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

Previous Work
- Accordion Drawing
  - TreeJuxtaposer [Munzner 02]
- Sequence Browsers
  - Ensembl [Hubbard 02], UCSC Genome Browser [Kent 02], NCBI [Wheeler 02]
  - MacClade [Maddison 90], 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

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™ Dekompressor "MPEG-4 Video" benötigt.
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 maintaining 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
  - SequenceJuxtaposer
    - olduvai.sf.net/sj
  - TreeJuxtaposer
    - olduvai.sf.net/tj

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