

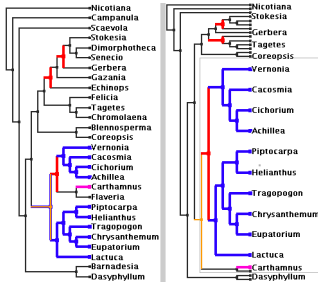
# Accordion Comparison of Evolutionary Trees and Genomic Sequences

James Slack, Kristian Hildebrand and Tamara Munzner  
Information Visualization, Imager Lab, UBC Computer Science



## TreeJuxtaposer

- Compare evolutionary trees



## Accordion drawing

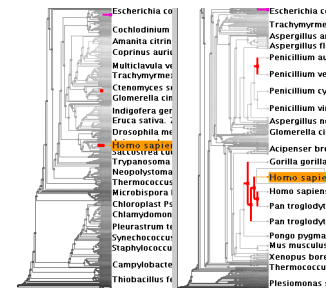
- Stretch and squish regions to navigate
- Focus on areas of interest in context

## Guaranteed interactive frame rates

- Fluid interactivity with accordion navigation
- Animated transitions of groups

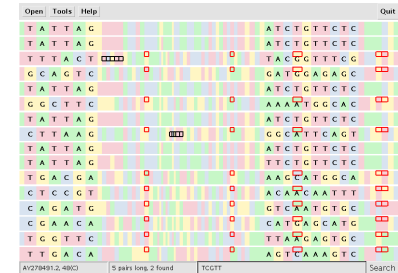
## Guaranteed visibility of marked regions

- Visual landmarks provide reference locations



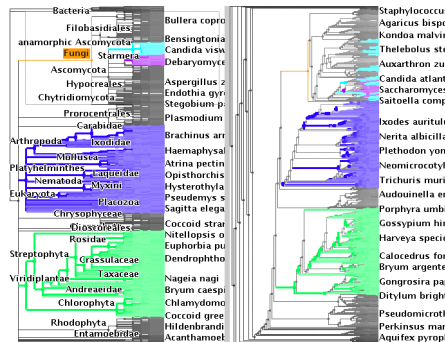
## SequenceJuxtaposer

- Compare DNA/RNA sequences



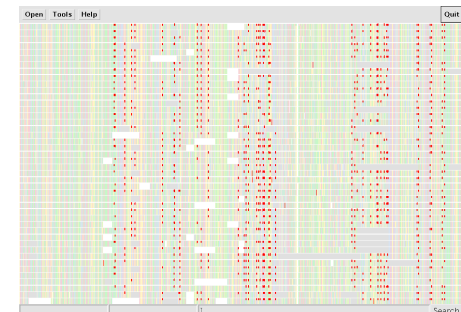
## Marking clades

- Exact differences highlighted with new best corresponding node algorithm
- Interactive mouse-over highlighting
- Incremental search for names



## Finding motifs

- User defined threshold for differences in aligned nucleotide positions
- Interactive mouse-over highlighting
- Search for text patterns

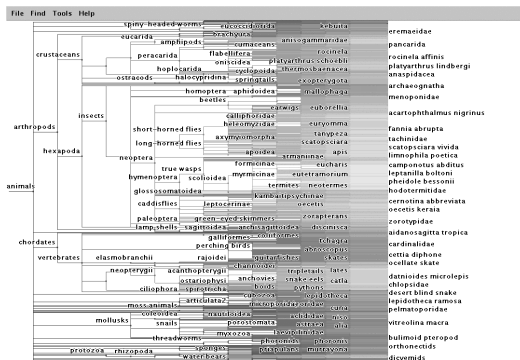


## Scalability

- Up to half a million nodes with interactive frame rates

## Scalability

- Over two million nodes with interactive frame rates



## TreeJuxtaposer topology

- Species (leaf node) right aligned structure
- Species initially have equal vertical space
- Edges dim with tree depth

## Combining trees with sequences

- Infrastructure allows for easy combination
- Build trees interactively from sequence data
- Speculate evolutionary genomic ancestors

