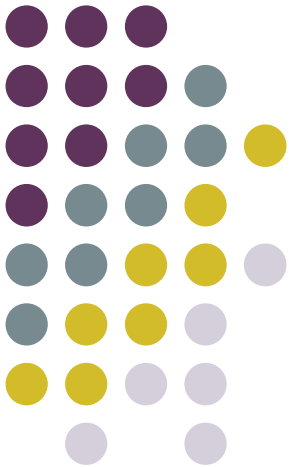
SequenceJuxtaposer: Fluid Navigation For Large-Scale Sequence Comparison in Context

James Slack*, Kristian Hildebrand*†, Tamara Munzner* and Katherine St.John¥

* University of British Columbia,

† Bauhaus University Weimar,

¥ City University of New York



Overview

- Introduction
- Previous Work
- Interaction Metaphor
- SequenceJuxtaposer
- Conclusion and Future Work

Introduction

- Sequence visualization tool
  - Exploration and comparison
- Accordion Drawing
  - Stretch and shrink rubber sheet
  - Borders tacked down

Introduction Video

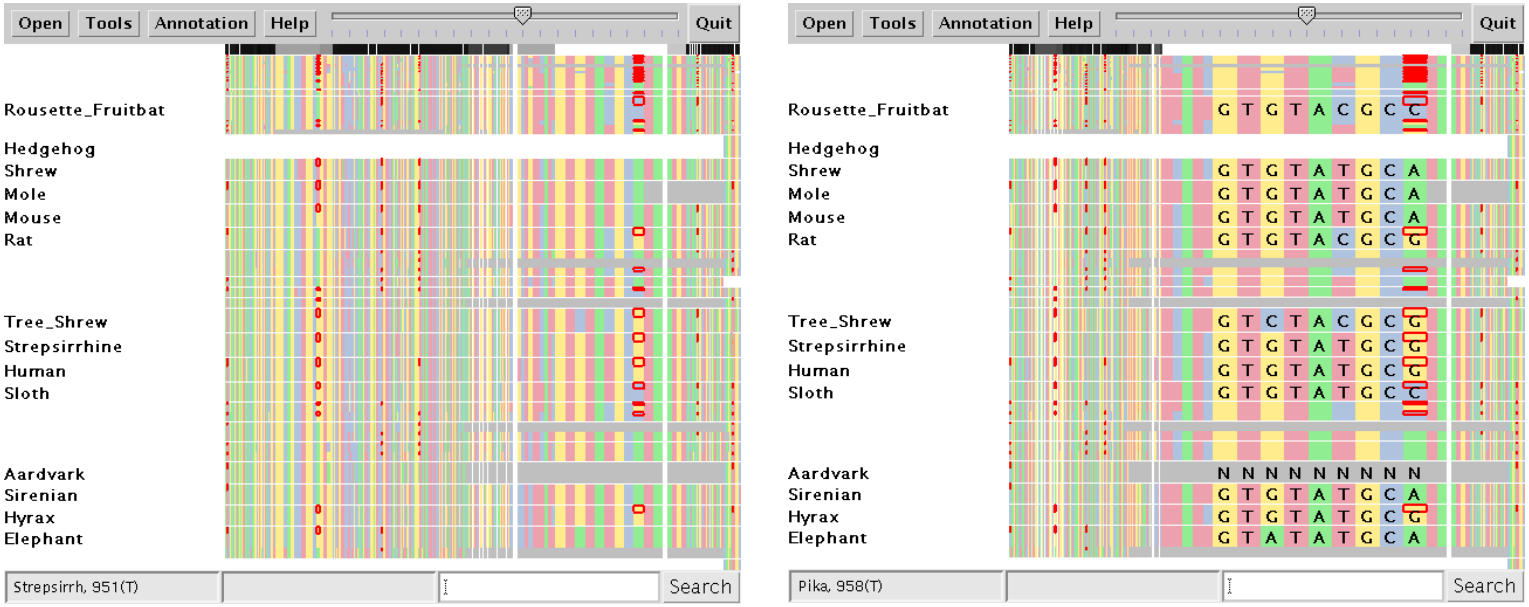
Zur Anzeige wird der QuickTime™
Dekompressor „MPEG-4 Video“
benötigt.

Previous Work

- Accordion Drawing
  - TreeJuxtaposer [Munzner 03]
- Sequence Browsers
  - Ensembl [Hubbard 02], UCSC Genome Browser [Kent 02], NCBI [Wheeler 02]
  - MacClade [Maddison 92], VISTA [Mayor 02], phylo-VISTA [Shah 03]
  - Artemis [Rutherford 00], LaInView [Duret 96], BARD [Spell 03], PipMaker [Schwartz 00]

Accordion Drawing

- SequenceJuxtaposer guarantees 3 key properties
  - Context
  - Visibility
  - Frame Rate



Guaranteed Context

- Focus+Context
  - Combine overview and detail into single view
  - More information visible simultaneously
  - Avoid getting lost while exploring
  - Major information visualization research theme
- Navigation metaphor
  - Rubber sheet with borders tacked down

Guaranteed Visibility

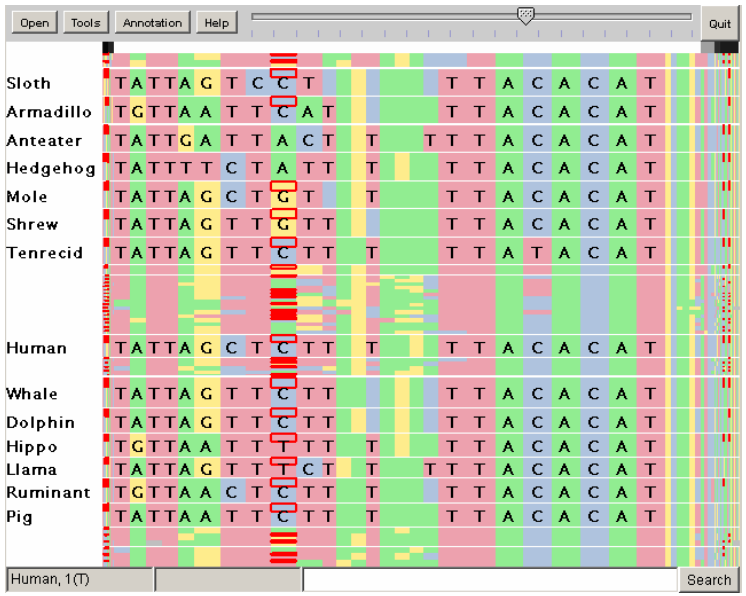
- Highlight marks always visible
  - Never fall outside of current view window
  - Never hidden by something in front
  - Never vanish, even if smaller than one pixel
- Requires efficient algorithms
  - Explicitly checking all items too slow
    - Linear in number of pixels, not number of items
  - Details in TreeJuxtaposer paper [Munzner et al, Siggraph03]

Guaranteed Frame Rate

- Need realtime update
  - Focus+Context interaction must be fluid
  - 20-30 frames per second
- Computer graphics challenge
  - Progressive rendering

SequenceJuxtaposer

- Fluid comparison of multiple sequences
- Handles DNA and RNA sequence data
- Provides searching, difference calculation



SequenceJuxtaposer Video

Zur Anzeige wird der QuickTime™
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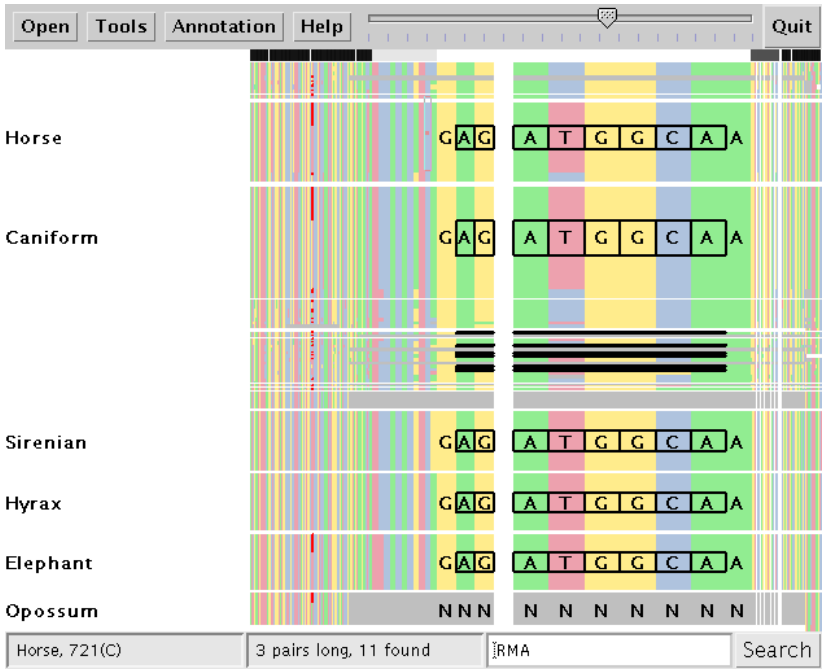
benötigt.

Algorithm Complexity

- Sublinear:
  - Runtime algorithms
- Linear:
  - User-initiated actions
- Subquadratic:
  - Preprocessing algorithms

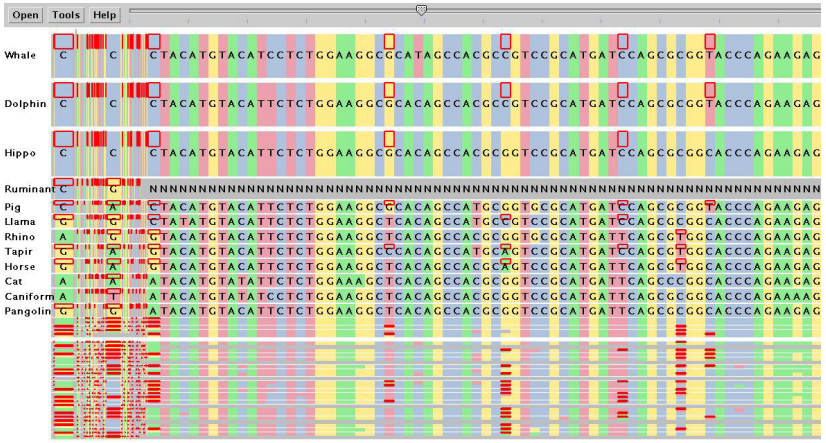
Searching

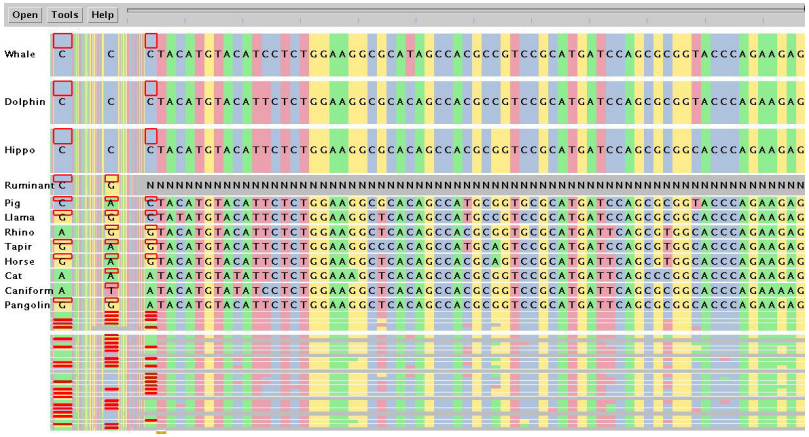
- Search for motifs
  - Protein/Codon search
  - Regular expressions supported
- Results marked with guaranteed visibility



Differences

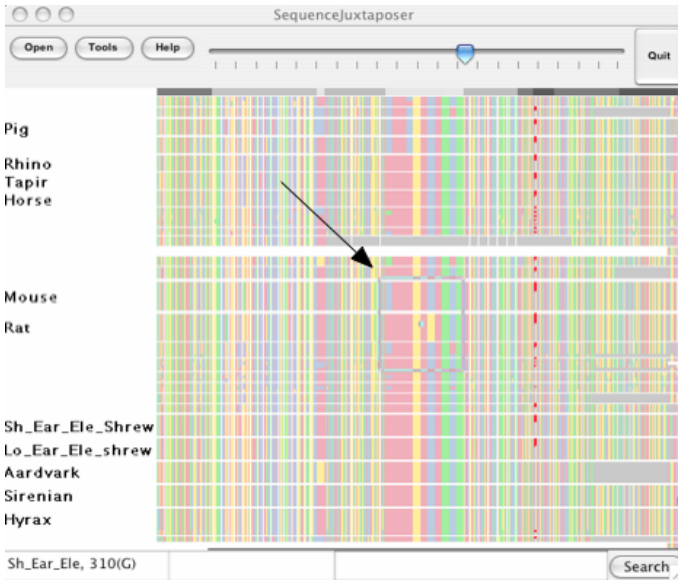
- Explore differences between aligned pairs
  - Slider controls difference threshold in realtime
- Results marked with guaranteed visibility





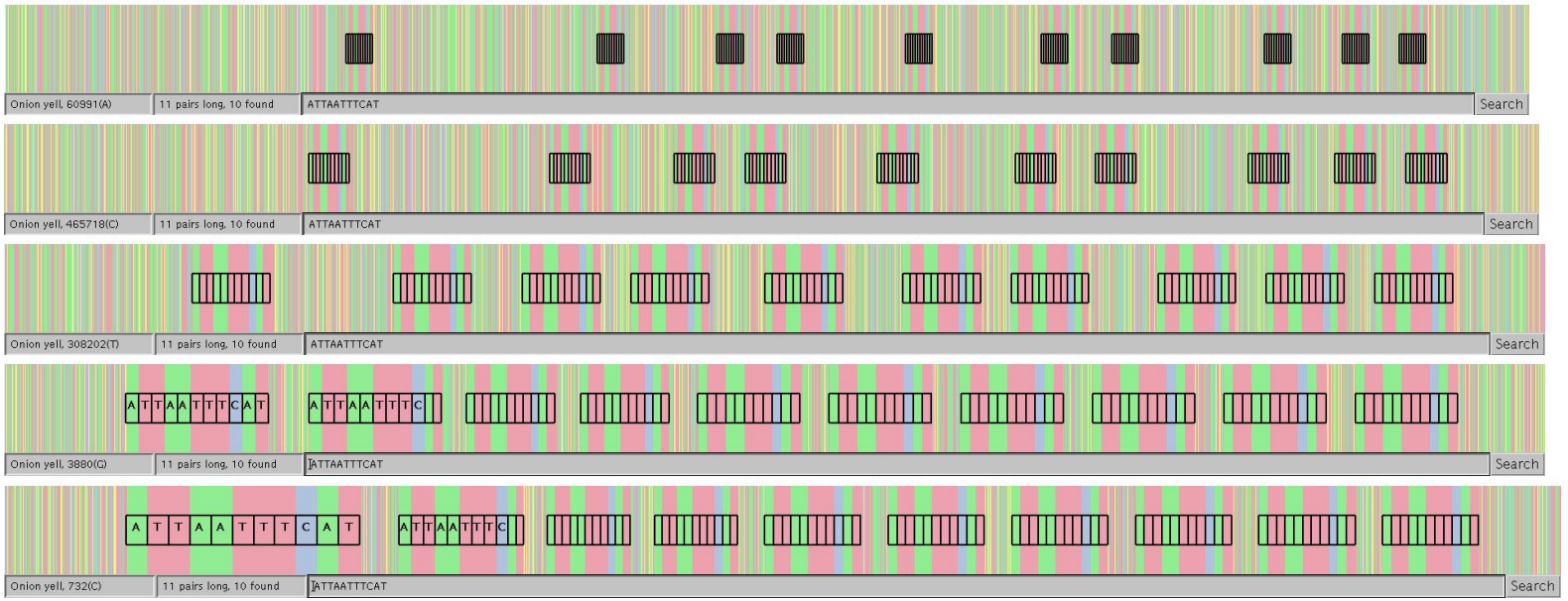
Interaction

- Resizing
  - Expand or contract rectangular areas
  - Drag visible rubberband interactively



Interaction

- Animated transitions
  - Grow and shrink groups
  - Allow user to track visual landmarks



Drawing

- Very high information density
- Avoid overdrawing in compressed areas
- Progressive rendering
  - Draw for fixed time, check for user interaction
  - Priority queue to draw items in order of current onscreen size

Drawing Video

Zur Anzeige wird der QuickTime™
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Results and Performance

- Java prototype using OpenGL, GL4Java
- Memory for AD data structures
  - significant, but linear
  - paper: 1.7 million base pairs
  - current: 20 Mbp

Conclusion

- Accordion Drawing for sequences
  - Powerful new information visualization technique
- Guarantees
  - Context for maintaing orientation
  - Visibility of landmarks: searches, differences
  - Frame rate for realtime response to interaction
- Fluid exploration of big datasets

Future Work

- Performance
  - Memory, speed
- Annotation
- Editing
- Connecting trees and sequences
- Other data types
  - BACs (bacterial artificial chromosomes)

Open Source

- Freely available from http://olduvai.sourceforge.net
  - SequenceJuxtaposer
    olduvai.sf.net/sj
  - TreeJuxtaposer
    olduvai.sf.net/tj

Acknowledgements

- Collaboration
  - David Hillis and lab members, UT-Austin
- Discussions
  - Wayne Maddison, David Haussler, Nina Amenta
- Technical writing
  - Ciáran Llachlan Leavitt
- Funding
  - NSF/DEB-0121651/0121682
  - German Academic Exchange Service