System Support for Collaborative Genomic Visualizations

Lars Ailo Bongo[12], Daniel Stødle[3], Grant Wallace[2], Tore Larsen[3], Kai Li[2], Olga G. Troyanskaya[12]
[1]Lewis-Sigler Institute for Integrative Genomics, Princeton University, [2]Department of Computer Science, Princeton University,
[3]Department of Computer Science, University of Tromsø, Norway

http://function.princeton.edu

Motivation: Analysis of functional genomics experiment often requires interactive collaborative investigation by biology and bioinformatics researchers. However, there is a need for computer systems designed to support such collaborative research.

Results: We present an integrated approach for collaborative data analysis. Remote users can analyze data on a server as if it was on their local machine. The system effectively supports cross-continent collaboration over the Internet, and takes full advantage of the powerful visualization capabilities of large-scale high-resolution display walls.

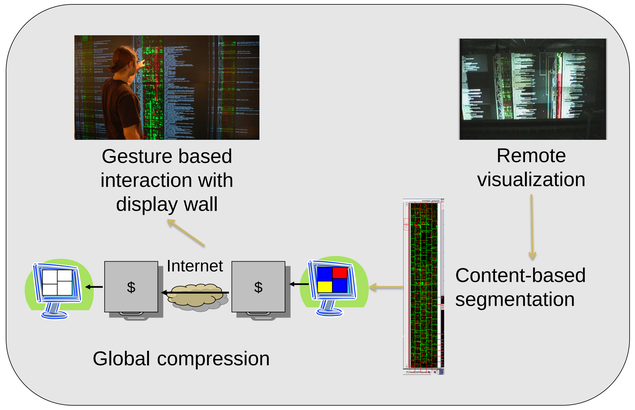
Gesture Based Microarray Analysis: we have developed a gesture library for the bioHIDRA system for visualization-based analysis of multiple microarray datasets. This allows using gestures to scroll panes, select clusters, and zoom into interesting regions.

System Overview

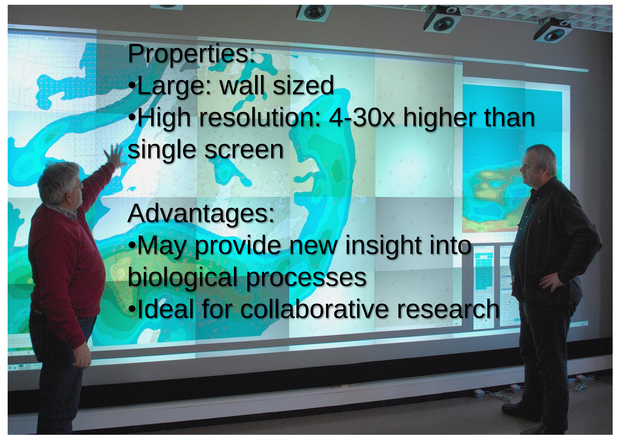
Share synchronized visualizations
•Regular displays or display walls
•Application independent
•Platform independent
•Raw data not shared

Smooth interaction with visualization intensive applications
•Location independent
•Over low-bandwidth Internet links

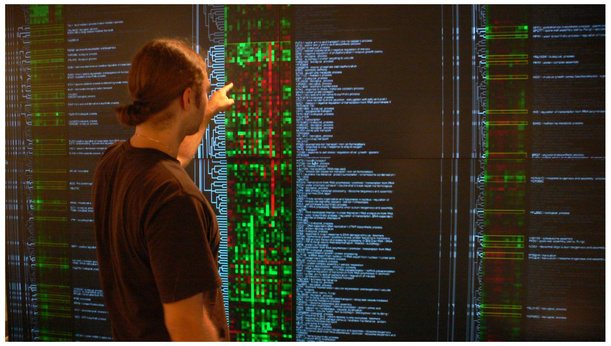
Multi-user gesture based interaction:
•Device free
•Interact using your arms and fingers



Display Wall

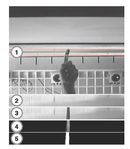


Gesture Based Collaborative Interaction

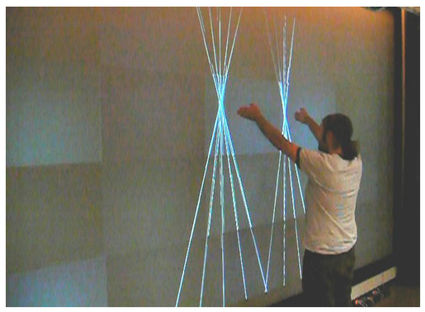


Gesture based interaction with interactive performance and multi-user support

Cameras on floor in front of display wall records images

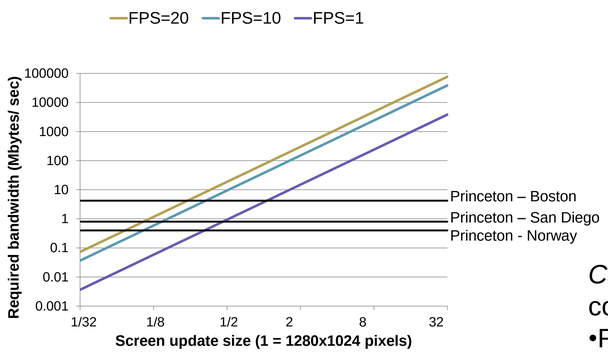


Captured images are analyzed to detect objects



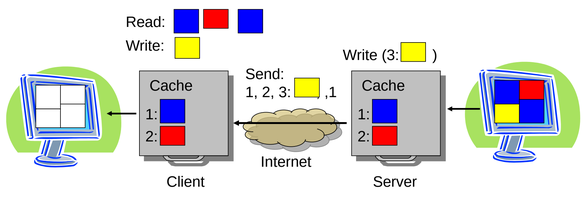
Triangulation is used to get 2-D object positions.

Canidae - Application Specific Compression

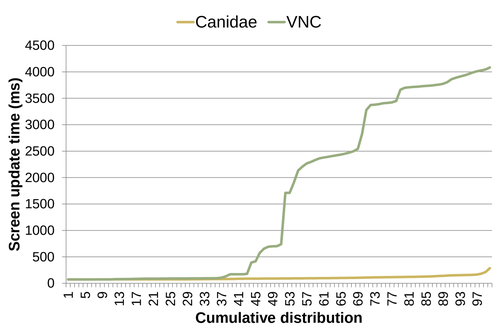


Current Internet connections do not have the application-level bandwidth necessary for visualization intensive applications

Compression:
•Detect redundancy
•Effectively encode (redundant) data



Canidae uses global compression for better compression ratio and lower compression time.
•Receiver side has cache with previously sent regions
•If a region is in the cache only a small token is sent over the network



Canidae compression significantly improves remote visualization performance for visualization intensive applications.

Content based segmentation for microarray visualizations:
Exploit two properties of microarray visualizations:
1. Data sets tend to be large
2. Display resolution limits view to a subset of genes

⇒Requires scrolling or zooming into regions
⇒Many redundant regions

Detect and efficiently encode regions that have been moved on screen or have been seen before.