



# Tree Comparison Contest: TreeJuxtaposer

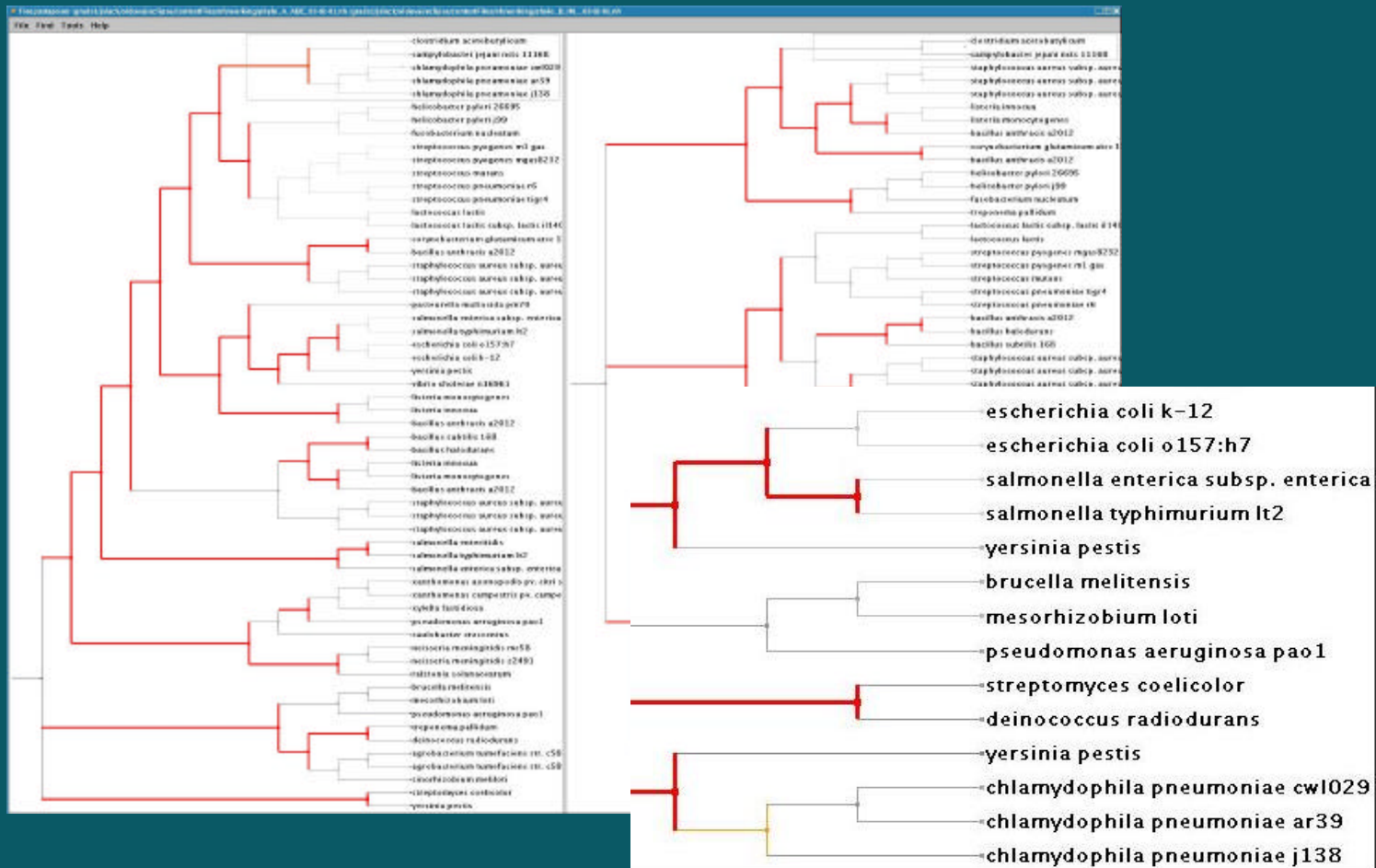
*James Slack, Tamara Munzner (UBC)*

*François Guimbretière (Maryland)*

*October 19, 2003*

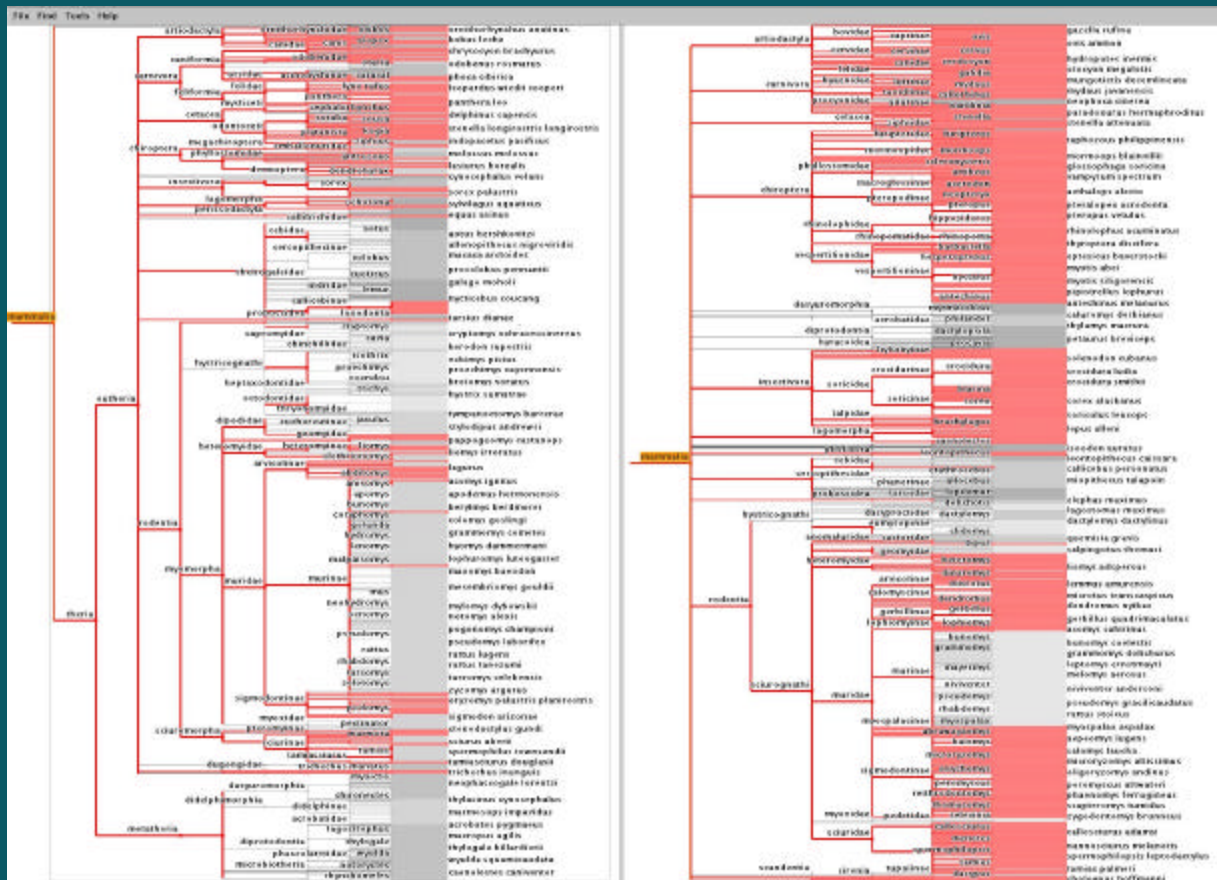
- [illegible]

- Differences marked automatically in red
  - Visually highlight exact points of topological change



- Figure 10. Phylogenetic tree of *Staphylococcus* species based on 16S rDNA sequences. The tree is rooted at the bottom and shows the relationships between various species. The species names are listed on the right side of the tree, and the bootstrap values are indicated at the nodes. The tree is color-coded to show different clades: red for *Staphylococcus aureus*, green for *Staphylococcus epidermidis*, blue for *Staphylococcus saprophyticus*, and purple for *Staphylococcus carnosus*.

- Mammalia subtree (6K nodes)
- Greedy label drawing algorithm, label not drawn if overlap

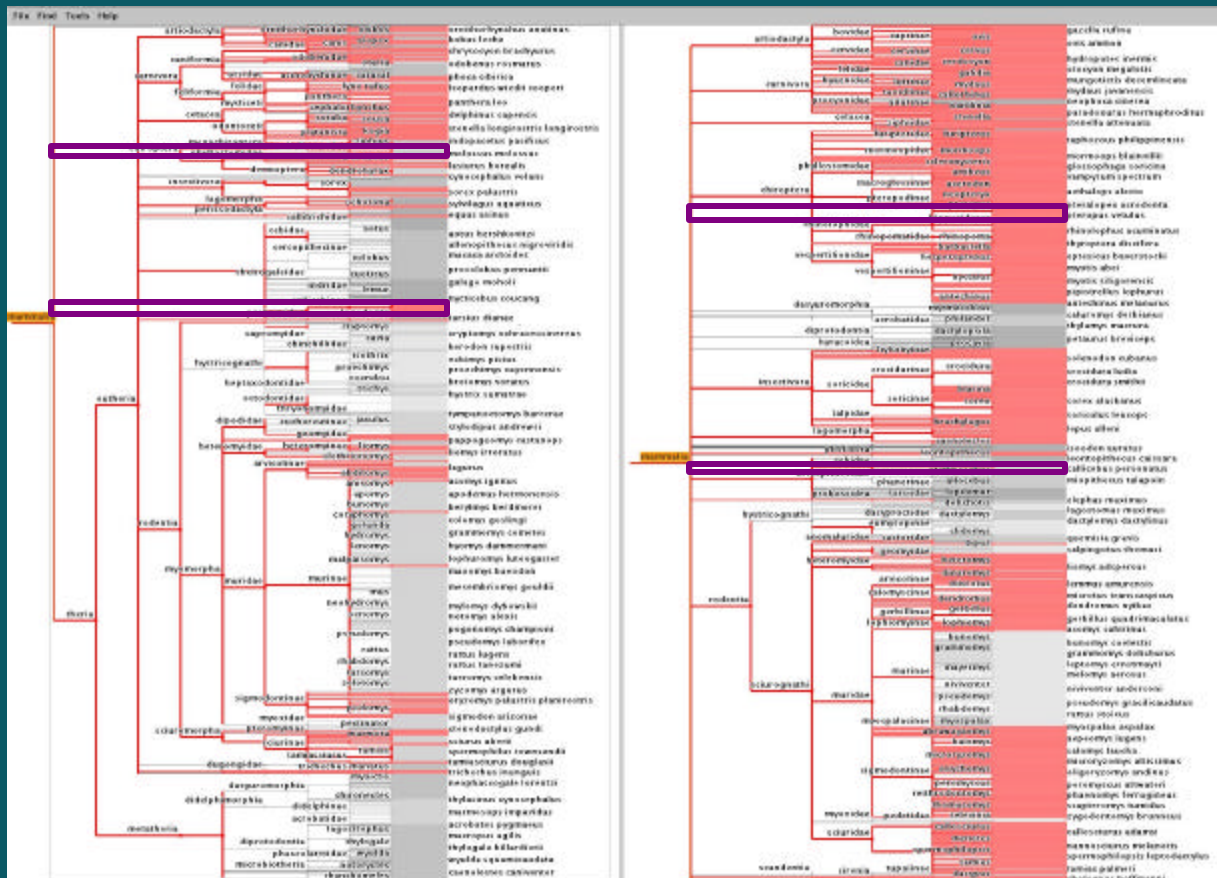




- [illegible]

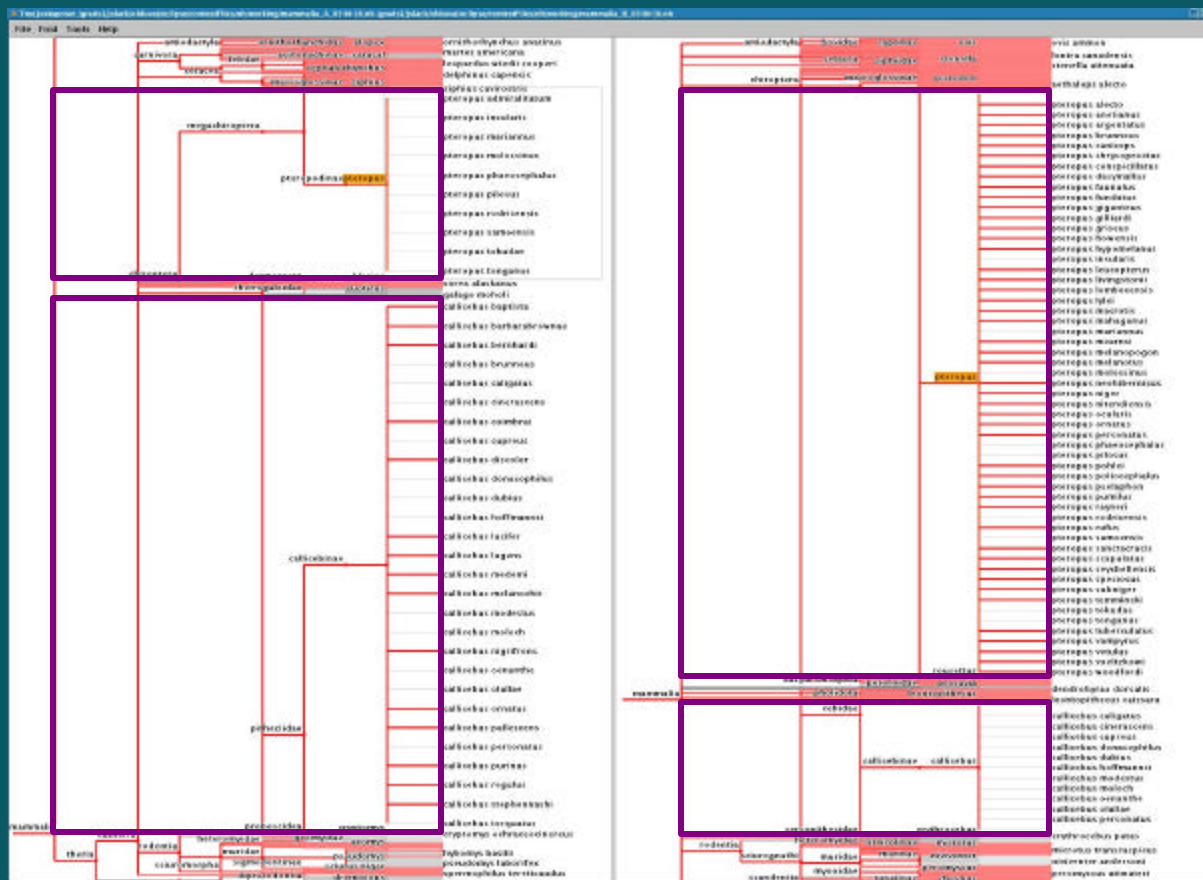
# Classification Trees

- Subtrees can be stretched (rubber sheet)
- Rest of tree compressed, remains in view (tacked borders)



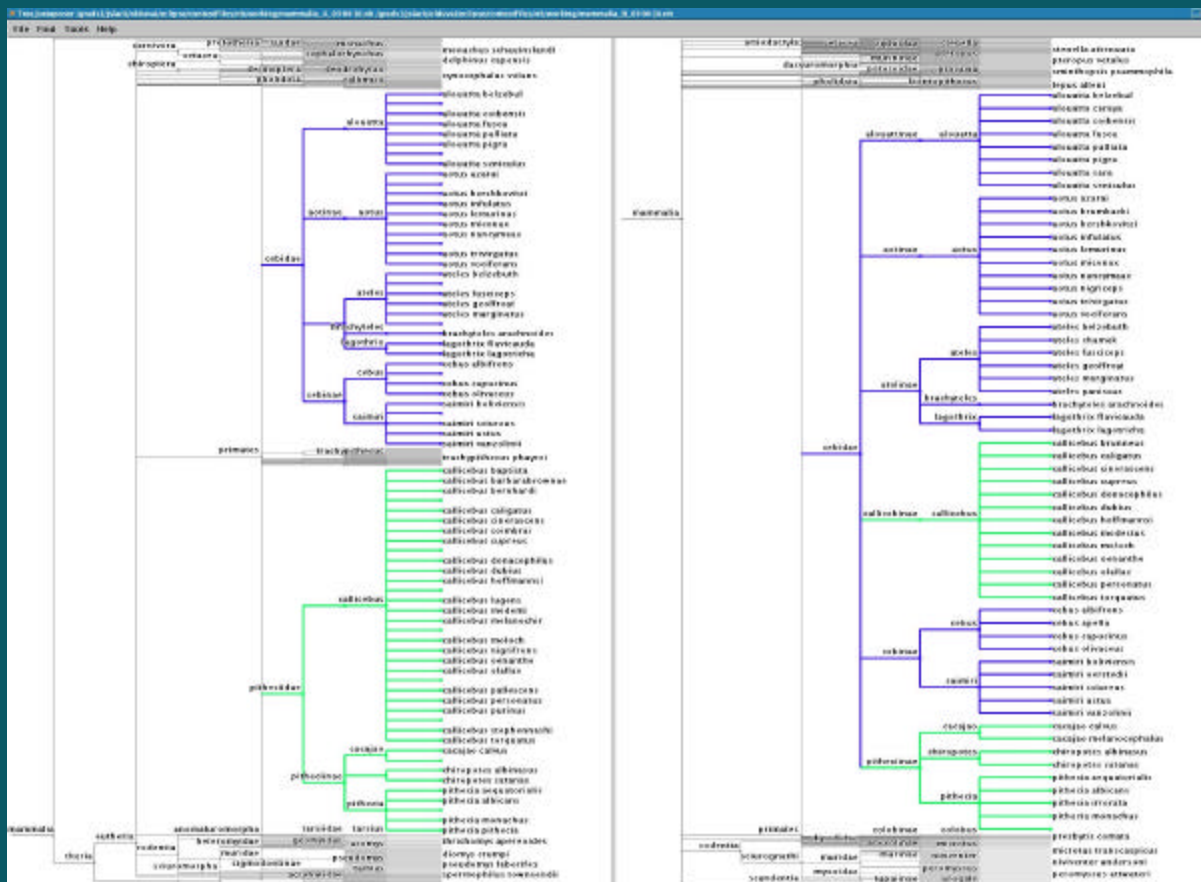
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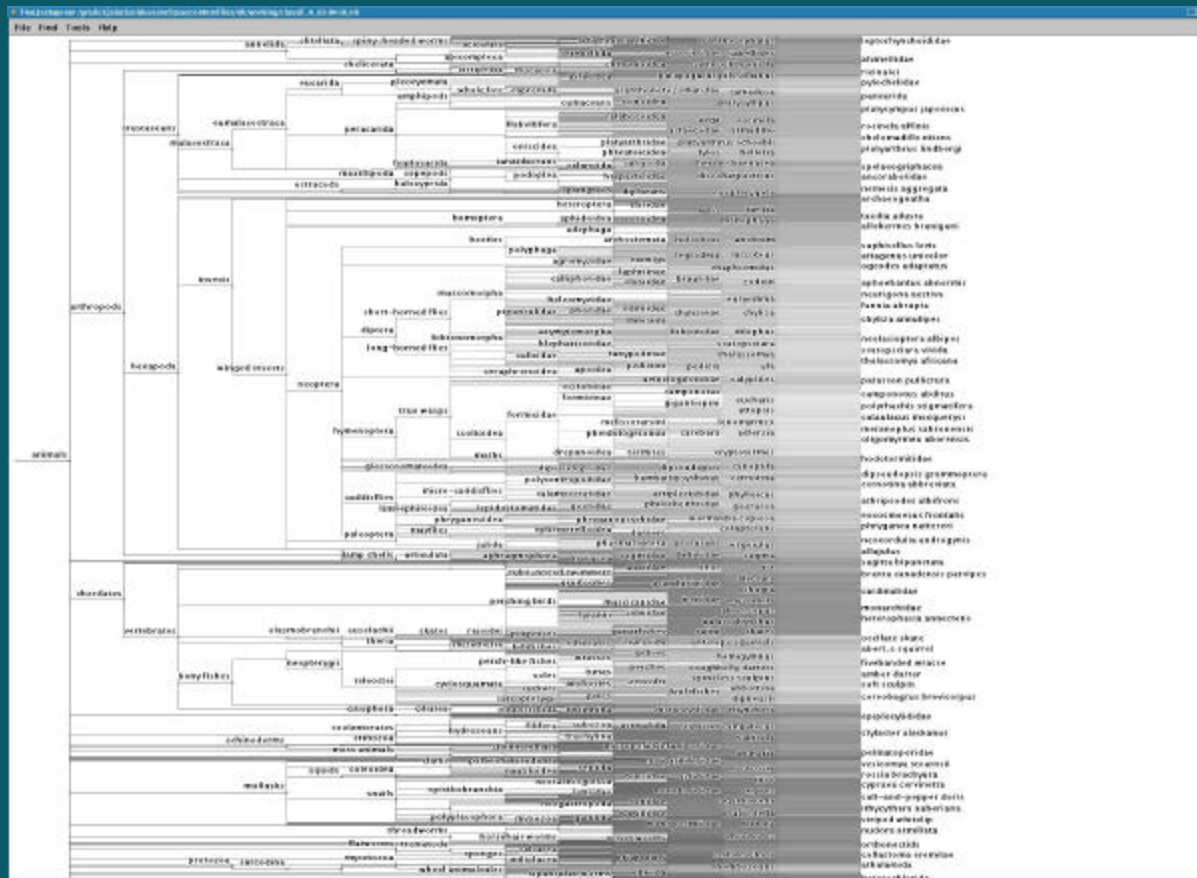


- Select subtree, preprocessed set of best nodes selected
  - Forest may result from best nodes, calculation in  $O(n \log^2 n)$



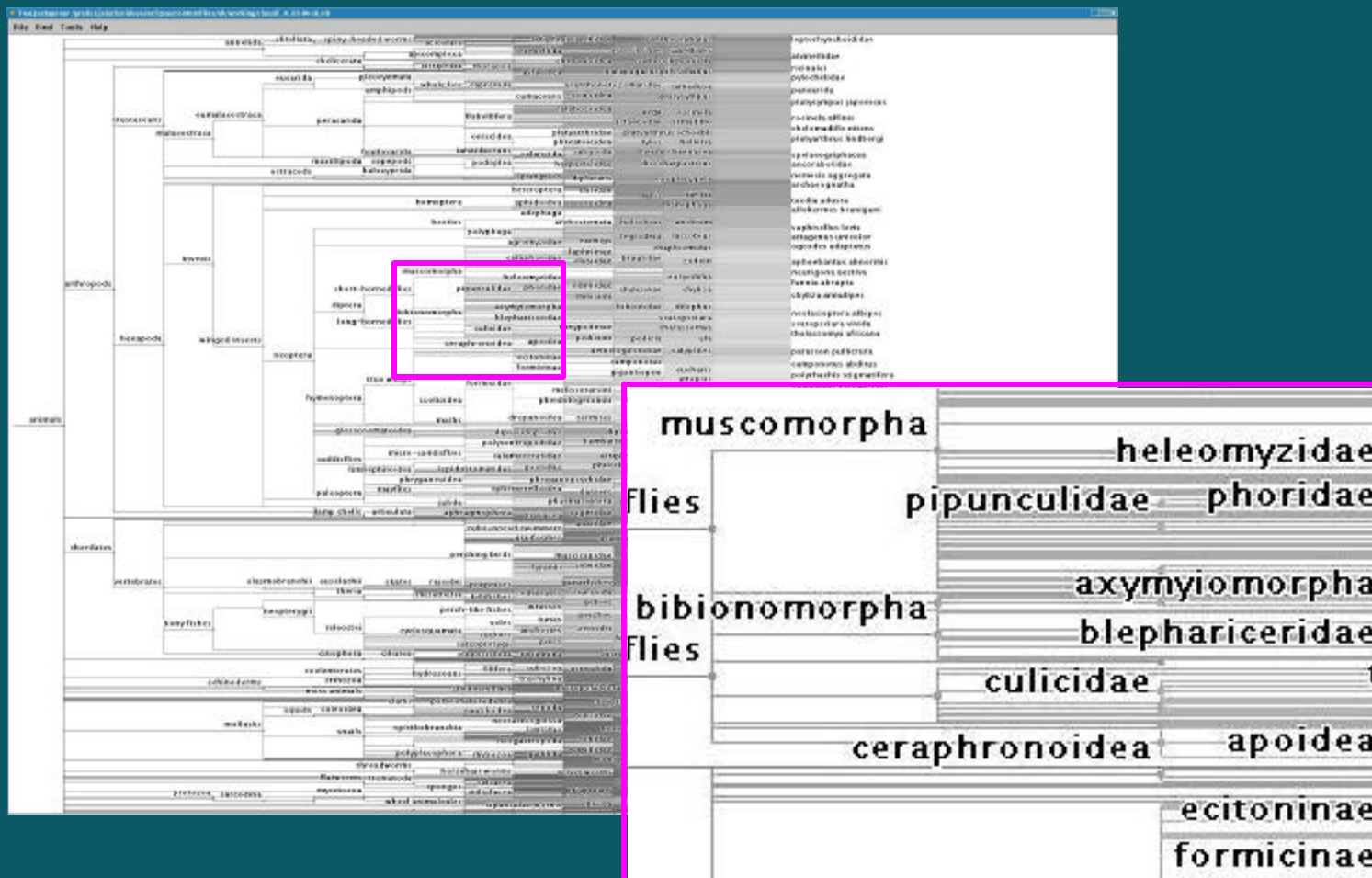
# Classification Tree Browsing

- Scalability: interactive browsing with 198K nodes
- Nodes initially given equal vertical screen space



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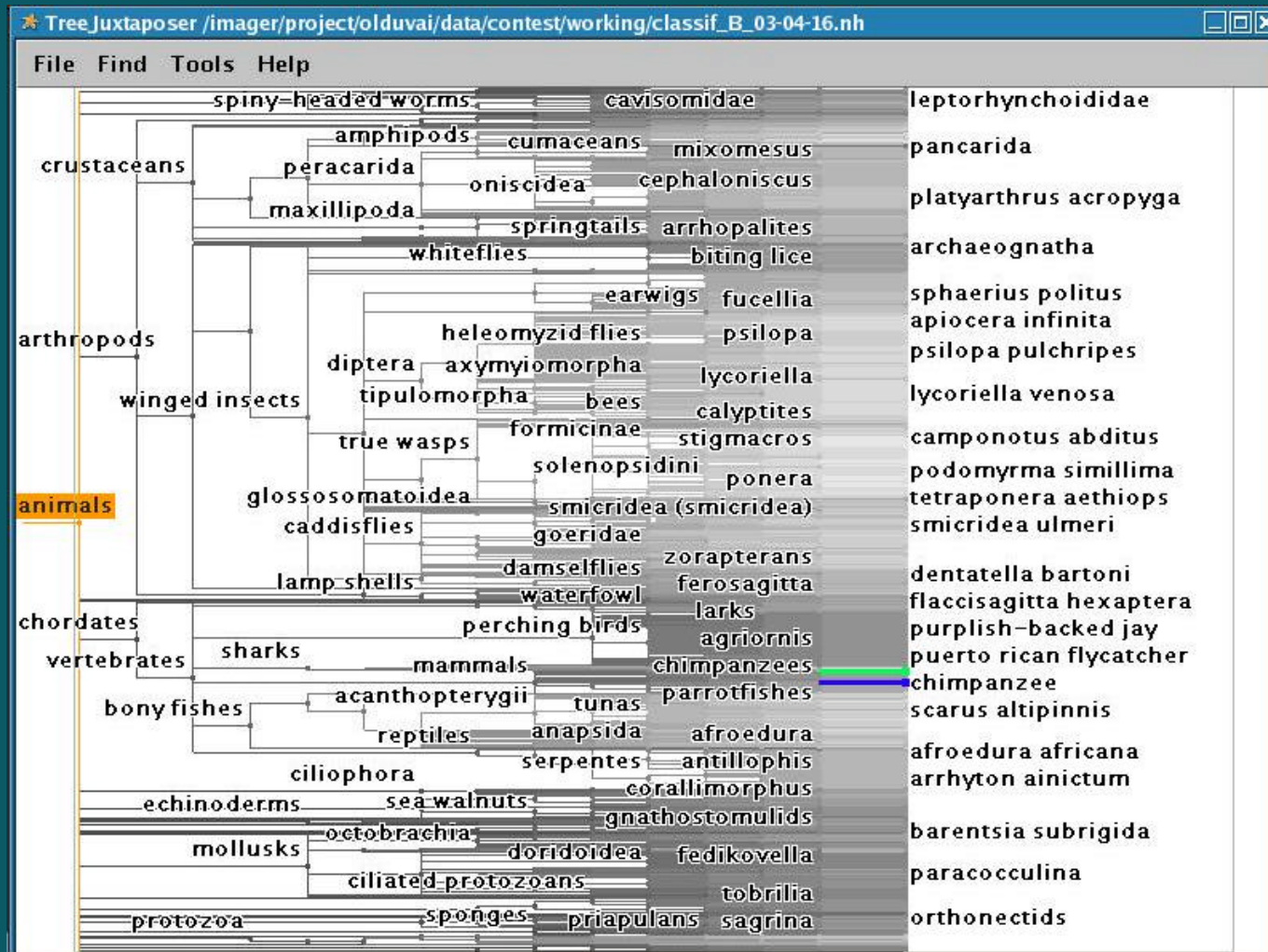


- Mouse browsing: spatial highlighting
- Keyboard browsing: topological highlighting
- cousin.mov (0:23)

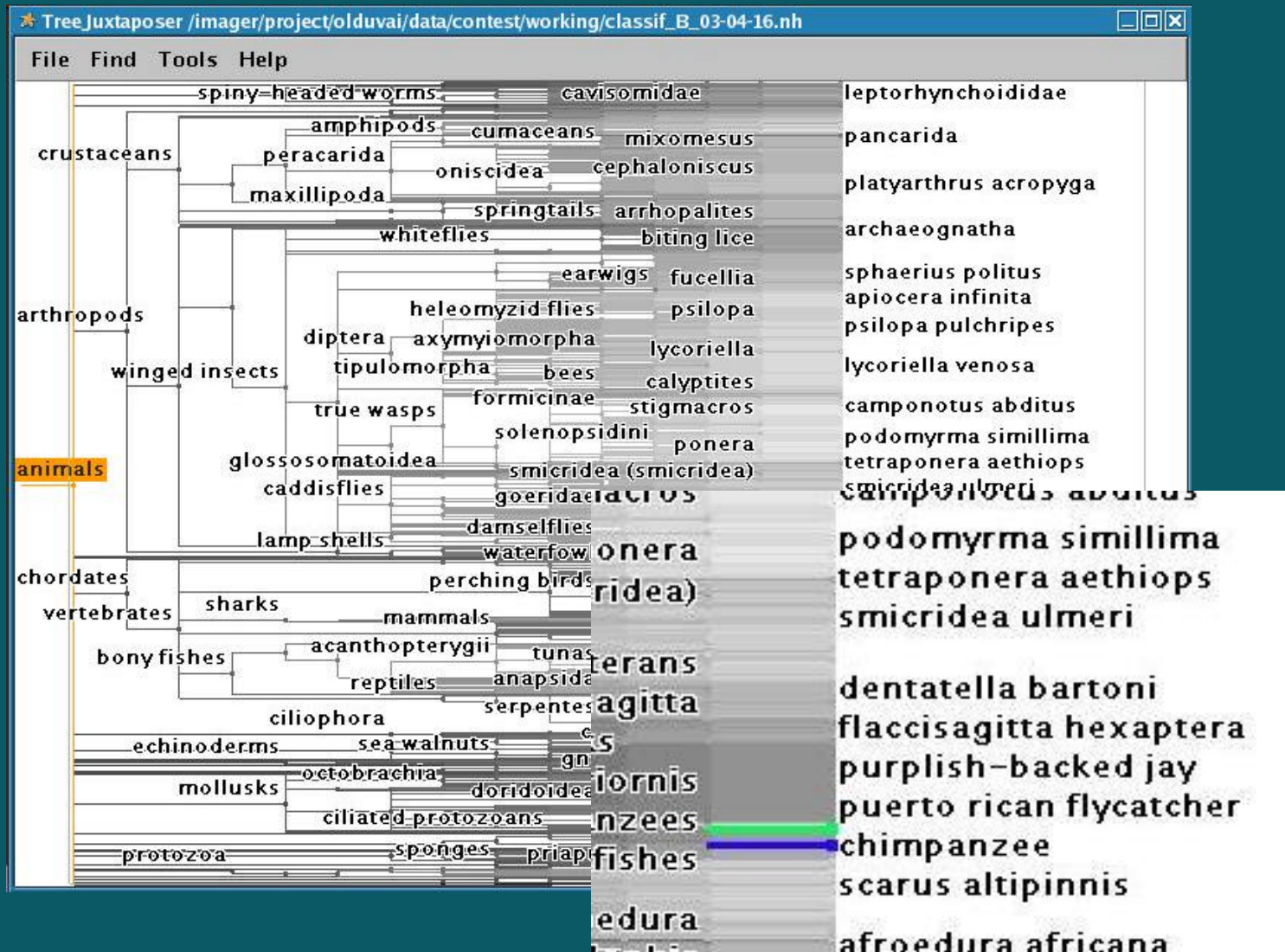
- Stretch subtrees with resize boxes using mouse
  - Browse to leaf nodes with mouse highlighting
- Traverse children of “mammal” to find ancestor
  - Arrow keys browse through topology
  - Resize ancestor with keyboard command, fine selection
- Progressive rendering for smooth animation
- browsing.mov (1:30)



# Classification Tree Browsing: Video 2

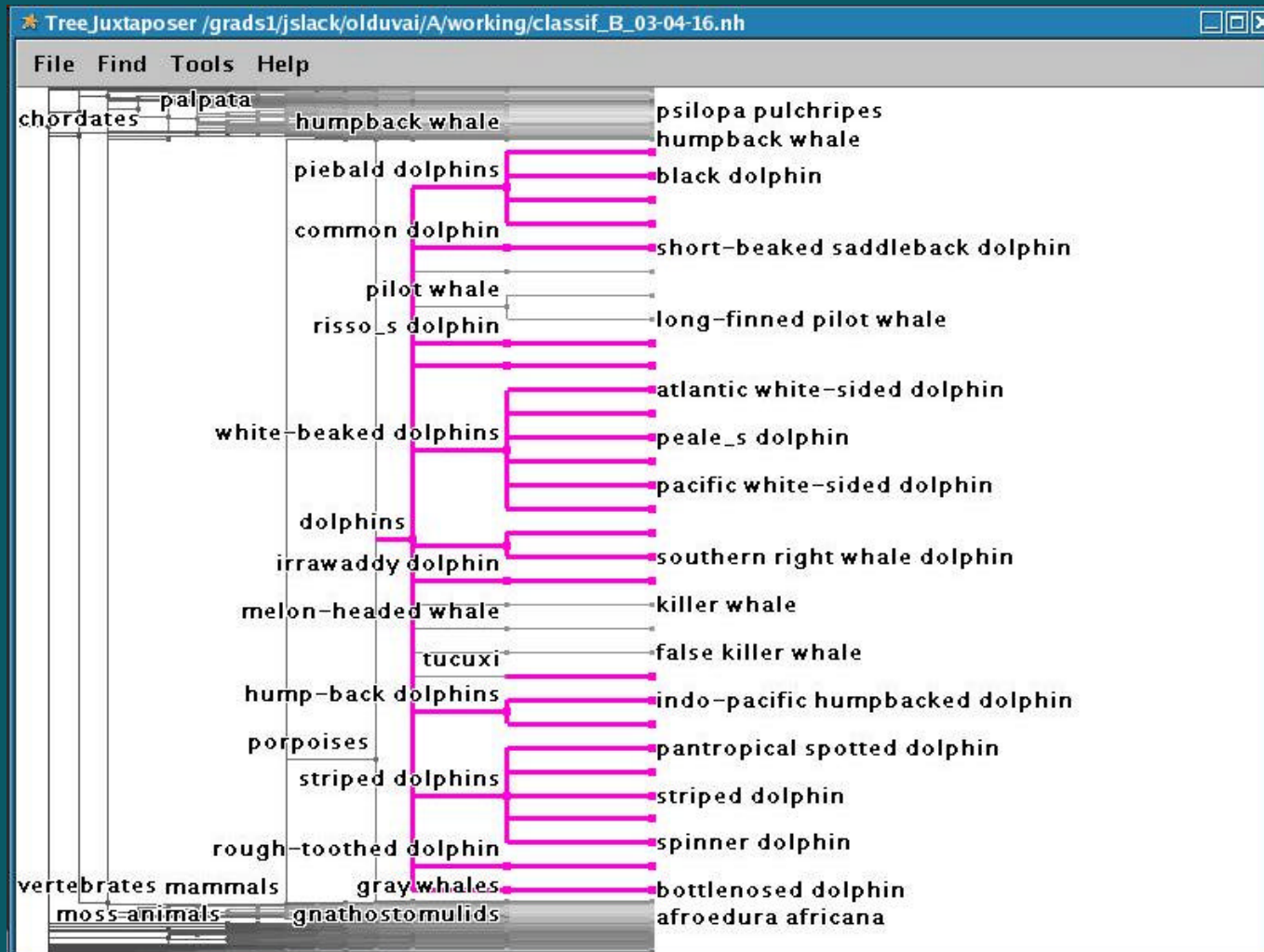


# Classification Tree Browsing: Video 2



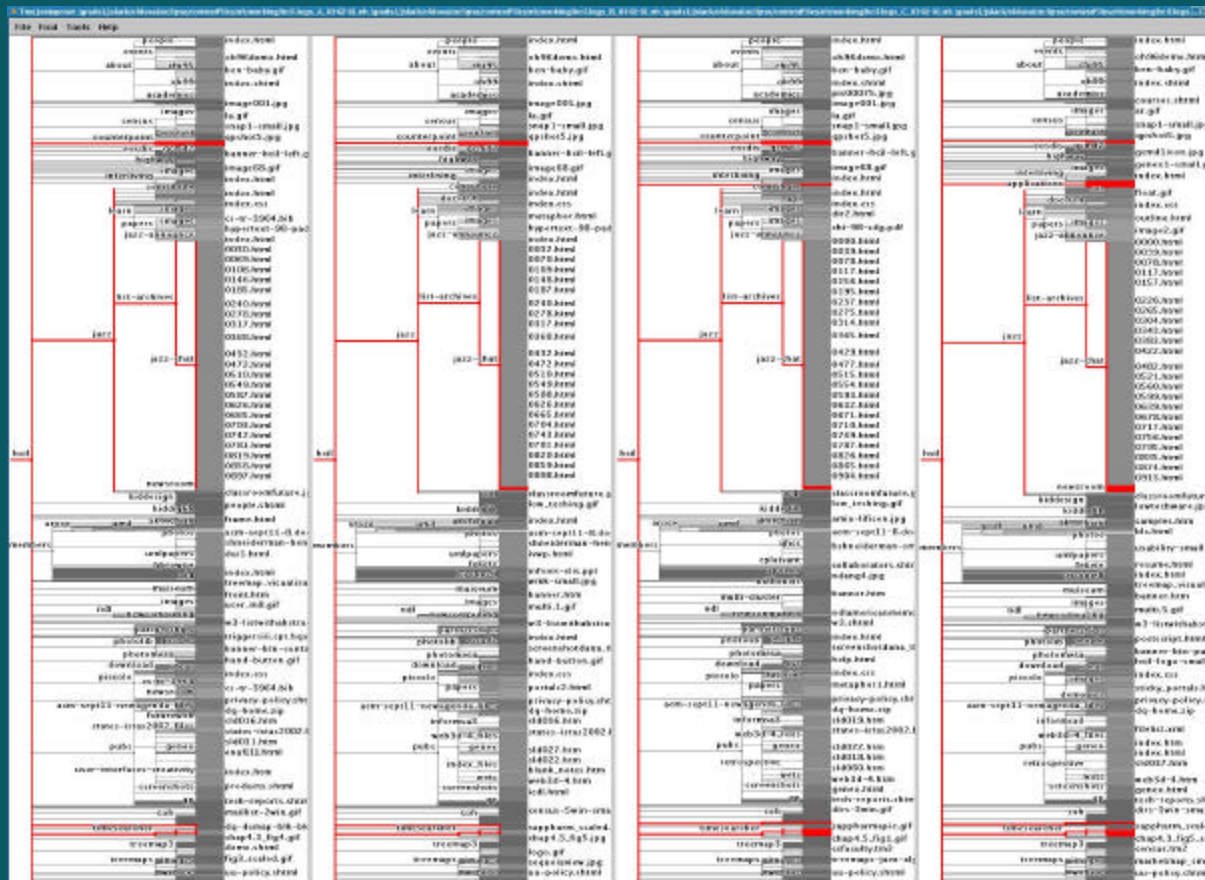
- Search for node with the find panel
  - Results relayed instantly as marked nodes
- dolphin.mov (0:57)

# Classification Tree Search: Video 3





- 4-way comparison of “hcil” subtree (3700 nodes)
  - Sparse differences are guaranteed to be visible





- Attributes for nodes not handled
- Trees can not be edited
  - Topology is static
  - Node name is static
  - No filtering
- No undo/playback functionality
- Large memory footprint
  - Unable to load two 200K node trees for comparison

- Guaranteed visibility of marked groups
  - Global overview to start, stretch to details
  - Focus+context (rubber sheet, tacked borders)
- Scalability
  - 4 way comparable: up to 75K nodes per tree
  - 2 way comparable: up to 140K nodes per tree
  - Single tree interactively browsing: up to 550K nodes
- Progressive rendering
  - Draw important animation updates first

- Difference computation automated, preprocessed
  - Visually highlight exact points of topological change
- Interactive search
  - Real-time visual feedback displayed in context during search
- Linked functionality
  - Highlighting: mouse-over reveals best corresponding nodes
  - Marking: is subtree on A best represented as a forest on B?
  - Navigating: stretch trees simultaneously

- TreeJuxtaposer: Scalable Tree Comparison using Focus+Context with Guaranteed Visibility
  - Tamara Munzner, François Guimbretière, Serdar Tasiran, Li Zhang, Yunhong Zhou, SIGGRAPH 2003
- Entry: <http://www.cs.ubc.ca/~tmm/papers/contest03>
- Visit our interactive poster for demonstration