Scalable Visualization with Accordion Drawing

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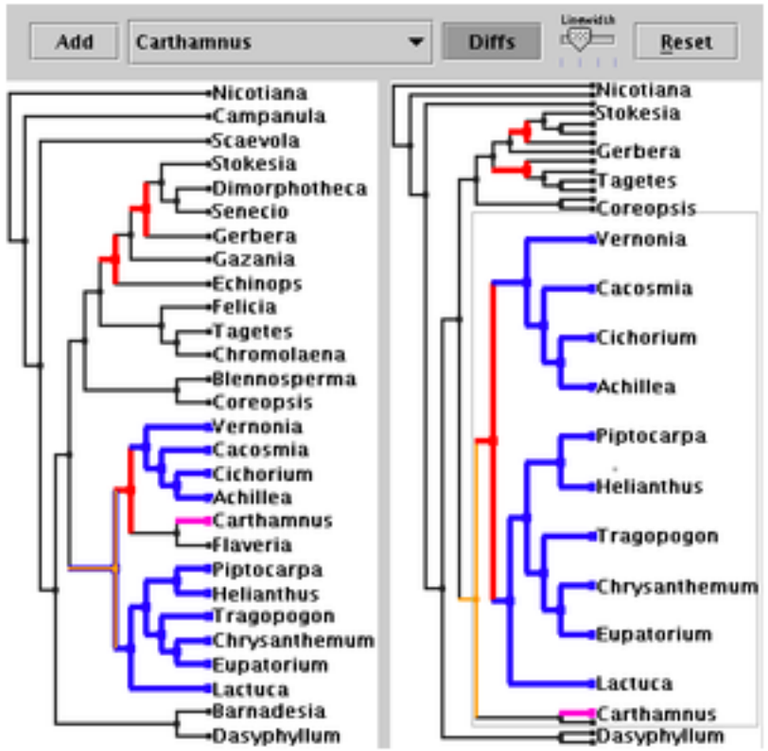
Accordion Drawing

rubber-sheet navigation

- stretch part of surface
- the rest squishes
- borders nailed down
- helps maintain orientation



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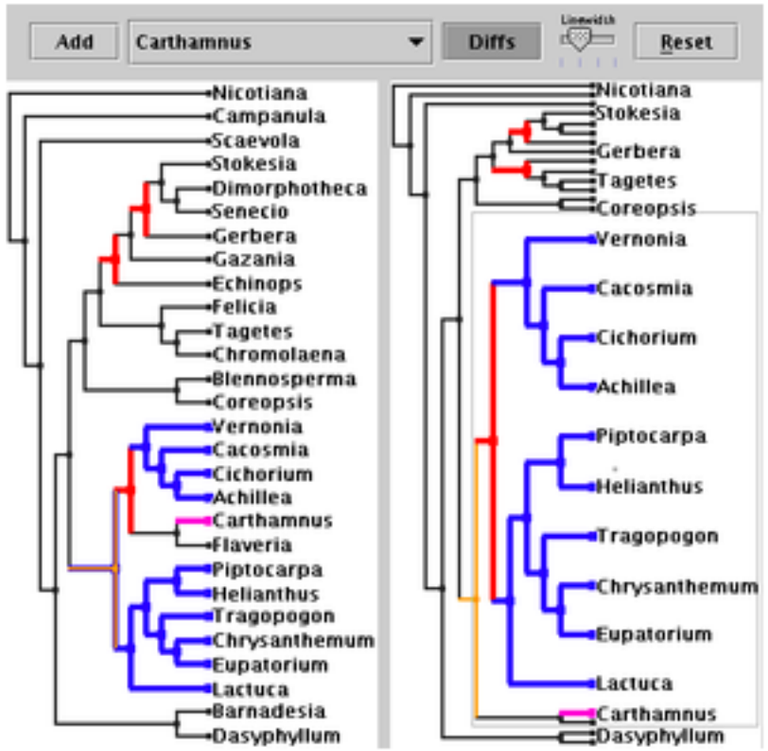
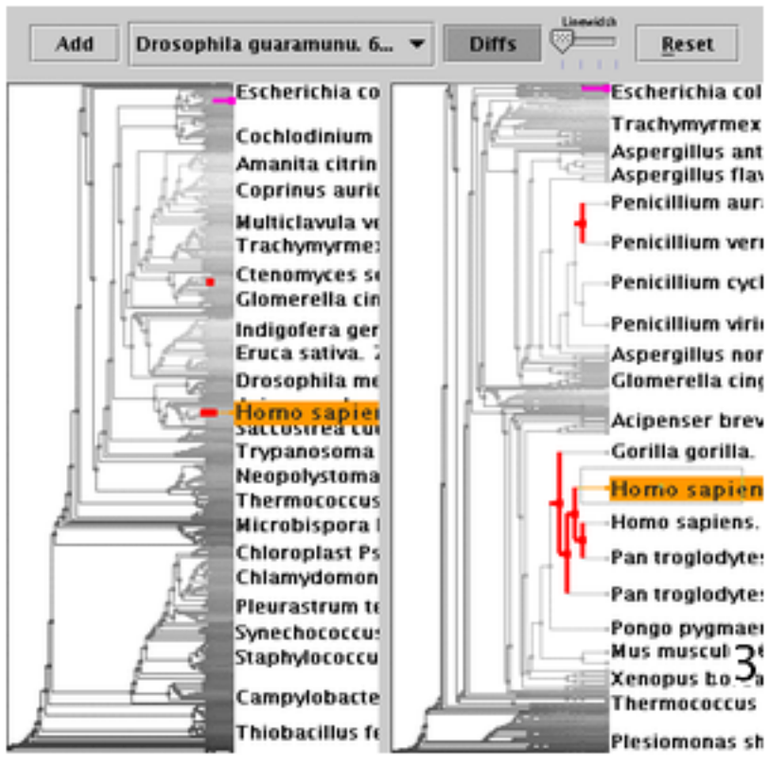


guaranteed visibility

- landmarks stay visible
- never offscreen
- visible mark even if very squished
- helps guide navigation choices



Accordion Drawing Framework

infrastructure for motion, marking, rendering

example datasets

- trees
  - built-in hierarchical structure
- gene sequences
  - dense, partially vertically correllated
- transactions in power set space
  - very sparse, huge space

[video]

Outline

Accordion Drawing

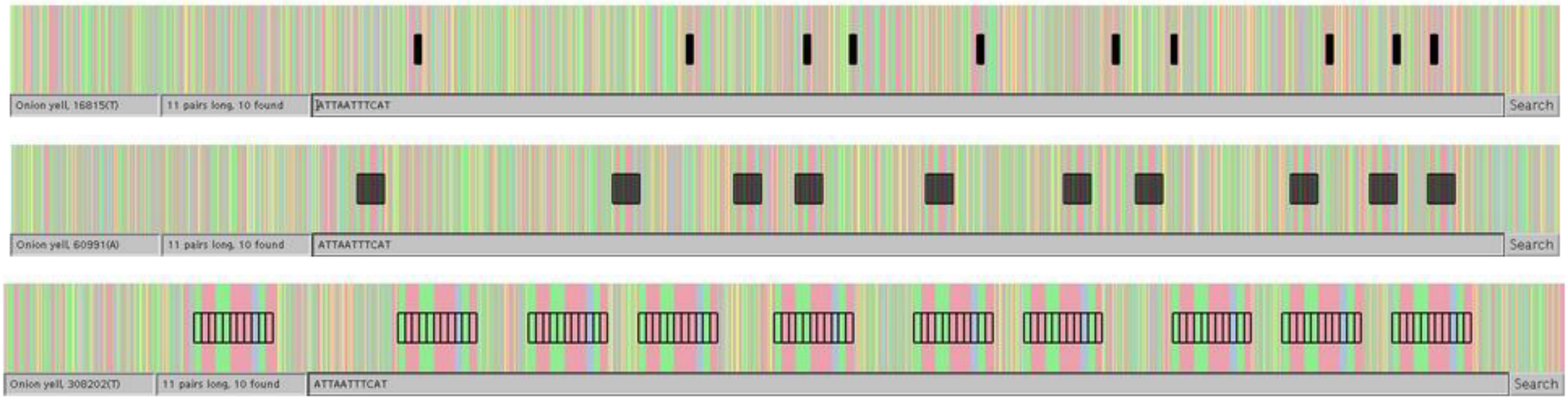
Example Applications

- Trees
- Sequences
- Power Sets

Rubber-Sheet Navigation

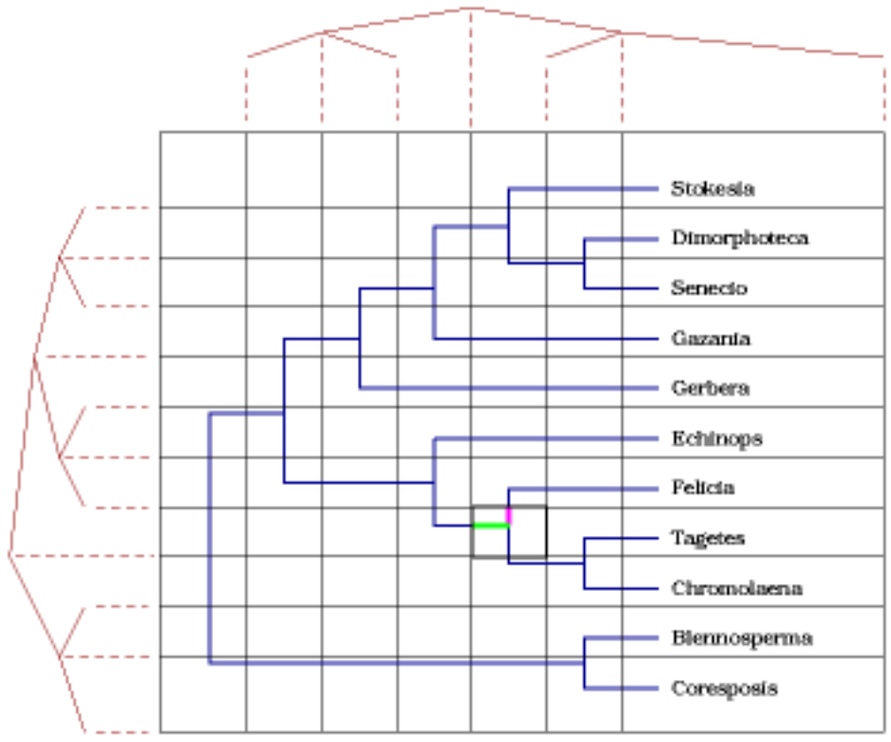
Focus+Context technique

- merge overview and details for single combined view
- rectilinear, multiple foci [Sarkar 94, Robertson 91]



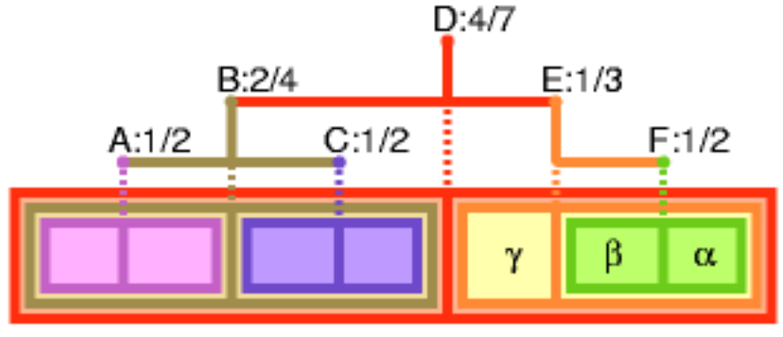
Hierarchical Grid

two directions, horizontal and vertical



two valid interpretations for SplitLines

- linear ordering
- hierarchical subdivision of space
  child splits parent in two



application maps from 2D layout to grid

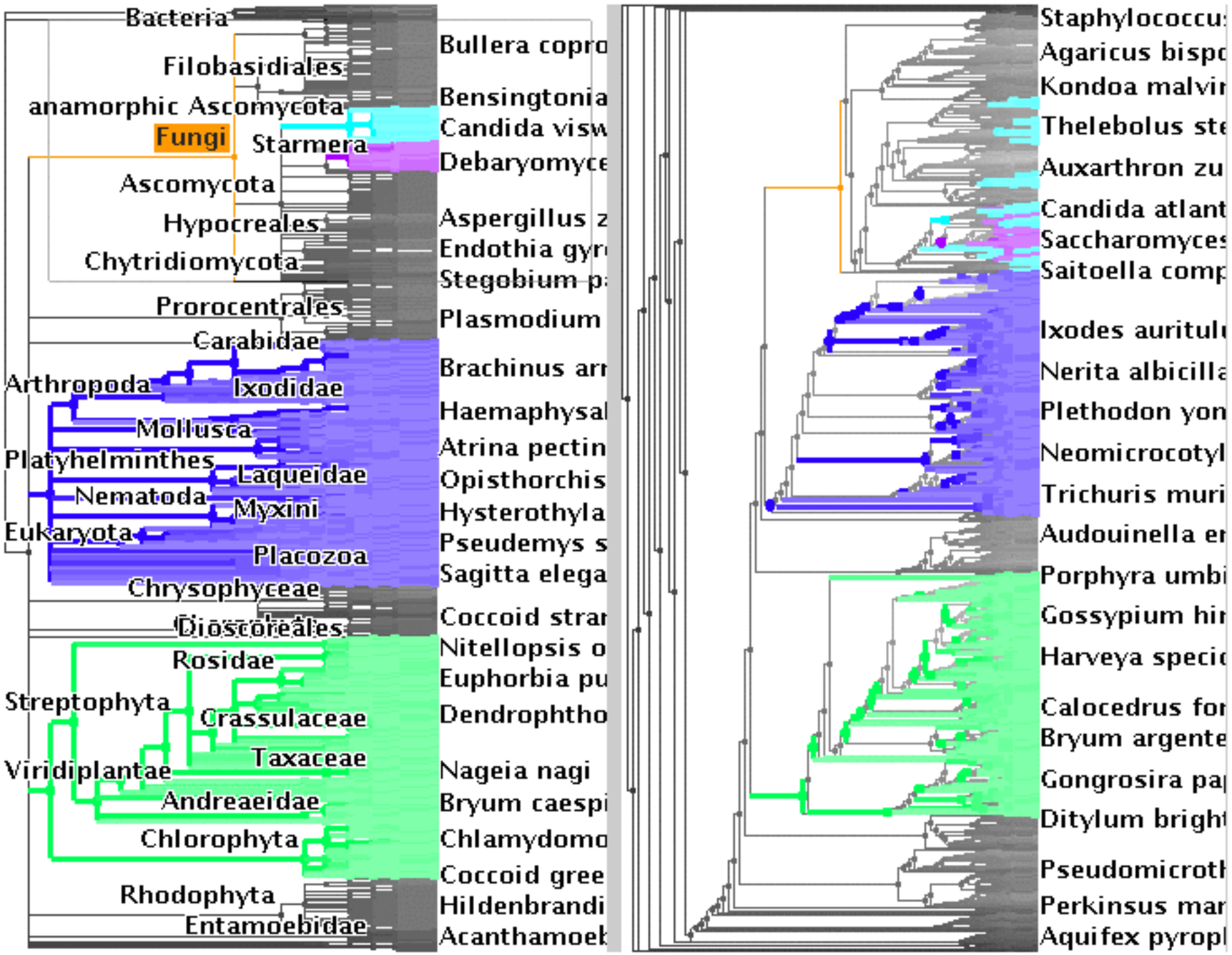
Grid Motion

move a set of SplitLines

- grow several regions simultaneously
- shrink the rest

- new O(k log n) algorithm
  - k = # lines to move
  - n = # lines total
- robust calculation, move each line only once

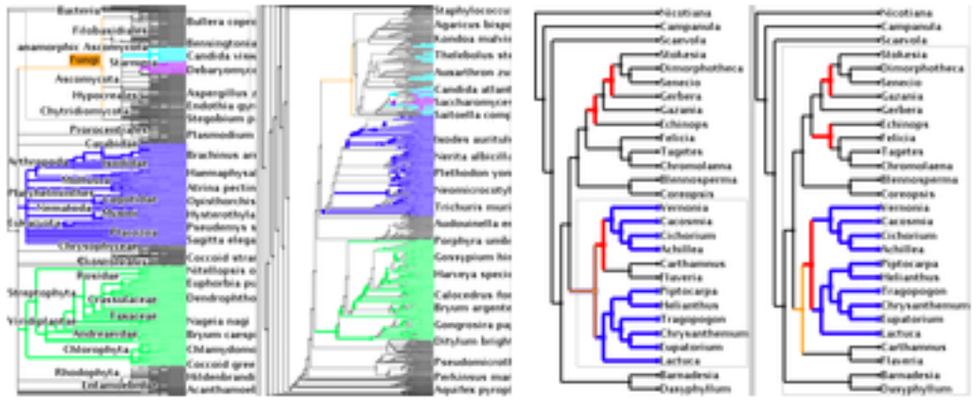
Guaranteed Mark Visibility



Marks

regions of interest shown with color highlight

- differences between datasets
- search results
- user selections



guide navigation

- safe to avoid empty places
  no false negatives, lack of mark meaningful
- investigate marked areas
  squished marks are visible placeholders
  seeing details still requires navigation

provide landmarks

- relative positions stay the same
- "green area I looked at first is underneath blue one"

Guaranteed Visibility

infrastructure needed for efficient computation

relief from exhaustive exploration

- missed marks lead to false conclusions
- hard to determine completion
- tedious, error-prone

compelling reason for Focus+Context

- controversy: does distortion help or hurt?
- strong rationale for comparison

constraint to fit everything in viewport

- instead could show indirectly
- ideas: Halo [Baudisch 03]

Guaranteed Visibility Previous Work

visibility of abstract information

- effective view navigation [Furnas 97]
- critical zones [Jul and Furnas 98]

How Could Marks Disappear?

moving outside viewport

- choose global Focus+Context navigation
  "tacked-down" borders
  as opposed to free camera motion

Focus+Context Previous Work

combine overview and detail into single view

Focus+Context

- large tree browsing
  - Cone Trees [Robertson et al 91]
  - Hyperbolic Trees [Lamping et al 95, Munzner 97]
  - Space Tree [Plaisant et al 03]
  - DOI Tree [Card and Nation 02]
- global
  - Document Lens [Robertson and Mackinlay 93]
  - Rubber Sheets [Sarker et al 93]

our contribution

- scalability, guaranteed visibility

How Could Marks Disappear?

moving outside viewport

- choose global Focus+Context navigation
  "nailed-down" borders
- as opposed to free camera motion

occlusion

- choose 2D++ layout
- as opposed to 3D layout

culling at subpixel sizes

- develop efficient check for marks when culling

Rendering

rubber sheet navigation challenges

- depth complexity changes quickly
- can be extremely high, thousands of objects per pixel

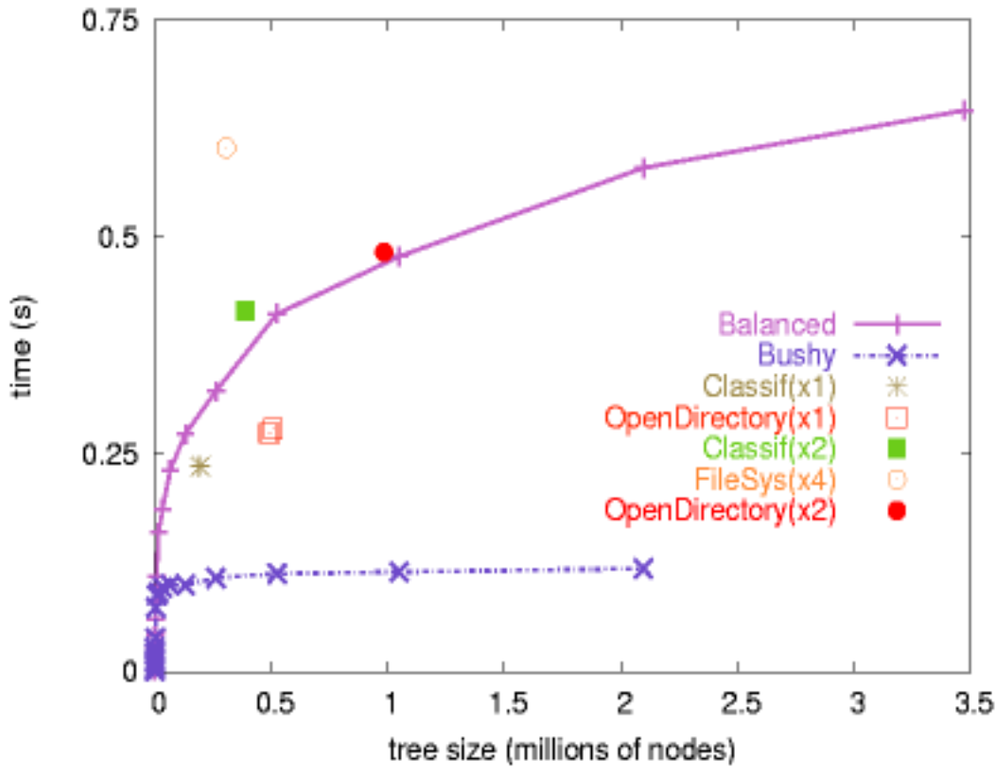
guaranteed visibility challenges

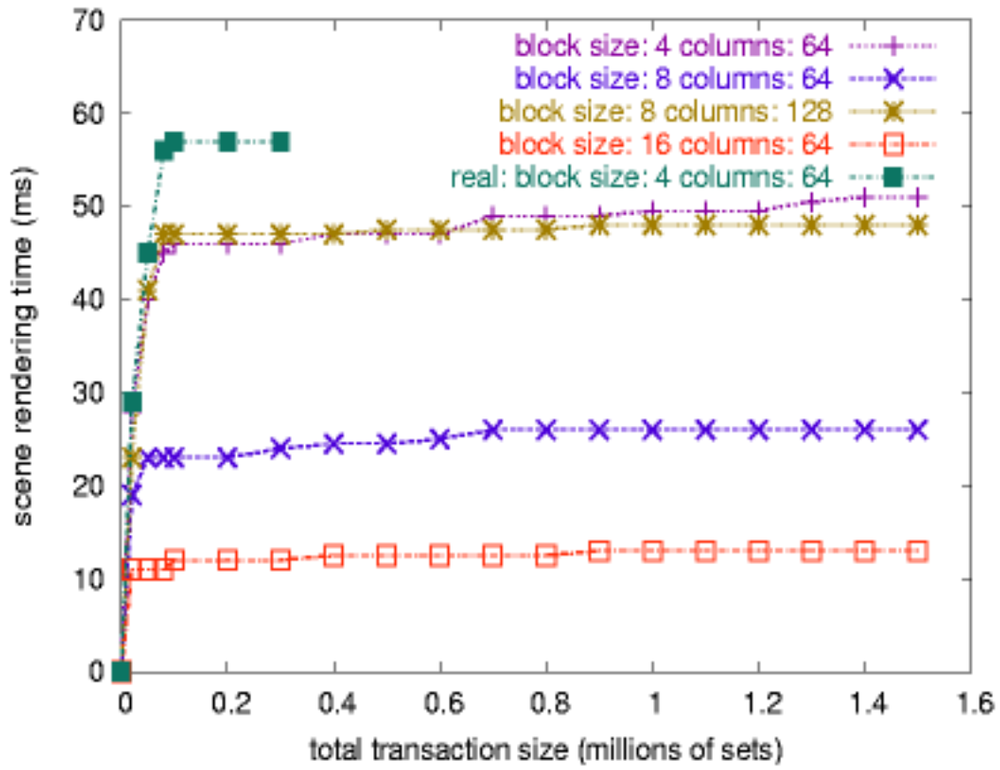
- avoid overculling
  violate guaranteed visibility constraint
- avoid underculling
  inefficient, overdraw same pixel multiple times

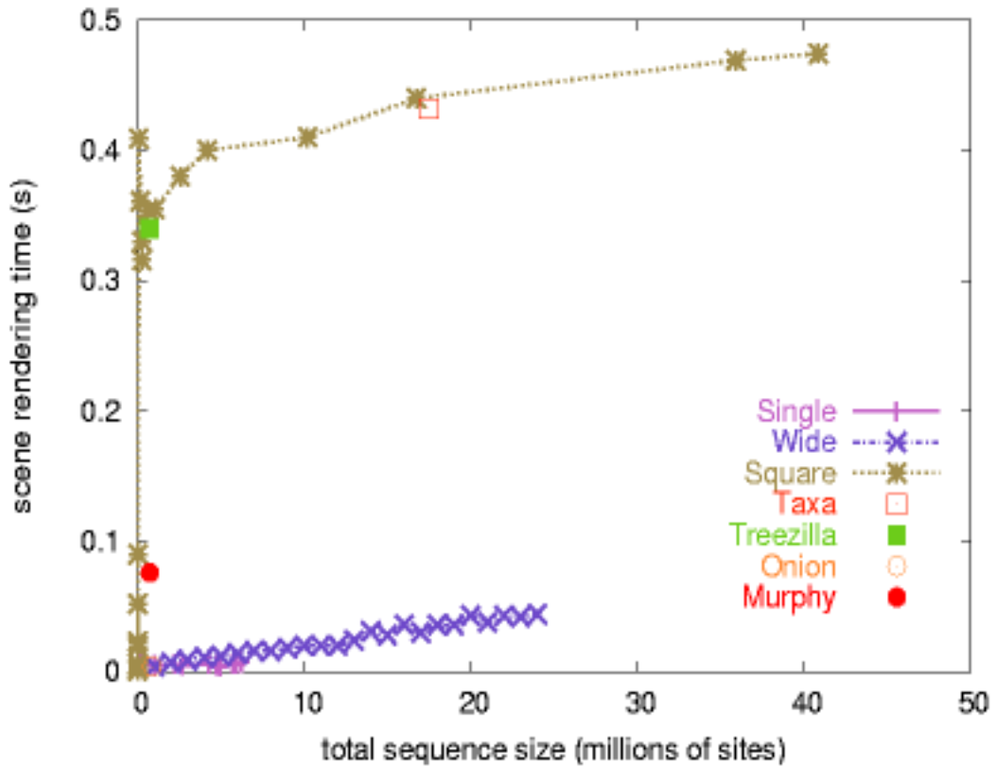
want render time to depend on screen area

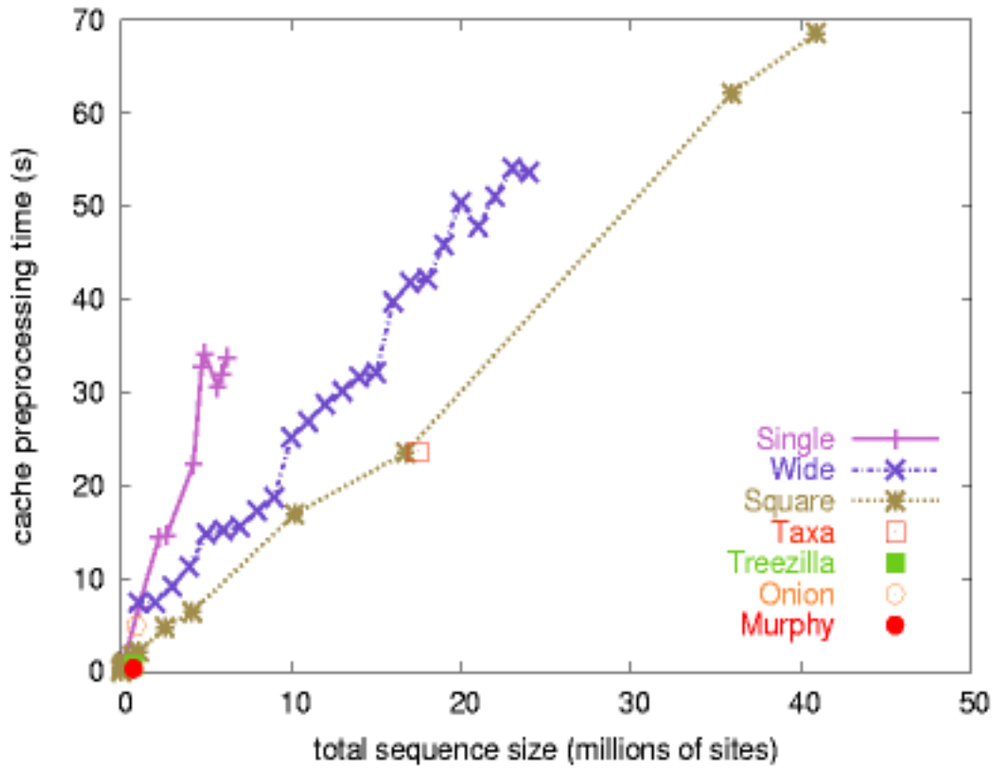
- not size of dataset

Near-Constant Rendering Time

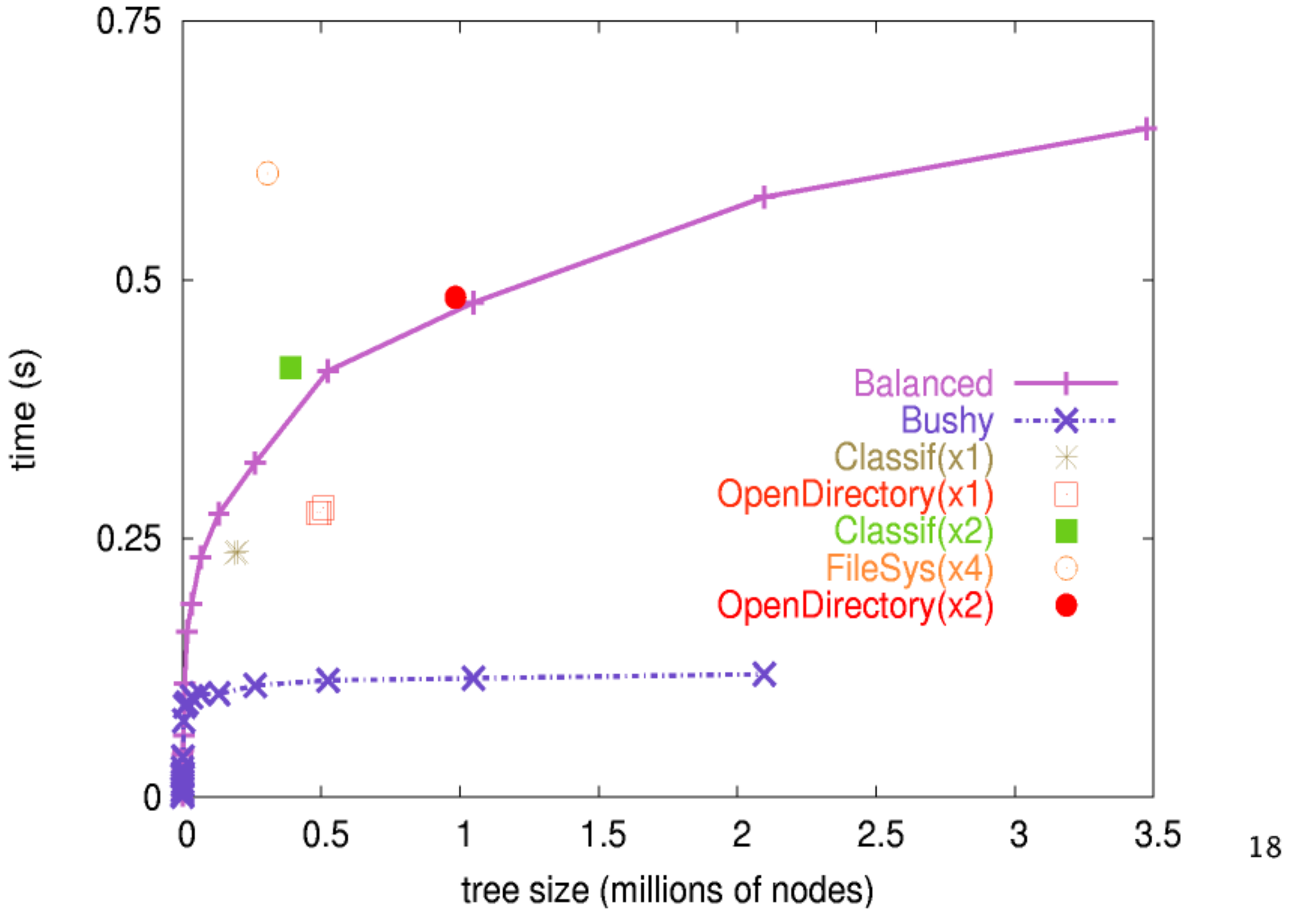




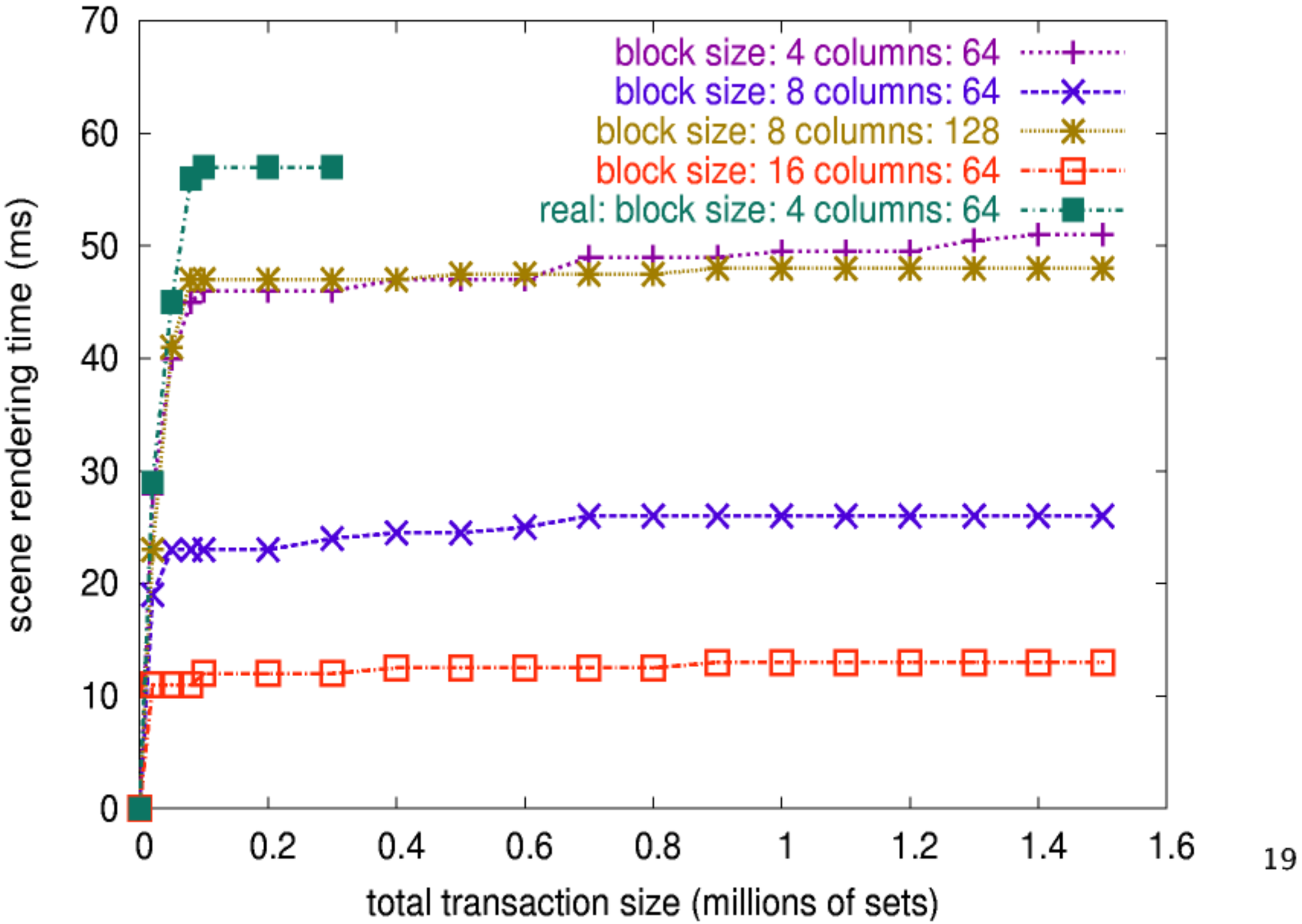




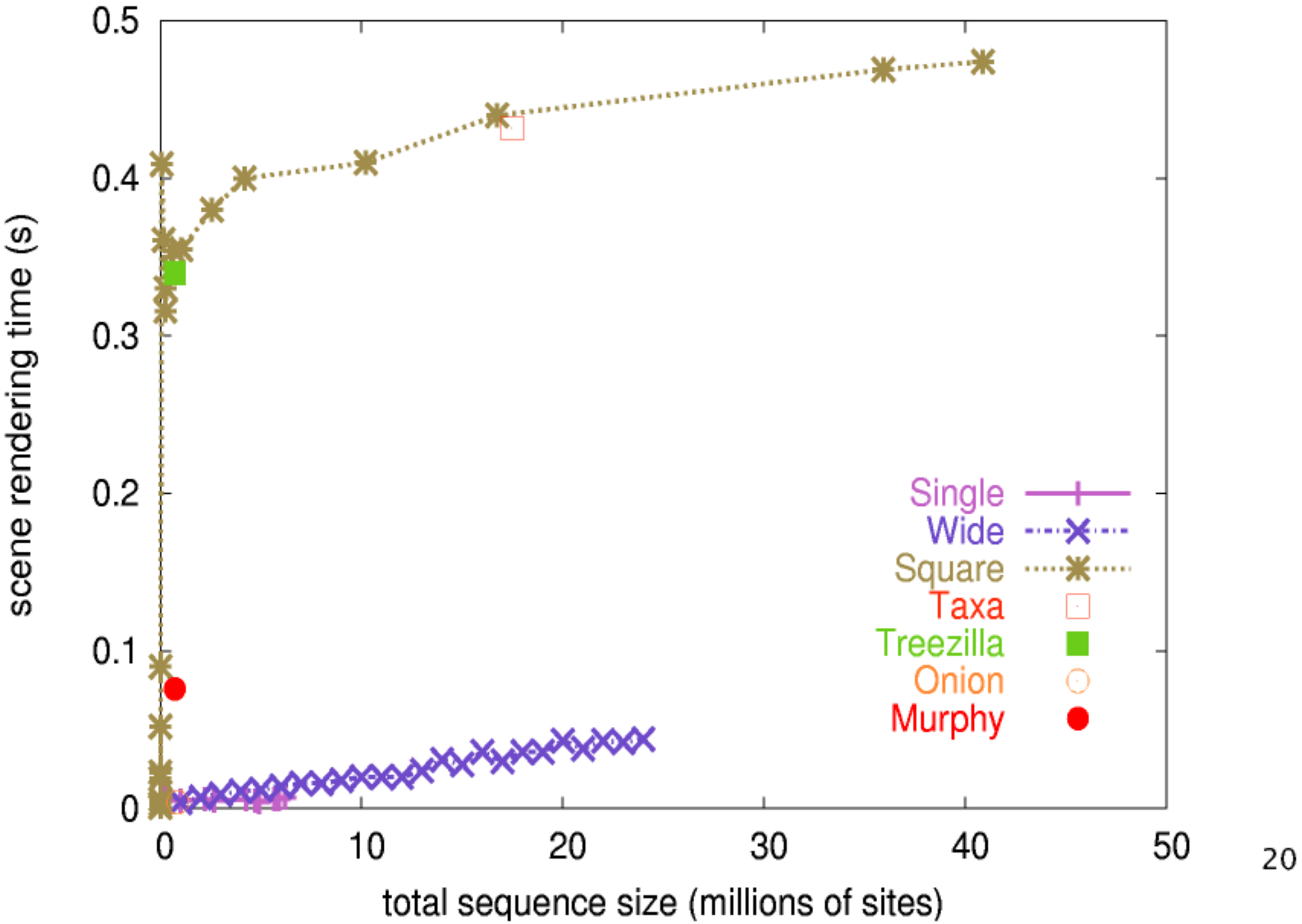
Rendering Time: Trees (3.5M)



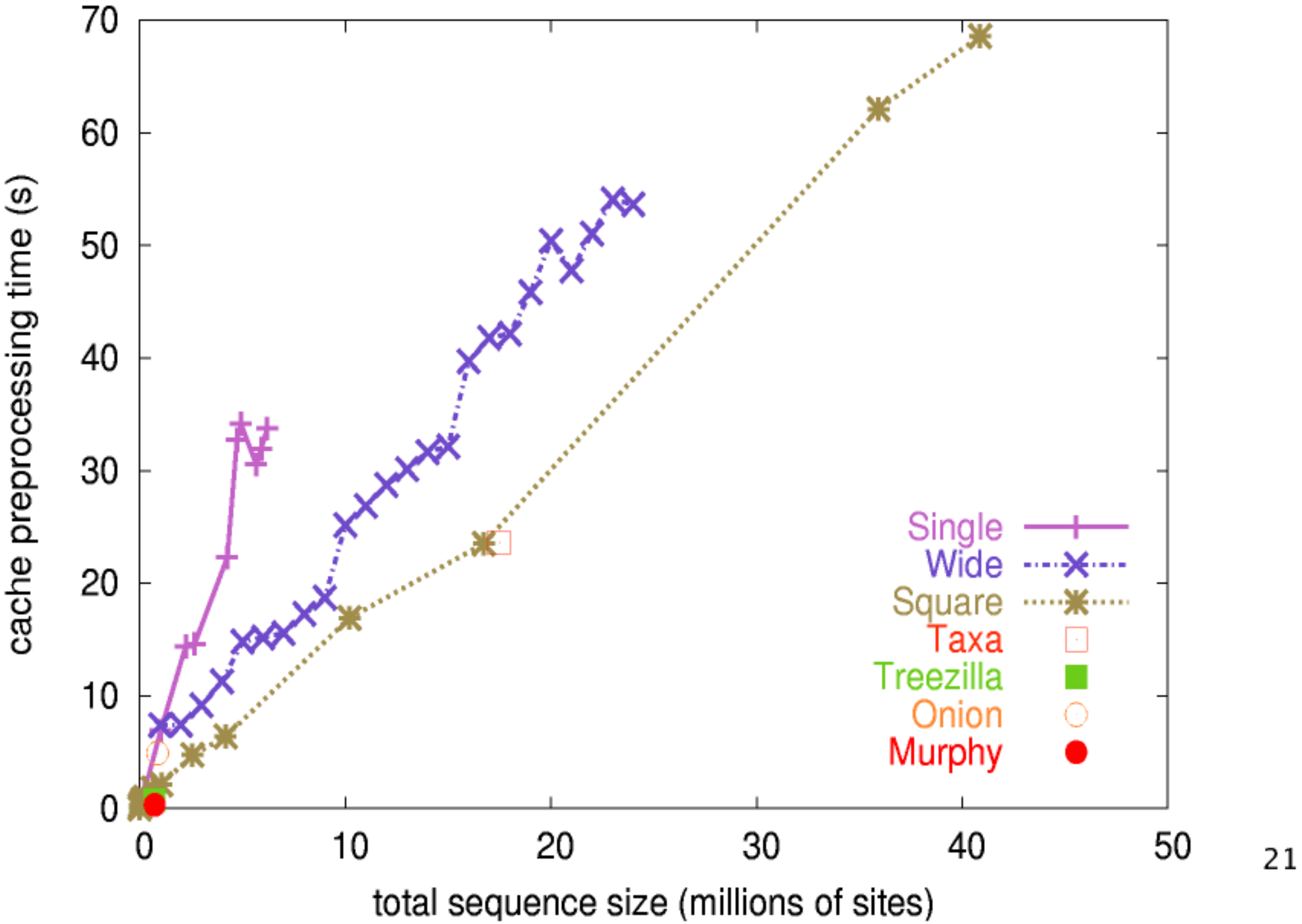
Rendering Time: Power Sets (1.5M)



Rendering Time: Sequences (40M)



Preprocessing Time: Sequences (70 sec)



Scalability Limits

memory footprint is limitation

- everything must fit into main memory

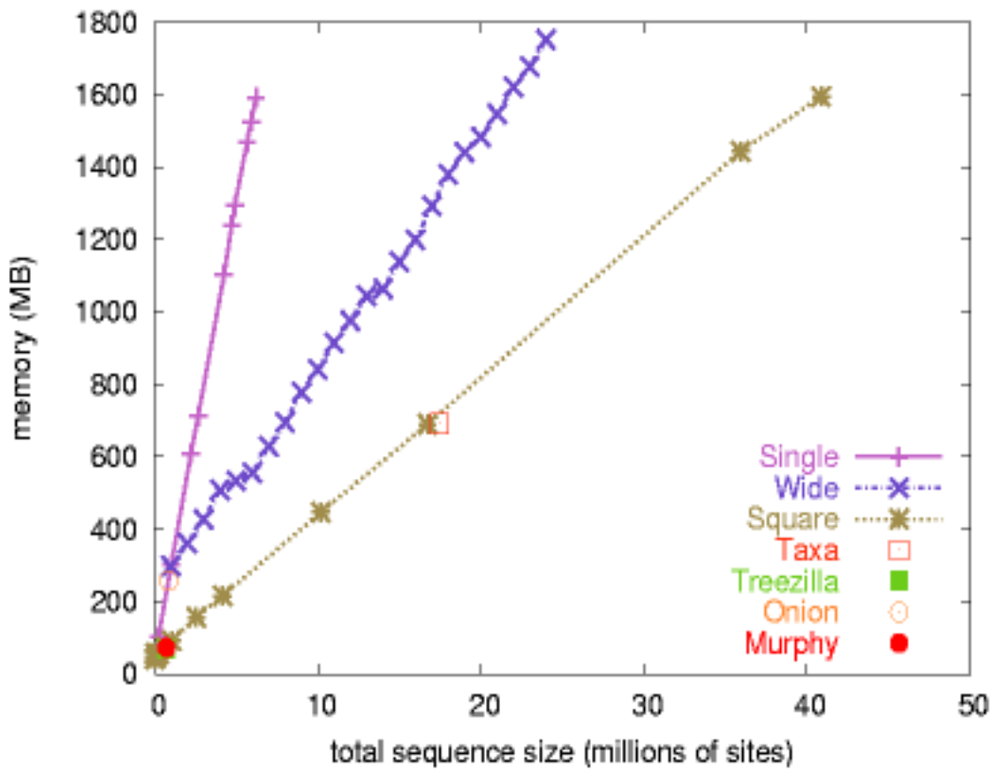
previous systems

- TJ: 250–500K nodes
- SJ 1.7M nodes

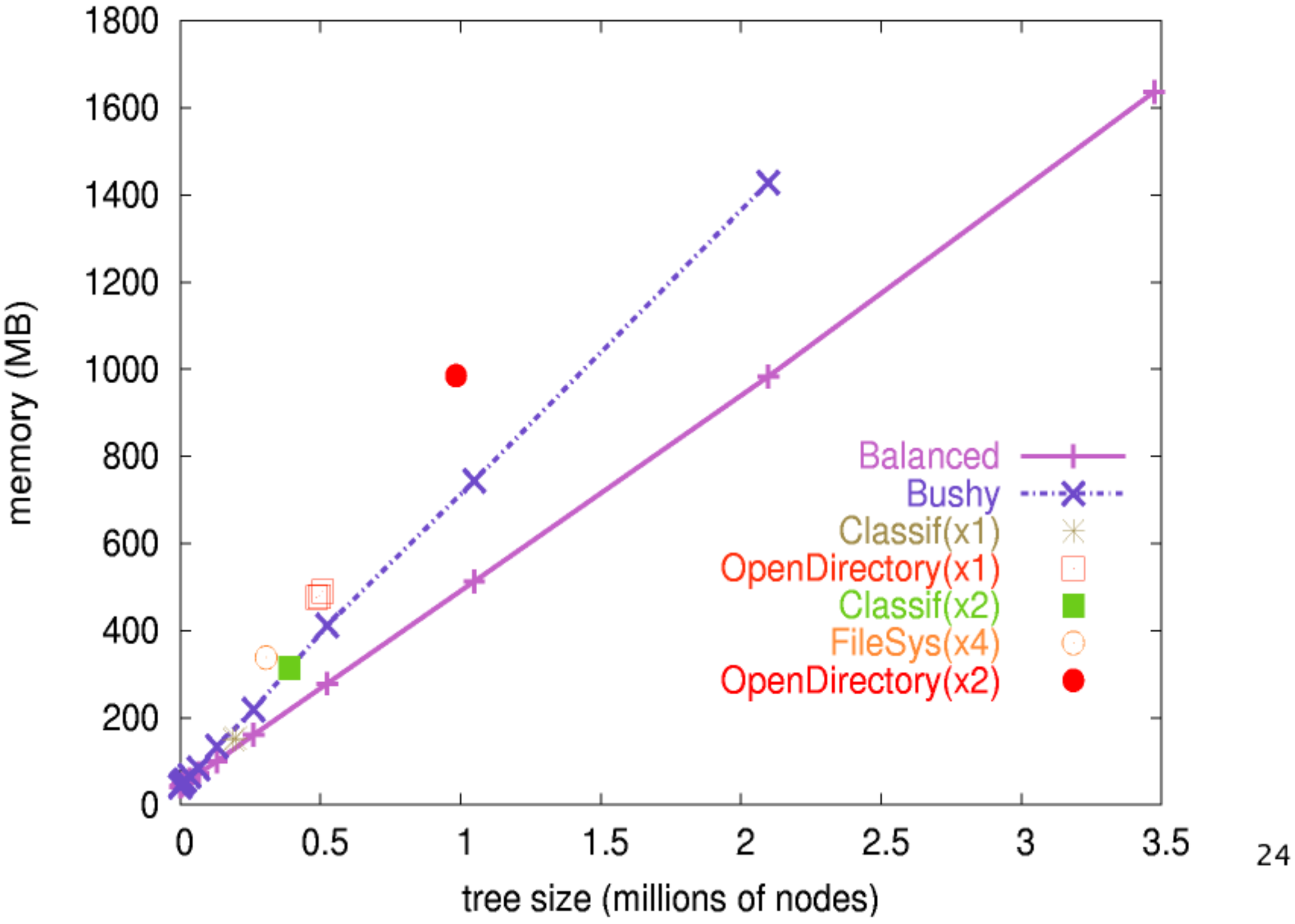
now

- TJ: 3.5M nodes
- SJ: 40M nodes
- PSV: 1.5M nodes

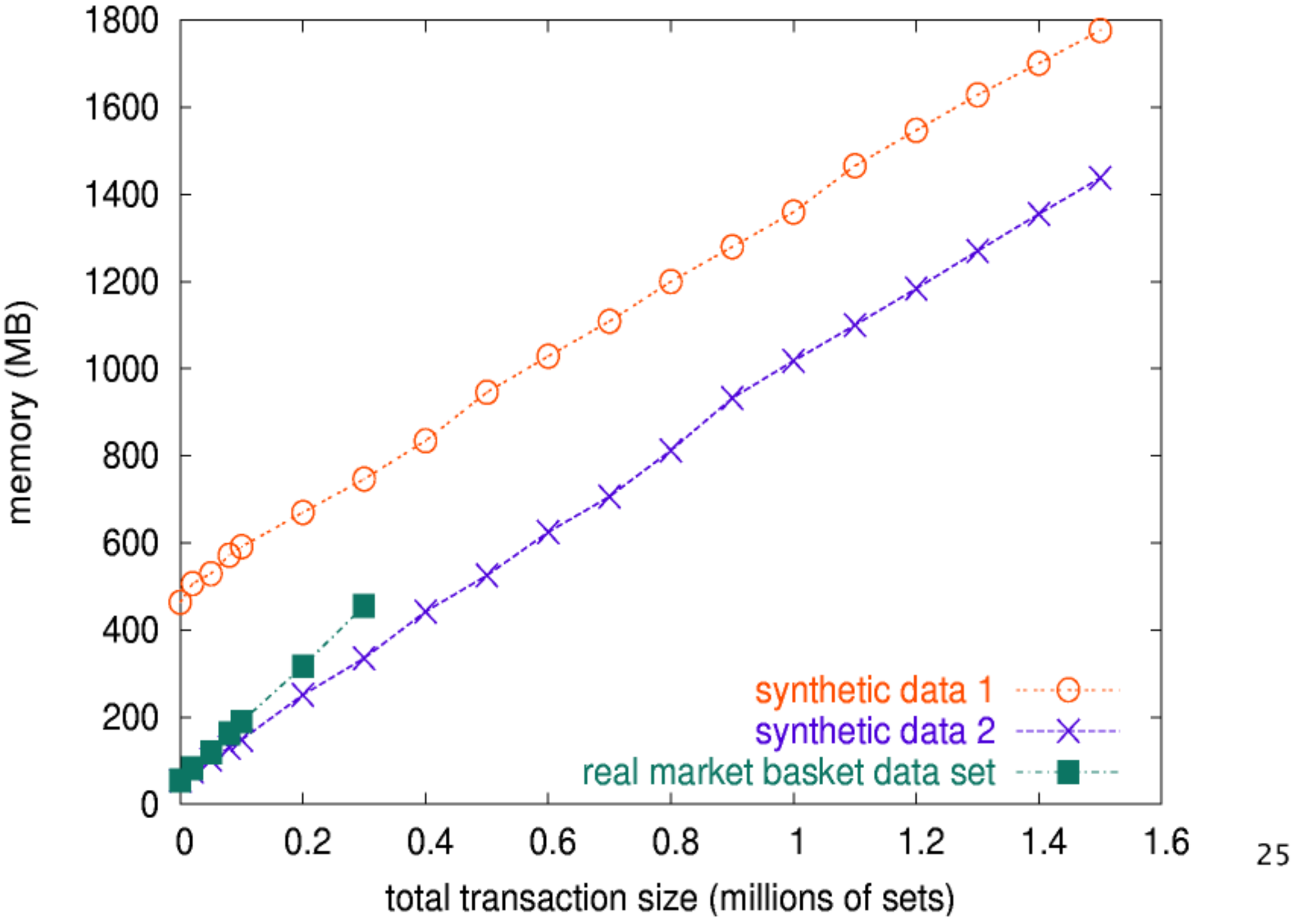
Linear Memory Usage



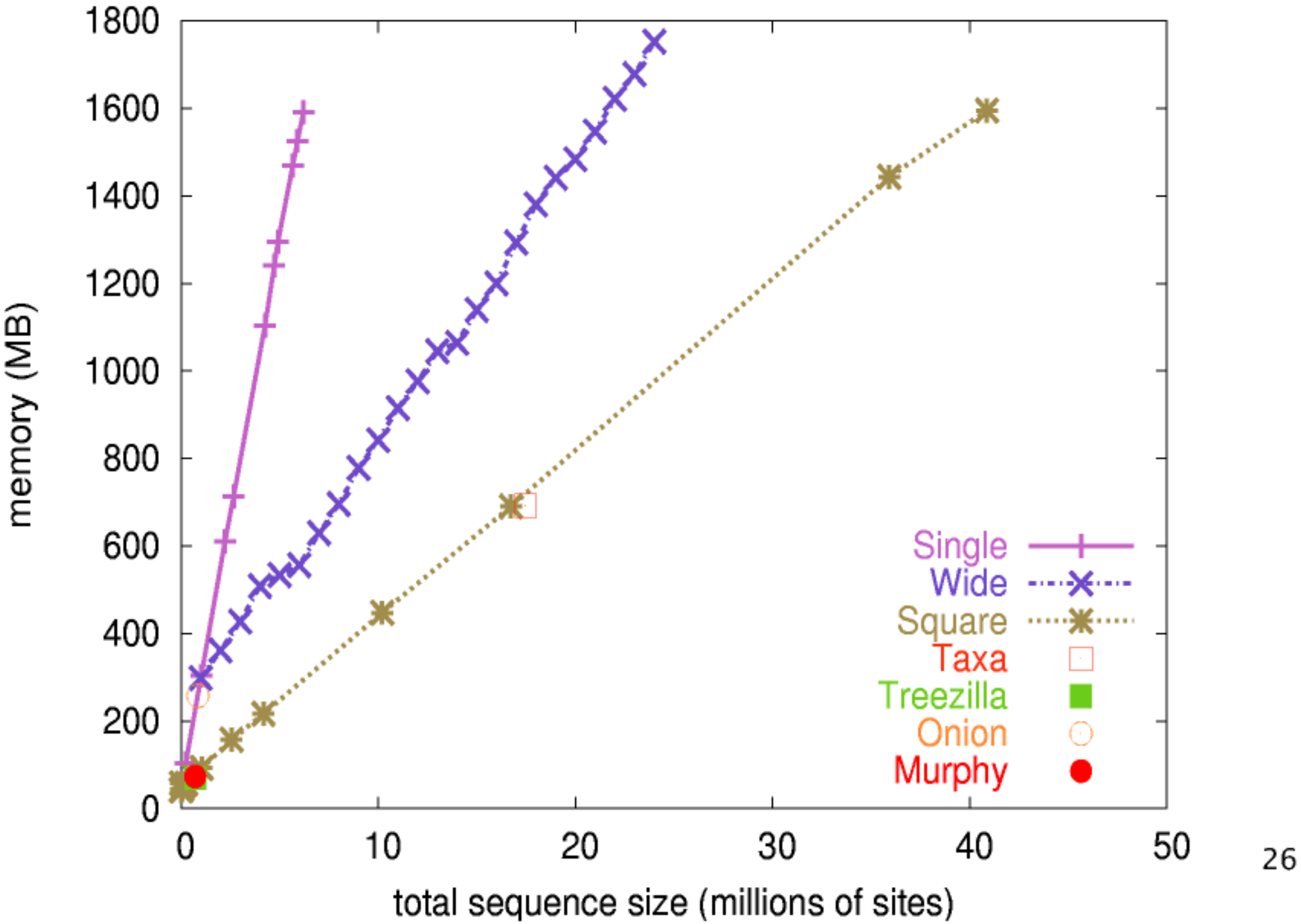
Memory Usage: Trees (3.5M)



Memory Usage: Power Sets (1.5M)



Memory Usage: Sequences (40M)



Outline

Accordion Drawing

Example Applications

- Trees
- Sequences
- Power Sets

TreeJuxtaposer

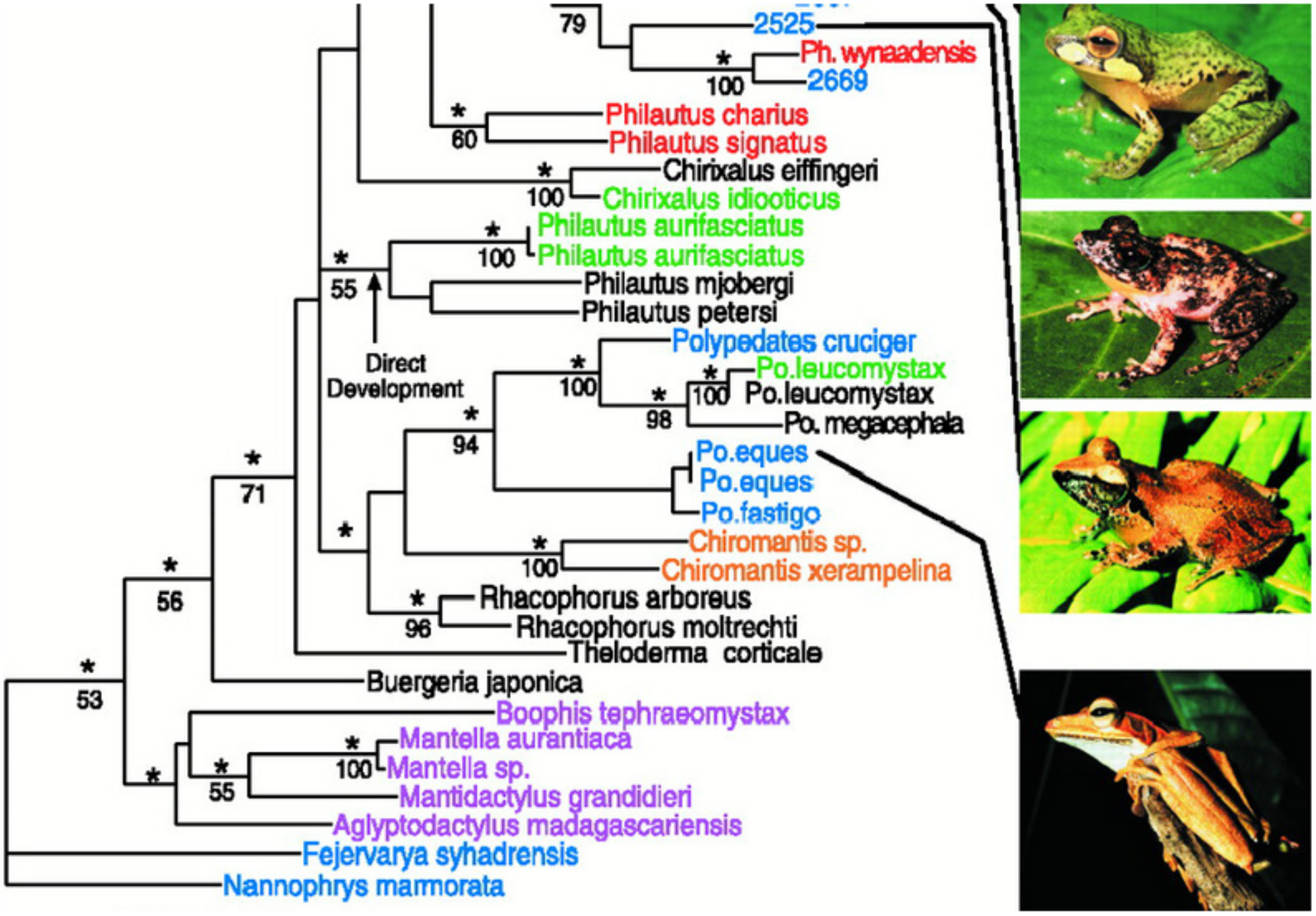
active area: hierarchy browsing

- previous work: browsing
- tree comparison was still open problem

bioinformatics application

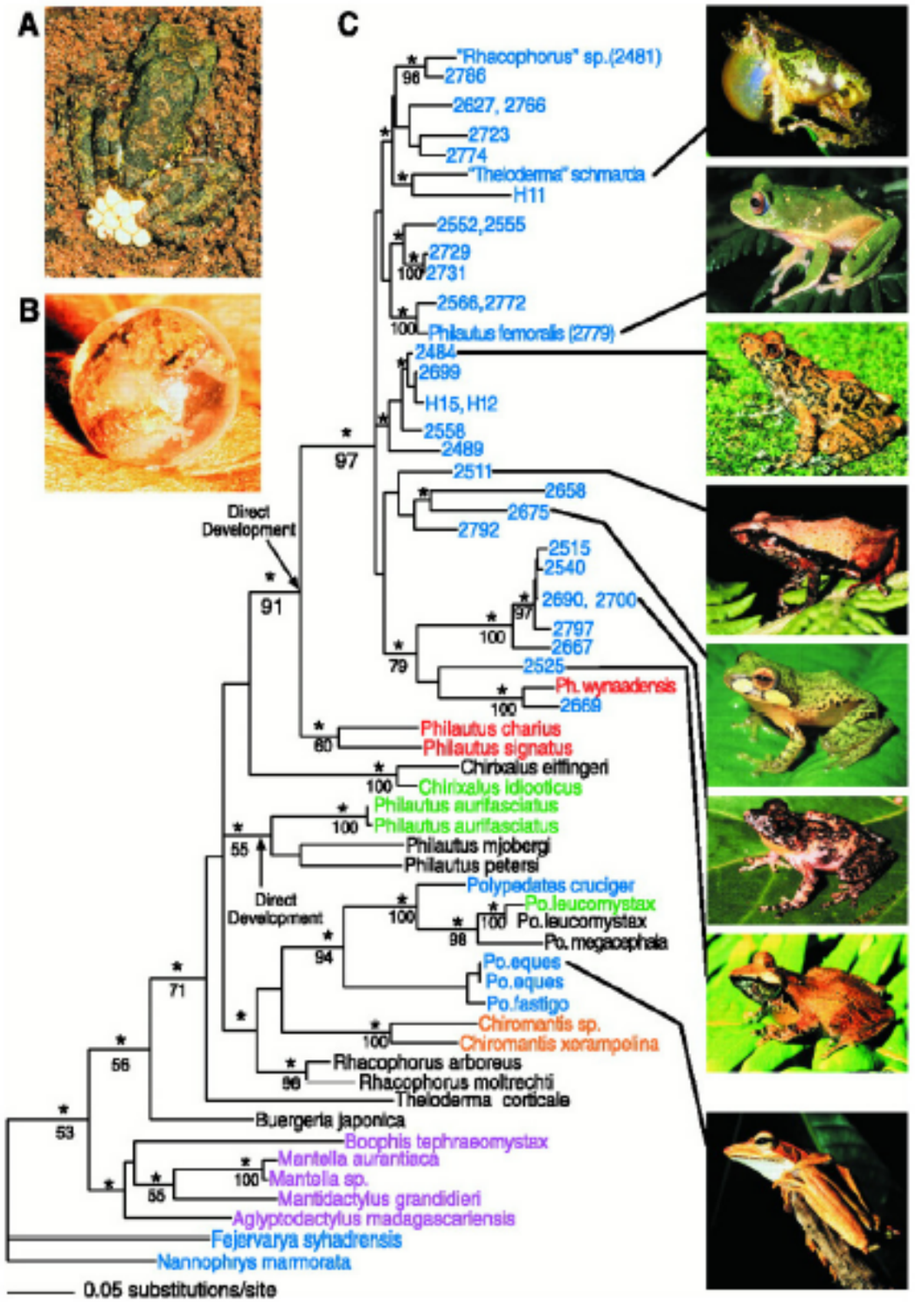
- phylogenetic trees reconstructed from DNA
- rectilinear layout, following conventions

Phylogenetic/Evolutionary Tree



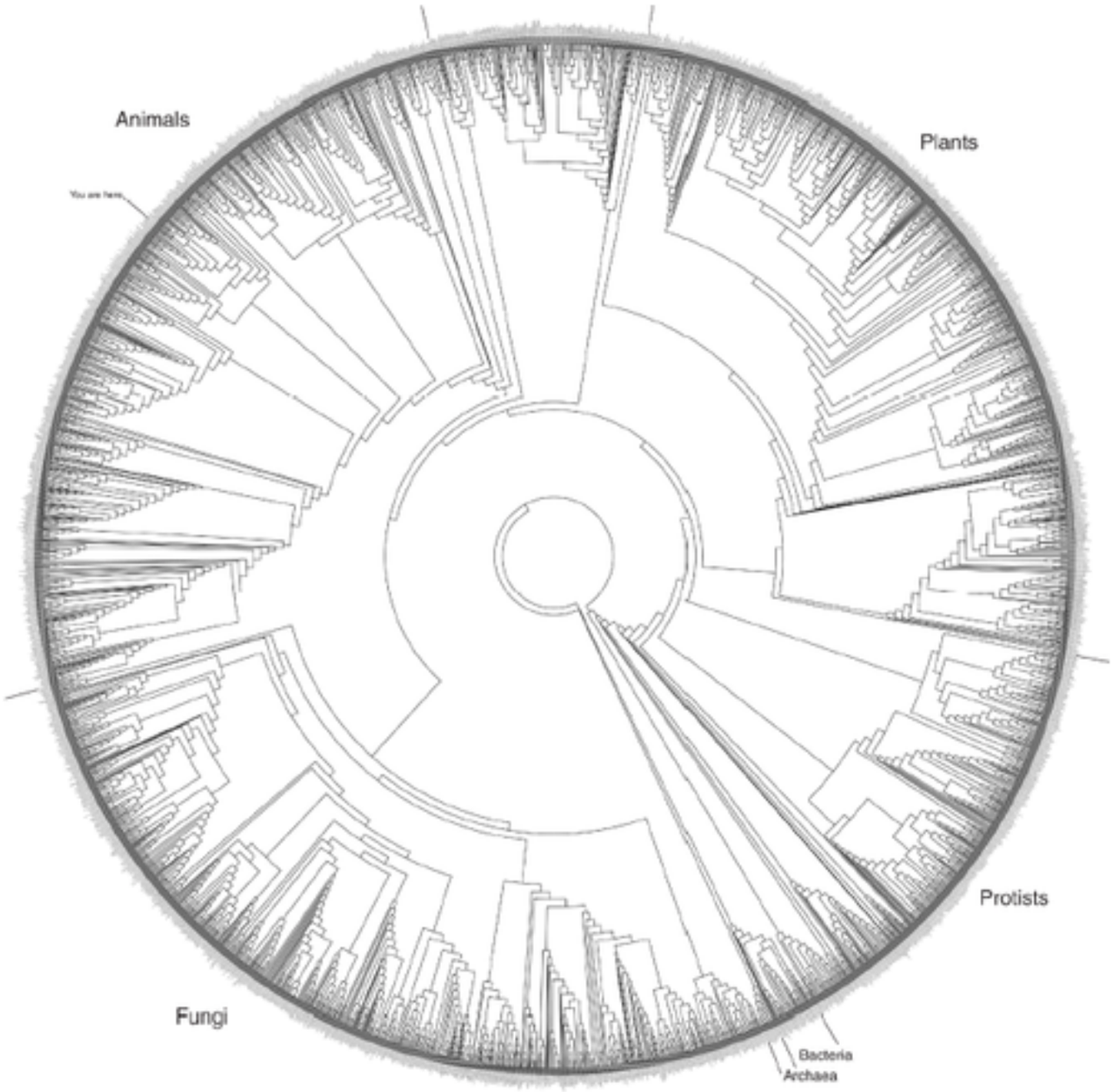
[M Meegaskumbura et al., Science, 298:379 (2002)]

Common Tree Size Now



[M Meegaskumbura et al., Science, 298:379 (2002)]

Tree of Life: 10M Species



[David Hillis, Science, 300:1687, 2003]

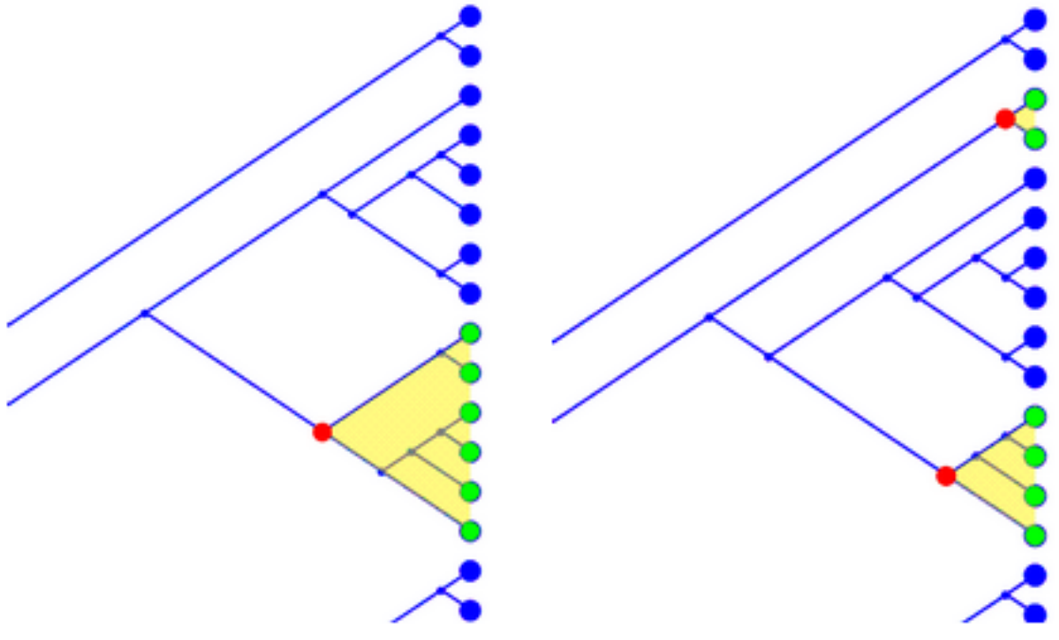
Comparing Trees

multiple trees

- from phylogenetic reconstruction
- algorithms returns many possibilities

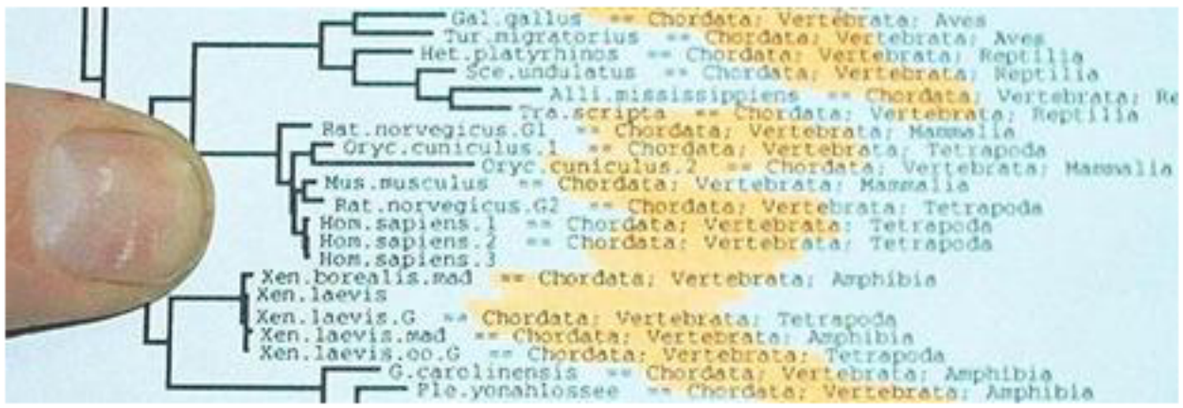
comparing contiguous groups

- clade: ancestor + all descendants
- is a clade in one tree also a clade in other?
- is some group a clade?



Paper Comparison

focus



context

Will Fischer, UT-Austin, May 2003

Biologists' Requirements

reliable detection of structural differences

- rapid identification of interesting spots

analyses of differences in context

- mostly side by side comparison

manipulation of increasingly larger trees

support for multiple platforms

- Java with OpenGL bindings

TreeJuxtaposer Contributions

first interactive tree comparison system
- automatic structural difference computation
- guaranteed visibility of landmark areas

scalable to large datasets
- 250,000 to 500,000 total nodes
  - new work: 3.5 million nodes
- all preprecessing subquadratic
- all realtime rendering sublinear

techniques broadly applicable
- not limited to biological trees

overall winner: InfoVis Contest 2003

Outline

Accordion Drawing

Example Applications

- Trees
- Sequences
- Power Sets

SequenceJuxtaposer

accordion drawing for DNA/RNA

previous work: web-based sequence browsers

- Ensembl, UCSC Genome Browser, NCBI MapViewer
- heavily used, huge server-side databases
- zoom or pan in jumps
- can't see context

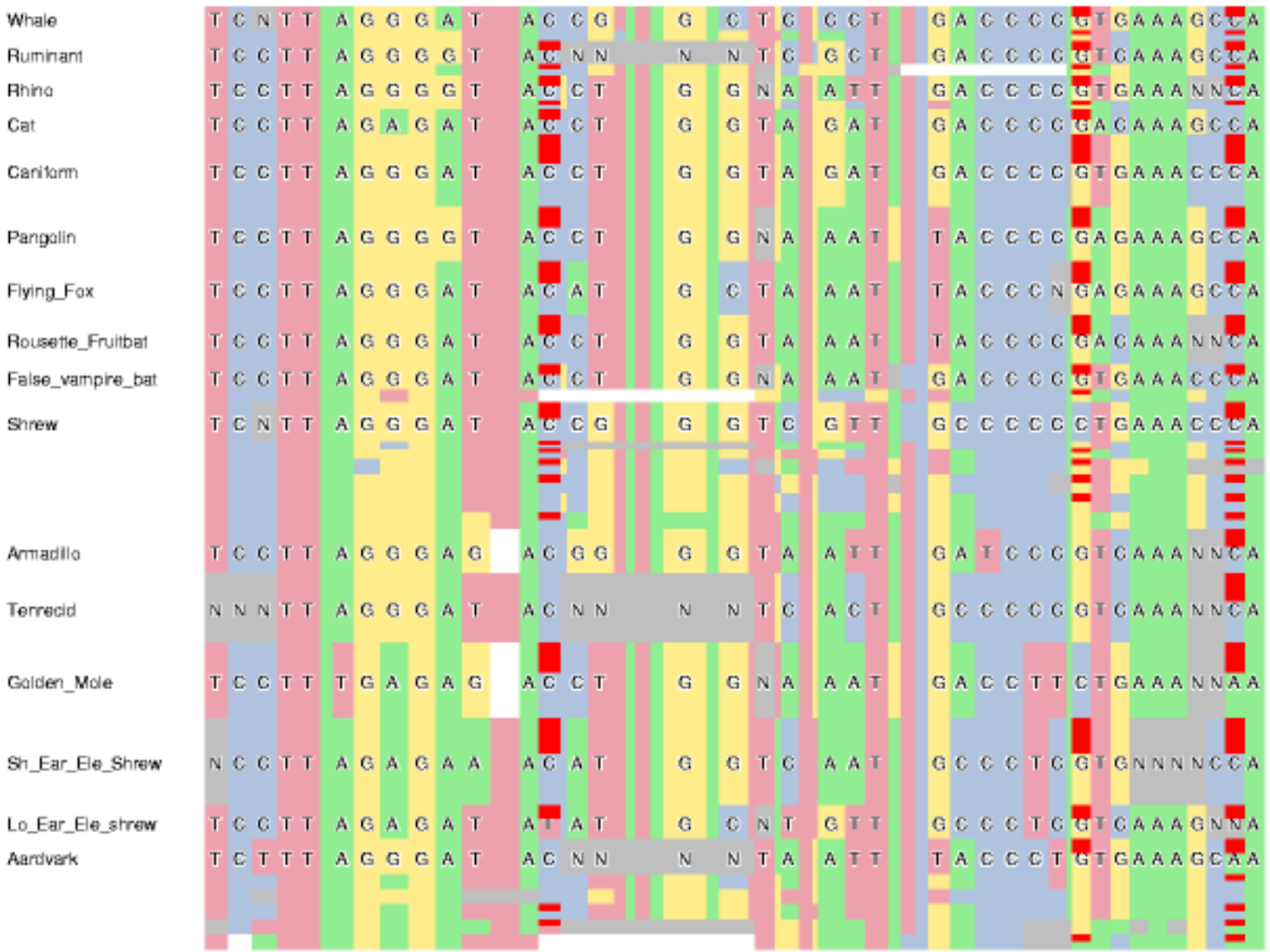
fluid Focus+Context navigation
guaranteed visibility

- establish when these features useful
- proof of concept prototype, eventually merge

SJ Layout

dense grid, following conventions

- rows of sequences
- partially correlated columns of aligned nucleotides



SJ in action

shown on publicly available data

- onion yellows phytoplasma: whole genome
  860 Kbp

- Murphy: 22 genes
  44 mammals x 17000 bp each = 748 Kbp

- Treezilla: single gene
  500 plants x 1428 bp each = 714 Kbp

[videos]

previous paper: 1.7 million nucleotides
currently: 40 million nucleotides

Outline

Accordion Drawing

Example Applications

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PowerSetViewer: Steerable Data Mining

investigating transaction logs

setting parameters for filtering operations

- classic problem: too much or too little
- engine allows parameter changes midstream

have a steering wheel: steerable data mining

need a windshield: visualization

- want meaningful spatial layout as parameters change
- scalability issue: what if filter is null?
  entire log passed through to viz client

Transactions As Sets

market-basket transactions are sets

- A bought {bread, milk, eggs}
- B bought {bread, chocolate, cat food}

alphabet: universe of possible items to buy

- all items in grocery store

space of all possible transactions

- set of all possible sets: power set
- huge, but only sparsely populated
- show distribution of log data within absolute space of possibilities
- accordion drawing preserves relative order

Enumeration of Power Set

order first by cardinality (set size)
within cardinality, order by alphabetical order

- {a},{b},{c},{ab},{ac},{bc},{abc}

very long linear list
wrap scanline-style, at a fixed width

- 128 columns, millions of rows

with conventional display, couldn't see anything

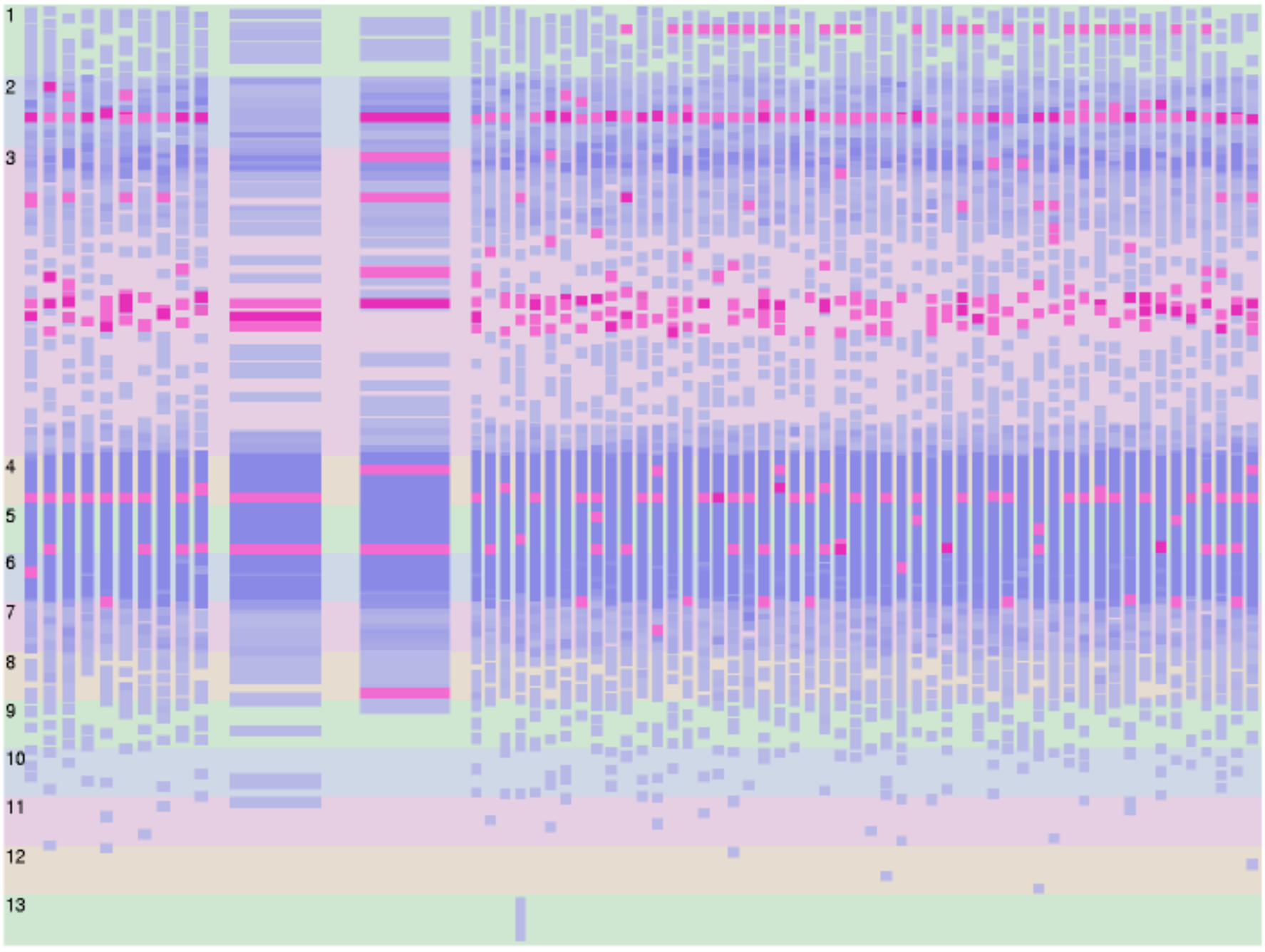
- everything smaller than a pixel

with guaranteed visibility, marks are visible

- construct hierarchical grid on the fly
- add and delete SplitLines as needed
- empty rows collapsed

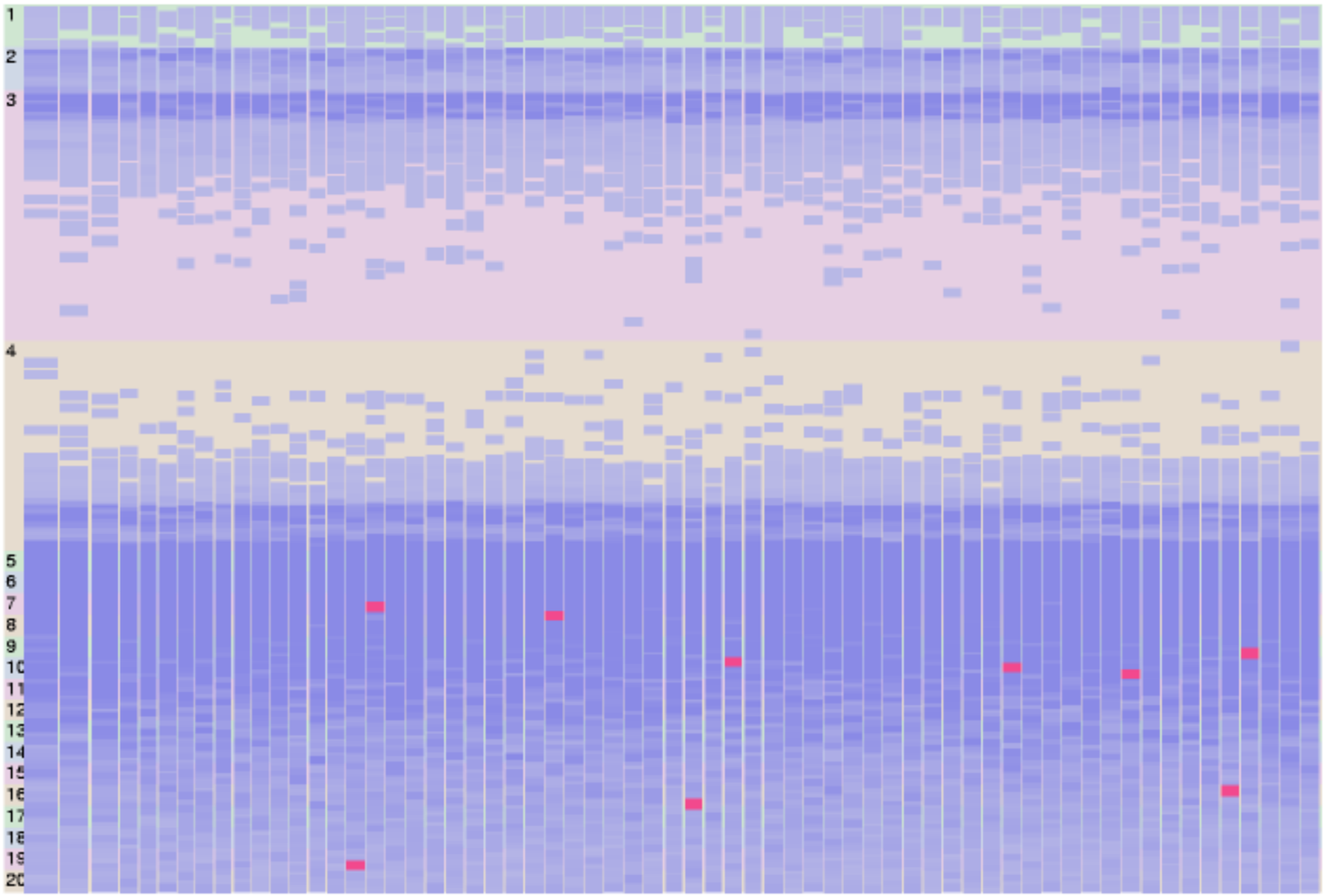
Distribution of Transactions: 90K Log

- alphabet: available courses
- transactions: courses taken by student in one term
- highlighting: grad CS courses



Distribution of Transactions: 300K Log

- alphabet: items in grocery store
- transactions: items bought at once
- highlighting: sets containing specific item



Future Work

trees with weighted edges

sequence alignment editing

protein sequences

linking tree and sequence navigation

open-source release of power set viewer

- data mining: transaction processing

More information

olduvai.sourceforge.net

- open-source release of TJ, SJ

www.cs.ubc.ca/~tmm/papers.html
www.cs.ubc.ca/~tmm/talks.html

- papers, slides, images, movies

Published Papers

TreeJuxtaposer: Scalable Tree Comparison using Focus+Context with Guaranteed Visibility
Tamara Munzner, Francois Guimbretiere, Serdar Tasiran, Li Zhang, and Yunhong Zhou.
SIGGRAPH 2003, published as ACM Transactions on Graphics 22(3), pages 453--462

SequenceJuxtaposer: Fluid Navigation For Large-Scale Sequence Comparison In Context
James Slack, Kristian Hildebrand, Tamara Munzner, and Katherine St. John.
Proc. German Conference on Bioinformatics 2004, pp 37-42

new: PowerSetViewer joint work with
Qiang Kong, UBC
Raymond Ng, UBC

new: TJC, TJC-Q joint work with
Dale Beerman, Virginia
Greg Humphreys, Virginia