

Accordion Comparison of Evolutionary Trees and Genomic Sequences

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TreeJuxtaposer

- Compare phylogenetic trees interactively and automatically
- Guaranteed visibility of marked regions provides visual landmarks
- Interactive frame rates and animated transitions give fluid navigation

Scalable for Laptops

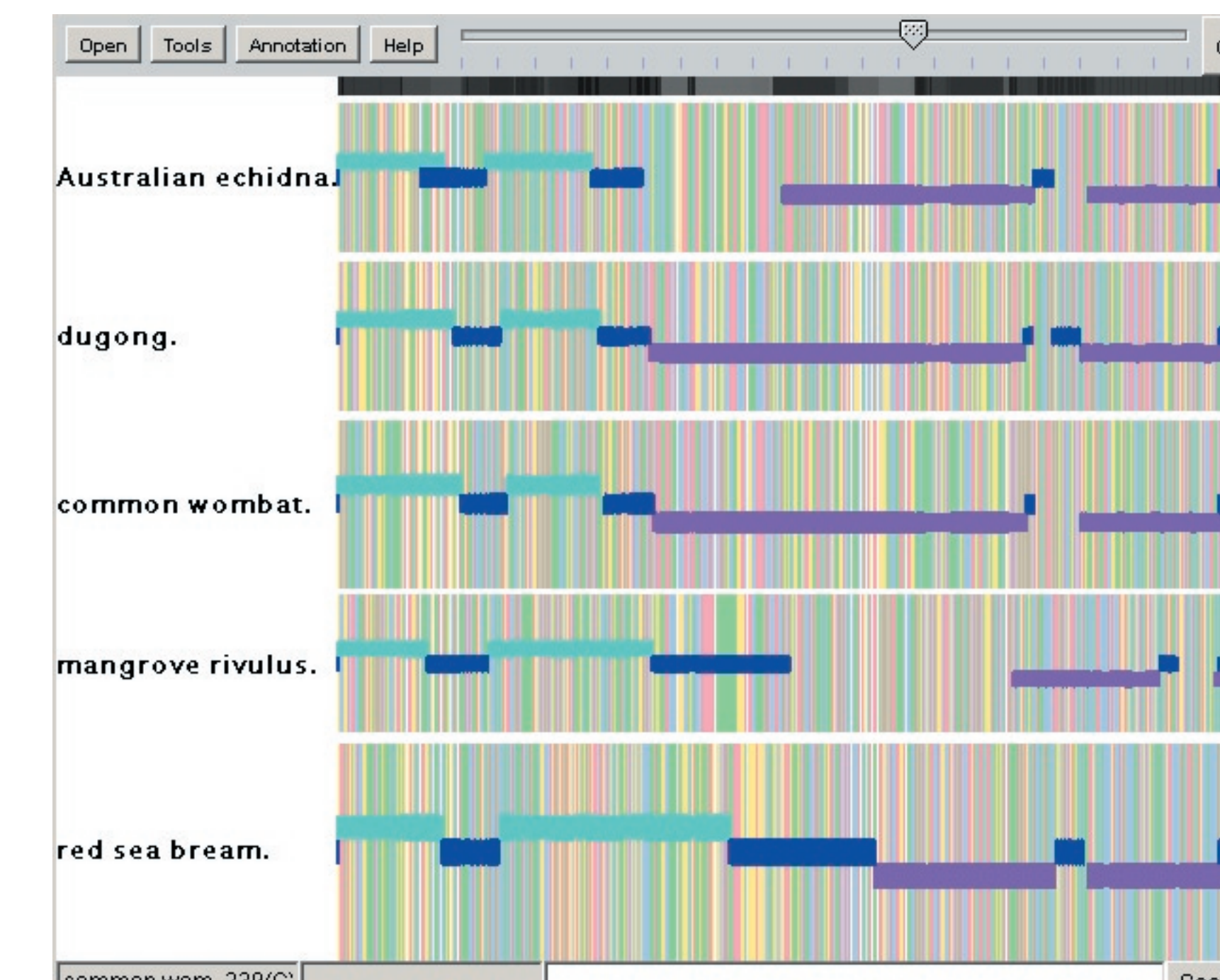
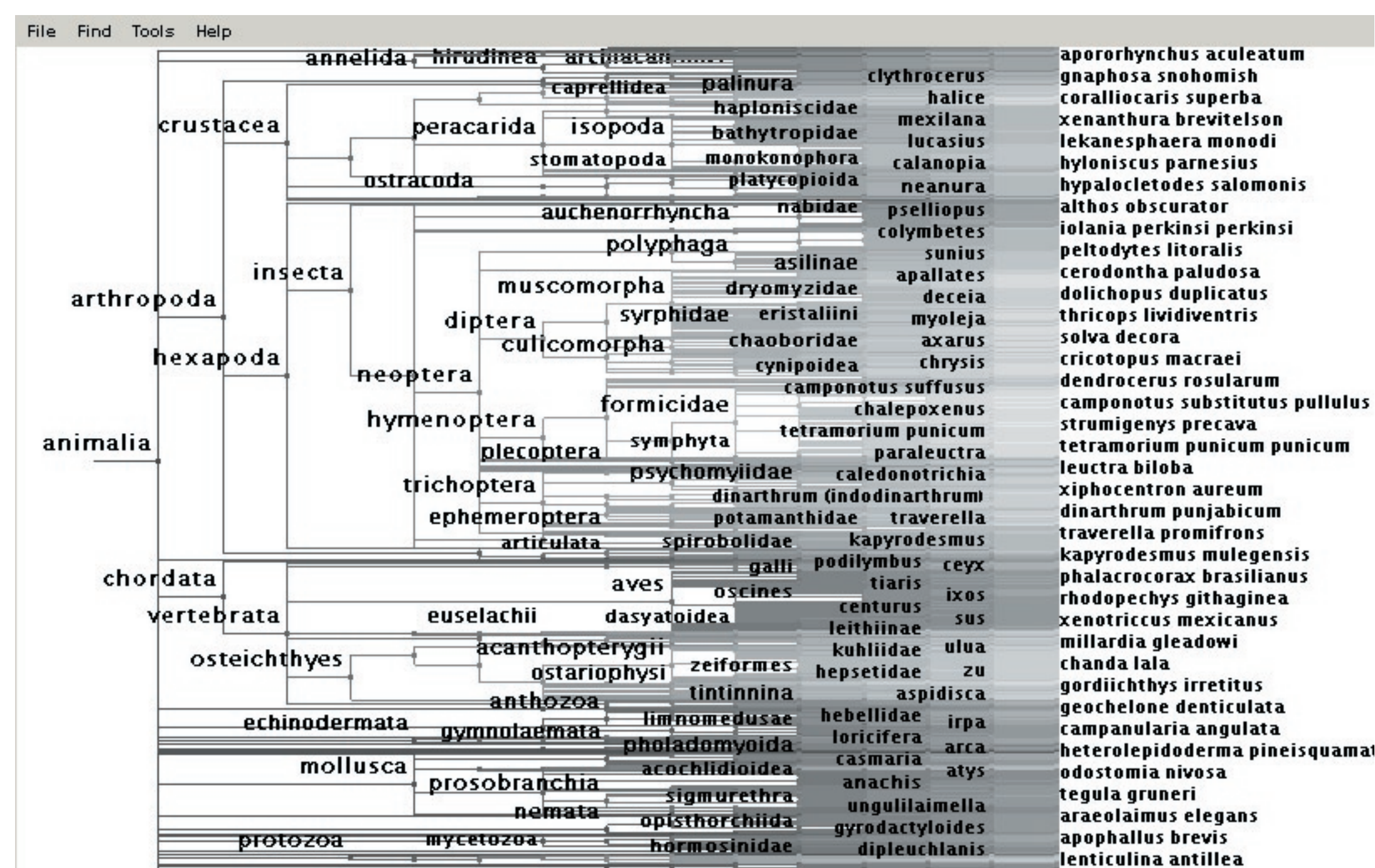
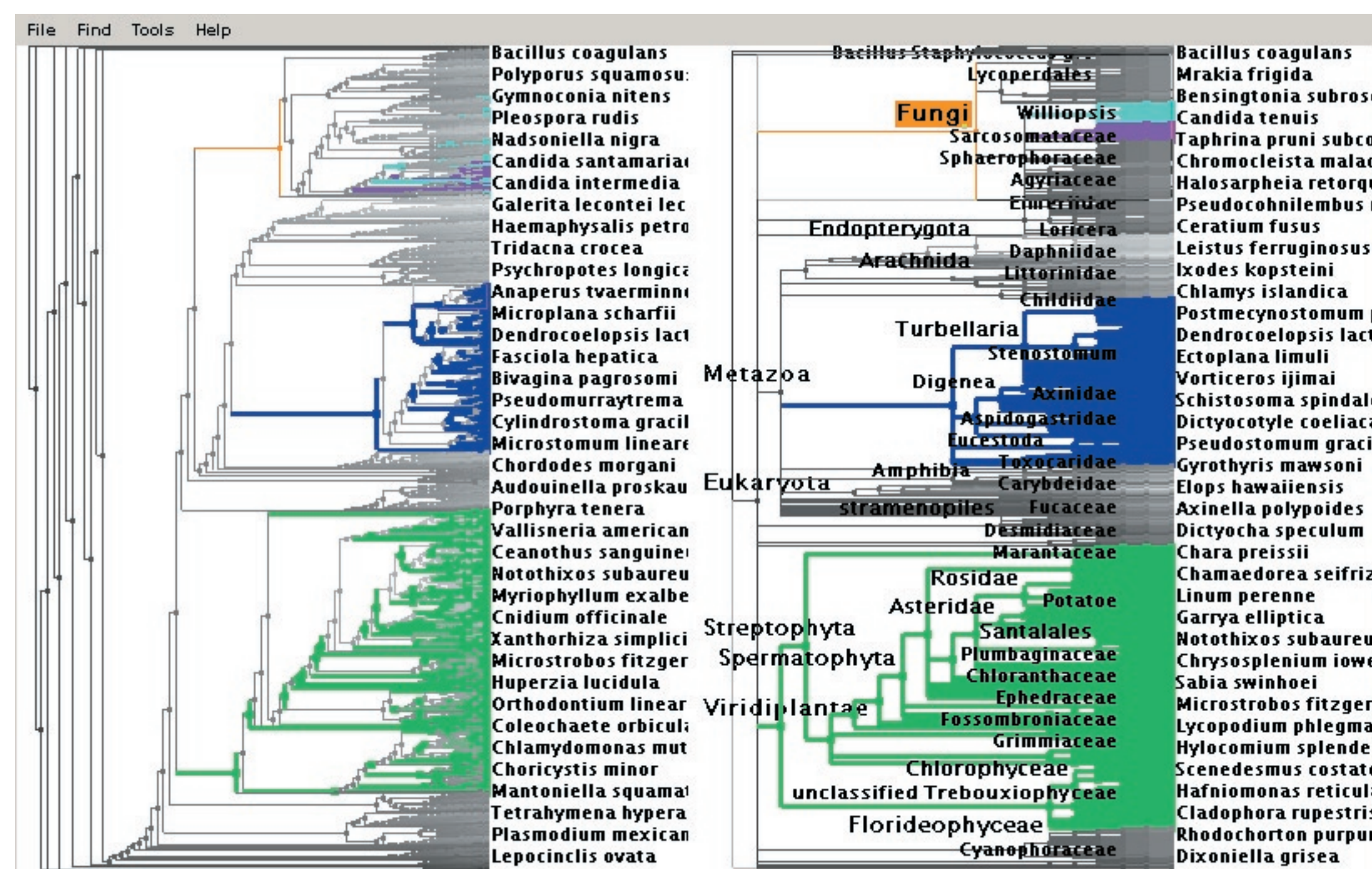
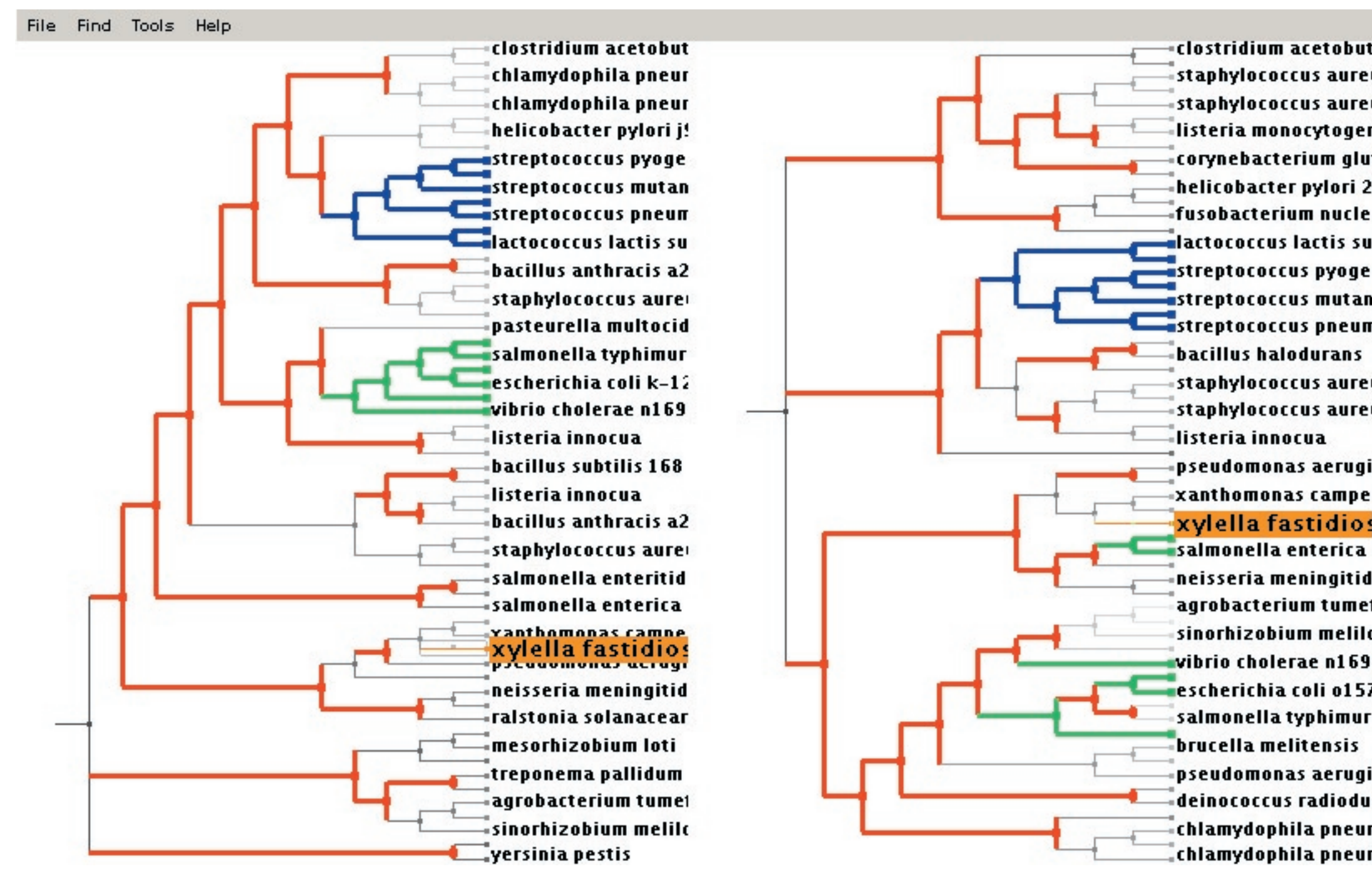
- Navigate through 500,000 nodes in a single tree
- 400,000 nodes in two tree comparison
- Draw whole trees in under a second with progressive rendering

Structural Differences

- Mouse-over highlighting shows matching nodes
- Marked clades highlight corresponding nodes on the trees
- Structural differences automatically marked

Marking Clades

- A clade in one tree could be discontinuous in another



SequenceJuxtaposer

- Compare DNA/RNA sequences
- Focus+Context: stretch “rubber sheet” to enlarge some areas, shrink other regions accordingly
- See individual nucleotides in the context of a sequence

Scalable for Laptops

- Navigate through 2 million base pairs in over 100 sequences
- Draw full frames in under a second with progressive rendering

Finding motifs

- Interactive mouse-over highlighting
- Search for nucleotide or codon strings
- Simple regular expressions for complex strings

Annotations

- High-level content rather than granular view
- Examples: Intron, Exon, t-RNA