SequenceJuxtaposer: Fluid **Navigation For Large-Scale Sequence Comparison in Context** James Slack*, Kristian Hildebrand*†, Tamara Munzner* and Katherine St.John¥ * University of British Columbia,

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Overview

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

Introduction



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

Introduction Video



Zur Anzeige wird der QuickTi Dekompressor "MFEG-4 Video" hendtige

Previous Work



- 1 Accordion Drawing
 - 1 TreeJuxtaposer [Munzner 03]
- Sequence Browsers
 - 1 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
- 1 Context
- 1 Visibility
- 1 Frame Rate



Guaranteed Context



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

Guaranteed Visibility



- 1 Highlight marks always visible
- Never fall outside of current view window
- 1 Never hidden by something in front
- Never vanish, even if smaller than one pixel
- 1 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
- 1 20-30 frames per second
- 1 Computer graphics challenge
 - Progressive rendering

SequenceJuxtaposer



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



SequenceJuxtaposer Video

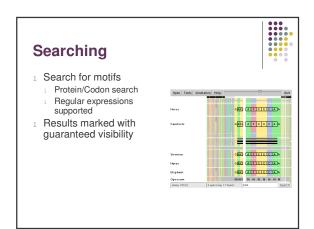


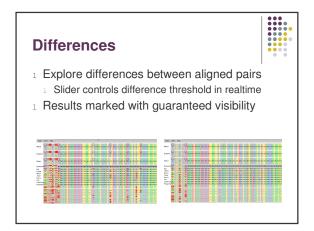
ur Anzeige wird der QuickTime™

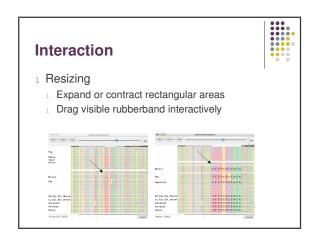
Algorithm Complexity

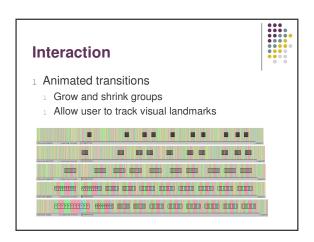


- 1 Sublinear:
 - Runtime algorithms
- 1 Linear:
 - User-initiated actions
- Subquadratic:
 - Preprocessing algorithms

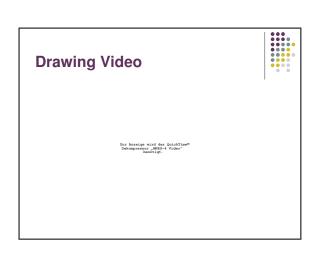








Drawing 1 Very high information density 1 Avoid overdrawing in compressed areas 1 Progressive rendering 1 Draw for fixed time, check for user interaction 1 Priority queue to draw items in order of current onscreen size



Results and Performance

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

Conclusion



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

Future Work



- 1 Performance
 - 1 Memory, speed
- Annotation
- 1 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

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