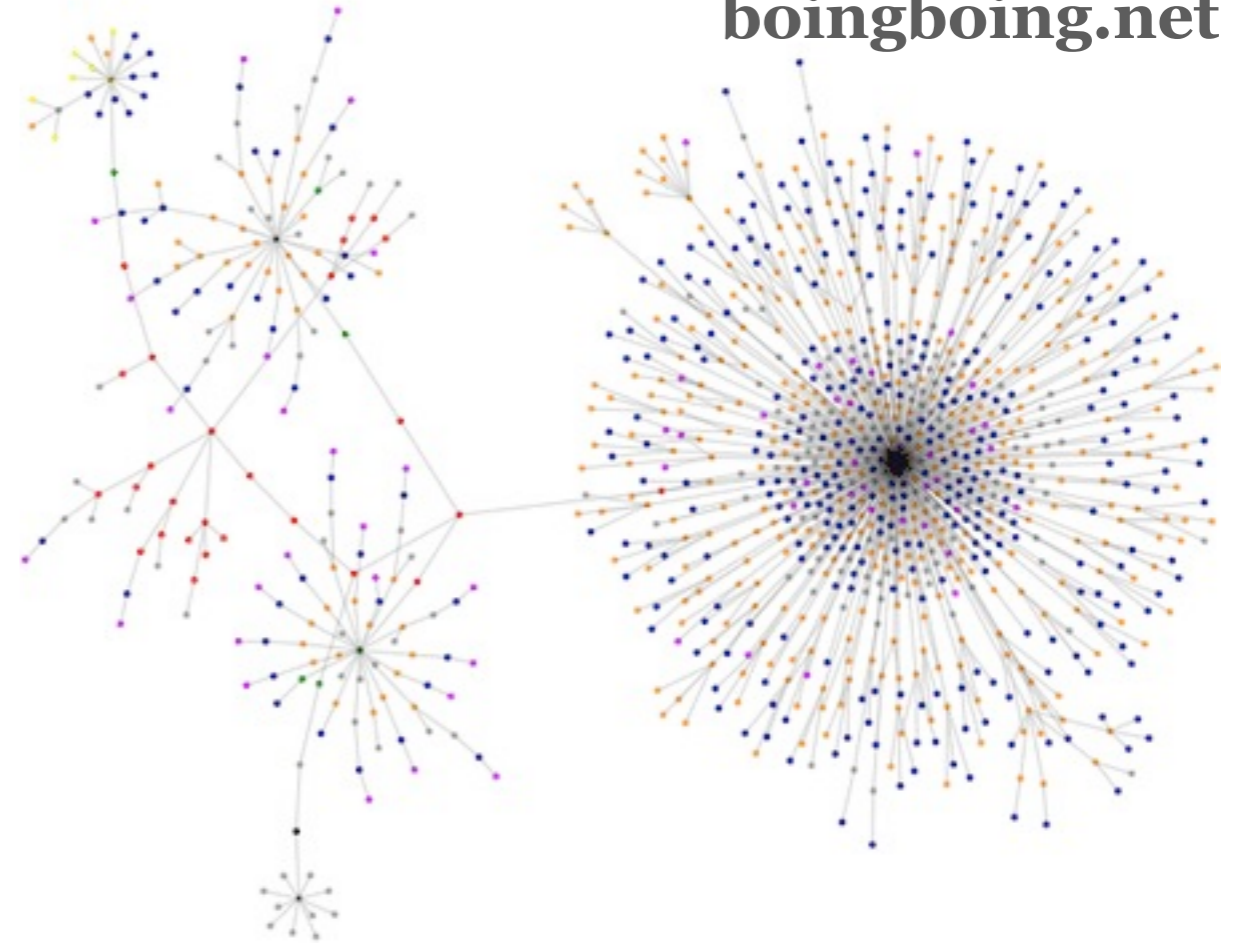
- blue:** for links (the A tag)
- red:** for tables (TABLE, TR and TD tags)
- green:** for the DIV tag
- violet:** for images (the IMG tag)
- yellow:** for forms (FORM, INPUT, TEXTAREA, SELECT and OPTION tags)
- orange:** for linebreaks and blockquotes (BR, P, and BLOCKQUOTE tags)
- black:** the HTML tag, the root node
- gray:** all other tags



**cnn.com**



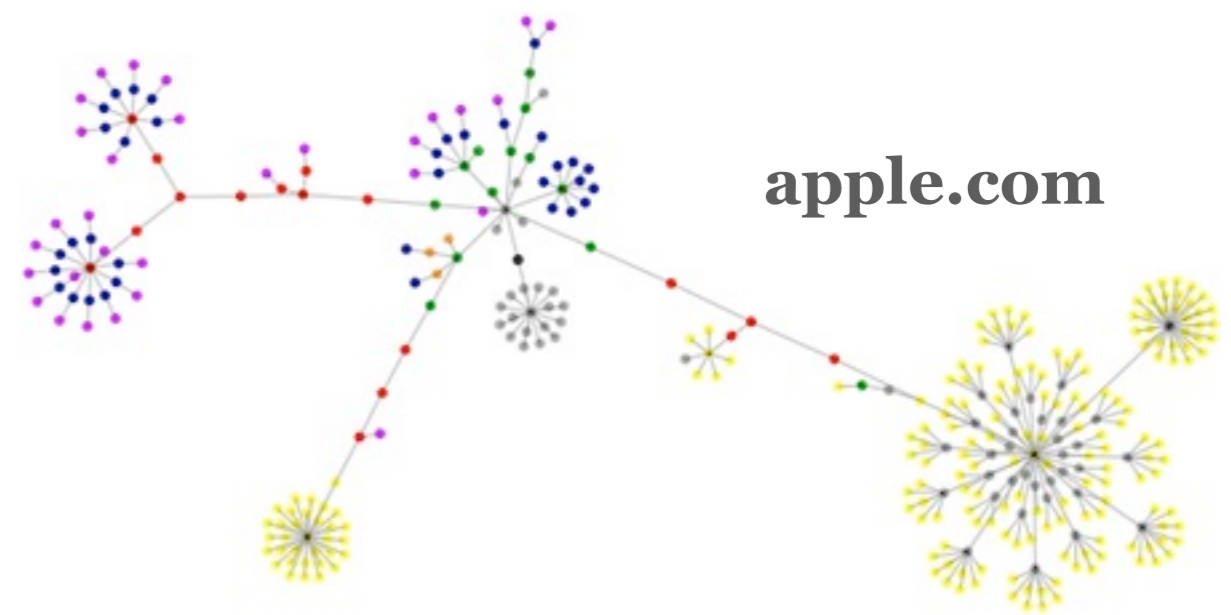
**boingboing.net**



**wired.com**



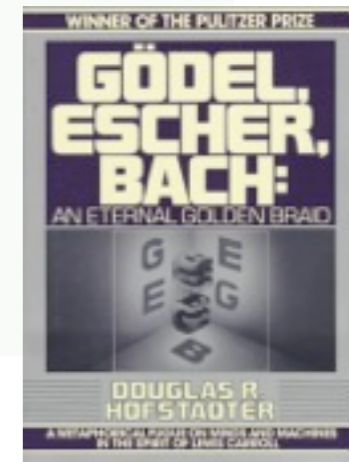
**apple.com**



# TOPIC GRAPH

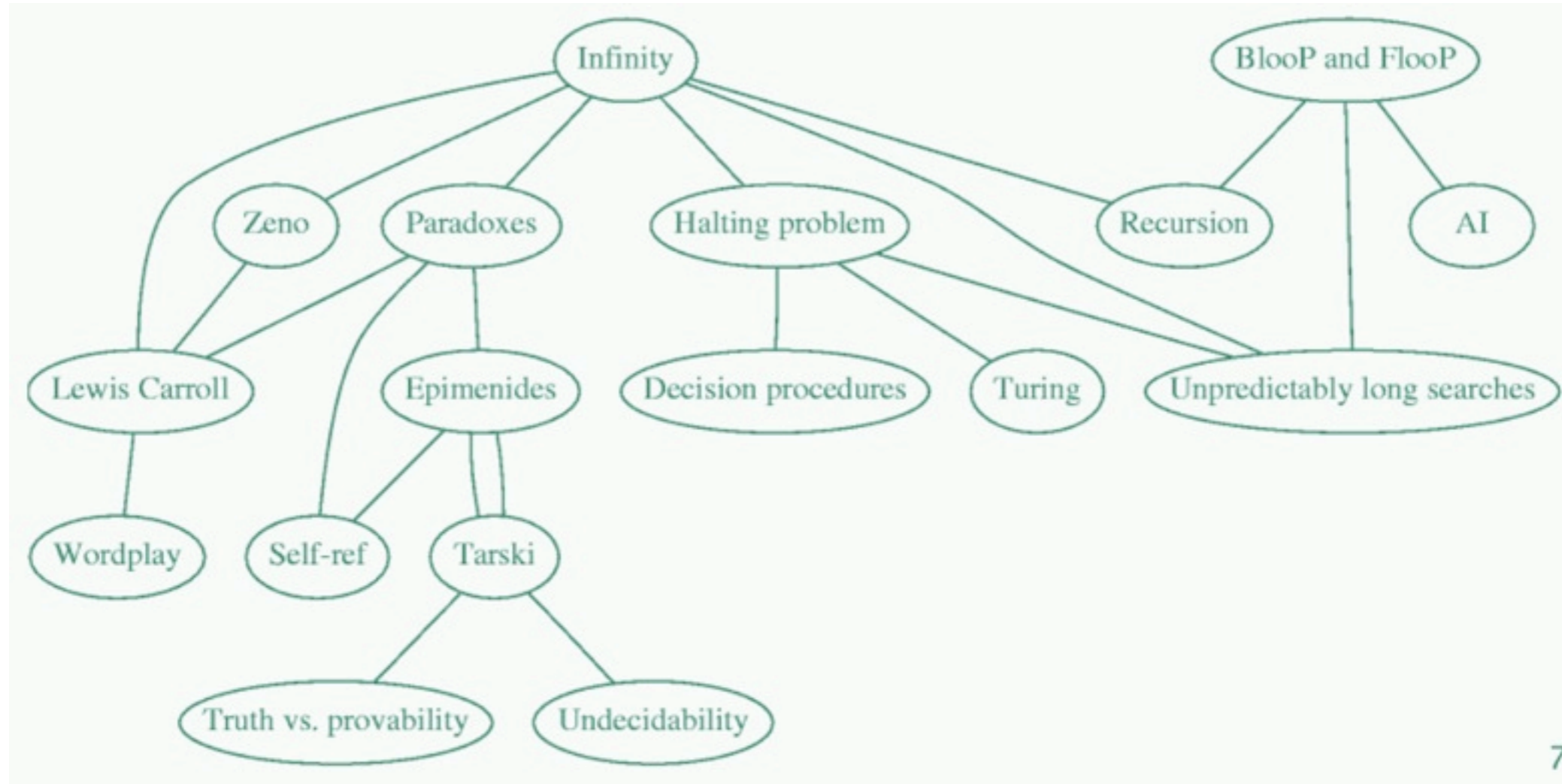
Turing – Halting problem  
Halting problem – Infinity  
Infinity – Paradoxes  
Paradoxes – Lewis Carroll  
Infinity – Lewis Carroll  
Infinity – Unpredictably long searches  
Infinity – Recursion  
Infinity – Zeno  
Infinity – Paradoxes  
Lewis Carroll – Zeno  
Lewis Carroll – Wordplay  
Halting problem – Decision procedures  
BlooP and FlooP – AI

Halting problem – Unpredictably long searches  
BlooP and FlooP – Unpredictably long searches  
BlooP and FlooP – Recursion  
Tarski – Truth vs. provability  
Tarski – Epimenides  
Tarski – Undecidability  
Paradoxes – Self-ref  
Epimenides – Tarski  
Epimenides – Paradoxes  
Epimenides – Self-ref  
[...]

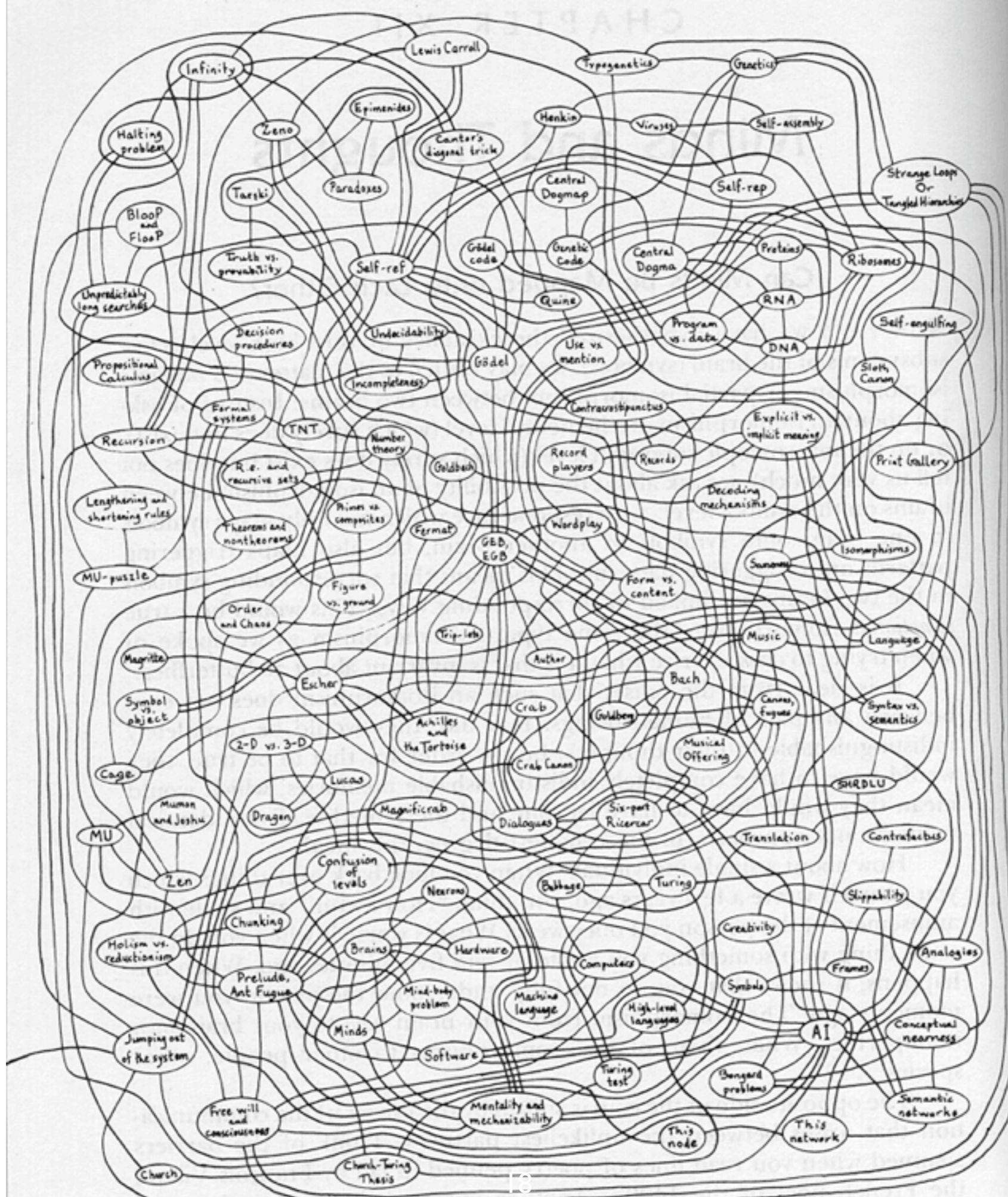


Hofstadter 1989

# TOPIC GRAPH







## **- definitions**

## **- visualizing trees**

- indented
- node link
- enclosure
- layered

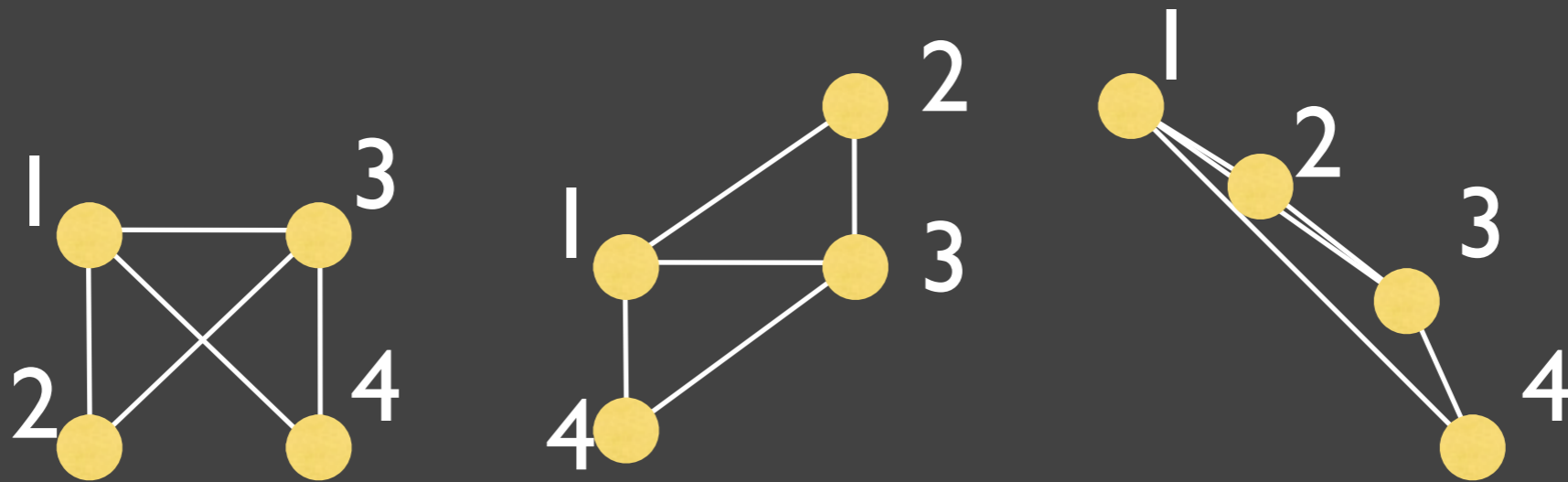
## **- visualizing graphs**

- node link
- matrix
- network summarizations

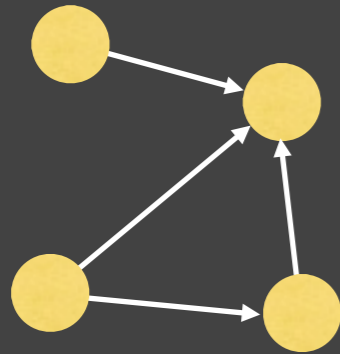
# DEFINITIONS

# GRAPH

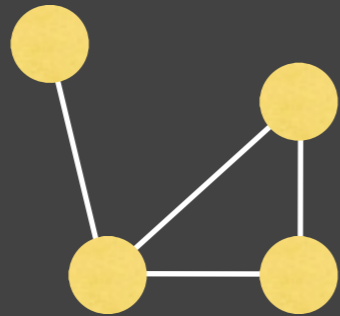
- **A graph  $G$  consists of a collection of vertices (or nodes)  $V$  and a set of edges  $E$ , consisting of vertex pairs.**
- **An edge  $e_{xy} = (x,y)$  connects two vertices  $x$  and  $y$ .**
  - for example:  $V=\{1,2,3,4\}$ ,  $E=\{(1,2),(1,3),(2,3),(3,4),(4,1)\}$



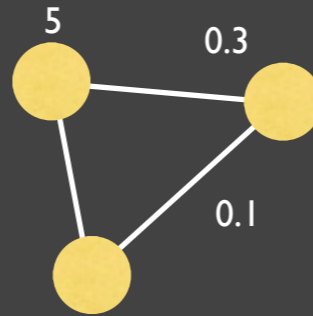
# a bunch of definitions



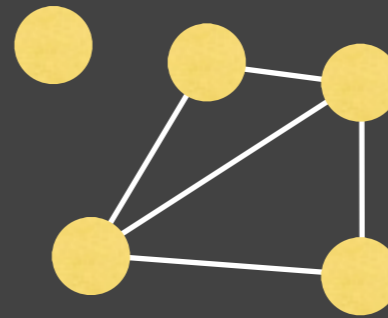
A directed graph



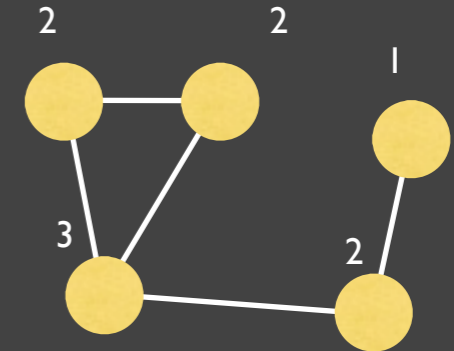
An undirected graph



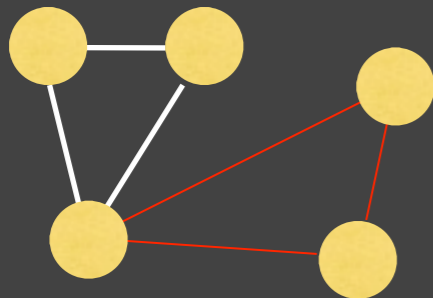
Weighted



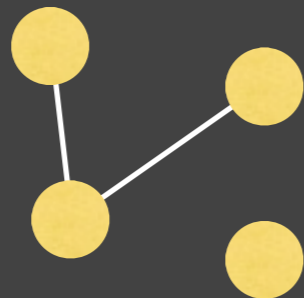
Unconnected



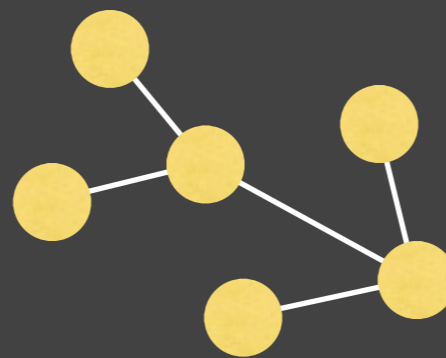
Node degrees



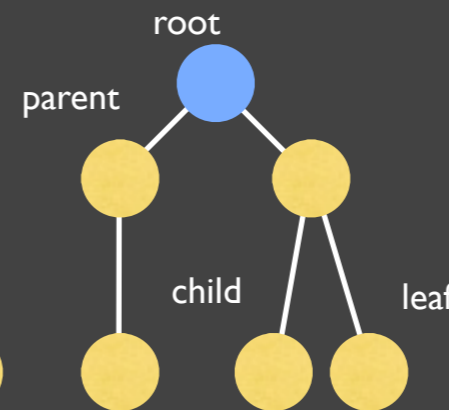
A cycle



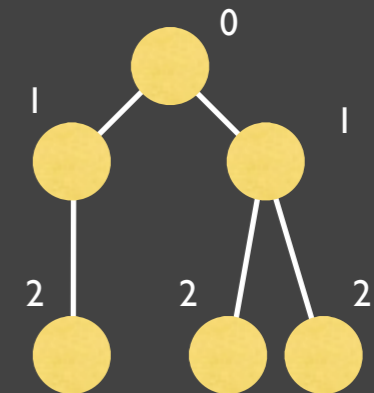
An acyclic graph



A connected acyclic graph,  
a.k.a. a tree



A rooted tree  
or hierarchy

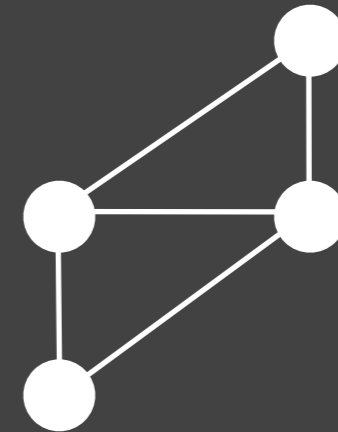


Node depths

# GRAPHS & TREES

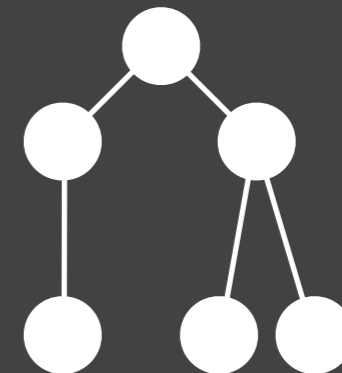
## -graphs

- model relations amount data
- nodes* and *edges*



## -trees

- graphs with hierarchical structure
  - connected graph with  $N-1$  edges*
- nodes as *parents* and *children*



# SPATIAL LAYOUT

- **primary concern of graph drawing is the spatial layout of nodes and edges**
- **often (but not always) the goal is to effectively depict the graph structure**
  - connectivity, path-following
  - network distance
  - clustering
  - ordering (e.g., hierarchy level)

# VISUALIZING TREES



# ROOTED TREES

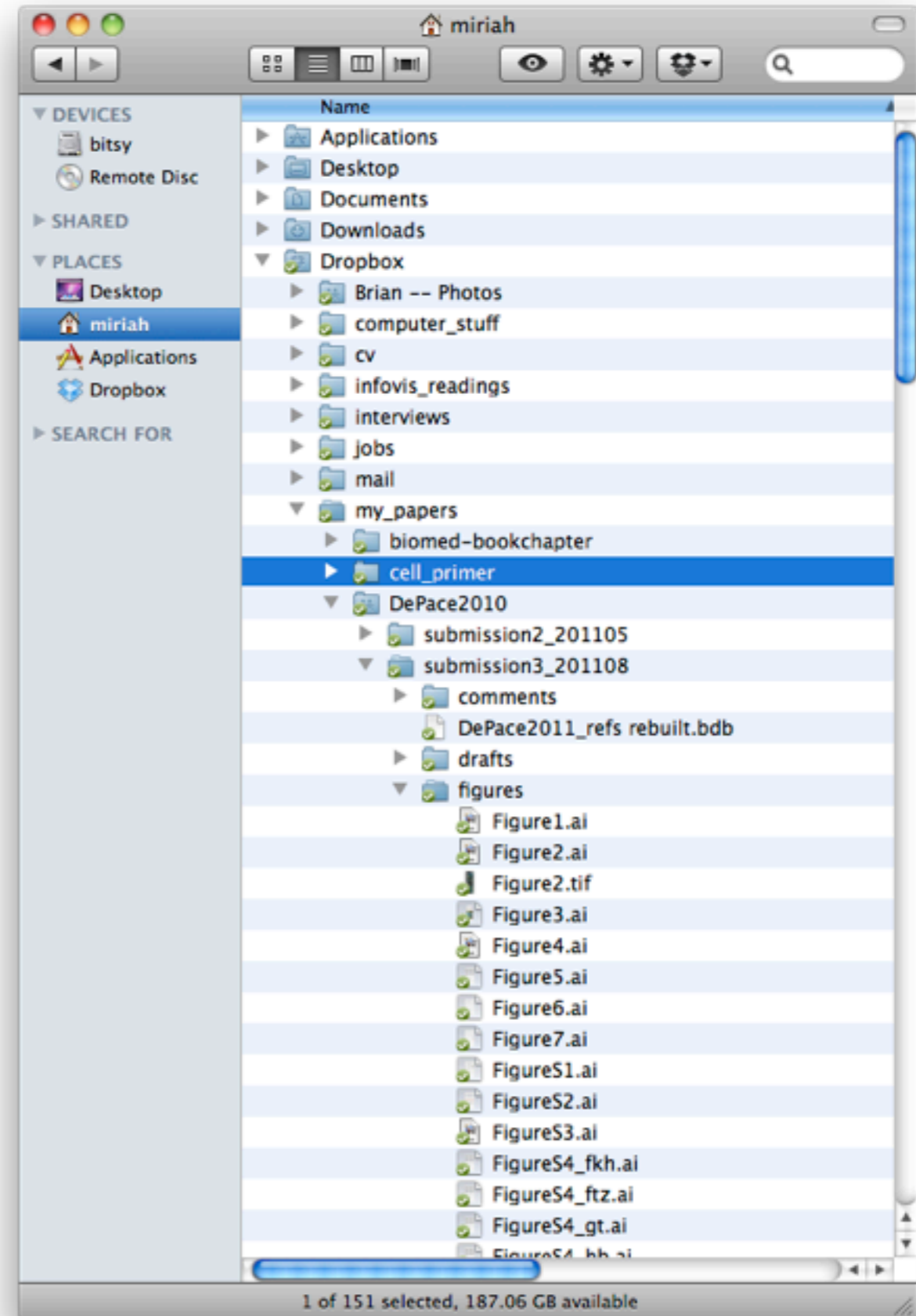
**-recursion makes it elegant and fast to draw trees**

**-approaches:**

- indentation
- node link
- enclosure
- layering

# INDENTATION

- **place all items along vertically spaced rows**
- **indentation used to show parent/child relationships**
- **commonly used as a component in an interface**
- **breadth and depth contend for space**
- **often requires a great deal of scrolling**



# WORD TREE

## Visualizations : definitions of visualization word tree

Uploaded by: mhaile

Created at: Wednesday May 21 2008, 11:37 PM

Tags: text



# NODE-LINK DIAGRAMS

- nodes are distributed in space, connected by straight or curved lines**
- typical approach is to use 2D space to break apart breadth and depth**
- often space is used to communicate hierarchical orientation**

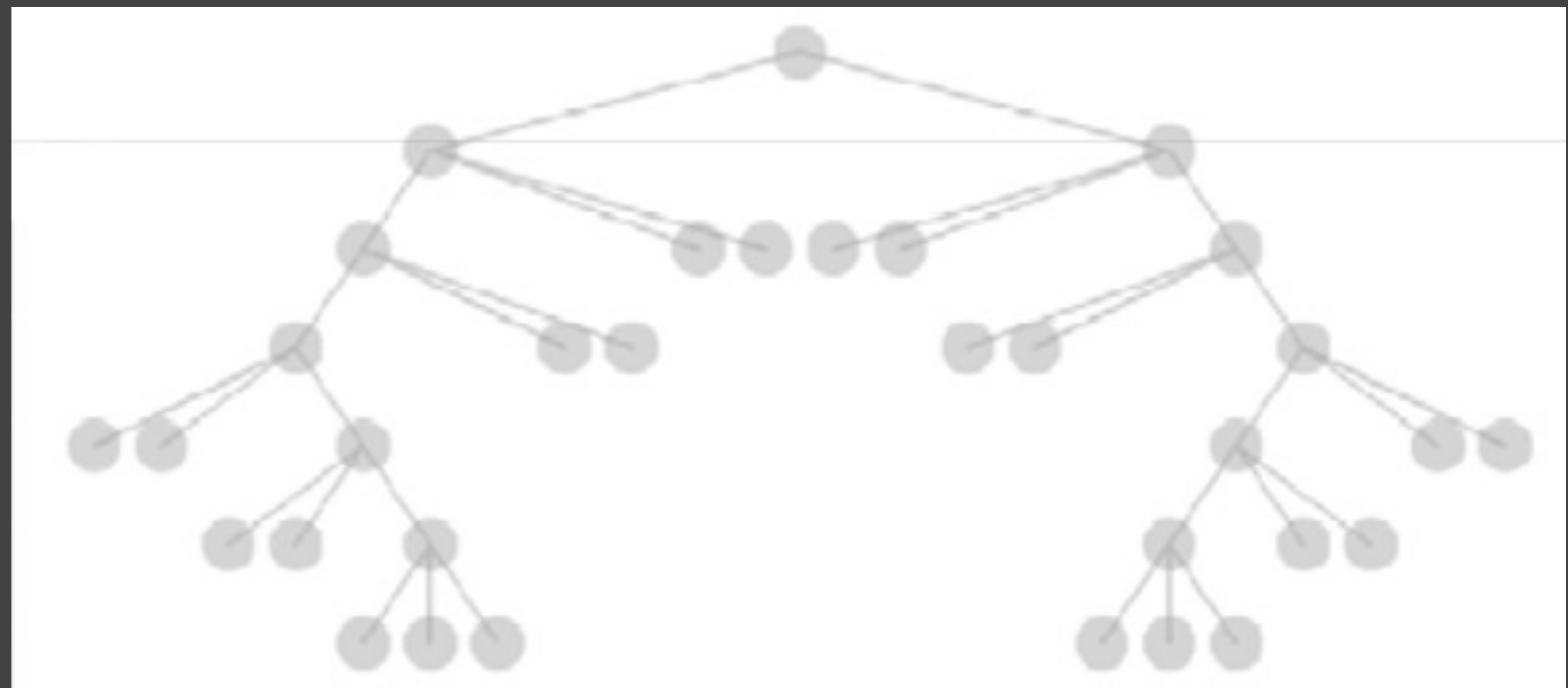
# BASIC APPROACH

- **repeatedly divide space for subtrees by leaf count**

- breadth of tree along one dimension

- depth along the other dimension

- **problem: exponential growth of breadth**



# REINGOLD-TILFORD type layouts

## - goal

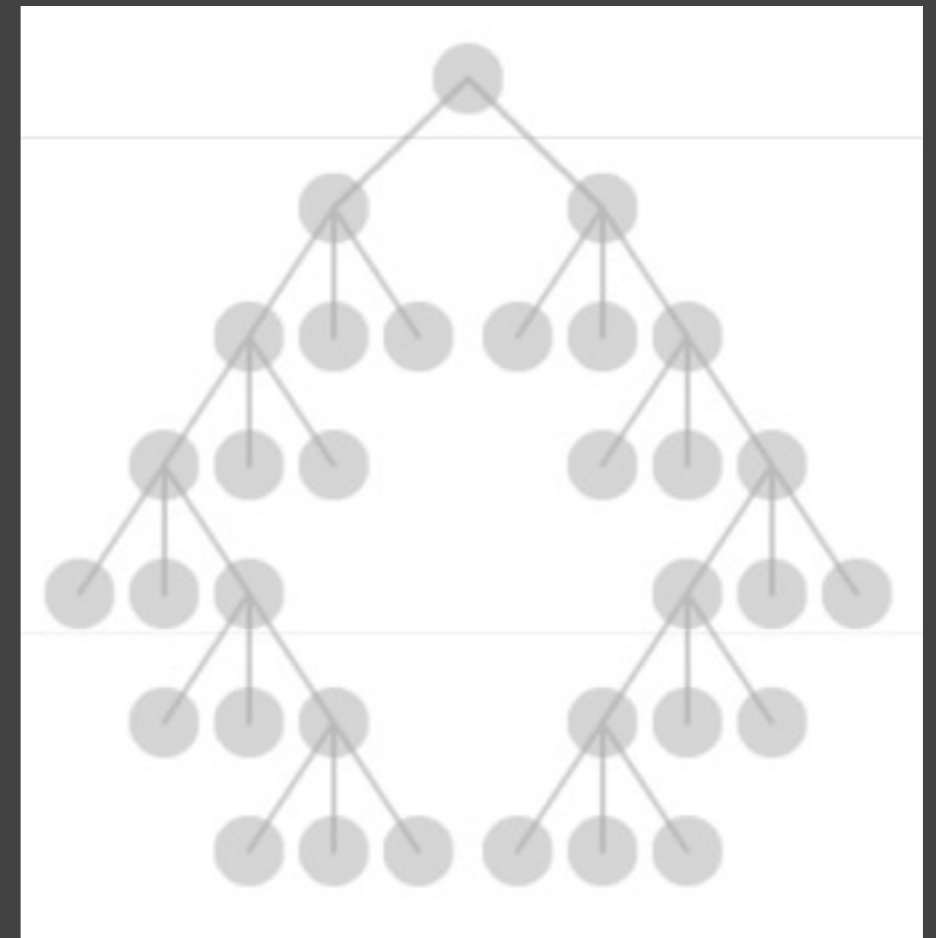
- make smarter use of space
- maximize density and symmetry

## - design concerns

- clearly encode depth level
- no edge crossings
- isomorphic subtrees drawn identically
- compact

## - approach

- bottom up recursive approach
- for each parent make sure every subtree is drawn
- pack subtrees as closely as possible
- center parent over subtrees



REINGOLD-TILFORD

REINGOLD-TILFORD





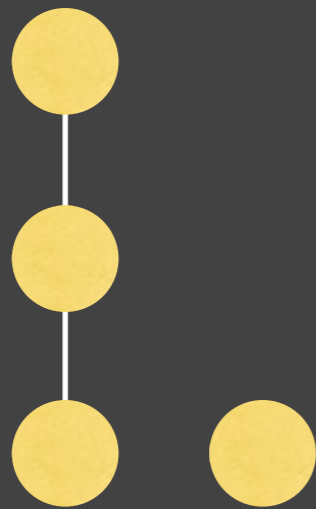
# REINGOLD-TILFORD



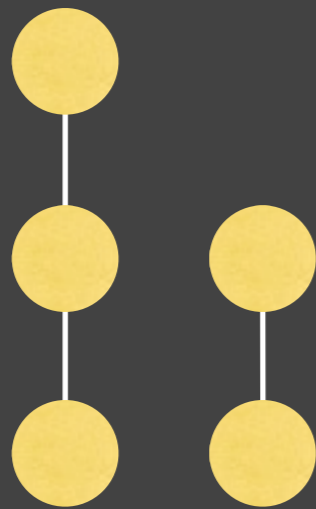
# REINGOLD-TILFORD



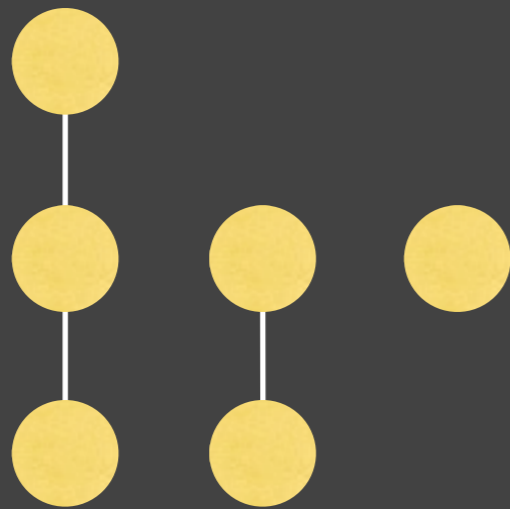
# REINGOLD-TILFORD



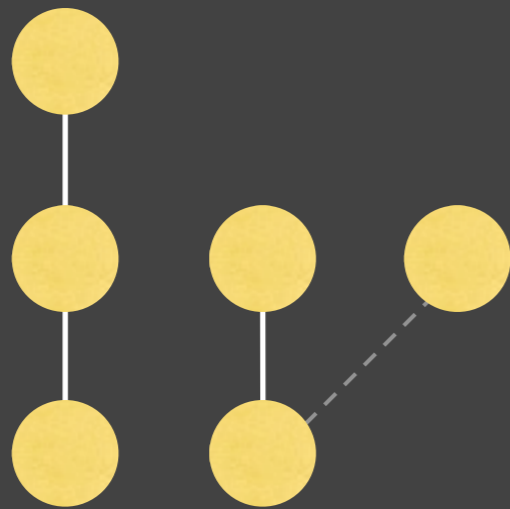
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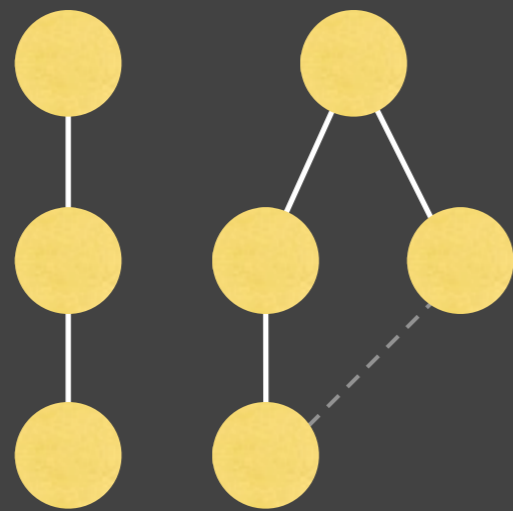
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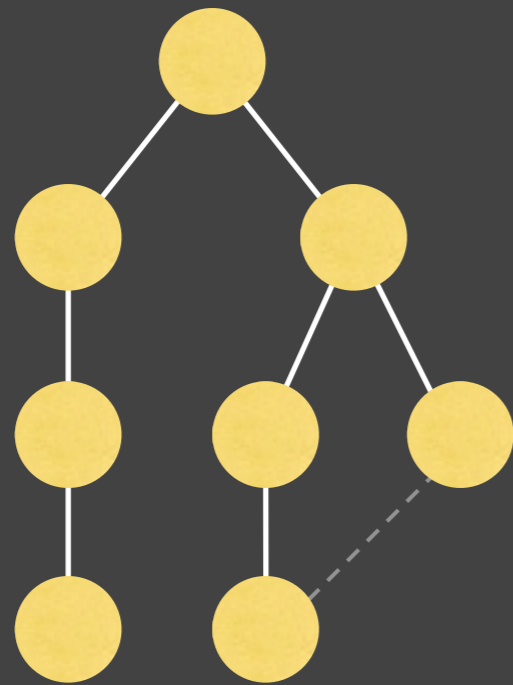
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# REINGOLD-TILFORD

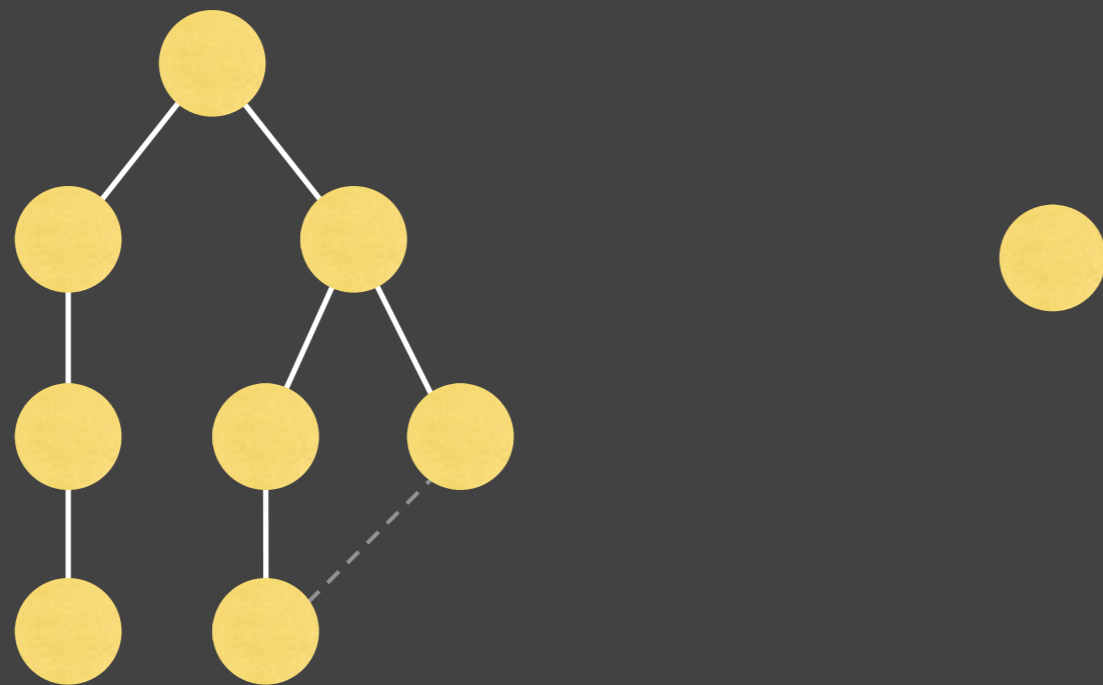


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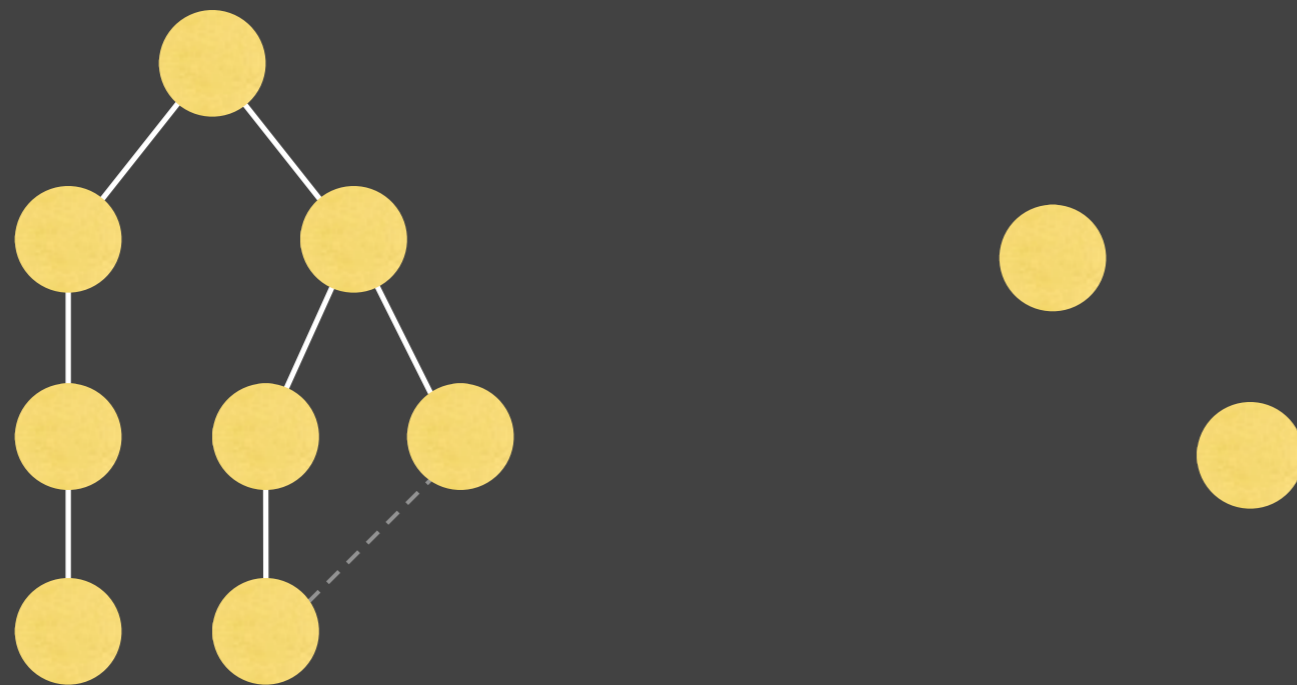




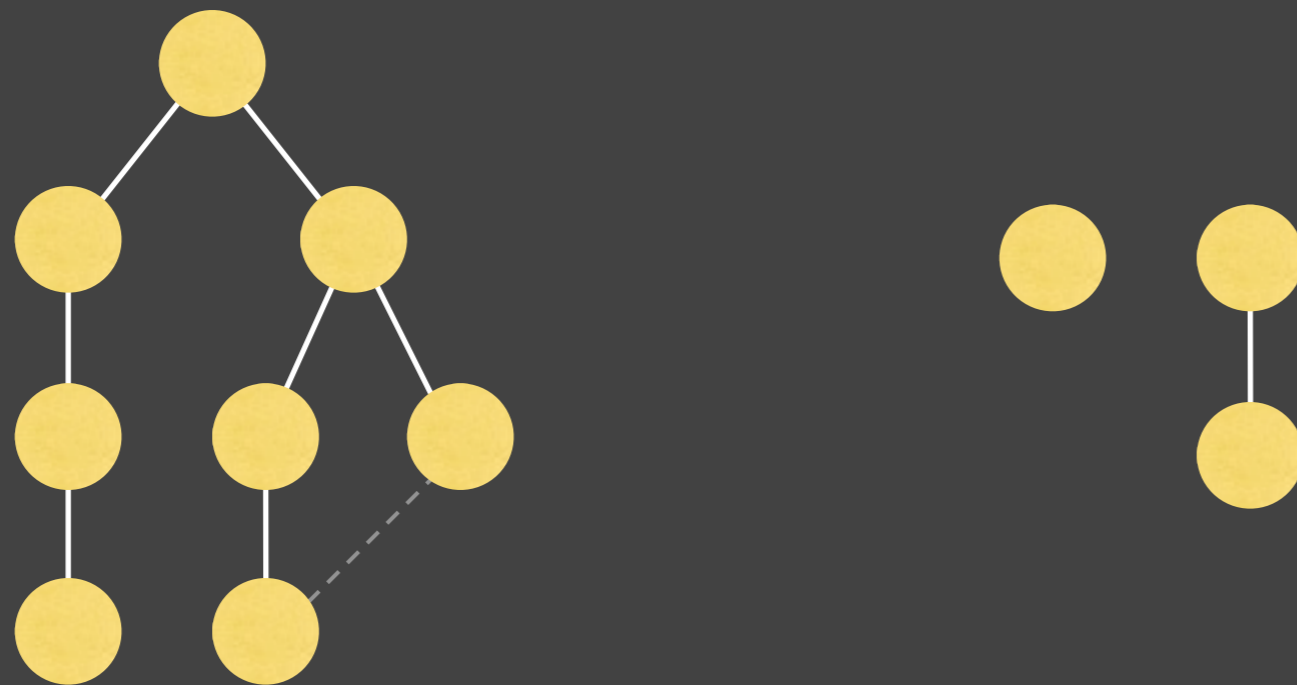
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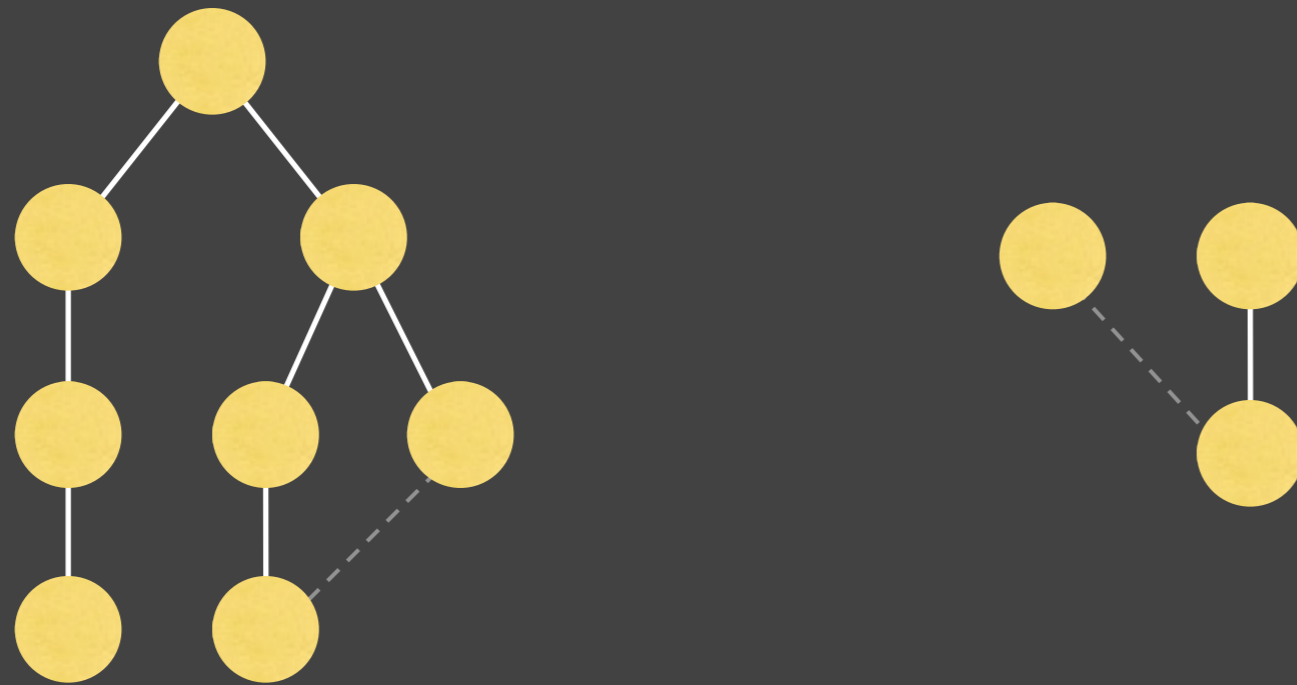
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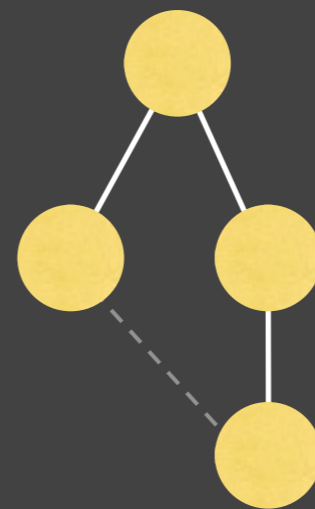
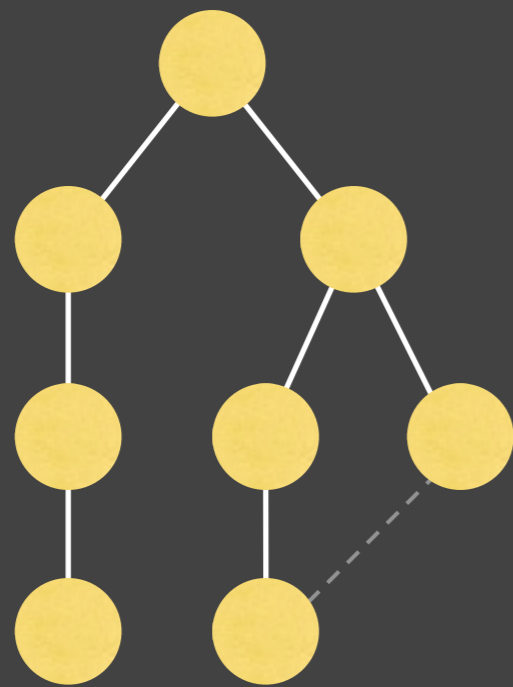
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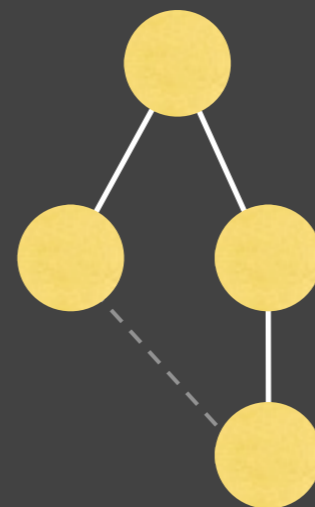
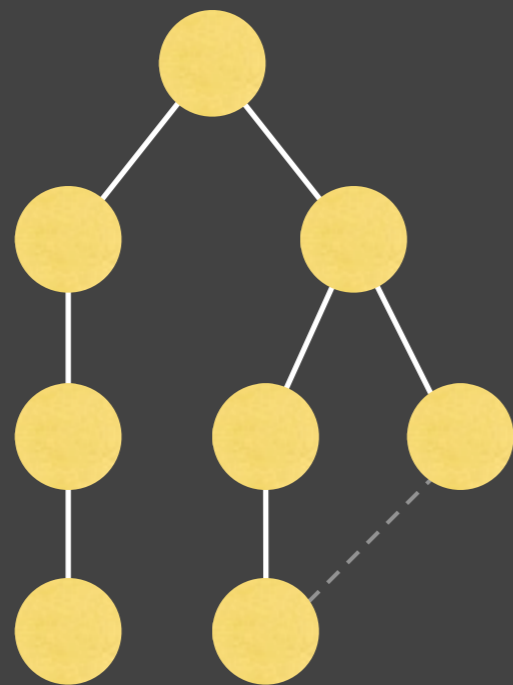
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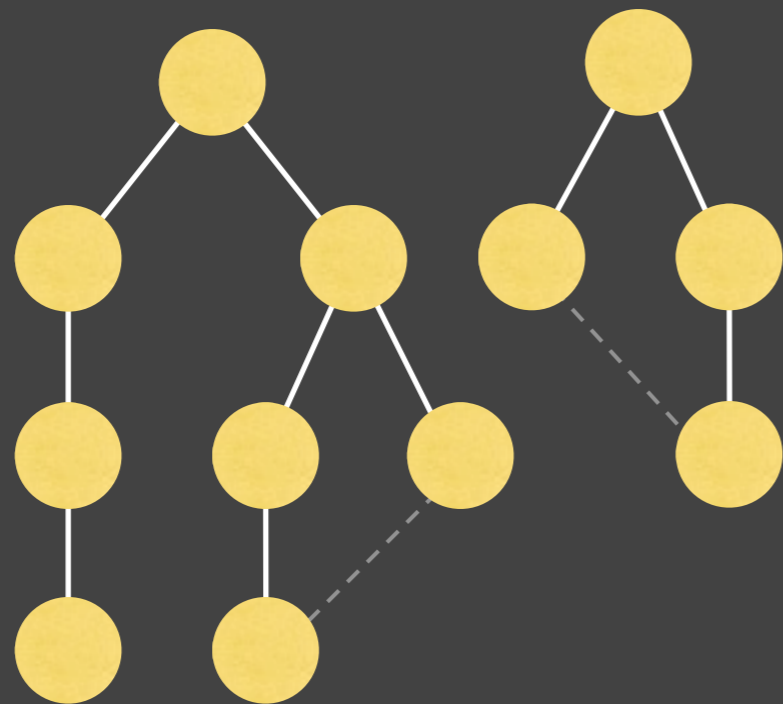
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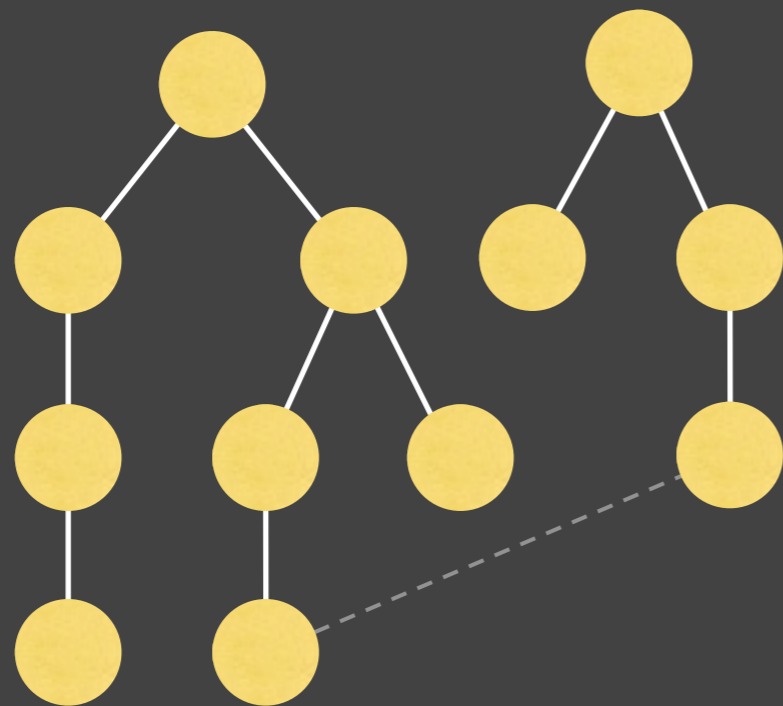
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# REINGOLD-TILFORD

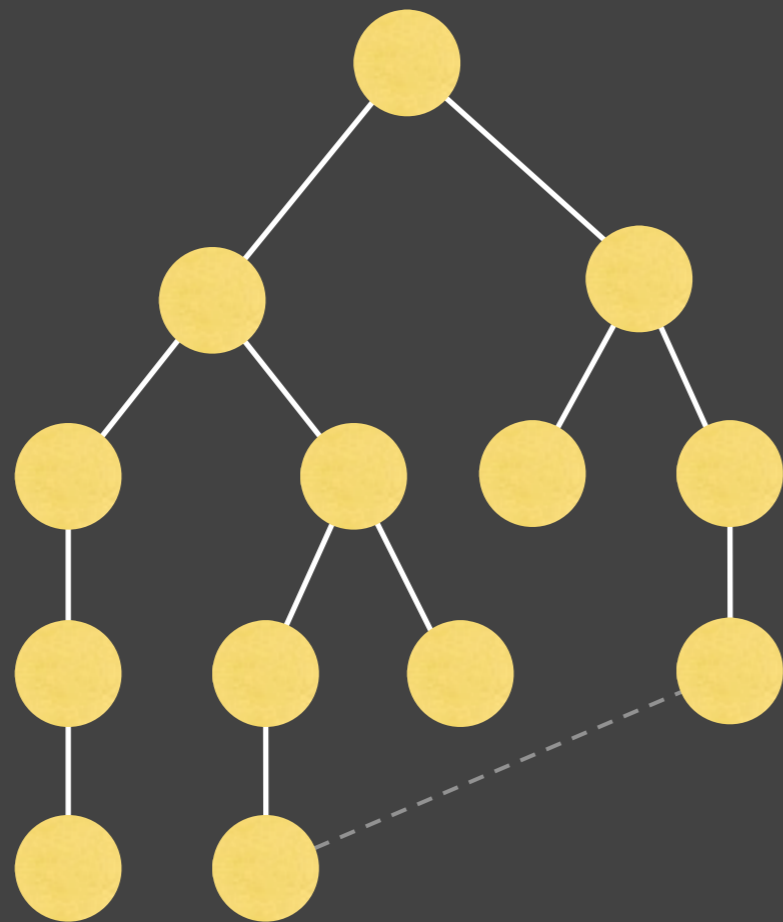


# REINGOLD-TILFORD





# REINGOLD-TILFORD

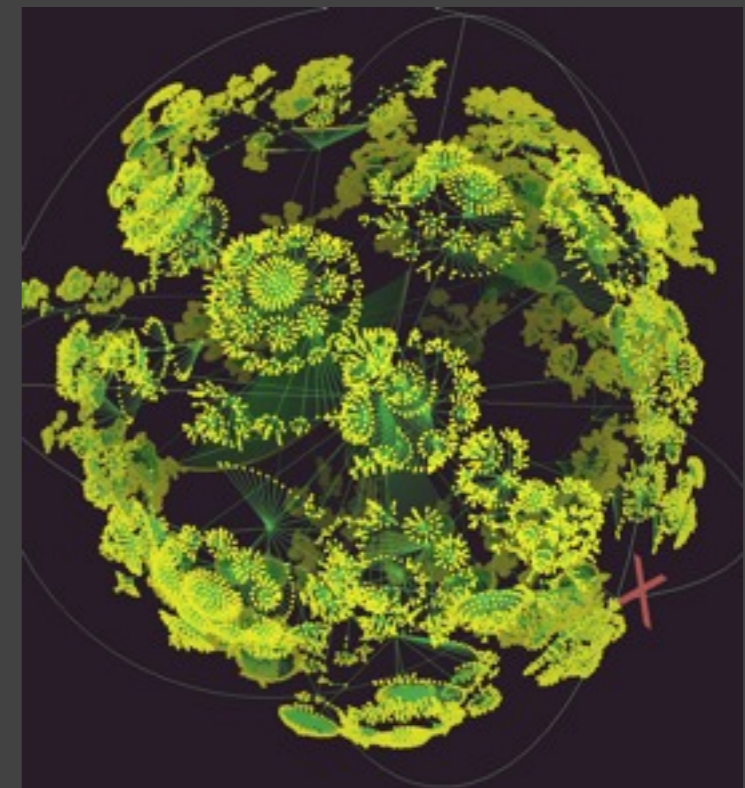




# NODE-LINK PROBLEMS

## -scale

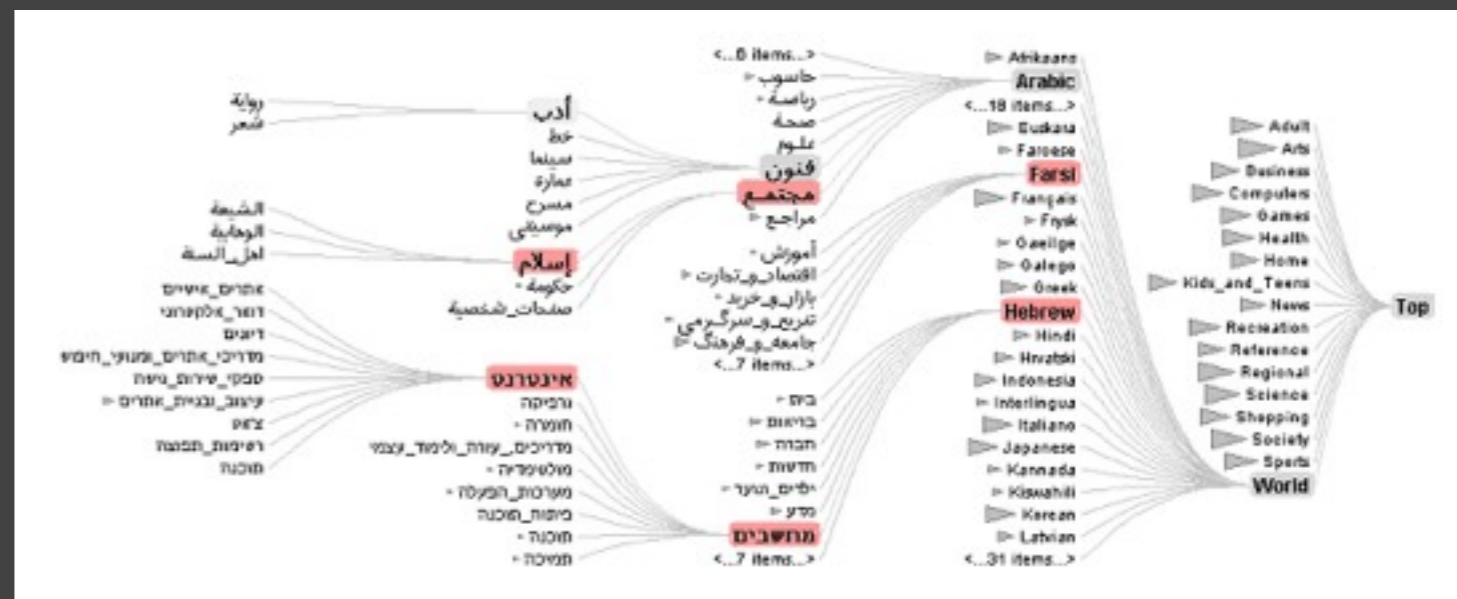
- tree breadth often grows exponentially
- quickly run out of space!



## -solutions

- hyperbolic layout
- filtering
- scrolling or panning
- zooming

<http://www.caida.org/tools/visualization/walrus/>



# ENCLOSURE DIAGRAMS

- **encode structure using spatial enclosure**

- often referred to as *treemaps*

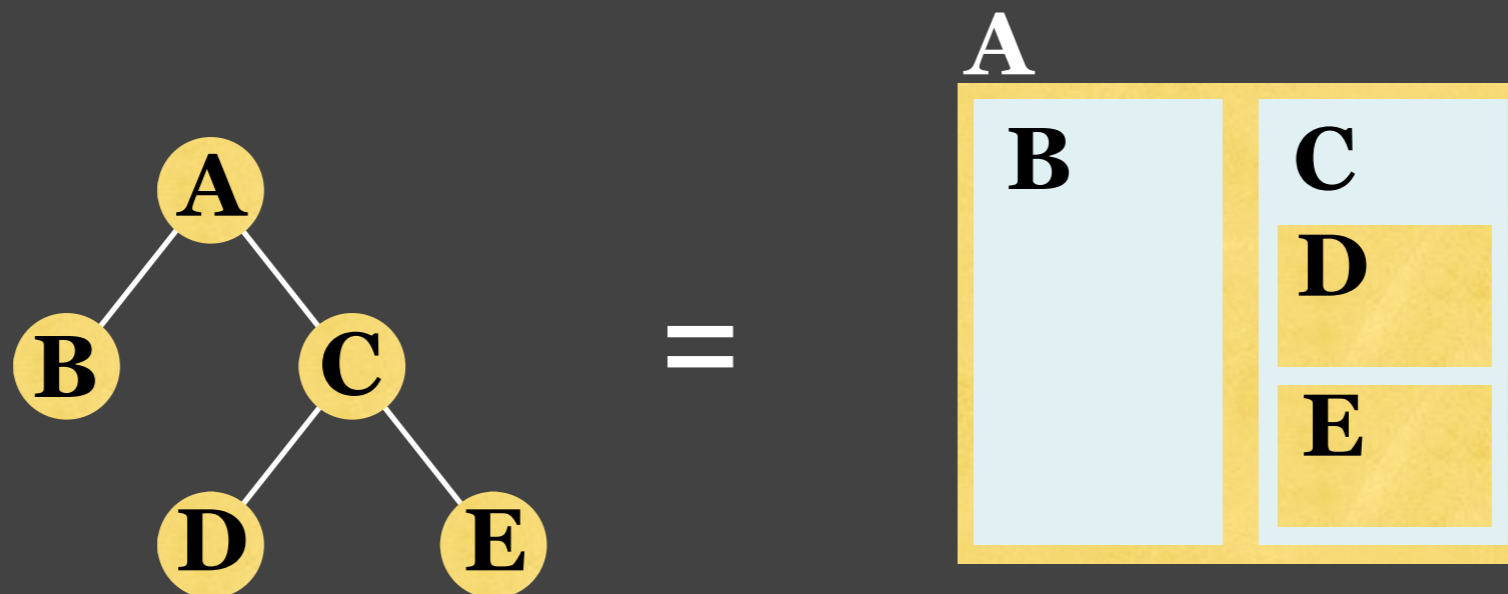
- **benefits**

- provides single view of entire tree

- easier to spot small / large nodes

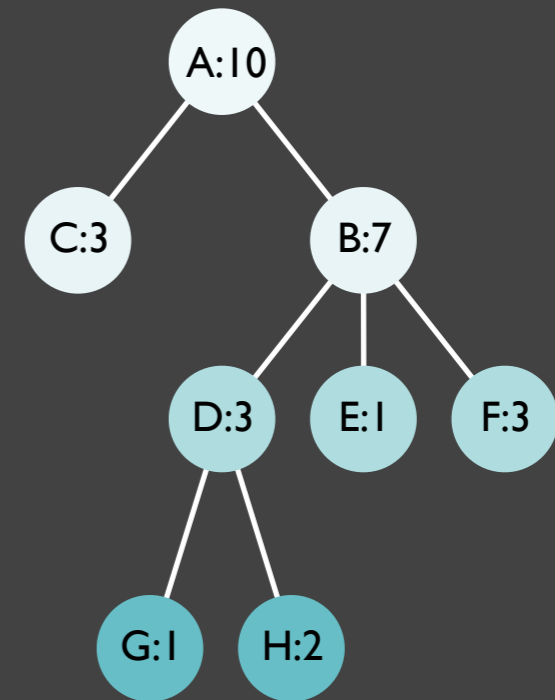
- **problems**

- difficult to accurately read depth



# TREEMAPS

- **recursively fill space based on a size metric for nodes**
- **enclosure indicates hierarchy**
- **additional measures can control aspect ratio of cells**
- **most often use rectangles, but other shapes possible**
  - square, circle, voronoi tessellation

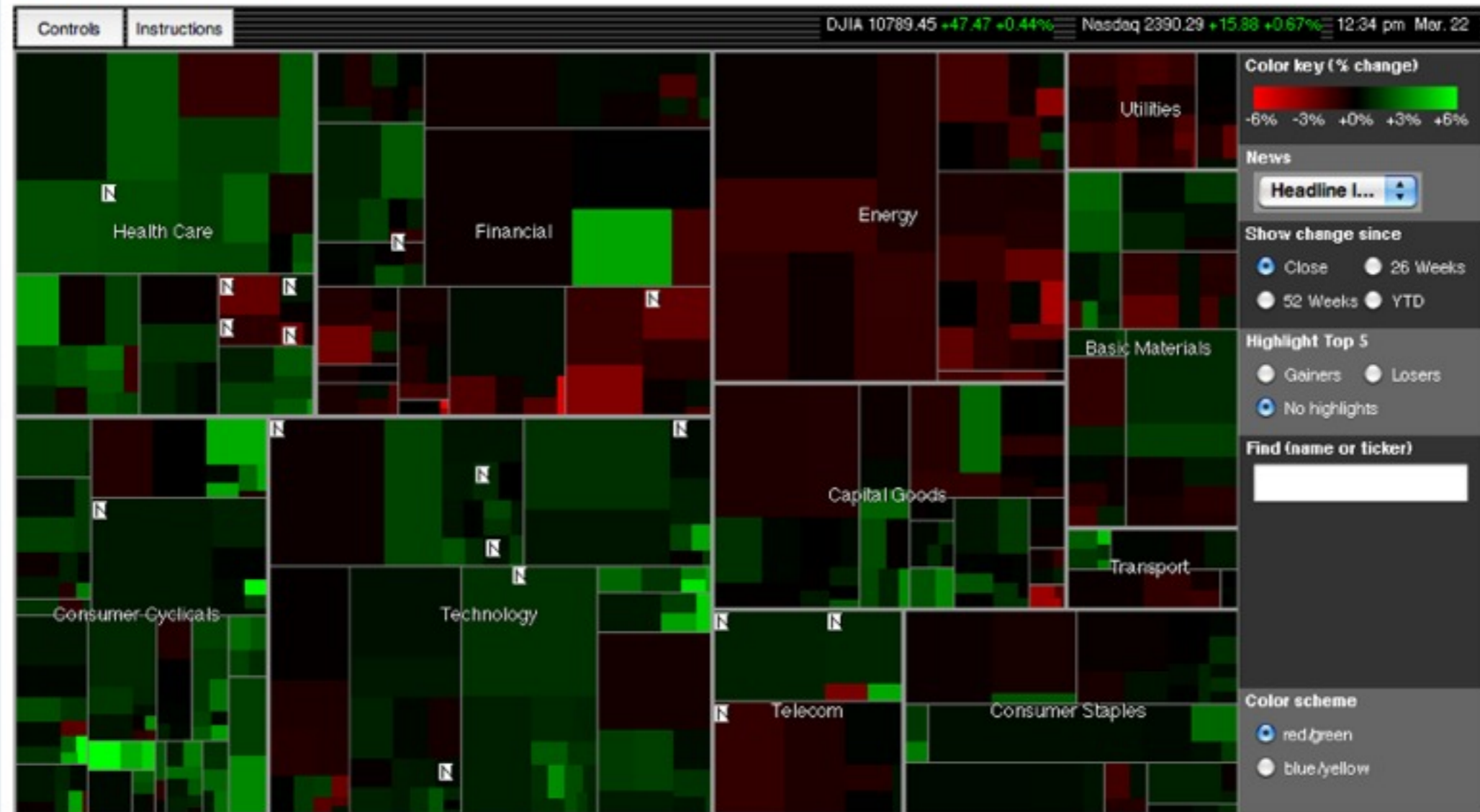


# Map of the Market

Launch Map in Separate Window 

SmartMoneySelect

Upgrade [here](#) to access the Market Map 1000 and search 1,000 companies with enhanced screening capabilities.



## MARKET NEWS

- [President Obama Hails Passage of Health Care Bill](#)
- [Health Bill Taxes Drug, Device Makers and the Rich](#)
- [Stock Screen: 3 Stocks With Big Dividends and Buybacks](#)

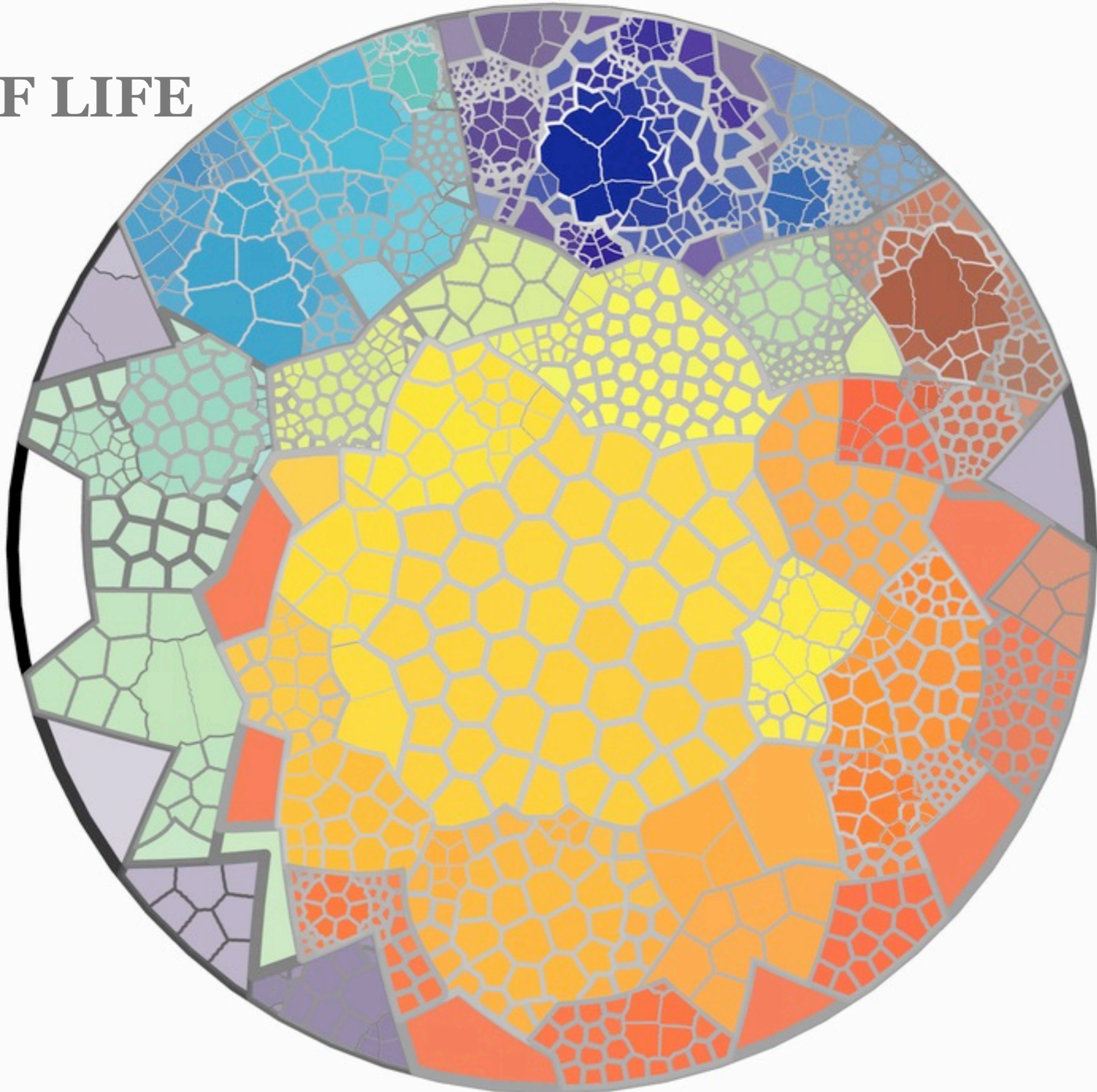
Patent No.: US 6,583,794 B1

[Click Here to License the Map Applet](#)



# TREE OF LIFE

mammals





# LAYERED DIAGRAMS

- **similar to node-link layouts without edges**

- structured encoded using:

- *layering*

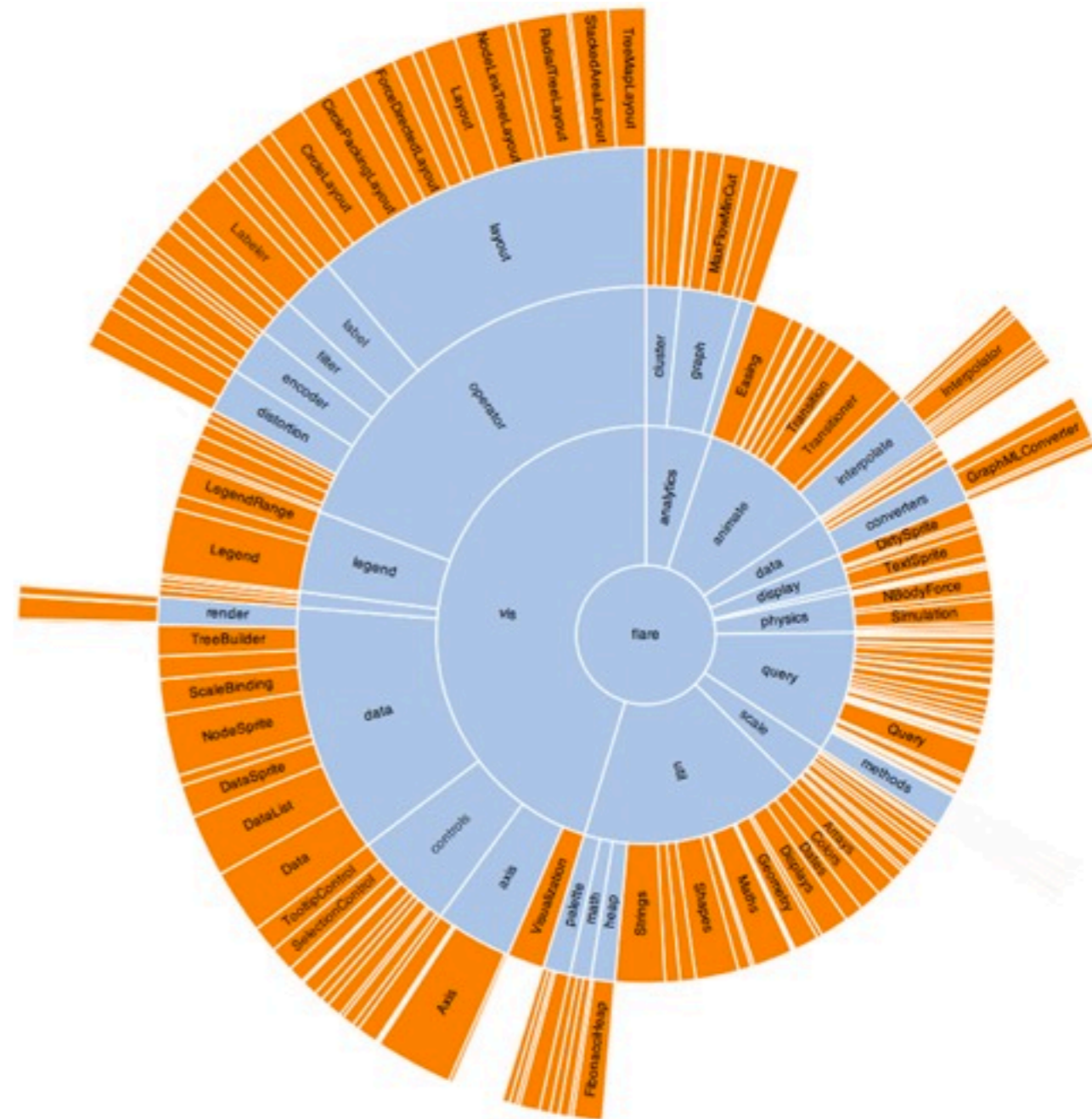
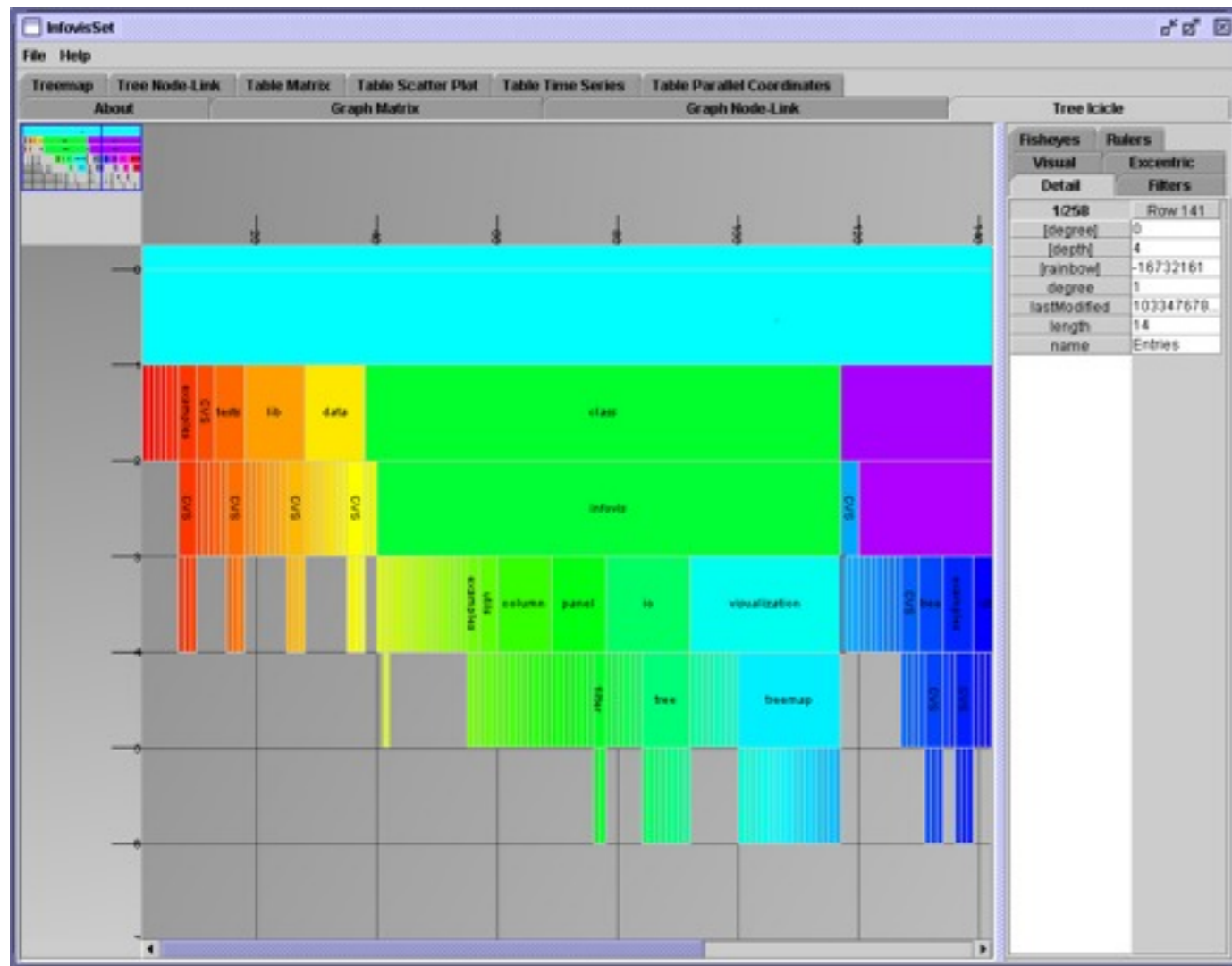
- *adjacency*

- *alignment*

- **recursive subdivision of space**

- **apply same set of approaches as in node-link layout**

# ICICLE & SUNBURST TREES



# Visualization of large tree structures

This project is about fast interactive visualization of large data structures organized in a tree.

This is an experimental software. If you have a feature request, or if you want to honour my work, send me an Amazon gift card or a donation.

## Project Goals

- Visualize the data structure in a way which allows to get an overview of the data structure within a short time.
- Provide guidance which allows to quickly drill down into points of interest in the data structure.
- Render the data structure fast enough so that real-time navigation is possible.

## Implemented Diagrams

The project currently consists of a file browser demo, which visualizes the file system with the following tree diagrams:

- Hyperbolic Tree
- Circular Treemap
- Rectangular Treemap
- Sunburst Tree
- Icicle Tree
- Sunray Tree
- Iceray Tree

## Try it out



Installs and launches Treeviz on all platforms. Needs a 64-bit JVM and at least 4 GB of RAM.

[Launch](#) with 32-bit JVM.

## Downloads

[1.0.4](#) (590 K)

Source code included.

The executable .jar file is located in the dist directory.

## Screenshots

The following pictures show all the same data set:

*Circular Treemap:*



*Rectangular Treemap:*



*Sunburst Tree:*



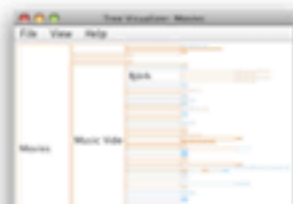
*Icicle Tree:*



*Sunray Tree:*



*Iceray Tree:*



*Hyperbolic Tree:*



## Examples

The demo application can visualize a directory structure or an XML file as illustrated in the following example files:

[Treeviz Example.xml](#)

[business.xml](#)

Please don't rely on the functionality of the demo application. Since this is an ongoing research project, the functionality and the format supported by the demo application is going to change in incompatible ways, even between minor versions.

## Licensing

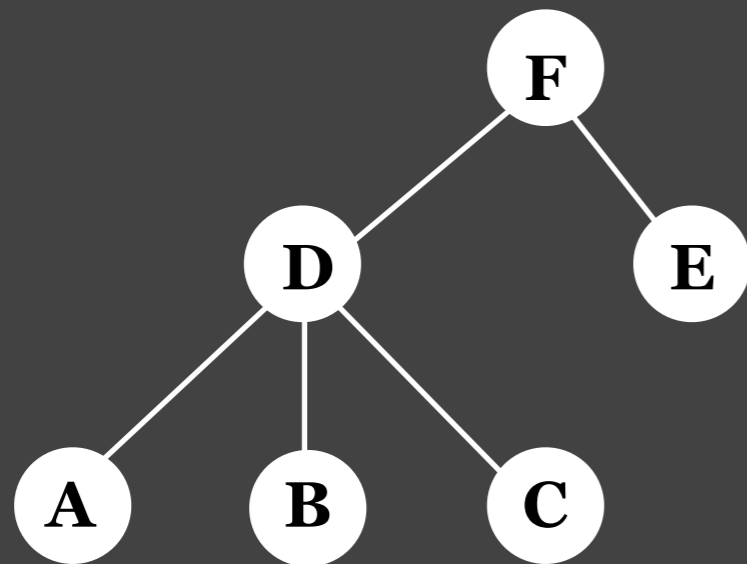
The Hypertree code is licensed under the MIT license.



exercise

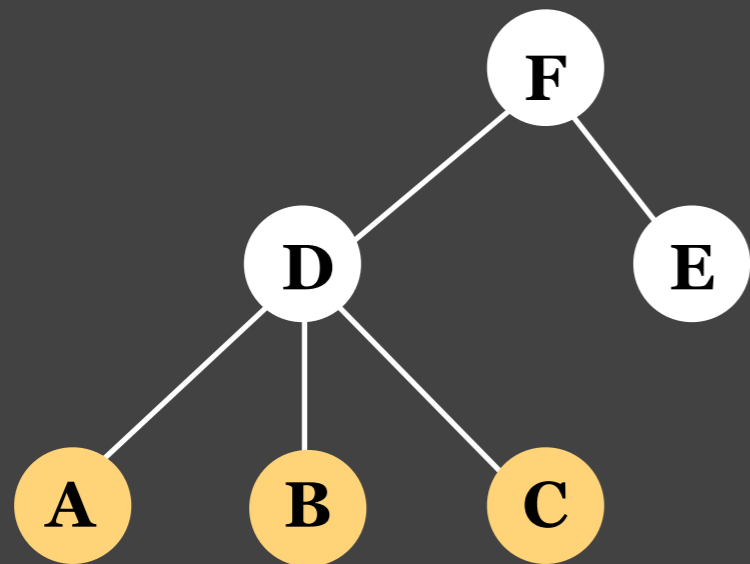
# NEWICK FORMAT

**-representation of trees using parentheses and commas**



# NEWICK FORMAT

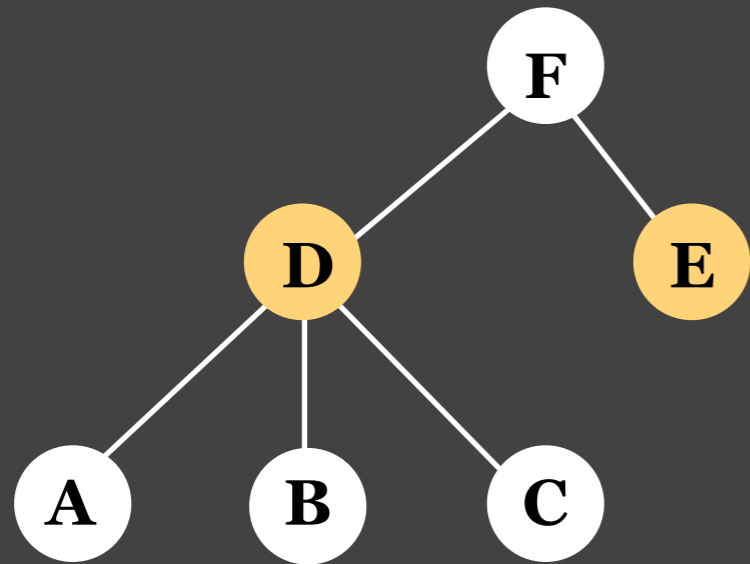
-representation of trees using parentheses and commas



A, B, C

# NEWICK FORMAT

-representation of trees using parentheses and commas

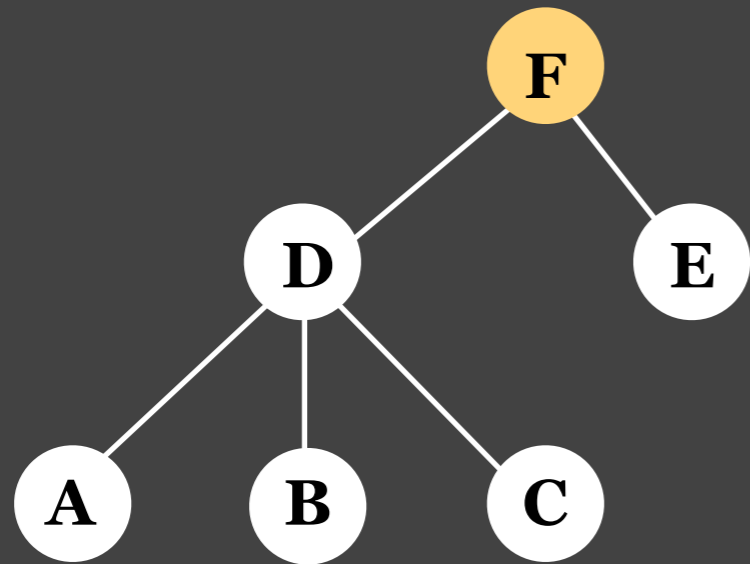


**( A, B, C ) D, E**



# NEWICK FORMAT

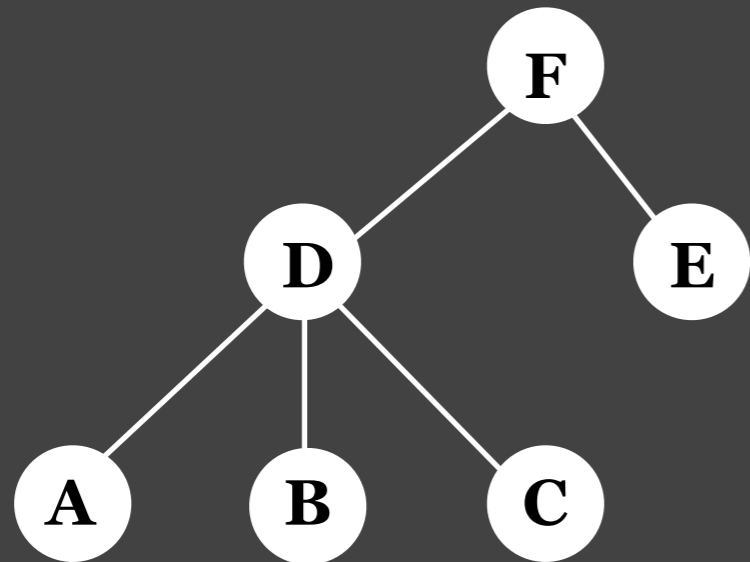
-representation of trees using parentheses and commas



**( ( A, B, C ) D, E ) F**

# NEWICK FORMAT

-representation of trees using parentheses and commas



**( ( A, B, C ) D, E ) F**

parentheses : child  
comma : sibling

## TREE DRAWING EXERCISE

newick format

(((((A, B) C) D) E, (((H, (L, M) N) I) J, (O, (((Q) R, (U, V) W) S, X) T) P) K) F, (Y) Z) G

## REINGOLD-TILFORD

- bottom up recursive approach
- for each parent make sure every subtree is drawn
- pack subtrees as closely as possible
- center parent over subtrees

L15: Trees & Graphs

**REQUIRED READING**

# Graph Visualisation and Navigation in Information Visualisation

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[CWI Information Visualization Home Page](#)

[ The preprint of an updated version of this article, published in IEEE Transactions on Visualization and Computer Graphics, 6(1), pp. 24-43, 2000. is also available [here in PDF](#). ]

**Abstract.** This is a survey on graph visualisation and navigation techniques, as used in information visualisation. Graphs appear in numerous applications, like web browsing, state-transition diagrams, computer data structures, etc. The ability to visualise and to navigate in these potentially very large, abstract graphs is often a crucial part of an application. Information visualisation has specific requirements, which means that this survey approaches the results of traditional graph drawing from a different perspective than the traditional surveys; as such it is a useful complementary survey to those.

Keywords: information visualisation, graph visualisation, graph drawing, navigation, focus+context, fish-eye, clustering.

1998 Computing Reviews Classification System: G.2.2., H.3.3, H.4.m, H.m, I.3.4, I.3.m, J.m

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- [Graph Layout](#)
- [Navigation and Interaction](#)
- [Clustering](#)
- [Systems](#)
- [Journals and Conferences](#)
- [References](#)

# Visual Exploration of Multivariate Graphs

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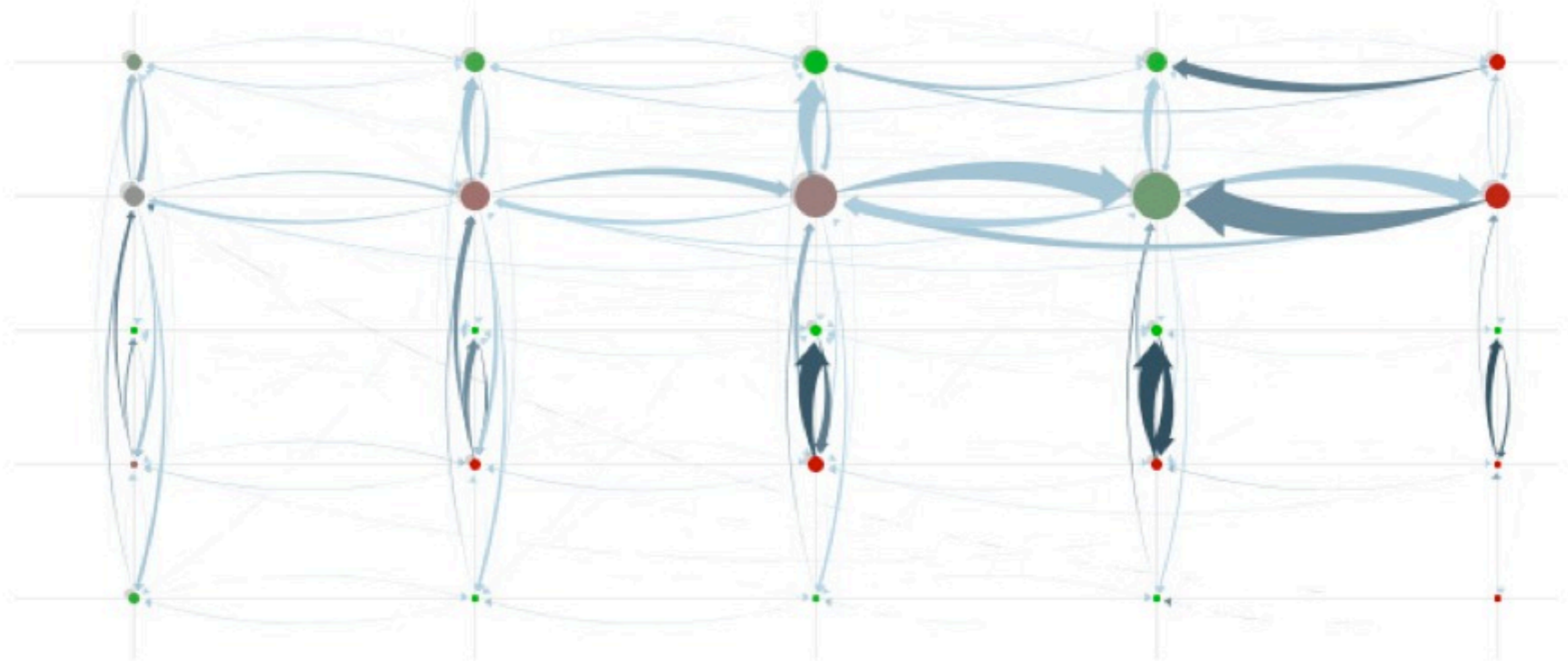


Figure 1. *A PivotGraph visualization of a large graph rolled up onto two categorical dimensions*

**ABSTRACT**

## **Author Keywords**

information visualization, graph drawing

ACM Classification Keywords

# ABySS-Explorer: Visualizing Genome Sequence Assemblies

Cydney B. Nielsen, Shaun D. Jackman, Inanç Birol, and Steven J.M. Jones

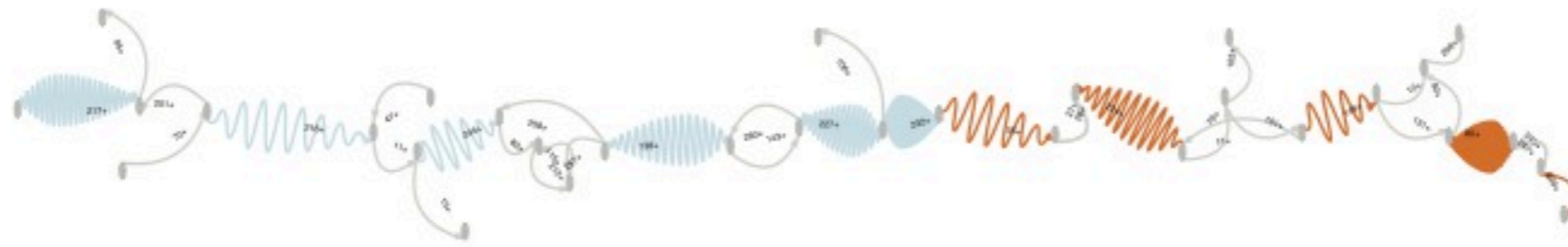


Fig. 1. ABYSS-Explorer employs a novel graph representation enabling biologists to examine the global structure of a genome sequence assembly.

**Abstract**—One bottleneck in large-scale genome sequencing projects is reconstructing the full genome sequence from the short sub-sequences produced by current technologies. The final stages of the genome assembly process inevitably require manual inspection of data inconsistencies and could be greatly aided by visualization. This paper presents our design decisions in translating key data features identified through discussions with analysts into a concise visual encoding. Current visualization tools in this domain focus on local sequence errors making high-level inspection of the assembly difficult if not impossible. We present a novel interactive graph display, ABYSS-Explorer, that emphasizes the global assembly structure while also integrating salient data features such as sequence length. Our tool replaces manual and in some cases pen-and-paper based analysis tasks, and we discuss how user feedback was incorporated into iterative design refinements. Finally, we touch on applications of this representation not initially considered in our design phase, suggesting the generality of this encoding for DNA sequence data.

**Index Terms**—Bioinformatics visualization, design study, DNA sequence, genome assembly.

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## 1 INTRODUCTION

Data generation used to be the expensive and time consuming step in biology research. Recent innovations in high-throughput techniques have transformed it into a cost-effective and rapid process, pushing the bottleneck of discovery into the analysis phase. There is increasing recognition in the field that improvements in visualization tools will be essential for understanding our growing wealth of data. This paper presents one such tool for a genome analysis problem.

The term “genome” refers to the genetic material of a cell and can be thought of as the cellular instruction set. A genome consists of

subjected to many rounds of automated improvement, but ultimately it is visually inspected and manually edited by specialists.

Our work was motivated by the needs of genome analysts and the shortcomings of existing visualization tools in this domain. A genome assembly consists of long contiguous sequences, called contigs, assembled from short sequencing reads. An analyst integrates diverse data types used by the assembly algorithm together with external meta-data to make final judgements about whether an assembly is correct and complete. It is useful to interpret these data in the context of the