A couple of UI prototypes*

Jonathan Crabtree
jcrabtree@som.umaryland.edu

Institute for Genome Sciences (IGS)
University of Maryland, Baltimore

* Dramatization: actual presentation may have been significantly less well-organized
1. New! Dojo tree widget, now with 100% more bar graphs.

- Took standard Dojo tree widget
- Added graphs of node-associated quantities
- Use case: Review counts of 454 sequence reads classified at different taxa in a taxonomic tree, using data from metagenomic survey sequencing classified using the RDP's Naïve Bayesian classifier and TOBA-based taxonomy.
Tree/graph widget features

- Synchronized scrolling of graph and tree panes
- Graphs dynamically update as tree nodes are expanded or collapsed.
- Clicking on a tree node loads a list of all the sequence reads classified at that node.
- Graph colors differentiate between: 1. sequences classified at a node and 2. sequences classified at OR below a node.
Tree/graph widget cons

- Not under active development
- No connection with chado tools (currently reads data in simple JSON format)
- Just an idea/prototype for the dynamic display of tree-associated abundance data in the context of a JavaScript framework.
2. An AJAX-Style Synteny Viewer

- Goal: produce a proof of concept of an interactive version of the “Sybil” synteny viewer (see http://sybil.sf.net)
- Under (extremely) sporadic development for several years now.
- Uses Nested Containment Lists like JBrowse, but only on the server side.
- Client uses Dojo, server is custom C app that uses libmicrohttpd, Cairo, NCLLists.
Synteny viewer example

• 13 sequence/6 genome example reading from a 10 genome PostgreSQL chado comparative database
• A protein clustering analysis is used for the comparative data.
• The current prototype displays single protein clusters in their genomic context.
• Sequences can be scrolled by dragging and the protein cluster display updates in real time.
• Color coding indicates source genome.
In the next slide...

- Click on the arrows to reorder the sequences, or pick them up and drag them directly.
- Here a sequence (the 5th from the top) is manually moved to be closer to those to which it is more similar (2 rows lower on the page.)
In the next slide...

- Zoom/change scale by using the mouse wheel or the zoom slider at the right edge of each sequence.
- Here we have zoomed out in 3 adjacent sequences.
- Scrolling and zooming is currently independently controlled in each sequence.
In the next slide...

- Double-click to open up control panel for each sequence.
- Control panel contains an overview of the entire sequence, which shows the currently-viewed position and can also be used as a scrollbar.
In the next slide...

- Click to display gene ids and/or gene product names.
- Gene ids and product names are retrieved asynchronously as needed.
Synteny viewer summary

- Still just a prototype/proof of concept, with a possible alpha release on the horizon if time permits.
- Similar in concept to proposed JBrowse_syn tool
- Current back-end is chado/PostgreSQL only
- No attempt to deal with 2\textsuperscript{nd} gen data here: assumes assembled and annotated sequence data.
- All the heavy lifting is done on the server side, which could potentially be distributed on the cloud (although the current app runs fine—for a small number of users—with client (browser), server, and back-end chado db all on the same laptop.)