Overview

- About Araport
- Extensions to JBrowse
  - Hybrid track selector plugin
  - Sequence viewer widget
- Araport on GitHub
- Useful tidbits for JBrowse users

About Araport

- Objectives
  - Develop community web interface
    - sustainable, fundable and community-extensible
    - hosts analysis modules, visualization tools, user data spaces
  - Practice data federation
    - integrate diverse data sets from distributed sources
    - consume and expose data via RESTful web services
  - Maintain “gold standard” Col-0 annotation
    - assemble tissue-specific transcripts from publicly available RNA-seq datasets
    - incorporate novel coding and non-coding genes

Araport

https://www.araport.org

- Explore data
  - ThaleMine
  - JBrowse
- Search data
  - Quick Search
  - BLAST
  - Raw data downloads
- Community
  - News & Events
  - Ask a question
  - Job Postings
  - Useful Links

Araport Architecture

Track selection in standard JBrowse installations

Hierarchical selector

Faceted selector
Tracks at Araport

• Combination of local and remotely located datasets
  • Local tracks generated from flat-files converted to JSON (in the near future, will be served by InterMine JBrowse web services)
    – Assembly, annotation, expression, similarity and variation related data
    – Normally associated with only a single unit of metadata (e.g. citation or text describing how data was generated)
  • Remote tracks are federated from CoGe via their RESTful API infrastructure
    – Epigenomics datasets collated from the EPIC project
    – Each dataset is associated with rich set of metadata tag/value pairs (such as experiment name, technique, conditions, etc.)

Using the JBrowse plugin architecture

ComboTrackSelector

Hierarchical selector

Faceted selector

Configuring and enabling the plugin

ComboTrackSelector

Hierarchical selector

• Uses the standard configuration file, trackList.json
• Usually generated programmatically using loading scripts like flatfile-to-json.pl, etc.
• Adding below plugin config stanza enables dual selectors:
  ```json
  "plugins": { "location": "./plugins/ComboTrackSelector", "name": "ComboTrackSelector" },
  ```

Faceted selector

• Relies on a new configuration file, trackList2.json
• Requires supporting comma-separated configuration file with metadata about the data
• Both files above are either hand curated or programmatically generated

Annotated sequence viewers

TAIR SeqViewer

Sequence viewer in JBrowse

• JBrowse feature details windows shows region sequence and subfeatures separately
• Members of the Arabidopsis community were used to working with TAIR SeqViewer and GBrowse2. But, Araport promotes usage of JBrowse over GBrowse2
• Users of our portal were missing this functionality at Araport and made requests during our portal “Preview” phase

Developing a sequence viewer for JBrowse

• Since JBrowse is client side application, widget would need to be lightweight JS for ease of integration
  BioJS (http://biojs.net) library of reusable JS components was the perfect fit
• Wide variety of components, not limited to:
  – Sequence, Chromosome karyotype
  – Tree, KEGGViewer
  – Cytoscape, Interaction Table
**Sequence viewer widget for JBrowse**

**SeqLighter**

- Can be configured as a right-click menu option for any track providing gene structure features. 

```javascript
menuTemplate : [ 
  { 
    label : "View Sequence",
    iconClass : "dijitIconDatabase",
    action : "contentDialog",
    content : "function(track,feature,div){ return SequenceViewer(track,feature,div)}"
  }
],
```

- Allows toggling annotation of various gene features (exon, intron, start/stop, UTR)
- Flanking region sequences can be added (0.5 to 4 KB)
- Results can be exported to SVG, PNG and JPG

---

**Araport on GitHub**

- GitHub organization: [https://www.github.com/Arabidopsis-Information-Portal](https://www.github.com/Arabidopsis-Information-Portal)
- Relevant repositories
  - GMOD/browse (fork)
  - browse-contrib (track config)

---

**Tidbit (1)**

**Generate screenshots programmatically**

- JBrowse does not currently have feature analogous to `gbrowse_img` to generate an image of desired region and set of tracks
- It is possible however to disable nav/tracklist/ruler elements from the view, by setting appropriate URL parameters
- Example:
  
  ```
  http://path/to/jbrowse/?tracks=A,B,C&nav=0&tracklist=0&overview=0
  ```

---

**Tidbit (2)**

**Streaming data files from iPlant**

- iPlant Data Store (iDS) provides cloud storage to researchers (initial allocation 100GB)
- Several methods can be used to transfer data to and from iDS
  - Discovery Environment web interface
  - iDrop GUI toolkit
  - iCommands command line interface
- Instructions on wiki page describing method used to generate link(s) to BAM/BAI, VCF, GFF file on the iDS
  - [https://pods.iplantcollaborative.org/wiki/display/DEmanual/Sending+Genome+Files+to+the+Genome+Browser](https://pods.iplantcollaborative.org/wiki/display/DEmanual/Sending+Genome+Files+to+the+Genome+Browser)

---

**Tidbit (1)**

**Generate screenshots programmatically**

- Possible to do so, with server side JavaScript technology, `nodejs` ([http://nodejs.org](http://nodejs.org)) and a headless webkit browser, PhantomJS ([http://phantomjs.org](http://phantomjs.org))
- Wrapped in command line toolkit, pageres
- Example:
  
  ```
  $ pageres <url> <resolution>
  ```

---

**Tidbit (2)**

**Streaming BAM files from iPlant**

- [https://pods.iplantcollaborative.org/wiki/display/DEmanual/Sending+Genome+Files+to+the+Genome+Browser](https://pods.iplantcollaborative.org/wiki/display/DEmanual/Sending+Genome+Files+to+the+Genome+Browser)
Acknowledgements

- JCVI Team Members
  - Engineers: Maria Kim
  - Analysts: Chia-Yi Cheng, Benjamin Rosen
- Awesome dev community
- Matt Bomhoff, Eric Lyons from CoGe
- iPlant Collaborative
- Funding Agencies

THANK YOU!