Visualization and Interaction: Enabling Efficient Data Exploration

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roadmap

research in visualization

SyntenyViewer

ExpressionExplorer

visualizing and meshing surfaces
why visualize?

big data
complex relationships

replace cognition with perception
why interact?

big data
complex relationships
enable real-time data exploration
why interact?

big data
complex relationships
enable real-time data exploration

visualization + interaction = increased efficiency
vis research?
in science
computer science

data types

operations on data types

algorithms

visualization

hypotheses

experiments

science

measured data

domain knowledge
characterization of measured data to data types
abstraction of scientific questions to operations on data types
represent data operations as visual components

incorporate interaction for data exploration
visualization challenges

- language barriers
- what questions to ask?
- correct abstractions of data and operations
- design decisions
- validation of visualization system
SyntenyViewer

**goal:** visualize conserved syntenic blocks to answer questions about evolution

**requirement:** visualize emergent patterns of conservation (where and how large), and strength of conserved relationships

**challenge:** multiple scales, from genome to genes (100,000X)
Stickleback

Tetraodon

http://fish.dnr.cornell.edu/nyfish/Gasterosteidae/stickleback.html

http://win.vergari.com/acquariofilia/salmastro02.asp
Rhizopus
previous work

genome/chromosome view

Apollo, Lewis et al.

Cinteny, Sinha et al.
previous work

block view

Ensemble, Clamp et al.
previous work

block view

Ensemble, Clamp et al.

SyntanyVista, Hunt et al.
previous work

generalizations

use color beyond visual distinguishability

built on top of existing genome browsers

limited by traditional chromosome representation

no visualization of conservation strength (exception, scatterplots)
SyntenyViewer
**conserved element**
- chromosome, coordinates, orientation, id, pair element, pair value, pair orientation

**conserved syntenic block**
- list of conserved elements

**where? how many? how strong?**
- show pairings, filter, drill-down
circle view for explicitly showing conservered relationships in stable way

histograms for conservation strength

d{}\textbf{edge bundles} for emergent relationships

color coding and \textbf{inversion} for orientations
ExpressionExplorer

**goal**: enable discovery of differences (and similarities) between space-time expression patterns

**requirements**: visualize differences spatially and temporally to facilitate exploration, and derive metrics to characterize differences

**challenge**: high dimensional data
for each species:
for each cell:
expression level of 12 genes at 6 time points
in the beginning...
in the beginning...
in the beginning...
species, cells, genes
  categorical data / parameter

time points, position
  quantitative data / parameter

expression level
  quantitative data / measurement

what and where are differences?
  derive measurements, browse
framework for deriving measurements of spatial time-series data

measurement overview and selection

measurement summary

neighborhood overview and selection

neighborhood summary

expression summary